PEEBEDU

Variant Ventures

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

> Open **peebedu.com** and navigate to **Variant Ventures**. Click the **Start Outbreak** button to begin. Read the introduction popup, which explains how RNA viruses mutate and how three codons determine viral traits: Spread Radius, Antigen Shape, and Infection Duration.

Part 1 — Model Evaluation (MAPP Framework)

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

M — Mode

What type of model is Variant Ventures? Describe how this computational simulation represents viral evolution and host-pathogen interactions. In your answer, identify at least three specific simulation elements and explain what each one is designed to show about how viruses evolve.

A — Accuracy

(a) Identify two things this simulation represents **accurately** about viral evolution and host immunity. For each, name the specific simulation feature and explain what biological concept it demonstrates.

(b) Identify two things this simulation **oversimplifies or leaves out** about viral evolution. Consider what you cannot observe in the simulation that would be important for a complete understanding of how real viruses mutate and spread.

P — Purpose

What is the learning goal of this simulation? Explain how Variant Ventures is designed to help you understand how random mutations in viral RNA create new variants that may be selected for or against based on host immunity. In your answer, connect at least one specific simulation feature to a real-world example of viral evolution.

P — Permanency

Could this model change with new scientific evidence? Describe one way that new discoveries about viral evolution might change or improve a simulation like Variant Ventures. 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 viral evolution?
- 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 molecular-level mutations to population-level changes in viral variants?

Part 2 — NGSS Questions

1.

> *Simulation Task: Start a new simulation with 30 pigs in the Free Range environment. Click Start Outbreak and watch for the first few days. Click on an infected pig to view its viral RNA sequence and note the three colored codons.*

Describe how the three RNA codons in the simulation map to specific viral traits (spread radius, antigen shape, and infection duration). Explain why a change in even one nucleotide can alter the virus's phenotype.

HS-LS4-2

2.

> *Simulation Task: Let the simulation run until the Variants counter reaches at least 5. Click View Variants to see the list of active variants and their population sizes.*

Explain how random mutations during viral replication produce new variants. Describe why some variants become more common in the population while others disappear.

HS-LS4-2

3.

> *Simulation Task: Click on a recovered (green-outlined) pig to view its antibody panel. Then observe what happens when a new variant with a different antigen shape infects nearby pigs.*

Explain how host antibodies create selective pressure on the viral population. Describe why a variant with a new antigen shape has an advantage over the original variant in a population with existing immunity.

HS-LS4-3

4.

> *Simulation Task: Reset the simulation. Run one outbreak using Free Range Organic (15 pigs) and note the final number of variants and infections. Then reset and run using Indoor Minimum (50 pigs) and compare.*

Compare how the two farming environments affected viral evolution. Explain how population density and contact rate influence the speed of mutation and the emergence of new variants.

HS-LS4-4

5.

> *Simulation Task: Run a simulation in the Indoor Minimum environment until a ZOONOTIC TRANSFER alert appears. Click View Genealogy to see the evolutionary tree of all variants.*

Explain how the simulation demonstrates zoonotic transfer from pigs to humans. Describe what conditions made this cross-species infection possible and why this is a concern in real-world agriculture.

HS-LS4-4

6.

> *Simulation Task: Click View Genealogy after running a simulation that has produced at least 6 variants. Study how variants branch from their parent variants.*

In the box below, draw a simplified genealogy tree showing how an ancestral virus variant gives rise to descendant variants through mutation. Include at least three generations, label each variant with a letter, and use arrows to show where mutations occurred.

Draw your diagrams here.

HS-LS4-2

7.

> *Simulation Task: Run one final simulation from start to finish. Observe how the virus population changes over time as hosts develop immunity and new variants emerge to evade that immunity.*

Using evidence from the simulation, construct an argument that natural selection acts on viral populations through the interaction between random mutation and host immunity. Explain how this process is similar to natural selection acting on any population of organisms in a changing environment.

HS-LS4-3