

# Unit Seven:

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Evolution



Name \_\_\_\_\_

Date \_\_\_\_\_

## Analyzing Amino-Acid Sequences to Determine Evolutionary Relationships

<b>Skills</b>	<ul style="list-style-type: none"> <li>• comparing and contrasting sequences of amino acids</li> <li>• interpreting data</li> </ul>
<b>Objectives</b>	<ul style="list-style-type: none"> <li>• <i>Identify</i> the differences in the amino-acid sequences of the cytochrome c and hemoglobin molecules of several species.</li> <li>• <i>Infer</i> the evolutionary relationships among several species by comparing amino-acid sequences of the same protein in different organisms.</li> </ul>
<b>Materials</b>	<ul style="list-style-type: none"> <li>• paper</li> <li>• pencil</li> </ul>
<b>Purpose</b>	<p>You are a zoologist who specializes in the classification of vertebrates according to their evolutionary relationships. In your research, you examine the amino-acid sequences of particular protein molecules found in vertebrates to determine the degree of biochemical similarity between vertebrate species. Today you will compare portions of human cytochrome c and hemoglobin molecules with the same portions of those molecules in other vertebrate species. Your goals are to determine the differences in the amino-acid sequences of the molecules and to deduce the evolutionary relationships among the species.</p>
<b>Background</b>	<p>The biochemical comparison of proteins is a technique used to determine evolutionary relationships among organisms. Proteins consist of chains of amino acids. The sequence, or order, of the amino acids in a protein determines the type and nature of the protein. In turn, the sequence of amino acids in a protein is determined by the sequence of nucleotides in a gene. A change in the DNA nucleotide sequence (mutation) of a gene that codes for a protein may result in a change in the amino-acid sequence of the protein.</p> <p>Biochemical evidence of evolution compares favorably with structural evidence of evolution. Even organisms that appear to have few physical similarities may have similar sequences of amino acids in their proteins and be closely related through evolution. Researchers believe that the greater the similarity in the amino-acid sequences of two organisms, the more closely related they are in an evolutionary sense. Conversely, the greater the time that organisms have been diverging from a common ancestor, the greater the differences that can be expected in the amino-acid sequences of their proteins.</p> <p>Two proteins are commonly studied in attempting to deduce evolutionary relationships from differences in amino-acid sequences. One is cytochrome c, and the other is hemoglobin. <b>Cytochrome c</b> is a protein used in cellular respiration and found in the mitochondria of many organisms. <b>Hemoglobin</b> is the oxygen-carrying molecule found in red blood cells.</p>

## Analysis Questions

1. Why can it be said that proteins behave like molecular clocks? Hint: clocks tell time!
2. When the portions of the gorilla and human hemoglobin molecules were compared, there was only one difference in the amino acid sequence. What could have been responsible for this change?
3. Examine the data table you completed in step 2 of part 1. The values listed for the chicken and the horse differ by only one. However, this does NOT indicate that the chicken and the horse are closely related to each other. Explain.
4. How is biochemical comparison different from other methods of determining evolutionary relationships?



## Part 2—Hemoglobin

3. Look at the amino-acid sequences shown below. These sequences are portions of the hemoglobin molecules of five organisms. The portion of the chains shown are from amino acid number 87 to amino acid number 116 in a sequence of 146 amino acids.

4. Compare the amino-acid sequence of human hemoglobin molecules with that of each of the other four vertebrates. For each vertebrate's sequence, count the number of amino acids that differ from the human sequence and list them in the table below. Be sure to list the animal species in descending order according to their degree of evolutionary closeness to humans.

### Hemoglobin Amino-Acid Sequence Similarities Between Humans and Other Vertebrate Species

Species	Number of differences from human hemoglobin

◆ In the study of hemoglobin, which vertebrate is most closely related to humans? Least closely related?

### Hemoglobin Amino-Acid Sequences

AA #	Human	Chimpanzee	Gorilla	Monkey	Horse
87	THR	THR	THR	GLN	ALA
88	LEU	LEU	LEU	LEU	LEU
89	SER	SER	SER	SER	SER
90	GLU	GLU	GLU	GLU	GLU
91	LEU	LEU	LEU	LEU	LEU
92	HIS	HIS	HIS	HIS	HIS
93	CYS	CYS	CYS	CYS	CYS
94	ASP	ASP	ASP	ASP	ASP
95	LYS	LYS	LYS	LYS	LYS
96	LEU	LEU	LEU	LEU	LEU
97	HIS	HIS	HIS	HIS	HIS
98	VAL	VAL	VAL	VAL	VAL
99	ASP	ASP	ASP	ASP	ASP
100	PRO	PRO	PRO	PRO	PRO
101	GLU	GLU	GLU	GLU	GLU
102	ASN	ASN	ASN	ASN	ASN
103	PHE	PHE	PHE	PHE	PHE
104	ARG	ARG	LYS	LYS	ARG
105	LEU	LEU	LEU	LEU	LEU
106	LEU	LEU	LEU	LEU	LEU
107	GLY	GLY	GLY	GLY	GLY
108	ASN	ASN	ASN	ASN	ASN
109	VAL	VAL	VAL	VAL	VAL
110	LEU	LEU	LEU	LEU	LEU
111	VAL	VAL	VAL	VAL	ALA
112	CYS	CYS	CYS	CYS	LEU
113	VAL	VAL	VAL	VAL	VAL
114	LEU	LEU	LEU	LEU	VAL
115	ALA	ALA	ALA	ALA	ALA
116	HIS	HIS	HIS	HIS	ARG

