

## PHYLOGENETIC ANALYSIS

In the discussion of molecular evolution we learned that mutations that arise in an ancestral species will be passed on to descendant species, who will themselves become subject to natural selection. Thus, the ancestor and all of its descendents form an evolutionary unit called a **monophyletic group**. A monophyletic group is defined by **derived characters** that all its members share, but which other organisms do not.

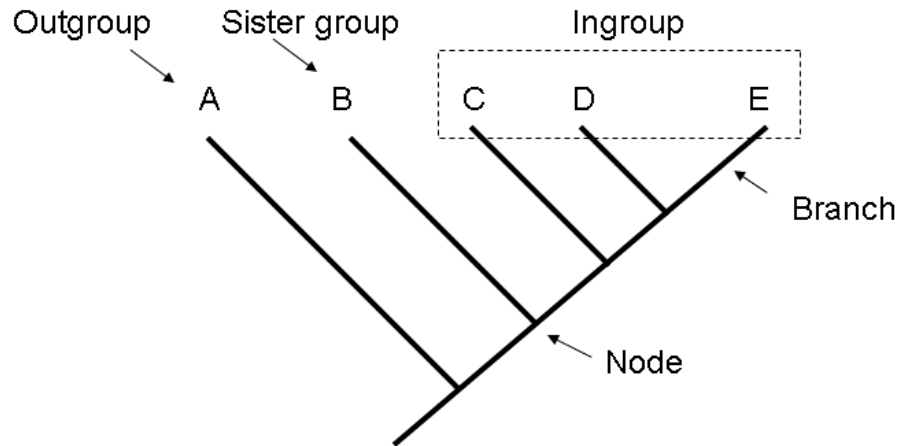
A **phylogeny** is the pattern of relationships among monophyletic groups. The simplest, most parsimonious, pattern of phylogeny is a system of dichotomous branching. Each branch represents a **clade** (monophyletic group), and the method of resolving phylogeny into a pattern of dichotomous branching is called **cladistic analysis**.

First, a few more definitions:

**Systematics** – the study of the evolutionary relationships among taxa

**Taxon** – a monophyletic group of organisms at any hierarchical level (i.e., genus, species, family, order)

**Shared derived characters** – features of a group of organisms that are an evolutionarily novelty in their common ancestor, passed on to them as descendants, but not present in taxa outside the group. Shared derived characters are a reflection of genetic change and its subsequent inheritance by descendant species. Therefore, the possession of shared derived characters defines monophyletic groups.



**Cladogram** – the graphical representation of phylogeny as determined through cladistic analysis. Cladograms ignore time, expressing instead the fewest number of steps needed to produce a branching pattern among monophyletic groups. The result is a nested hierarchy of monophyletic groups, becoming more inclusive toward the root of the cladogram, less inclusive toward the terminal branches. Even though cladograms ignore time, their topology (shape) implies a sequence of hypothetical common ancestors because of the sequence of branching events showing the first occurrence of shared derived characters.

**Node** – the common point on a cladogram from which two branches diverge. A node can be considered the point at which evolutionary novelties arise. They can be used to represent the position of a hypothetical common ancestor for the sister clades because all the descendants on each of the two branches arising from a node will share the derived character that appears for the first time on the cladogram at that node. Cladistic analysis does not seek real ancestors, but rather groups organisms by their shared derived characters.

**Sister groups** – closest relatives in a cladistic analysis. The two branches deriving from a common node.

**Primitive character** – a phylogenetically uninformative character because it is more widely distributed among taxa, and hence present in the sister group to that under investigation. Note that a primitive character for one phylogenetic analysis is a derived character for a more inclusive phylogenetic analysis.

**Outgroup** – the primitive sister group to the set of organisms that are the subject of a phylogenetic analysis. Outgroups help to determine the polarity of a character (whether it is primitive or derived) because the state of a character in a more inclusive suite of organisms suggests its primitive condition.

Sources of phylogenetic information: living organisms, fossil organisms.

Cladistic (phylogenetic) analysis rests on algorithms that determine the fewest number of evolutionary steps needed to produce a cladogram. The goal is maximum parsimony and the result is the shortest cladogram possible.

The discussion above is rudimentary and does not reflect the statistical complexity involved with the simultaneous evaluation of many characters in many taxa.

Here are next week's quiz questions: How many possible cladograms can be drawn for a group of three taxa (A, B, C)? How many can be drawn for a group of four taxa (A, B, C, D)? How would you choose the correct one? You may draw the cladograms and count them if you wish.

For our purposes, for the remainder of the semester the relationships of organisms will be shown in the form of cladograms with one or a few derived characters at each node, thereby expressing the sister group relationship of monophyletic groups. The monophyletic groups will thus be arranged in a nested hierarchy.