



Classification and cladistics: practice questions

7 questions • 22 marks • mark scheme at the back

For IB Diploma Biology, Standard Level and Higher Level (first assessment 2025). **HL only** is additional higher level content, for HL students only.

Name

Total / 22

1 PAPER 1A STYLE

[1 mark]

HL only

What does a node on a cladogram represent?

- A. ☐ A species alive today
- B. ☐ A hypothetical common ancestor
- C. ☐ A mutation in a single base
- D. ☐ The time since a species became extinct

2 PAPER 1A STYLE

[1 mark]

HL only

Which evidence led to the classification of all organisms into three domains?

- A. ☐ Comparisons of cell wall structure
- B. ☐ Base sequences of ribosomal RNA
- C. ☐ Numbers of chromosomes
- D. ☐ Fossils of the earliest cells

3 PAPER 1A STYLE

[1 mark]

HL only

Why can the molecular clock only give an estimate of when two clades diverged?

- A. ☐ Sequence differences stop accumulating once two clades have diverged.
- B. ☐ Only amino acid sequences, not base sequences, can be used.
- C. ☐ Mutation rates are affected by generation time, population size and selective pressure.
- D. ☐ The number of sequence differences decreases as time passes.

4 PAPER 2A STYLE

[4 marks]

HL only

(a) Outline the need for classification of organisms. [2] (b) Explain one advantage of classifying organisms according to evolutionary relationships. [2]

5 PAPER 1B STYLE

[5 marks]

HL only

The table shows the number of amino acid differences in a protein between four species, P, Q, R and S (practice data). (a) Identify the two most closely related species. [1] (b) Assuming differences accumulate at 1 difference per 10 million years, estimate when P and S diverged. [1] (c) Deduce the sequence in which the species diverged, and describe the most probable cladogram. [2] (d) Suggest why the estimate in (b) may be inaccurate. [1]

Amino acid differences between species				
	P	Q	R	S
P	–	9	10	12
Q	9	–	3	8
R	10	3	–	7
S	12	8	7	–

Answer =

PAPER 2A STYLE

HL only

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PAPER 2B STYLE

HL only

[illegible]

Mark scheme

One mark for each point unless a maximum is given. Words in brackets are not needed for the mark.

1. [1] **HL only**

B B [1]

2. [1] **HL only**

B B [1]

3. [1] **HL only**

C C [1]

4. [4] **HL only**

- (a) immense diversity of species / very large number of species [1]
- (a) classification makes diversity manageable / allows identification [1]
- (a) after classification, further study is facilitated / information about related species can be found [1]
- (b) all members of the group have evolved from a common ancestor [1]
- (b) characteristics of members can be predicted [1]
- (b) because characteristics are shared within a clade [1]
- (b) e.g. a species related to one that produces a useful drug may produce it too [1]
- max 4

5. [5] **HL only**

- (a) Q and R [1]
- (b) $12 \times 10 = 120$ million years ago [1]
- (c) P diverged first / P is the outgroup [1]
- (c) then S; Q and R share the most recent common ancestor [1]
- (c) cladogram: P branches from the root, then S, with Q and R as sister species at the last node [1]
- (d) mutation rate may not be constant / varies with generation time / population size / selective pressure [1] Accept: P-Q differences (9) give a different date (90 million years) for the same divergence, so rates differ between lineages
- max 5

6. [3] **HL only**

- (a) node 2 [1]
- (b) two (the clade from node 1 and the clade from node 2) [1] Accept three if B alone is counted as a clade
- (c) D [1]

7. [7] **HL only**

- traditional hierarchy of kingdom, phylum, class, order, family, genus, species [1]
- fixed ranks are arbitrary / do not reflect gradation of variation / do not always match patterns of divergence [1]
- cladistics uses unranked clades: an ancestor and all its descendants [1]
- evidence from base sequences of genes / amino acid sequences of proteins [1]
- sequence evidence is more objective than morphology [1]
- morphology can mislead because of convergent evolution [1]
- cladograms built using parsimony / fewest sequence changes [1]
- traditional groups found not to be clades were reclassified [1]
- e.g. figwort family / Scrophulariaceae: many species moved to other families [1]
- e.g. birds lie within the reptiles, so the class Reptilia is not a clade [1]
- rRNA base sequences led to three domains: Bacteria, Archaea, Eukarya (1977) [1]
- a new level above kingdoms / prokaryotes split into two domains [1]
- paradigm shift / earlier classifications falsified [1]
- but cladograms are hypotheses; different criteria / data can give different trees [1]
- max 7