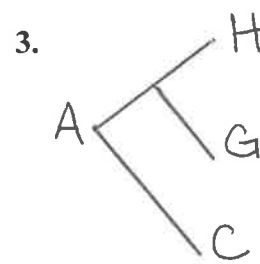
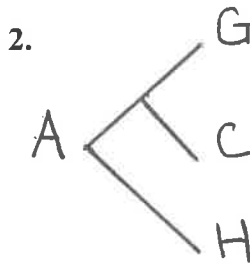
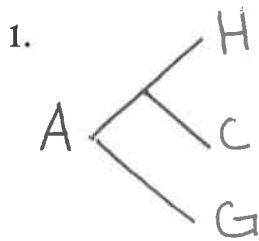
Name \_\_\_\_\_

Date \_\_\_\_\_

### Investigating Common Descent

#### Part I: Morphological Trees

Morphological trees show the relationship between organisms. The following three morphological trees show possible relationships between humans (h), chimpanzees (c), gorillas (g), and a common ancestor (a).



Part II: Working in your lab groups, “synthesize” strands of DNA according to the following specifications.

Blue = adenine (A)  
Yellow = thymine (T)

Green = guanine (G)  
Pink = cytosine (C)

Each student will synthesize one strand of DNA. The strand represents a small section of a gene that codes for hemoglobin protein. Circle each letter (A, G, T, C) with an even, small circle and color in each circle according to the color chart above.

EXAMPLE: A - C - G - T - A

#### Strand #1 – Human DNA

A - G - G - C - A - T - A - A - A - C - C - A - A - C - C - G - A - T - T - A

#### Strand #2 – Chimpanzee DNA

A - G - G - C - C - C - C - T - T - C - C - A - A - C - C - G - A - T - T - A

#### Strand #3 – Gorilla DNA

A - G - G - C - C - C - C - T - T - C - C - A - A - C - C - A - G - G - C - C

#### Strand #4 – Common Ancestor DNA (hypothetical gene)

A - G - G - C - C - G - G - C - T - C - C - A - A - C - C - A - G - G - C - C

**Questions:**

**1. Compare the human DNA to the chimpanzee DNA. Count the number of bases that are the same and then count the number of bases that are not the same. Put the data in the table below. Then compare the human DNA to the gorilla DNA.**

**(# of matched + # of unmatched = 20)**

<b>Human DNA compared to:</b>	<b># of Matched Bases</b>	<b># of Unmatched Bases</b>
<b>Chimpanzee DNA</b>		
<b>Gorilla DNA</b>		

**2. What do these data suggest about the relationship among humans, gorillas, and chimpanzees?**

**3. Which of the three hypothesized morphological trees from Part I, if any, is supported by the data? Why or why not?**

**4. What further investigation could be done to provide additional support for your hypotheses?**

**5. Now compare the common ancestor DNA to the other three. Record the data in the table. (# of matched + # of unmatched = 20)**

<b>Common Ancestor DNA Compared to:</b>	<b># of Matched Bases</b>	<b># of Unmatched Bases</b>
<b>Chimpanzee DNA</b>		
<b>Gorilla DNA</b>		
<b>Human DNA</b>		

**6. Which DNA is most similar to the common ancestor DNA?**

**7. Which two DNA strands were most similar in the way they compared to the common ancestor DNA?**

**8. Which hypothesized morphological tree from Part I is best supported by your data?**

**9. Do your findings PROVE that this hypothesis is correct? Explain**



Name \_\_\_\_\_

# I.D. That Tree!

## **Background:**

What is a dichotomous key? A dichotomous key is one tool that can be used to identify trees. This type of key is also used for flowers, animals, rocks, fish, and more! A dichotomous key contains a series of choices that lead the user to the correct name of an item. "Dichotomous" means "divided into two parts." Therefore, a dichotomous key will always give you two choices in each step.

To find the website you will use, go to *google*, and search: ***uwsp leaf tree to identify***. You will utilize the website indicated by the first link, which should be...

[www.uwsp.edu/cnrap/leaf/Pages/TreeKey/treeToidentify.aspx?feature](http://www.uwsp.edu/cnrap/leaf/Pages/TreeKey/treeToidentify.aspx?feature) to learn how a dichotomous key works. Identify the first 20 tree species and write each tree's name in the chart provided (recopy chart into your lab notebook).

## **Procedure:**

Choose a tree to identify on the left-hand side of the page. Click on each number and follow the steps to identify each tree. Record your findings in the chart below.

Number	Common Name of Tree
1	
2	
3	
4	
5	
6	
7	
8	
9	
10	
11	
12	
13	
14	
15	
16	
17	
18	
19	
20	

## **Analysis:**

- 1) Describe the difference between a deciduous and coniferous tree.
- 2) Describe at least 4 characteristics of a tree that may be useful in identifying it.
- 3) Why do you think it is important that trees be identified? (Think about why trees are important to humans or other animals)

