AP® BIOLOGY
2015 SCORING GUIDELINES

Question 3

The amino-acid sequence of cytochrome *c* was determined for five different species of vertebrates. The table below shows the number of differences in the sequences between each pair of species.

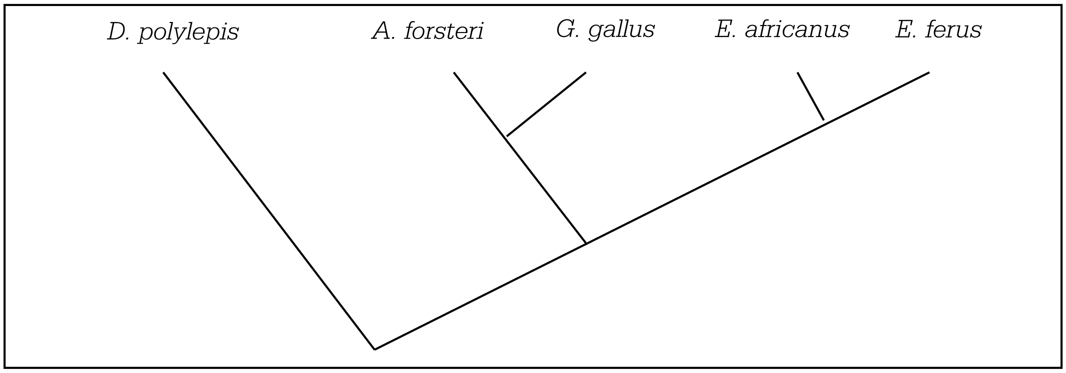
THE NUMBER OF AMINO ACID DIFFERENCES
IN CYTOCHROME *c* AMONG FIVE SPECIES

	E. ferus	*D. polylepis*	*G. gallus*	*A. forsteri*	*E. africanus*
E. ferus	0	21	11	13	1
D. polylepis		0	18	17	20
G. gallus			0	3	10
A. forsteri				0	12
E. africanus					0

(a) Using the data in the table, **create** a phylogenetic tree on the template provided to reflect the evolutionary relationships of the organisms. **Provide reasoning** for the placement on the tree of the species that is least related to the others.

Phylogenetic tree (1 point)

NOTE: There can be free rotation around the nodes in the tree.



Reasoning (1 point)

- D. polylepis has the most differences in amino acids (or changes in DNA or proteins as they relate to amino acids).

(b) **Identify** whether morphological data or amino acid sequence data are more likely to accurately represent the true evolutionary relationships among the species, and **provide reasoning** for your answer.

Question 3 (continued)

Identification (1 point)

- Amino acid/molecular data

Reasoning (1 point)

- Morphology may be similar (due to convergent evolution/analogous structures) even if there are differences in amino acid/DNA sequences.
- Molecular data (e.g. amino acid changes, DNA changes) directly show genetic make-up/ reveal evolution.

OR

Identification (1 point)

- Morphological data

Reasoning (1 point)

- Similar molecular sequences may result in different morphologies.
- An example of species with similar proteins but different morphology (e.g., chimps and humans).

3A1

3. The amino acid sequence of cytochrome *c* was determined for five different species of vertebrates. The table below shows the number of differences in the sequences between each pair of species.

