

6.1 Diversity, classification and a branching model

Name: _____ Class: _____ Date: _____

Total: 10 marks

KEY WORDS taxon • clade

Objective

Diversity, classification and a branching model. Supported HL concept preparation; original classroom practice, not an official IB paper or assessed learner work.

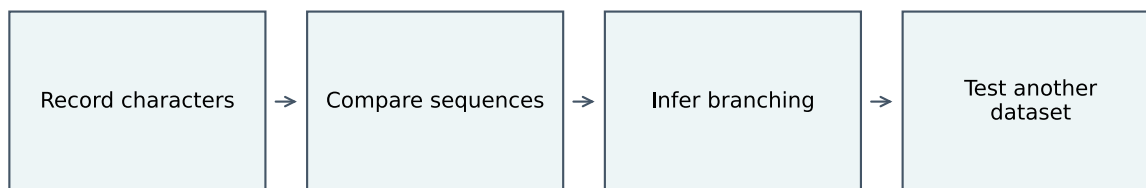
1 Key knowledge and worked examples

■ What would explain this observation?

- Two species look similar but their DNA comparison places them in different branches. Classification uses several kinds of evidence rather than appearance alone.
 - Start with a prediction. State the quantities or features you would compare, then decide what evidence could distinguish two explanations.
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■ Build the model

- A species is a biological grouping; a **taxon** is a named classification group. A cladogram represents a hypothesis of relationships based on shared derived characteristics or molecular evidence. A branch point represents a common ancestor, not an individual alive today.
- taxon: A named group in a classification; **clade** : A common ancestor and all its descendants.



■ Choose evidence that can test it

- Read relationships from the branching order. Rotating branches at a node does not change ancestry. A branch length represents time or change only when the diagram gives a scale.
- Record character states in a matrix before drawing a tree. Define which state is ancestral using an appropriate comparison. Test whether a new molecular dataset supports the same grouping.

■ Work from known quantities

- State the known values and their units. Choose the relation because its assumptions fit this case, then rearrange before substitution.
- Known: an alignment contains 40 sites, with 6 differences. Difference proportion = $6/40 = 0.15$, or 15%. This is an observed comparison, not a calibrated molecular clock unless rate assumptions and corrections are supplied.

Example:

There are 8 differences in 50 aligned sites. Calculate percentage difference. Use the same sequence: known quantities → model → relation → substitution → unit and interpretation.

■ Check the conclusion and its limits

- A modern species is not automatically the ancestor of another modern species. Similarity caused by convergent evolution can mislead a classification based on one trait.
- Return to the original observation. Explain what the result supports, which conditions it assumes, and one way to test a competing explanation.

Warn:

Every cladogram branch length is a measurement of elapsed time. This claim is false: A modern species is not automatically the ancestor of another modern species. Similarity caused by convergent evolution can mislead a classification based on one trait.

Key:

Diversity, classification and a branching model: Read relationships from the branching order. Rotating branches at a node does not change ancestry. A branch length represents time or change only when the diagram gives a scale.

2 Practice

2.1 What remains the same when branches rotate around a node? Choose one answer.

- **A** The evolutionary relationships
- **B** Every printed tip position
- **C** An unstated time scale

[1]

2.2 There are 8 differences in 50 aligned sites. Calculate percentage difference. Show the relation, substitution and units.

[2]

2.3 Decide whether this claim is true and justify: Every cladogram branch length is a measurement of elapsed time.

[2]

2.4 A named group in a classification: write the technical term.

[1]

3 Exam-style questions

3.1 Alignment A has 6 differences in 60 sites; B has 9 in 30. Compare proportions. Explain why these two values alone cannot date a divergence. [4]
