Virtual PCR

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

> Open **peebedu.com** and navigate to **Virtual PCR**. Read the introduction popup, which describes PCR as a technique that makes millions of copies of specific DNA sequences. Select **Standard Mode** to begin exploring the laboratory bench.

Part 1 — Model Evaluation (MAPP Framework)

Scientific models are simplified representations of complex biological phenomena. Use the MAPP framework below to evaluate the Virtual PCR simulation as a scientific model.

M — Mode

What type of model is the Virtual PCR simulation? Describe how this computational simulation represents the process of polymerase chain reaction. In your answer, identify at least three specific simulation elements (e.g., the thermocycler workflow, primer reagents, DNA template rack) and explain what each one is designed to show about PCR.

A — Accuracy

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

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

P — Purpose

What is the learning goal of this simulation? Explain how the Virtual PCR laboratory is designed to help you understand how DNA fragments are amplified by denaturing DNA, annealing primers to the original strand, and extending the new DNA molecule. In your answer, connect at least one specific simulation feature to a real-world application of PCR in biology or medicine.

P — Permanency

Could this model change with new scientific evidence? Describe one way that new discoveries in molecular biology might change or improve a simulation like Virtual PCR. 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 the PCR process?
- What are its limitations?
- If you could add one feature to improve this simulation, what would it be and why?
- How does the simulation help you connect laboratory procedures to the molecular events occurring during each PCR cycle?

Part 2 — Free Response Questions

Conceptual Analysis

Question 1 — PCR Amplification and Primer Specificity

> *Simulation Task: Select the **Sickle Cell** case study. Load the **Control AA**, **Control AS**, and **Control SS** DNA templates into separate test tubes. Add Master Mix and primers to each tube, centrifuge, and run the PCR thermocycler. Observe how the same primers amplify DNA from individuals with different HBB genotypes.*

(A) (1 pt) **Describe** how PCR amplifies a specific DNA fragment through three repeated steps: denaturing the double-stranded DNA, annealing primers to complementary sequences on the original strands, and extending new DNA molecules using DNA polymerase.

(B) (1 pt) **Explain** why specific primers are necessary for PCR to amplify only the target region of DNA, rather than copying the entire genome.

(C) (1 pt) **Predict** what would happen to the PCR results if the annealing temperature were set too high, preventing the primers from binding to the template DNA.

(D) (1 pt) **Justify** your prediction by explaining how each of the three PCR steps (denaturation, annealing, and extension) depends on the successful completion of the preceding step, and why failure at the annealing step would prevent DNA amplification.

EK 6.8.A.1 (ii)

Analyze Model / Visual Representation

Question 2 — Forensic DNA Analysis and Genetic Variation

> *Simulation Task: Select the **CSI Analysis** case study. Load the **Crime Scene** DNA sample and at least two **Suspect** samples into separate test tubes. Add Master Mix and primers to each, centrifuge, and run PCR. After the thermocycler completes, click **Load VLDS** to compare the amplified DNA fragment patterns across samples.*

(A) (1 pt) **Describe** how PCR is used in forensic DNA analysis to amplify small amounts of DNA collected from a crime scene into quantities large enough for comparison and identification.

(B) (1 pt) **Explain** how the use of specific primers in PCR targets particular regions of DNA that vary between individuals, allowing forensic scientists to generate a DNA profile that can distinguish one person from another.

(C) (1 pt) **Represent** the three steps of one PCR cycle.

Draw your diagram here.

(D) (1 pt) **Explain** how genetic variation detected by PCR connects to the concept of natural selection acting on phenotypic variation in populations.

EK 6.8.A.1 (ii)