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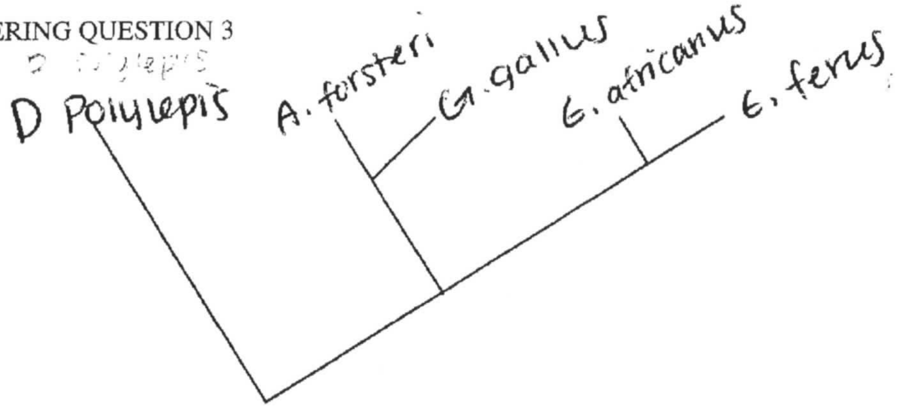
D. polylepis	21	0	18	17	20
G. gallus	11	18	0	3	10
A. forsteri	13	17	3	0	12
E. africanus	1	20	10	12	0

(a) Using the data in the table, **create** a phylogenetic tree on the template provided to reflect the evolutionary relationships of the organisms. **Provide reasoning** for the placement on the tree of the species that is least related to the others.

(b) **Identify** whether morphological data or amino acid sequence data are more likely to accurately represent the true evolutionary relationships among the species, and **provide reasoning** for your answer.

PAGE FOR ANSWERING QUESTION 3



The reason that I labeled D Polylepis as the outgroup- the one that shares the least amount of similarities- is because it had the greatest number of differences in ~~DNA~~ the amino acid sequences from all the others. It was relatively unlike any of the others. If it's lineage diverged from the other organisms' earlier, there would

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3A$_2$

ADDITIONAL PAGE FOR ANSWERING QUESTION 3

be more time for the lineages to grow apart, experience environmental pressures, and genetic mutations. The ~~differences~~ more closely related organisms are, the more recently they shared a common ancestor.

Amino acid sequence data is more likely to accurately represent the true evolutionary relationships among organisms. Morphological data can be deceiving — some structures that appear to be derived characteristics may really just be analogous structures. Analogous structures are similar in appearance or function, but do not ~~common~~ come from a common ancestor. Similar environmental pressures, for example, may have selected both flying, winged insects and birds, but their wings do not indicate their relatedness. ~~Nucleotide se~~ Amino acid sequences are more specific and similarities are less likely to occur by chance.

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3B1

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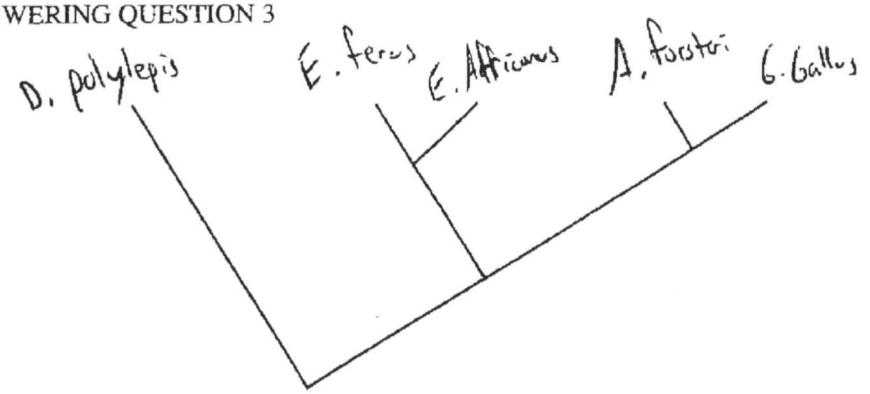
A. forsteri				0	12
E. africanus					0

(a) Using the data in the table, **create** a phylogenetic tree on the template provided to reflect the evolutionary relationships of the organisms. **Provide reasoning** for the placement on the tree of the species that is least related to the others.

(b) **Identify** whether morphological data or amino acid sequence data are more likely to accurately represent the true evolutionary relationships among the species, and **provide reasoning** for your answer.

PAGE FOR ANSWERING QUESTION 3



a) D. polylepis demonstrates the most amino acid differences from all other species, therefor it is the least evolutionarily related.

b. Amino Acid data is more accurate at demonstrating evolutionary relatedness because it is more specific, objective, and may be [illegible] [illegible] measured and held values.

