

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 Verdera 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: NGSS Questions

1.

Simulation Task: In Phase 1 (First Contact), click each organism card to expand it and check off its traits in the trait matrix. Compare the traits of organisms B and F to the traits of organisms C, D, and E.

Describe how shared physical traits can be used as evidence for common ancestry. Explain why organisms B and F are grouped together in one clade while organisms C, D, and E are grouped in a separate clade, using specific trait data from Phase 1 to support your answer.

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2.

Simulation Task: In Phase 1, examine the outgroup organisms A, A-spikes, and A-leaves. Compare their traits to the ingroup organisms B, C, D, E, and F. Note which traits the outgroup organisms lack entirely.

Explain the role of the outgroup in constructing a cladogram. Describe how comparing organism A (which lacks all derived traits) to the ingroup organisms allows you to determine which traits are ancestral and which are derived, and why this distinction is necessary for correctly grouping related lineages.

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3.

Simulation Task: Advance to Phase 2a (The Molecular Transmission). Read the aligned DNA sequences displayed for all eight organisms. Identify which nucleotide positions differ between organism A (outgroup) and the ingroup organisms B, C, D, E, and F.

Describe how shared mutations at the same positions in a DNA sequence provide evidence for common ancestry. Explain why two organisms that share a mutation at the same position are likely descended from a common ancestor that acquired that mutation, rather than having each developed the same mutation independently.

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4.

Simulation Task: After completing Phases 1, 2a, and 2b, use the Check Tree button after each phase to verify your cladogram. Observe that your cladogram passes validation using morphological traits, DNA sequences, and protein amino acid sequences.

Explain what it means that three independent lines of evidence (morphology, DNA, and protein sequences) all support the same phylogenetic tree. Describe how this convergence demonstrates that the evolutionary relationships shown in the cladogram are well-supported, and why scientists use multiple types of evidence rather than relying on a single data source.

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5.

Simulation Task: In Phase 3a (Fossil Placement), examine the two partial fossil specimens shown in the left panel. Notice that each fossil displays only some of the traits seen in the living ingroup organisms. Drag each fossil to what you believe is its correct location on the cladogram.

Describe how a fossil organism that possesses some but not all of the derived traits of a living clade can be placed on a phylogenetic tree. Explain how the traits a fossil does and does not have — even in fragmentary form — serve as evidence for where that organism fits in the evolutionary history of a lineage.

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6.

Simulation Task: In Phase 3c (Carbon-14 Dating), read the C-14 percentage remaining for each fossil from the spectrometer readout shown in the left panel. Use the interactive decay graph to find the corresponding age in years for each fossil.

Explain how radiocarbon dating works as a method for determining the age of fossil organisms. Describe what the percentage of carbon-14 remaining in a fossil tells you about how long ago the organism lived, and explain why a fossil that is deeper in the cladogram (representing an older lineage) is expected to have a greater age than one placed at a more recent branch.

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7.

Simulation Task: Review your completed cladogram from all phases. The five ingroup organisms are B, C, D, E, and F. Recall the traits that define each clade: all ingroup organisms share Trait 1 (eye stalks); B and F share Trait 4 (mandibles); C, D, and E share Trait 2 (antennae); D and E share Trait 3 (wings).

In the box below, draw the cladogram for the five ingroup organisms (B, C, D, E, F). Label each internal node with the shared derived trait that first appeared at that branching point. Then, below your drawing, explain how the same branching pattern was independently supported by DNA sequences in Phase 2a and protein sequences in Phase 2b, and what this convergence tells us about the reliability of the phylogenetic hypothesis.

Draw your cladogram here.

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