2024 Bi H2 Q4

Section: DNA and the Genome

Topic: Genomic Sequencing / Phylogenetics

Question Summary

A phylogenetic tree of land plants is used to read evolutionary relationships and timing of common ancestors. You must identify another evidence source used in phylogenetics, read approximate dates from the timeline, and justify relatedness from common-ancestor positions. The ACS gene example then asks for the definition of a genome and how one gene can give rise to different enzymes.

Worked Solution

- (a)(i) Besides fossils, use molecular evidence (for example, DNA or protein sequence comparisons, molecular clocks, or genomic data).
- (a)(ii) From the timeline, the last common ancestor of Amborella (a basal angiosperm) and Osmunda (a fern) lies deep in the tree, around the early diversification of land plants. Reading from the scale gives an approximate value of about 420-450 million years ago (mya).
- (a)(iii) At 200 mya, count the lineages that share a node with monocots at or more recently than this date. From the diagram this is a small number - monocots share a relatively recent common ancestor mainly with the other angiosperms (for example,

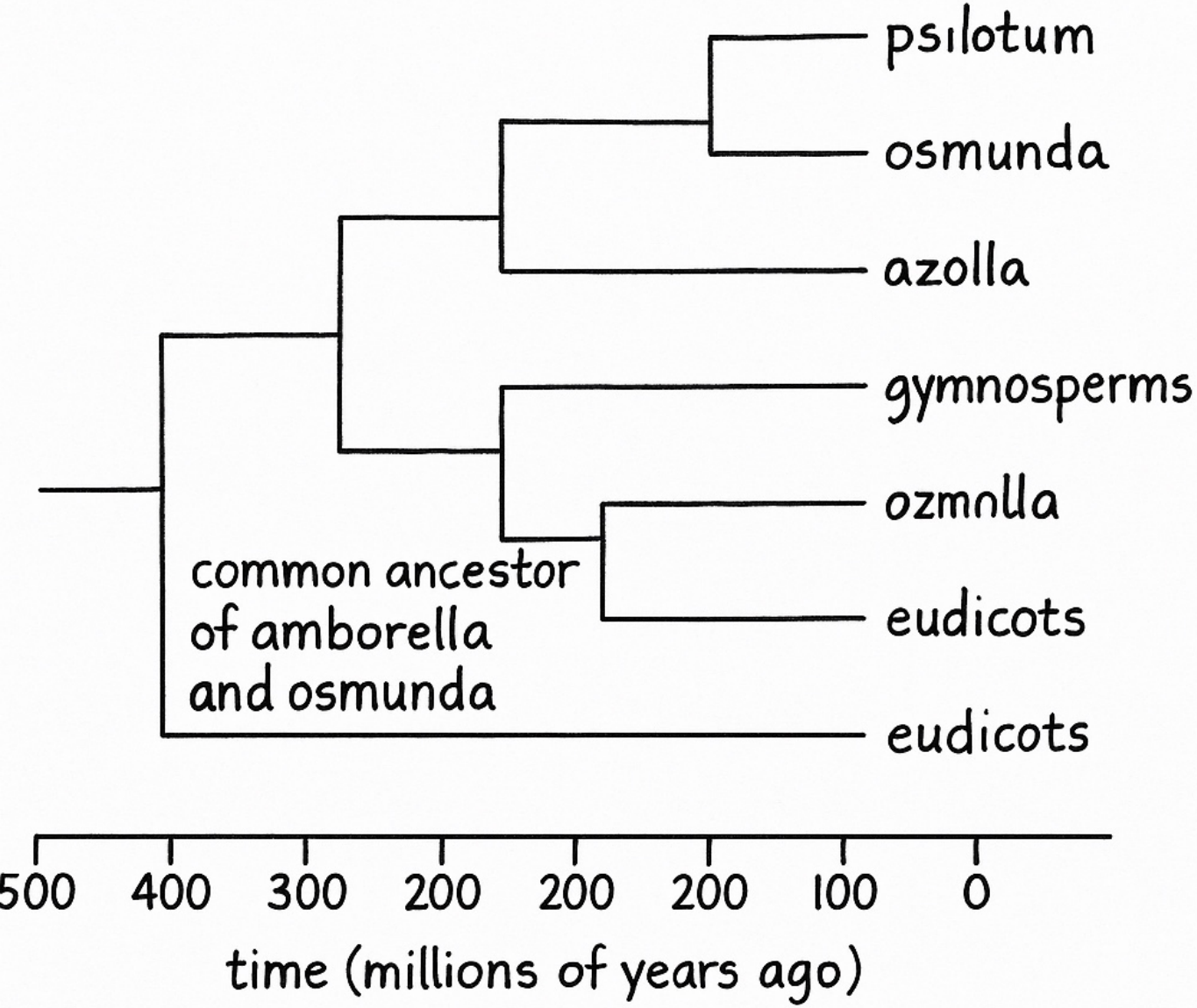
eudicots), so the answer is one group (the other major angiosperm lineage) at that time point.
- (a)(iv) Monocots are closer to gymnosperms than to lycopodiophyta because the node joining monocots and gymnosperms is more recent than the node joining monocots and lycopodiophyta - they share a more recent common ancestor on the diagram.
- (b)(i) A genome is the complete set of genetic material (DNA) of an organism, including all genes and non-coding sequences.
- (b)(ii) Different enzymes from one ACS gene can arise through alternative RNA splicing producing different mRNAs, and further post-translational modification (for example, proteolytic cleavage) generating different active enzymes.

Final Answer

-> (a)(i) Molecular (DNA/protein) evidence
-> (a)(ii) 420-450 mya (approx. from the scale)
-> (a)(iii) One group at about 200 mya (the other angiosperm lineage)
-> (a)(iv) Monocots share a more recent common ancestor with gymnosperms than with lycopodiophyta
-> (b)(i) Entire DNA content of an organism (all genes and non-coding DNA)
-> (b)(ii) Alternative splicing + post-translational modification -> different enzymes

Revision Tips

- On phylogenetic trees, recency of the common node indicates closer relatedness.
- Molecular data (DNA/protein sequences) often refine fossil-based trees.
- A genome includes coding and non-coding DNA; a gene can yield multiple proteins via alternative splicing and processing.
- When reading dates, give values directly from the timeline and state that they are approximate.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common ancestor
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500
400
300
200
200
200
100
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time (millions of years ago)