

APOLLO

Classification and cladistics

HL

Biology

First assessment 2025

10 questions | mark schemes

Mark-scheme answers

Biology HL | Paper 1A | May 2025 TZ1 | Q21 | 1 marks

21. C

Biology HL | Paper 1A | May 2025 TZ2 | Q22 | 1 marks

22. B

Biology HL | Paper 1A | May 2025 TZ3 | Q22 | 1 marks

22. C

9.	a	a. (homologous structures are) similar features/structures/anatomy that can have different functions; b. (homologies are) result of divergent evolution/adaptive radiation OR (homologies are) result of different selection pressures/natural selection; c. (organisms evolve) from a common ancestor / show evolutionary relationships; d. can be seen in ancient organism remains / fossils; e. can be seen in similarities among organism limbs/structures/vestigial organs/embryos/DNA alive today; f. an example of homologous structures are pentadactyl limbs;		4 max
9.	b	<i>conditions [2 max]:</i> a. no mutation; b. random mating; c. no migration / gene flow; d. large population size / no genetic drift; e. no selection / (natural) selection does not favour one phenotype <i>use [2 max]:</i> f. p and q denote the two allele frequencies; OR p denotes frequency of dominant allele <u>and</u> q denotes frequency of recessive allele; g. p and q add up to 1 / $p + q = 1$; h. $p^2 + 2pq + q^2 = 1$; i. the frequency of the 2 homozygous genotypes are p^2 and q^2 OR the frequency of the heterozygous genotype is $2pq$;	Max 2 for conditions and Max 2 for use.	3 max

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Question		Answers	Notes	Total
9.	c	a. classification needed because of immense diversity of species/further study is facilitated/helps in identification of species; b. (ideal) classification follows/is based on evolutionary relationships (between species that have a common ancestor); c. (classification based on evolutionary relationships) allows characteristics of organisms within a group to be predicted because they are shared; d. relationships can be inferred using different kinds of evidence such as morphology/development/molecular markers/presence/absence of genes/DNA/RNA/protein/amino acid sequences; e. organisms that share similar structures/genetic sequences/DNA/RNA tend to be more closely related; f. differences in (DNA/amino acid) sequence are due to mutation; g. cladograms are branching diagrams/trees connected to a common ancestor OR the branches (in a cladogram) represent the evolutionary path of a group of organisms from a common ancestor; h. <u>cladograms</u> are based on phylogeny/evolutionary relationships OR <u>cladograms</u> are built from multiple sequence alignments/ base sequences of genes / base sequences of amino acids in proteins; Marking points for 9c continued on next page....	<i>g. can be awarded through a labelled diagram.</i>	8 max

Question 9c continued....

9.	c	i. a clade is a group of organisms that have evolved from a common ancestor OR a clade includes a single common ancestor and all of its descendants/all species evolved from it; j. the <u>root</u> is the base of the cladogram / the hypothetical common ancestor <u>of all the clades</u>; k. the <u>node</u> of the branch shows the most recent common ancestor between two species of a clade OR the <u>node</u> represents a (hypothetical) common ancestor OR the <u>node</u> is a branching point indicating that a group of organisms are related; l. the <u>terminal branches</u> are ends that represent individual clades / species / group of closely related species;	j, k. and l. can be awarded in a clearly annotated diagram.	
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Question	Answers	Notes	Total
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7.	a	a. root is the (last/initial) common ancestor of all the organisms / earliest ancestor (in the cladogram); b. node represents the most recent common ancestor (of two species/two clades) OR node is a branching point indicating that a group of organisms are related OR node is a point where species/clades branch off;	<i>a. It must be clear that all of the organisms/clades in the cladogram came / evolved / descended from the root.</i>	2
7.	b	a. mutations change base sequence of DNA; b. changes to DNA/base sequence cause changes to amino acid sequence; c. sequence differences accumulate (gradually/slowly) over time; d. species with more differences in amino acid sequences diverged longer ago / fewer differences means more recent divergence from a common ancestor; e. more objective than using morphology/physical traits / <i>OWTTE</i>; f. species with similar amino acid sequences are more closely related;		3 max
7.	c	a. base sequence of genes / DNA (base) sequences OR base sequence of rRNA OR comparing karyotypes; b. morphological/physical/anatomical/homologous traits/characteristics / specific example of morphology/homology that could be used;		1 max

Question		Answers	Notes	Total
7.	d	a. choose the simplest explanation for observations; b. choose the cladogram that requires the smallest number of sequence/genetic/ trait changes/fewest mutations;		1 max

Mark-scheme answers

Biology HL | Paper 1A | Nov 2025 TZ1 | Q21 | 1 marks

21. C

Biology HL | Paper 1A | Nov 2025 TZ1 | Q22 | 1 marks

22. D

Biology HL | Paper 1A | Nov 2025 TZ3 | Q21 | 1 marks

21. A

Biology HL | Paper 1A | Specimen 2025 | Q24 | 1 marks

24. C

Biology HL | Paper 1A | Specimen 2025 | Q25 | 1 marks

25. D