

The image is a colorful, hand-drawn cover for a biology resource. It features a central light green rounded rectangle on a white grid background. The text 'AP Bio' is in large, dark green, bubbly letters with a pink shadow, and 'FRQ Fridays' is in large, purple, bubbly letters with a pink shadow. Below this, '2015 #3' and 'Phylogeny' are written in a simple black font. A small, cute penguin character with a bow tie and the word 'Hi!' above it is positioned to the right of the text. The cover is decorated with various biology-related icons: a DNA double helix in red and blue, a yellow pencil, a purple spiral notebook labeled 'NOTES', yellow paper clips, teal clouds, and teal exclamation marks. On the right side, there are also orange and green squiggly lines and more yellow paper clips.

AP Bio

FRQ Fridays

2015 #3
Phylogeny



FRQ Friday #24

2015 #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

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



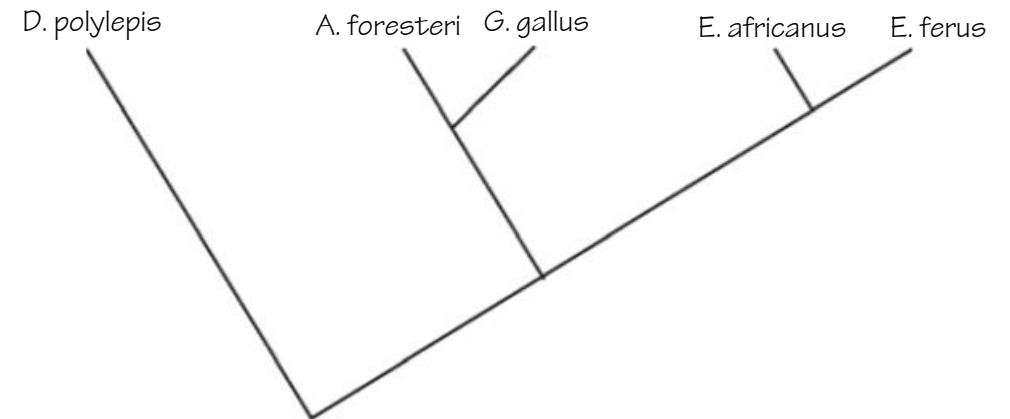
FRQ Friday #24

2015 #3

- (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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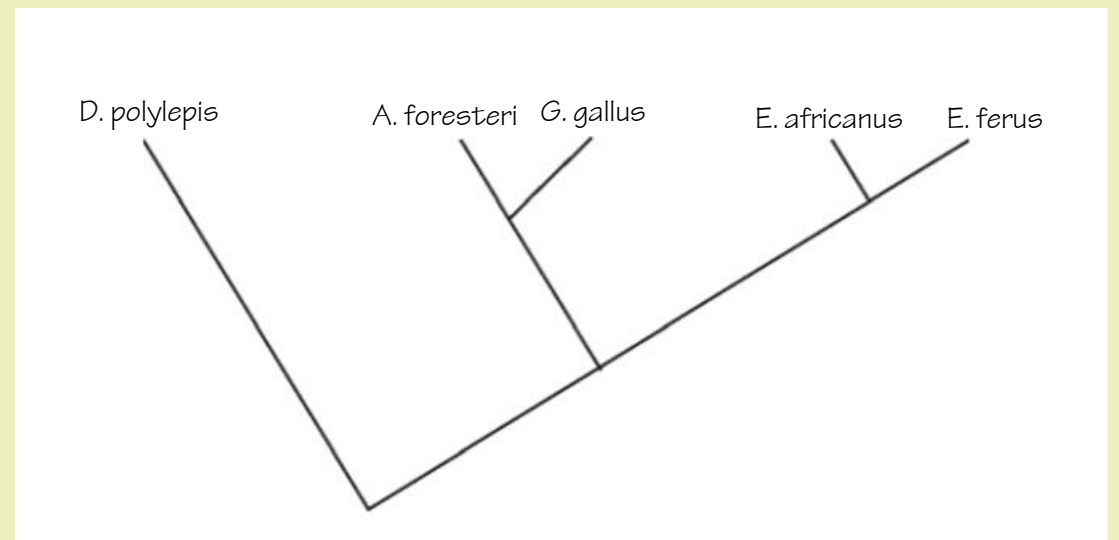
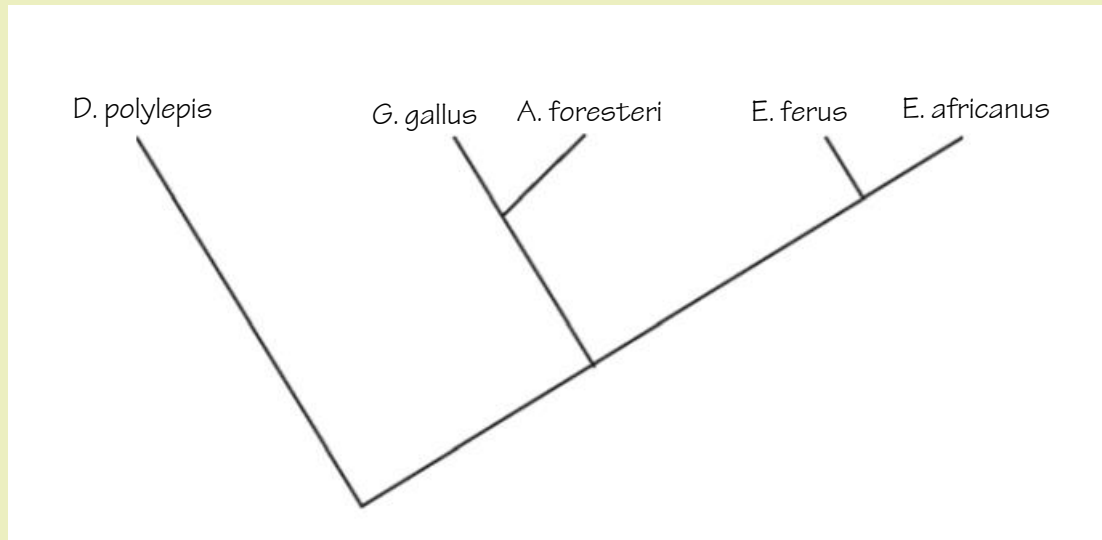
	<i>E. ferus</i>	<i>D. polylepis</i>	<i>G. gallus</i>	<i>A. forsteri</i>	<i>E. africanus</i>
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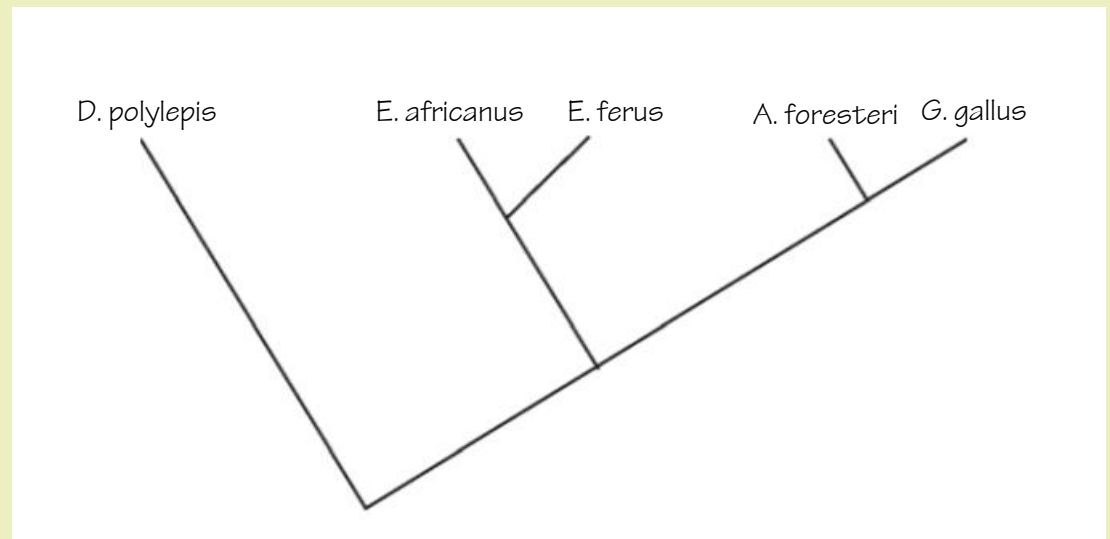
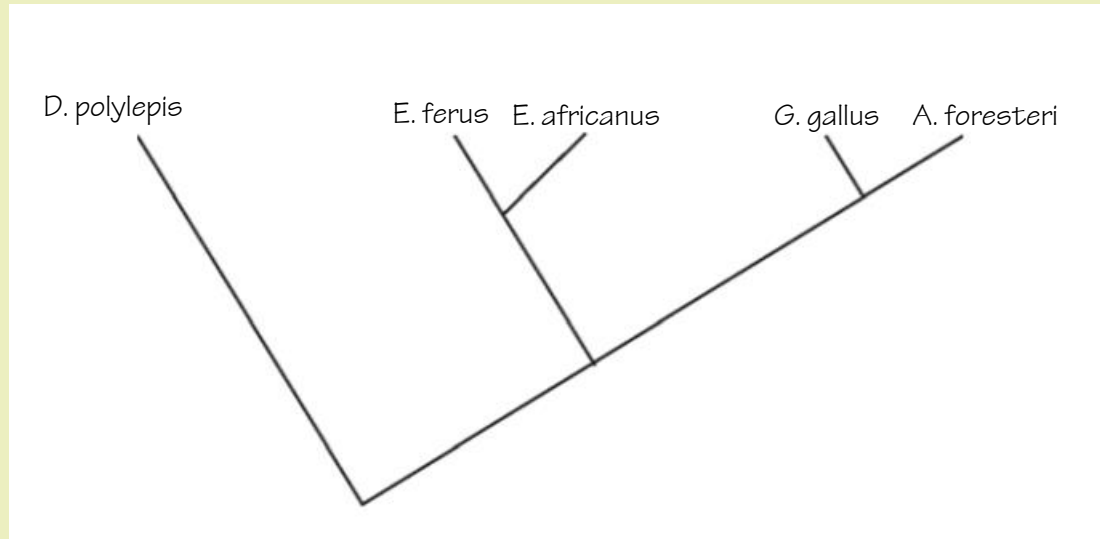
Based on the rotating points, this is also acceptable



