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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

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**BIOLOGY**

**HL - IB**

Key skills

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### Answer 1

The correct answer is C. The organisms with the least number of differences (compared to humans) are the most closely related. This list provides the order from the least number of differences (most closely related) to the most number of differences (least closely related).

### Answer 2

The correct answer is B; the latest analysis suggests that the eukaryotes originated from within the archaea rather than sharing a common ancestor with them. This can be seen in the two domains tree from the fact that the node that leads to the eukaryotes occurs after the node that leads to the archaea.

A clade contains all of the descendants of a common ancestor, and in both trees the eubacteria form a single branch from their most recent node rather than containing all of the descendants from that node.

The archaea form a clade in the three domains tree but do not form a clade in the two domains tree; to make a clade in the two domains tree the eukaryotes would need to be included.

While it is correct to say that the eukaryotes are more closely related to the lokiarchaeota than to any other group in the two domains tree it is not correct to say that the eukaryotes are more closely related to the euryarchaeota than to any other group in the three domains tree. In the three domains tree the eukaryotes are equally closely related to all of the archaea.

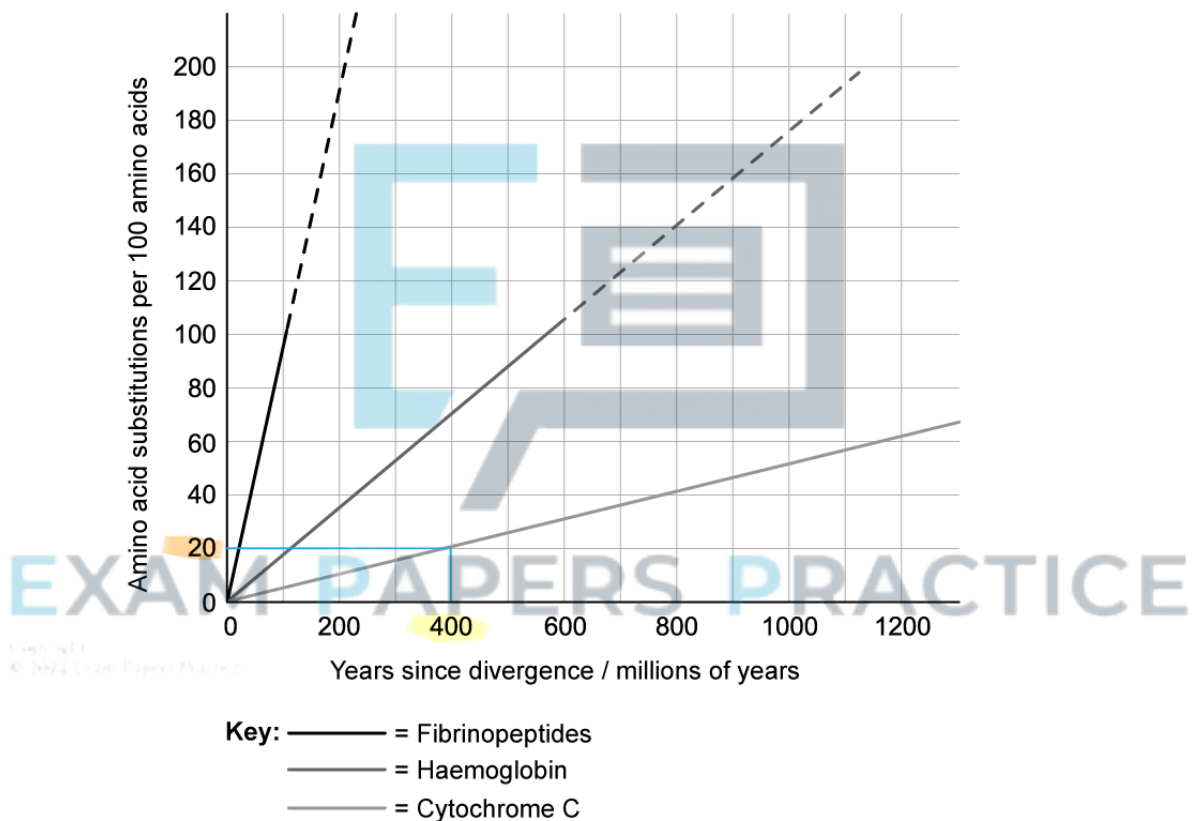
### Answer 3

The correct answer is B.



It can be seen from the graph that amino acids in cytochrome C are substituted at a rate of 20 per 400 million years. To get to a rate of substitution per 100 million years we divide each of these numbers by 4, giving a rate of substitution of 5 amino acids per 100 million years:

Substitution rate per 400 million years can be read from the graph as follows:



Amino acids are substituted at a rate of 20 per 400 million years.

convert this to substitution rate per 100 million years by dividing each number by 4:  $400 \text{ million} \div 4 = 100 \text{ million}$

$$\frac{20}{4} = 5 \quad \frac{400}{4} = 100$$

20 substitutions per 400 million years = 5 substitutions per 100 million years

Cytochrome C has been present in living organisms since before the divergence of plants and animals, and has a slow rate of change in comparison to other proteins, even important ones such as haemoglobin. This suggests that it has been around and doing the same job for a very long time. In fact cytochrome C is involved with the process of respiration, which is common to all organisms.

Not all proteins are equal when it comes to using their rate of divergence to provide a molecular clock. Some proteins have only evolved relatively recently, meaning that they are less useful for studying ancient lineages of organisms.

Arthropoda include the insects, and we have been told in the question stem that insects evolved around 400 million years ago; this is before the emergence of fibrinopeptides, meaning that it is likely that insects do not have this type of protein in their bodies.

#### Answer 4

The correct answer is D. The appearance of the two plant groups is very similar; both have succulent stems and spines instead of leaves. While the cladogram shows that the two plant groups do share a common ancestor (which might make you think the features are homologous), the horizontal lines on the branches show that succulent stems and leaf loss evolved separately in succulent cacti and euphorbias and were not a feature of their shared common ancestor. This has enabled the plant groups to adapt to similar dry environmental conditions and is known as convergent evolution.

Option A would be correct if spines and succulent stems were a feature of the common ancestor, but the cladogram shows that this is not the case.

Options B and C describe homologous and analogous traits rather than explaining their appearance.

### Answer 5

The correct answer is A. The table shows that there are more differences between the DNA base sequences of species 1 and 2 and between species 2 and 3 than there are between species 1 and 3. This tells us that species 1 and 3 are more closely related to each other than either species is to species 2. This relationship is represented by cladogram A as it shows that species 1 and 3 share a more recent common ancestor.

Species	Base sequence
1	ATCTGC
2	CCTGGT
3	ACCTAC

5 differences between species 1 + 2

Species	Base sequence
1	ATCTGC
2	CCTGGT
3	ACCTAC

2 differences between 1 + 3

Species	Base sequence
1	ATCTGC
2	CCTGGT
3	ACCTAC

5 differences between 2 + 3

Cladogram B shows that species 1 and 2 are more closely related to each other than either is to 3 as they are shown to share a more recent common ancestor.

Cladogram C shows that species 2 and 3 are closely related to each other than either is to 1 as they are shown to share a more recent common ancestor.



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Cladogram D shows an equal level of relationship between all three species as they all diverge from the common ancestor at the same time. A cladogram like this will only be used if there is not enough evidence to conclude which species are more closely related to each other.



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