

# PHYLOGENY & CLADISTICS ACTIVITY

## Background:

One way to discover how groups of organisms are related to each other (phylogeny) is to compare the anatomical structures (body organs and parts) of many different organisms.

Corresponding organs and other body parts that are alike in basic structure and origin are said to be homologous structures (for example, the front legs of a horse, wings of a bird, flippers of a whale, and the arms of a person are all homologous to each other). When different organisms share a large number of homologous structures, it is considered strong evidence that they are related to each other. When organisms are related to each other, it means they must have had a common ancestor at some time in the past. If there are specific modifications of those features shared by different groups of organisms, we say that those features are “shared derived characters”.

When we do studies in comparative anatomy, and find different numbers of shared derived characters exist between different groups, we can draw a diagram of branching lines which connect those groups, showing their different degrees of relationship. These diagrams look like trees and are called "phylogenetic trees" or "cladograms" (CLAY-doe-grams); see examples provided by your teacher. The organisms are at the tips of the stems. The shared derived features of the homologous structures are shown on the cladogram by solid square boxes along the branches, and common ancestors are shown by open circles. The more derived structures two organisms share, the closer is their evolutionary relationship -- that is, the more recently their common ancestor lived. On the cladogram, close relationships are shown by a recent fork from the supporting branch. The closer the fork in the branch between two organisms, the closer is their relationship.

1. GAPDH (glyceraldehyde 3-phosphate dehydrogenase) is an enzyme that catalyzes the sixth step in glycolysis, an important reaction that produces molecules used in cellular respiration. The following data table shows the percentage similarity of this gene and the protein it expresses in humans versus other species. For example, according to the table, the GAPDH gene in chimpanzees is 99.6% identical to the gene found in humans, while the protein is identical.

Species	Gene Percentage Similarity	Protein Percentage Similarity
Chimpanzee ( <i>Pan troglodytes</i> )	99.6%	100%
Dog ( <i>Canis lupus familiaris</i> )	91.3%	95.2%
Fruit fly ( <i>Drosophila melanogaster</i> )	72.4%	76.7%
Roundworm ( <i>Caenorhabditis elegans</i> )	68.2%	74.3%

- Why is the percentage similarity in the gene always lower than the percentage similarity in the protein for each of the species? (Hint: Recall how a gene is expressed to produce a protein.)
- Draw a cladogram depicting the evolutionary relationships among all five species (including Humans) according to their gene or protein percentage similarity in the GAPDH gene shown in the table below.

2. Use the following data to construct a cladogram of the major plant groups.

Organisms	Vascular Tissue	Flowers	Seeds
Mosses	0	0	0
Pine trees	1	0	1
Flowering plants	1	1	1
Ferns	1	0	0
Total	3	1	2

3. The following table shows the percentage similarity in sequences of nucleotides from a homologous gene derived from five different species of mammals compared to that of a homologous human gene. In simpler terms, the percentage similarity between the Human gene and the Chimpanzee gene is 99.7%.

Draw a cladogram depicting the evolutionary relationships among all six species (including Humans) according to their percentage similarity in the gene shown in the table.

SPECIES	% SIMILARITY
CHIMPANZEE	99.7
BABOON	97.2
RABBIT	93.7
RHESUS MONKEY	96.9
ORANGUTAN	98.6

An **Outgroup** is a species of organisms that acts as a reference group when determining the evolutionary relationships between three or more other species of organisms. It is hypothesized to be related to the species in question but less closely than any of the other species are to each other. Outgroup species therefore share more primitive characteristics with the group in question. In a phylogenetic tree, the line for the outgroup should branch from the ancestral lineage before any of the other groups. It gives you an overall comparison between a distantly related species and those that are more closely related.

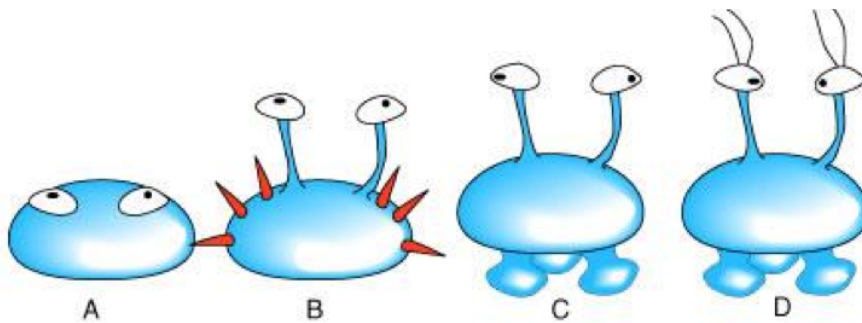
4. What probably explains the inclusion of rabbits in this research from question #3?
- Their short generation time provides a ready source of DNA.
  - They possess all of the shared derived characters as do the other species.
  - They are the closest known relatives of the rhesus monkeys.
  - They are the outgroup.
  - They are mammals.
5. What conclusions can be drawn from the data shown in question #3?
- Humans and other primates evolved from rabbits within the past 10 million years.
  - Most of the genes of other organisms are similar to human genes.
  - Among the species listed, humans shared a common ancestor most recently with chimpanzees.
  - Humans evolved from chimpanzees somewhere in Africa within the last 6 million years.

6. Draw a cladogram based on the characters in the table below. Place hatch marks on the tree to indicate the origin(s) of each of the characters.

CHARACTER	LANCELET	LAMPREY	TUNA	SALAMANDER	TURTLE	LEOPARD	DOLPHIN
BACKBONE	0	1	1	1	1	1	1
HINGED JAW	0	0	1	1	1	1	1
4 LIMBS	0	0	0	1	1	1	1
AMNION	0	0	0	0	1	1	1
MILK	0	0	0	0	0	1	1
DORSAL FIN	0	0	1	0	0	0	1

Notice that the character “dorsal fin” is included in the table, a character possessed by both the Tuna and the Dolphin. Why should the “dorsal fin” character not be used to construct the cladogram even though it is a shared character by both the Tuna and the Dolphin?

7. The following four alien species were discovered, and it was realized that species “A” is very primitive. Use the pictures of each species to complete the table and construct a cladogram.



Physical Characteristic	SPECIES			
	A	B	C	D
eyes present				
spines present				
eyes on stalks				
“feet” present				
antennae present				