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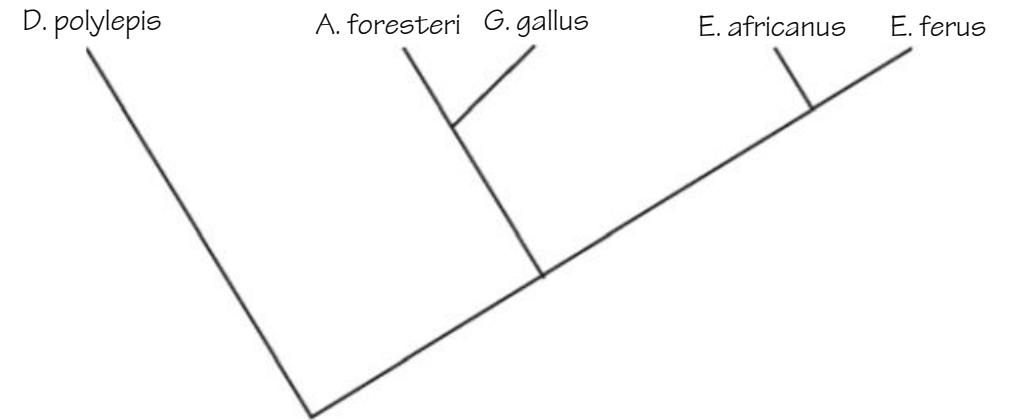
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Reasoning (1 point)

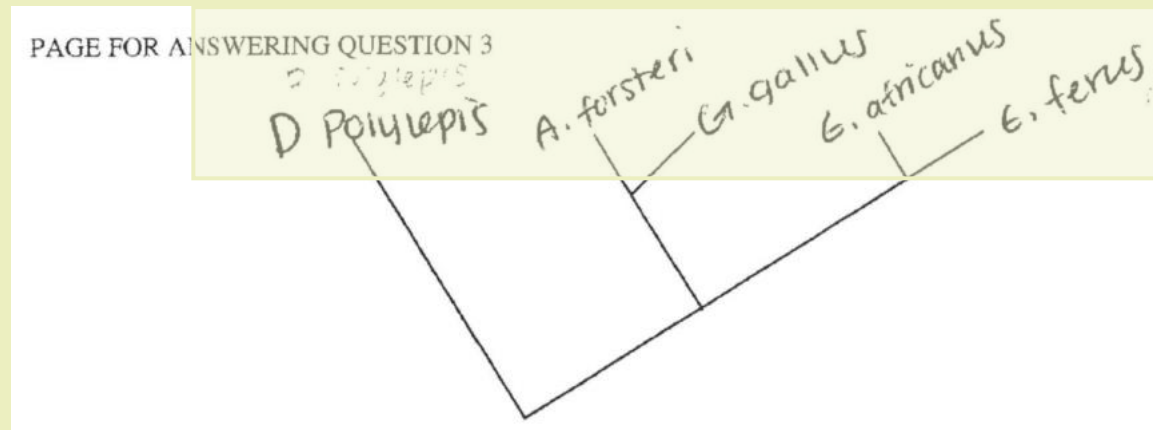
- *D. polylepis* has the most differences in amino acids (or changes in DNA or proteins as they relate to amino acids).



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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 ~~the~~ the amino acid sequences from all the others. It was relatively unlike any of the others. If its lineage diverged from the other organisms' earlier, there would 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.



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(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.

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.

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).



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"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 ~~form~~^{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~~ Amino acid sequences are more specific and similarities are less likely to occur by chance.

