**PEEBEDU**

# Alien Evolution Lab

Unit 7: Natural Selection
and Evolution

**Name:** ______________________ **Period:** ________ **Date:** ______________

> Open **peebedu.com** and navigate to **Alien Evolution Lab**. Read the introduction popup, which explains that NASA's Kepler-9 rover has landed on exoplanet Verdara and transmitted photographs of eight life forms back to Earth. Your mission: classify these organisms by building and validating a cladogram using three independent lines of evidence (morphological traits, DNA nucleotide sequences, and protein amino acid sequences), then apply your tree to interpret fossil evidence.

## Part 1: Model Evaluation (MAPP Framework)

*Scientific models are simplified representations of complex biological phenomena. Use the MAPP framework below to evaluate the Alien Evolution Lab simulation as a scientific model.*

### M: Mode

What type of model is the Alien Evolution Lab simulation? Describe how it represents the process of constructing and testing a phylogenetic hypothesis. Identify at least three specific elements of the simulation and explain what aspect of cladistic analysis each one is designed to illustrate.

### A: Accuracy

**(a)** Identify two things this simulation represents **accurately** about how scientists construct cladograms. For each, name the specific simulation element and explain what aspect of cladistics it demonstrates.

**(b)** Identify two things this simulation **oversimplifies or leaves out** about real phylogenetic analysis. Consider what aspects of constructing and testing evolutionary trees in the field or laboratory cannot be represented in this simulation.

### P: Purpose

What is the learning goal of this simulation? Explain how experiencing three independent phases of evidence (morphological traits, DNA sequences, and protein sequences) is designed to build understanding of how scientists gain confidence in a phylogenetic hypothesis. Connect one specific simulation feature to how real biologists use multiple lines of evidence to test evolutionary relationships.

### P: Permanency

Could this model change with new scientific evidence? Describe one way that the discovery of new Verdara organisms, additional molecular data, or new fossil specimens could require the cladogram to be revised. Explain why phylogenetic trees are considered scientific hypotheses rather than established facts.

### Small-Group Discussion

With your group, discuss the following:

- What are the strengths of this simulation as a model for phylogenetic analysis?
- What are its limitations?
- If you could add one feature to improve the simulation, what would it be and why?
- How does the convergence of morphological, DNA, and protein evidence in this simulation reflect how real scientists build and test evolutionary hypotheses?

## Part 2: Free Response Questions

### Conceptual Analysis

### Question 1: Shared Derived Characters and Cladogram Construction

> *Simulation Task: In Phase 1 (First Contact), click each organism card to expand it and check off its traits in the trait matrix. Pay close attention to Trait 2 (antennae) and Trait 3 (wings). Identify which organisms share these traits, and which organisms share Trait 4 (mandibles) but not Trait 2.*

**(A)** (1 pt) **Identify** the process that produces new, derived traits in organisms that share an ancestral body plan with other members of their clade.

**(B)** (1 pt) **Explain** why organisms C, D, and E are grouped together in the same clade on the Verdara cladogram, using the trait matrix data from Phase 1 to support your answer.

**(C)** (1 pt) **Predict** where a newly discovered Verdara organism that possesses Trait 1 (eye stalks) and Trait 4 (mandibles) but not Traits 2, 3, or 5 would be placed on the existing cladogram.

**(D)** (1 pt) **Justify** your prediction by explaining how shared derived characters, not shared ancestral characters, determine branching patterns on a cladogram.

EK 7.1.A.1, 7.9.A.1, 7.9.A.3

## Analyze Model / Visual Representation

### Question 2: Convergence of Multiple Lines of Evidence

> *Simulation Task: Complete Phases 1, 2a, and 2b of the simulation. After each phase, use the Check Tree button to confirm your cladogram. Observe that the same groupings of organisms are supported independently by morphological traits, DNA nucleotide sequences, and amino acid sequences.*

**(A)** (1 pt) **Identify** the two biological processes that connect a DNA nucleotide sequence to the amino acid sequence of the protein it encodes.

**(B)** (1 pt) **Explain** why three independent lines of evidence (morphology, DNA, and protein sequences) all supporting the same phylogenetic tree increases scientific confidence in the cladogram as an accurate representation of evolutionary relationships.

**(C)** (1 pt) **Represent** the five ingroup organisms (B, C, D, E, F) as a cladogram. Label each internal node with the shared derived character(s) that unite the clade above it.

*Draw your cladogram here.*

**(D)** (1 pt) **Explain** how a change in an amino acid sequence can lead to a change in a morphological trait.

EK 6.3.A.1, 6.3.B.1, 7.6.B.2, 7.9.A.3, 7.9.B.2