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 — NGSS Questions

1.

> *Simulation Task: Select Topoisomerase from the enzyme panel and click on the DNA. Then select Helicase and click again. Watch the double helix unwind and the two strands separate at the replication fork.*

Describe what happens to the DNA molecule when the strands are separated at the replication fork. Explain why the cell must unwind and separate the two strands before it can copy its genetic information.

HS-LS1-1

2.

> *Simulation Task: After unwinding the DNA, select Primase and click on the DNA to add RNA primers. Then apply DNA Polymerase to the leading strand (click the bottom half of the canvas). Drag the correct complementary nucleotides from the free nucleotide pool to match each template base. Pay attention to the "Need: X" label and the feedback messages.*

Explain how the base-pairing rules (A pairs with T, G pairs with C) ensure that each new DNA strand is an accurate copy of the original. Describe the evidence you observed in the simulation that supports complementary base pairing.

HS-LS1-1

3.

> *Simulation Task: Now apply DNA Polymerase to the lagging strand (click the top half of the canvas). Drag complementary nucleotides to build this strand. Notice how synthesis proceeds in separate short sections rather than as one continuous strand. Compare how the leading strand and lagging strand were built.*

Describe how the leading strand and the lagging strand are built differently during DNA replication. Explain why the lagging strand must be assembled in short sections that are later joined together.

HS-LS1-1

4.

> *Simulation Task: After completing synthesis on both strands, select Ligase and apply it. Observe how the separate fragments on the lagging strand are connected into a continuous strand. Look at the two completed daughter DNA molecules and compare the original template strands (blue) with the newly synthesized strands (green).*

Explain what semiconservative replication means based on what you observe in the simulation. Describe how each completed daughter molecule is composed of one old strand and one new strand, and explain why this method of copying DNA is important for passing genetic information to new cells.

HS-LS1-1

5.

> *Simulation Task: Reset the simulation and run through the full replication process again. This time, intentionally drag a wrong nucleotide to a highlighted position and read the error feedback message. Then correct it by placing the right nucleotide.*

Predict what would happen to the daughter DNA molecule if a wrong nucleotide were permanently inserted during replication and not corrected. Explain how such a change in the DNA sequence could affect the structure of a protein made from that gene.

HS-LS3-2

6.

> *Simulation Task: Observe the completed replication in the simulation. Note the two daughter molecules, the color difference between original and new strands, and the base pairs connecting each strand.*

In the box below, draw a diagram showing one parent DNA molecule replicating into two daughter molecules. Label the original template strands and the newly synthesized strands. Show at least four base pairs in each daughter molecule using correct base-pairing rules.

Draw your diagram here.

HS-LS3-2

7.

> *Simulation Task: Reset and replicate the DNA one more time. Consider that every time a cell divides, it must copy all of its DNA. Think about what happens when copying errors are not repaired and are passed on to offspring over many generations.*

Explain how mistakes made during DNA replication can introduce new variations in a population. Describe how these inherited variations could give some individuals advantages or disadvantages in a particular environment and lead to changes in a population over many generations.

HS-LS4-2