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Level: HL IB in Biology

Subject: Biology

Topic: IB HL Biology

Type: Mark Scheme

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All International Baccalaureate IB Topic Questions HL Biology

BIOLOGY

HL - IB

Key skills

Answer 1

The correct answer is B. There is nothing wrong with the use of common names, in fact it is good to hold onto historical language and cultural individuality; the time when it is essential to use shared terminology is when scientists are communicating with each other about their work.

A, C and D are all important reasons for the development of the binomial system of naming organisms. Note that D is an example of having many different names for the same species, which can occur between countries, localities, and cultures.

Answer 2

The correct answer is B. The development of RNA analysis allowed scientists to show that the ribosomal RNA of archaea was different from that of the rest of the prokaryotes.

The size of a taxonomic group is irrelevant if the classification is correct; larger groups will only be split into smaller ones if they are discovered to be evolutionarily distinct. The archaea do have a similar cell structure to the rest of the prokaryotes (this is why they were originally classified along with them) but it is their differences, such as their distinct ribosomes, that have led to their being reclassified as a separate domain.

Answer 3

The correct answer is C because these two bird species both belong to the same genus *Poecile*.

The birds in option B share a species name, but this is likely to be a descriptive name and tells us nothing about how closely related they are given that their genus is different (if they had the same species name and genus name then they would be the same species).

Other birds on the list may share a taxon higher up the hierarchy, but these species will all be more distantly related than those sharing a genus.

Answer 4

The correct answer is A because there are 62 base matches between sperm whales and humpback whales, 59 between sperm whales and harbour porpoises, and 53 between sperm whales and bottlenose dolphins. The greater similarity between the sequences of the two whales shows a closer evolutionary relationship.

B is incorrect because there are the same number of matches (59) between harbour porpoises and sperm whales and between harbour porpoises and humpback whales; we therefore cannot tell from this analysis which is the closer relationship.

C and D are incorrect because we do not have enough information to reach these conclusions. We would need to be able to compare these four marine mammals with all other marine mammals to assess their genetic relationships. Note that the conclusions given in C and D are in fact the same; if these four species were more closely related to each other than to any other species, then they would be the only descendents of a common ancestor, and therefore would also form a clade.

Answer 5

The correct answer is C because while homologous characteristics can be useful in identifying clades, they can also be misleading (if analogous traits are falsely identified as homologous). For this reason, sequencing technology e.g. DNA, RNA, or protein sequencing, is usually used to identify clades.

Members of a clade are descendants of a common ancestor, and clades must contain all of the descendants of that common ancestor; none can be missing, and no members can be descended from a different ancestor. Species that share a common ancestor are evolutionary relatives, meaning that clades are built on the basis of evolutionary relationships.

Answer 6

The correct answer is D because gorillas are also descended from the common ancestor of all of these species, and therefore this would not be a clade.

A is a correct statement; the common ancestor of chimps and bonobos is only one node away, showing that they share a recent common ancestor, and so are more closely related to each other than any other species.

B is a correct statement; chimps, bonobos, humans, and gorillas are all descended from a common ancestor, and no other descendants of that ancestor have been missed off this list.

C is a correct statement; the node at which the lemurs diverge from the rest of the primates can be seen to be located at around 56 million years ago on the time scale.