PEEBEDU DNA Replication Simulator

Unit 6: Gene Expression and Regulation

Name: _____ **Period:** _____ **Date:** _____

> Open **peebedu.com** and navigate to **DNA Replication Simulator**. Click **Unzip the Mystery!** to begin. Read the introduction popup, which describes how DNA unzips and replicates in real-time. Review the five enzyme tools on the right panel and the progress checklist in the header.

Part 1 — Model Evaluation (MAPP Framework)

Scientific models are simplified representations of complex biological phenomena. Use the MAPP framework below to evaluate the DNA Replication Simulator as a scientific model.

M — Mode

What type of model is the DNA Replication Simulator? Describe how this computational simulation represents the process of DNA replication. In your answer, identify at least three specific simulation elements and explain what each one is designed to show about how DNA is copied.

A — Accuracy

(a) Identify two things this simulation represents **accurately** about DNA replication. For each, name the specific simulation feature and explain what aspect of DNA replication it demonstrates.

(b) Identify two things this simulation **oversimplifies or leaves out** about DNA replication. Consider what you cannot observe in the simulation that would be important for a complete molecular-level understanding of the replication process.

P — Purpose

What is the learning goal of this simulation? Explain how the DNA Replication Simulator is designed to help you understand the sequence of enzymatic steps and the structural differences between leading and lagging strand synthesis. In your answer, connect at least one specific simulation feature to a biological reason why accurate DNA replication matters for living organisms.

P — Permanency

Could this model change with new scientific evidence? Describe one way that new discoveries might change or improve a simulation like the DNA Replication Simulator. Explain why scientific models, including computational simulations, are revised as new evidence becomes available.

Small-Group Discussion

With your group, discuss the following:

- What are the strengths of this simulation as a model for DNA replication?
- What are its limitations?
- If you could add one feature to improve this simulation, what would it be and why?
- How does the drag-and-drop nucleotide matching help you understand complementary base pairing?

Part 2 — Free Response Questions

Conceptual Analysis

Question 1 — Leading and Lagging Strand Synthesis

> *Simulation Task: Apply Topoisomerase, then Helicase to unwind the DNA. Add RNA primers with Primase. Apply DNA Polymerase to the leading strand (click the bottom half of the canvas) and then to the lagging strand (click the top half). Drag complementary nucleotides from the free nucleotide pool to build the leading strand continuously. Then build the lagging strand, noting how synthesis proceeds in separate Okazaki fragments.*

(A) (1 pt) **Describe** how DNA polymerase synthesizes new DNA in the 5' to 3' direction and why RNA primers are required for DNA polymerase to initiate synthesis.

(B) (1 pt) **Explain** why the leading strand is synthesized continuously toward the replication fork while the lagging strand must be synthesized discontinuously as Okazaki fragments in the opposite direction.

(C) (1 pt) **Predict** what would happen to DNA replication if a mutation in the gene encoding ligase produced a nonfunctional protein.

(D) (1 pt) **Justify** your prediction by explaining the specific role of ligase in joining Okazaki fragments and why this step is essential for producing a complete, continuous daughter strand on the lagging strand.

EK 6.2.A.1

Analyze Model / Visual Representation

Question 2 — Semiconservative Replication and Enzyme Coordination

> *Simulation Task: Complete a full replication cycle from start to finish. After applying Ligase, observe the two completed daughter DNA molecules. Compare the original template strands (blue) with the newly synthesized strands (green) in each molecule. Reset and repeat if needed to observe the full process again.*

(A) (1 pt) **Describe** how DNA replication is a semiconservative process.

(B) (1 pt) **Explain** the relationship between the sequential action of the five replication enzymes (topoisomerase, helicase, primase, DNA polymerase, and ligase) and the accurate copying of genetic information from parent to daughter DNA molecules.

(C) (1 pt) **Represent** a replication fork.

Draw your diagram here.

(D) (1 pt) **Explain** how errors during DNA replication can introduce mutations that increase genetic variation in a population.

EK 6.2.A.1