

Name: _____

Lab: Classification using Molecular Homologies

BACKGROUND: You just have completed an activity in which you made a phylogenetic tree showing the evolutionary relationships between seven organisms. The data used to draw that evolutionary tree were homologous structures that were inherited from their ancestors. In this activity, you will use molecular data to determine evolutionary relationships.

Molecular homologies are similarities in nuclear DNA, mitochondrial DNA, or protein structure. If there is strong agreement between the patterns produced using anatomical similarities and those produced by using molecular homologies, it provides what we call "independent confirmation" of the phylogenetic tree. Independent confirmation is where two or more sources of evidence that are not dependent on each other produce the same pattern. The more independent confirmation that is available, the more confidence we have that the evolutionary relationships shown in the phylogenetic tree are correct.

In this activity, we will examine and compare the amino acid sequence of a protein. All seven of the organisms used in the previous activity produce this protein (it is a homologous protein). The complete sequence of amino acids for this protein has been determined for many organisms, including six of those seven animals. We assume that if we find fewer differences in the amino acid sequences, those animals are more closely related.

PROCEDURE: You will be provided with a chart showing the amino acid sequence in a protein that is homologous for the 20 organisms shown, including six of the seven organisms already studied (data on this protein is not available here for the lamprey). The name of the protein is cytochrome-c. It is an enzyme that is important in the breakdown of food molecules by a cell. It helps release the energy in food molecules so that it can be used by the cell. Each amino acid is represented by a unique letter in the chart.

Compare the sequence of amino acids (letters) in human cytochrome-c to the sequences for each of the 5 remaining animals (shown in the diagram below) by counting the number of differences. HINT: Highlight or underline the organism being checked, then circle each amino acid which is different from the one in the human sequence. It helps to use a ruler or other straight edge. When an organism has a "-" instead of an amino acid, that means there is no amino acid there. When comparing a "-" to an organism that has an amino acid at the position, it should be considered as a difference. When both organisms have a "-" at that spot, it is not considered as a difference. Amino acids with no differences are shown in lighter print.

Record the number of differences next to each animal's name. Compare your numbers with those of your team members. If there is a discrepancy, repeat the scan and count. Record the confirmed number of amino acid differences in the appropriate hexagon on the evolutionary tree below (below the vertical arrow pointing to that animal).