How do amino acid sequences provide evidence for evolution?

BACKGROUND :

Homologous structures—those structures believed to have a common origin but not necessarily a common function—provide some of the most significant evidence supporting the theory of evolution. For example, the forelimbs of vertebrates often have different functions and outward appearances, yet the underlying similarity of the bones indicates a common origin. While homologous structures can be used to demonstrate relationships between similar organisms, they are of little value for determining evolutionary relationships among those structures that are dissimilar.

Another technique used to determine evolutionary relationships is to study the biochemical similarity of organisms. Though molds, aardvarks, and humans appear to have little in common physically, a study of their proteins reveals certain similarities. Biologists have perfected techniques for determining the sequence of amino acids in proteins. By comparing the amino acid sequences in homologous proteins of similar organisms and of diverse organisms, evolutionary relationships that might otherwise go undetected can be determined. Biologists believe that the greater the similarity between the amino acid sequences of two organisms, the closer their relationship. Conversely, the greater the differences, the more distant the relationship. Further, biologists have found that such biochemical evidence compares favorably with other lines of evidence for evolutionary relationships.

In this investigation you will compare amino acid sequences in proteins of several vertebrates. You will also study amino acid differences and infer evolutionary relationships among some diverse organisms.

OBJECTIVES -

After completing this investigation, you will be able to

- Recognize evolutionary relationships by studying the sequences of amino acids in the hemoglobin of several vertebrates.
- Describe evolutionary relationships by interpreting graphs showing differences in the cytochrome c molecules of several organisms.

MATERIALS

Prelab

Investigation

needed

 no special materials
 no special materials needed

PROCEDURE •

Prelab: Technique—Comparing Amino Acid Sequences

- 1. Review pages 188 through 194 in your text.
- 2. Examine Figure 19-1 on page 94, which compares corresponding portions of hemoglobin molecules in humans and five other vertebrate animials. Hemoglobin, a protein composed of several long chains of amino acids, is the oxygen-carrying molecule in red blood cells. The sequence shown is only a portion of a chain made up of 146 amino acids. The numbers in Figure 19-1 indicate the position of a particular amino acid in the chain.
- 3. In number I on the Answer Sheet, notice that the abbreviated names of the amino acids in human hemoglobin are printed.
- 4. In the appropriate spaces in number 1, write the abbreviated name of each amino acid in chimpanzee hemoglobin that is different from that in human hemoglobin. If there are no differences. leave the spaces blank.
- 5. For the remaining organisms, write the abbreviated names of any amino acids that do not correspond to those in human hemoglobin. NOTE: Always be sure that you compare the amino acid sequence for each organism with that of the human, and not the organism on the line above. Complete numbers 2 through 5 on the Answer Sheet.

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Fig. 19-1

Investigation—Inferring Evolutionary Relationships from Differences in Amino Acid Sequences

1. Another commonly studied protein is cytochrome c. This protein, consisting of 104 amino acids, is located in the mitochondria of cells. There it functions as a respiratory enzyme. Examine Figure 19-2. Using human cytochrome c as a standard, the amino acid differences between humans and a number of other organisms are shown.

Species Pairings	Number of Differences
Human - chimpanzee Human - fruit fly Human - horse Human - pigeon Human - rattlesnake Human - red bread mold Human - rhesus monkey Human - screwworm fly Human - snapping turtle Human - tuna fish Human - wheat Fig. 19-2	0 29 12 12 14 48 1 27 15 21 43

- Complete number 1 on the Answer Sheet by making a bar graph to show the amino acid differences between humans and the other organisms. You will have one bar for each difference.
- 3. Next examine Figure 19-3. In this figure the cytochrome c of a fruit fly is used as a standard in comparing amino acid differences among several organisms. Use the grid in number 2 to construct a bar graph of these differences. Then complete Answer Sheet numbers 3 through 9.

	Species Pairings	Number of Differences
1	Fruit fly - dogfish shark	` 26
1	Fruit fly - pigeon	25
1	Fruit fly - screwworm fly	2
1	Fruit fly - silkworm moth	_
1	Fruit fly - tabacco hornworm moth	15
l	Fruit fly - wheat	14
	, and a second	47
L	Fig. 19-3	

FURTHER INVESTIGATION

Conduct an investigation on the means by which amino acid sequences are used to construct phylogenetic, or evolutionary, trees. Then, using an appropriate reference, make a large bulletin-board drawing showing an example of a phylogenetic tree.

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3.	3. In how many positions are the amino acids the same in each organism?	
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On the basis of their Explain your answer.					
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5. Among the organisms that you compared, which one appears to be least closely related to humans?

Investigation

1. Use the information from Figure 19-2 to complete the following graph.

Number of Differences

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2. Use the information from Figure 19–3 to complete the following graph.

Number of Differences

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. W	That organisms appear to be least closely related to humans?	
. C	heck the pair of organisms that appears to be most closely related to each other	
	snapping turtle—tuna fish	
	snapping turtle—rattlesnake	
	snapping turtle—pigeon	•
G	ive a reason for your answer.	S 6
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7. Name the pair of organisms that appears to be equally related to humans on the basis of cytochrome c similarity.

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Agree or disa	agree with the following statement. "Fruit flies and humans have about the same evol	lutio
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There is a diffe	erence of only one amino acid in one chain of the hemoglobin of humans and gorillas. Wh	at m
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