



ANSWER BOOK

Classification and phylogeny: sorting by ancestry, not by looks

Classification, biodiversity and conservation · Unit B18

AQA 3.4.5 · OCR A 4.2.2 · Edexcel A Topic 4 (biodiversity and natural resources) · CAIE 18.1

6 questions · 18 marks

NAVY EDITION

SECTION A · Short, 1 to 2 marks

- A1** **B1** domain, kingdom, phylum, class, order, family, genus, species. **B1** the genus takes a capital letter and the specific name does not, and both are printed in italics or underlined when written by hand. [2]
- A2** **B1** organisms that do not reproduce sexually, such as bacteria and archaea, never interbreed at all, so the test cannot be carried out and prokaryotes are grouped instead by how similar their genomes are. **B1** fossils cannot be bred, so the interbreeding test cannot be applied to them and the species are assigned from morphology instead. [2]

SECTION B · Standard, 3 to 5 marks

- B1** **B1** a phenetic classification counts observable resemblances without asking where the resemblance came from. **B1** unrelated lineages exposed to the same selective pressure end up with similar features, so a dolphin and a shark are both streamlined with fins because both hunt in open water; that is convergent evolution and the structures are analogous. **B1** a dolphin's flipper contains the pentadactyl limb: one upper arm bone, two forearm bones, wrist bones and five digits. That is the same plan as a bat's wing and a human hand, while a shark's fin has nothing of the kind. **B1** a shared underlying plan is homologous and can only be explained by inheritance from a common ancestor, so a phylogenetic classification uses homology as evidence of ancestry and discards analogy. [4]
- B2** **M1** calibrate first: rate = number of amino acid differences divided by the time since divergence, using the pair whose date is known. **A1** $4 \div 12 = 0.33$ amino acid differences per million years. **M1** time since divergence = number of differences divided by that rate, so $7 \div 0.33$. **A1** 21 million years. [4]
- B3** **B1** the base sequence of the RNA in the small subunit of the ribosome was compared across as many organisms as could be obtained. **B1** the prokaryotes fell into two groups whose sequences differed from each other about as much as either differed from those of eukaryotes. **B1** that supported a rank above kingdom, the domain, with Bacteria, Archaea and Eukarya, and with Archaea sharing a more recent common ancestor with Eukarya than with Bacteria. [3]

B4 **B1** every organism that has been sequenced has ribosomes, so the same [3]
molecule can be compared right across life, whereas haemoglobin is present in only
some animals. **B1** its job is the same in every organism, holding the ribosome together
and positioning the tRNAs, so equivalent positions in the sequence can be lined up
against one another. **B1** most of its sequence changes very slowly, because almost any
change breaks a working ribosome, so a readable signal survives across billions of
years, and it is long enough that the similarities are not coincidence.
