

# The De-riving Force of Cladogenesis<sup>1</sup>

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**Cladogenesis** is the term used to describe the branching off of new taxa. These branches — or *clades* — are based on several criteria which make the descendants along a particular branch different from their ancestors and from related taxa on other branches. Each new branch exhibits a combination of novel characteristics that are unique to that branch mixed with some "familial" characteristics which this branch shares with its evolutionary ancestors. Although certain novel traits may be diagnostic for members of an evolving lineage, it is often the *combination* of unique and shared characteristics that defines new branches.

The basis of constructing a valid cladogram is the ability to identify the characteristics of the ancestral population and those of the descendants ([http://evolution.berkeley.edu/evolibrary/article/0\\_0\\_0/evo\\_06](http://evolution.berkeley.edu/evolibrary/article/0_0_0/evo_06)). Characteristics found among the ancestors and shared by most or all members of related taxa are referred to as *primitive*. In cladistic studies this word is understood as "original" or "primal" and not as "crude" or "simple". In order to avoid confusion, some writers refer to these traits as *conservative* or simply *ancestral*. Shared, conservative traits link the members of related branches to a common ancestor. On the other hand, characteristics that are found in various evolutionary branches that differ from those of the ancestors are considered *derived*. In many cases these derived characteristics are unique modifications of widely shared ancestral characteristics. Derived traits distinguish the members of one evolutionary branch from the members of another branch.

A cladogram is constructed on these combinations of ancestral and derived characteristics in related taxa by organizing and diagramming the pattern and sequence in which they could have arisen. Ideally, we want a cladogram based on branches defined by uniquely derived characters that emerge once in an evolving lineage and are shared by all subsequent descendants. This helps us to test our hypotheses about common descent in evolving lineages. A branch that includes all the organisms descended from the same ancestral population is said to be *monophyletic*.

Because living organisms are a complex combination of traits, however, sometimes it is possible to draw more than one cladogram that might reflect the evolutionary history of a group of organisms. There is a variety of methods that researchers use to evaluate these options, and the appropriate choice depends on the kinds of data available and the specific hypothesis to be tested. The goal, however, is to find the tree that best explains the phylogenetic relationships among the organisms included in the tree.

Two fundamental principles used in evaluating cladograms are parsimony ([http://evolution.berkeley.edu/evolibrary/article/0\\_0\\_0/phylogenetics\\_08](http://evolution.berkeley.edu/evolibrary/article/0_0_0/phylogenetics_08)) and robusticity. First, when there is more than one way to draw a cladogram, *and* when there are no *other* data that suggest one of these is more likely than the others, we tend to choose the one in which derived traits are re-invented in different branches the fewest number of times. Second, we prefer trees that

maintain their basic form, even when different options are applied to the sequence of changes in one or more of their branches. However, when more data are available about the history or the origin of a particular feature, these data are more important tools in determining which of the alternative trees is better. In contrast to exercises in mere *classification*, we want to base our *taxonomy* on the cladogram. The guiding principle is that our taxa should be monophyletic. Each evolutionary branch must contain all descendants of a common ancestor. One of the chief criticisms against the "classical" taxonomy that places humans on one branch of the hominoid family tree and the great apes (African apes and the orang utan) on another is that this arrangement fails on the criterion of monophyly. Based on fossil data, comparative anatomy, and molecular biology, humans and African apes share a recent common ancestor and so a monophyletic clade would include humans and African apes together. Any branch that combines Asian apes (such as the orang utan) with African apes, but excludes the human branch, is invalid because it does not include *all* the descendants of the common ancestor of Asian and African apes (see <http://tolweb.org/hominidae/16299>).

There is, of course, a uniquely human clade containing all the hominins (species of the genera *Homo*, *Australopithecus*, and *Ardipithecus*) descended from the first upright walkers among the African apes; however, no clade that excludes humans but includes African and Asian groups is phylogenetically valid because it fails on the basic criterion of monophyly: it must include the most recent common ancestor of all the organisms in the tree and all the descendants of that most recent common ancestor.

Fossil data help to refine cladistic analysis by providing information about the sequence or order in which certain derived traits emerged. Cladistic analysis helps to resolve the "problem" of the so-called "missing links" or the intermediate specimens, because it does not require that fossil species *evolve into* any related species which emerge later. Instead, it represents the evolutionary history of an evolving lineage in terms of a collection of characteristics which can be passed along to descendant populations — or not!

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