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3C₁

3. The amino acid sequence of cytochrome *c* was determined for five different species of vertebrates. The table below shows the number of differences in the sequences between each pair of species.

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(a) Using the data in the table, **create** a phylogenetic tree on the template provided to reflect the evolutionary relationships of the organisms. **Provide reasoning** for the placement on the tree of the species that is least related to the others.

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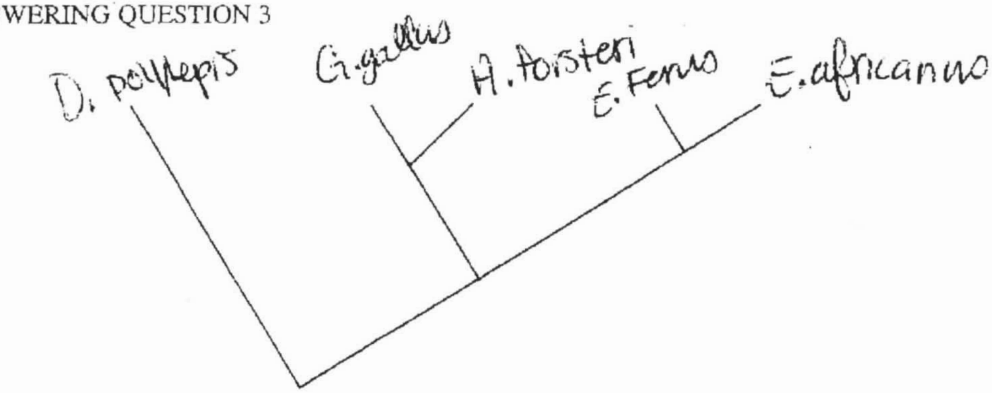

b.) Amino Acids are more usefull and better able to represent the evolutionary relationships accurately because an amino acid is literally that organisms DNA code. The amino acid sequence tells us what that organisms body is telling itself it needs to survive.

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AP® BIOLOGY
2015 SCORING COMMENTARY

Question 3

Question 3 was written to the following Learning Objectives in the AP® Biology Curriculum Framework: 1.9, 1.13, and 1.19.

Overview

This question focused on using evidence to support biological evolution. Students were asked to evaluate amino acid sequences from five related species to construct a phylogenetic tree reflecting the evolutionary relationships among them, and justify the placement on the tree of the species that is least related to the others. Students were then asked to identify whether morphological or amino acid sequence data was more likely to accurately represent the true evolutionary relationships among the species for constructing the most accurate phylogenetic tree and to provide reasoning to support their answer.

Sample: 3A
Score: 4

The response earned 1 point in part (a) for correctly drawing the phylogenetic tree. The response earned 1 point for providing reasoning that *D. polylepis* has the greatest number of differences in amino acid sequences.

In part (b) the response earned 1 point for identifying that amino acid sequences more accurately represent true evolutionary relationships. The response earned 1 point for providing the reasoning that morphological data can be deceiving because some structures that appear to be derived characteristics may just be analogous structures that do not come from a common ancestor and that amino acid similarities are less likely to occur by chance.

Sample: 3B
Score: 3

The response earned 1 point in part (a) for correctly drawing the phylogenetic tree. Note: The placement of *E. ferus* and *E. africanus* in the central part of the tree is a rotation of the node and still correctly reflects the evolutionary relationships of the organisms. The response earned 1 point for providing reasoning that *D. polylepis* has the greatest number of amino acid differences.

The response earned 1 point in part (b) for identifying that amino acid sequences more accurately represent true evolutionary relationships.

Sample: 3C
Score: 2

The response earned 1 point in part (a) for correctly drawing the phylogenetic tree. Note: The central node is rotated, but still correctly reflects the evolutionary relationships.

The response earned 1 point in part (b) for identifying that amino acid sequences are more useful for representing true evolutionary relationships.