4.1 Diversity, classification and a branching model

Name: _____ Class: _____ Date: _____ **Total: 10 marks**

KEY WORDS taxon • clade

Objective

Diversity, classification and a branching model. Original classroom practice for IB SL; not an official IB paper.

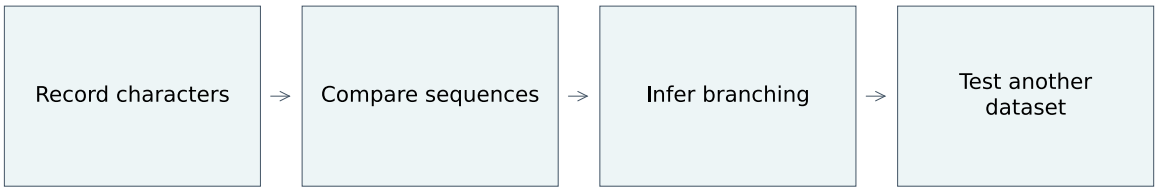
1 Key knowledge and worked examples

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.

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.

In the lab: 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

- 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.

Your turn: There are 8 differences in 50 aligned sites. Calculate percentage difference.

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.

Not true: Every cladogram branch length is a measurement of elapsed time. Branch lengths mean time only in trees explicitly drawn with a time or change scale. Many cladograms encode relationships only, with arbitrary lengths.

Key:

- A species is a biological grouping; a taxon is a named classification group.
- Read relationships from the branching order.
- Watch for: A modern species is not automatically the ancestor of another modern species.

Write from a difference of 22 percent

- There are 11 differences in 50 aligned sites.
- Find the percentage difference. A cladogram branch length is time only when the tree is drawn that way.

2 Practice

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

- **A** Every printed tip position
- **B** The evolutionary relationships
- **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: Branch lengths mean time only in trees explicitly drawn with a time or change scale. [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]

Solutions

2.1 B Rotating branches at a node changes only the drawing order; the branching pattern - which groups share which ancestors - is untouched. Tip order on the page is not a sequence of progress or time.

2.2 difference=8/50×100=16%.

2.3 True. True. Branch lengths mean time only in trees explicitly drawn with a time or change scale. Many cladograms encode relationships only, with arbitrary lengths.

2.4 taxon. taxon means A named group in a classification.

3.1 A=10%; B=30%. Site choice, substitution-rate assumptions and repeated substitutions affect interpretation; percentage difference alone supplies no calibrated time.