7.1 Classification and cladistics

Name: _____ Class: _____ Date: _____ **Total: 24 marks**

KEY WORDS taxon • domain • clade • cladogram • molecular clock • parsimony

Objective

Build the skills to answer exam questions on **classification and cladistics** : the hierarchy of taxa, the three domains, clades, cladograms and molecular clocks.

You must be able to:

- list the taxonomic ranks and explain why classification should follow evolutionary relationships
- describe the three domains and the evidence for them
- construct and interpret cladograms, using base or amino acid sequences
- explain molecular clocks and why groups are sometimes reclassified

1 Key knowledge and worked examples

■ Classification and cladistics

Ranks (taxa): domain → kingdom → phylum → class → order → family → genus → species. A good classification groups organisms by **common ancestry**, so it can **predict** features of a newly found member.

Three domains (from ribosomal RNA sequences): **Bacteria**, **Archaea** and **Eukarya**. Archaea look like bacteria (no nucleus) but their rRNA, membrane lipids and some enzymes are closer to eukaryotes. Viruses are not in any domain.

Clade: a common ancestor and **all** of its descendants. A **cladogram** shows clades: each **node** is a common ancestor; the **root** is the oldest ancestor. Fewer sequence differences → more recent common ancestor (closer relatives). Choose the tree with the fewest changes (**parsimony**).

Molecular clock: mutations build up at a roughly steady rate, so the number of differences estimates the time since two species split. Limits: the rate differs between genes and between groups.

Reclassification: when DNA evidence shows a family is not a clade, species are moved, e.g. the old figwort family was split into several families.

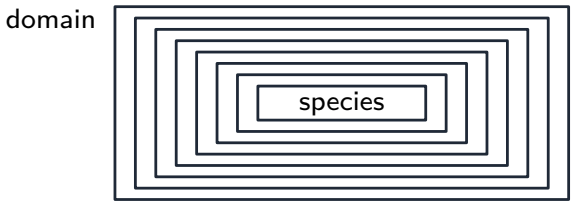
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Worked example. Cytochrome c differences from humans: rhesus monkey 1, horse 12, yeast 44. The **monkey** is the closest relative; yeast split off earliest.

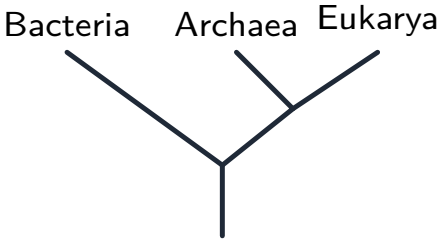
Answer shapes: "nodes show common ancestors"; "fewer differences, more recent split".

2 Practice

2.1 List the taxonomic ranks from domain to species, in order. [2]

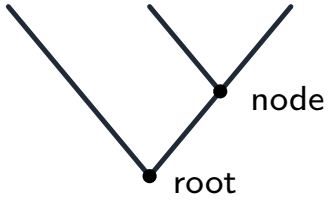


2.2 Explain why the Archaea are placed in a separate domain from the Bacteria. [3]

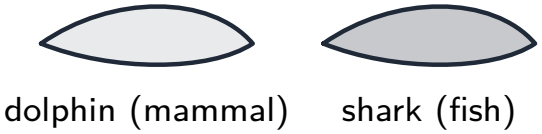


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2.3 State what is meant by a clade, and what a node in a cladogram represents. [3]



2.4 Explain why a classification based on common ancestry is more useful than one based on appearance. [2]



2.5 State one reason why a molecular clock gives only an estimate of when two species split. [2]

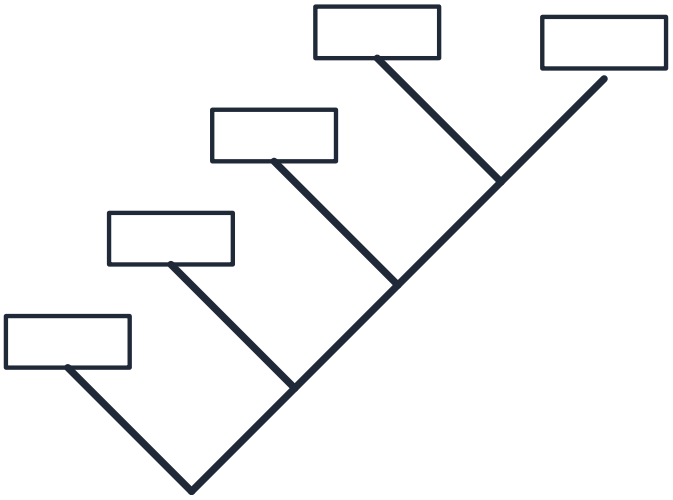


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3 Exam-style questions

3.1 The table shows the number of amino acid differences in cytochrome c between humans and four other organisms.

organism	differences from human
rhesus monkey	1
dog	11
chicken	13
yeast	44



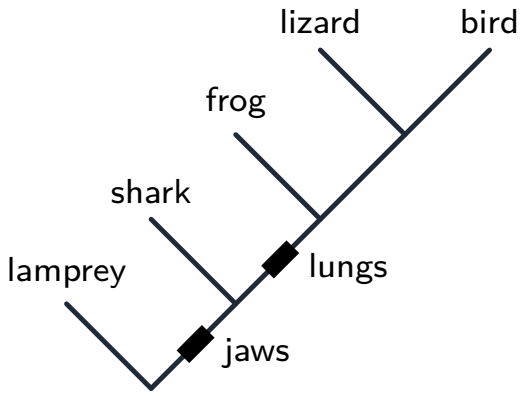
(a) State which organism is most closely related to humans, and give a reason. [2]

(b) Use the data to place the five organisms on the cladogram, from the root outwards. [2]

(c) Explain how cytochrome c differences can act as a molecular clock. [2]

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3.2 The cladogram shows five groups of animals.



(a) State the feature shared by all groups except the lamprey. [1]

(b) Name the group most closely related to birds. [1]

(c) State one group that, with its common ancestor, does **not** form a clade. Explain why. [2]

(d) Suggest why scientists now prefer DNA sequences to anatomy when drawing cladograms. [2]

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Solutions

Marking: **M1** a correct method, **A1** the correct answer, **B1** an independent mark.

Each answer shows the steps, then the **result**.

2.1

domain, kingdom, phylum, class, order, family, genus, species

2.2

ribosomal RNA sequences of Archaea differ greatly from those of Bacteria; Archaea have different membrane lipids / some enzymes and histones like eukaryotes; so they share a more recent common ancestor with Eukarya, despite having no nucleus

2.3

a clade is a common ancestor and all of its descendants; a node is a common ancestor / the point where two lineages split

2.4

organisms that look alike may not be related, e.g. analogous features from convergent evolution; grouping by ancestry predicts shared features of newly found members

2.5

mutation rates differ between genes; and between groups of organisms / over time, so the rate is not constant

3.1

(a) rhesus monkey; fewest differences, so the most recent common ancestor

(b) yeast branches first, then chicken, then dog, with monkey and human as the closest pair

(c) mutations in the gene build up at a roughly constant rate; so more differences mean a longer time since the two species shared an ancestor

3.2

(a) jaws

(b) lizard

(c) e.g. “reptiles without birds”, or lamprey + shark; a clade must contain all descendants of the common ancestor, and this group leaves some out

(d) sequences give many measurable characters / are objective; anatomy can mislead because of convergent evolution