

(For more example and diagram of the rooted, unrooted tree which we have already discussed in earlier lecture go through the **figure no. 8.13** from Dr. Gurcharan Singh's book)

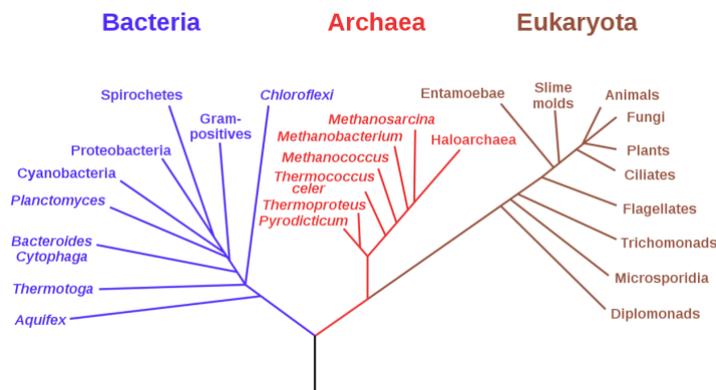
Phylogenetic tree

The phylogenetic tree is a commonly used diagram in relating the phylogenetic history. The vertical axis in such a diagram represents the geological time scale. In such a diagram, the origin of a group is depicted by the branch diverging from the main stock and its disappearance by the branch termination. Branches representing the fossil groups end in the geological time when the group became extinct, whereas the extant plant groups extend up to the top of the tree. The relative advancement of the living groups is indicated by their distance from the centre, primitive groups being near the centre, and advanced groups towards the periphery.

Tree types:

Dendrogram

A dendrogram is a general name for a tree, whether phylogenetic or not, and hence also for the diagrammatic representation of a phylogenetic tree.

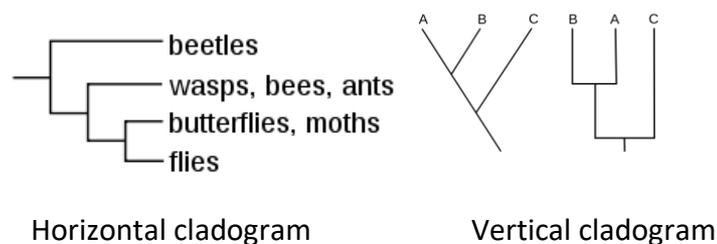


Cladogram

It is based on “**Principle of Parsimony**” (the most likely evolutionary route is the shortest hypothetical pathway of changes that explains the pattern under observation). Cladogram represents an evolutionary diagram utilizing cladistics method and representation of the historical connections between the entities as evidenced by synapomorphies.

The vertical axis of the cladogram is always an implied, but usually non-absolute time scale. Cladograms are ancestor-descendant sequences of populations. Each bifurcation of the cladogram represents a past speciation that resulted in two separate lineages.

A cladogram only represents a branching pattern; i.e., its branch lengths do not represent time or relative amount of character change, and its internal nodes do not represent ancestors. The least informative way of depicting a phylogenetic tree is as a cladogram. All that it shows is how the terminals are assumed to be related, nothing else. The branch lengths are meaningless and could be drawn with arbitrary length. But to show that this is the case, in practice people draw them either equal length or, as in the case of my example tree here, as all ending flush. If you are unsure if you are dealing with a cladogram, it might be useful to check if there is a scale bar on the diagram. If there isn't, it is probably a cladogram.



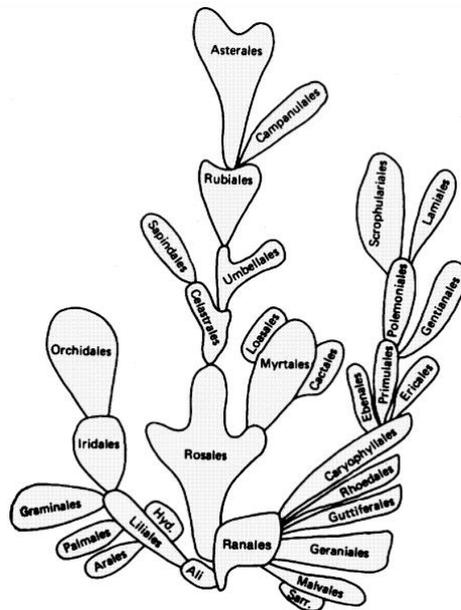
Wiley (1981) defines a **cladogram** as a branching diagram of entities where the branching is based on inferred historical connections between the entities as evidenced by synapomorphies. It is, thus, a phylogenetic or historical dendrogram.

He defines a phylogenetic tree as a branching diagram portraying hypothesized genealogical ties and sequences of historical events linking individual organisms, populations, or taxa

Phylogram

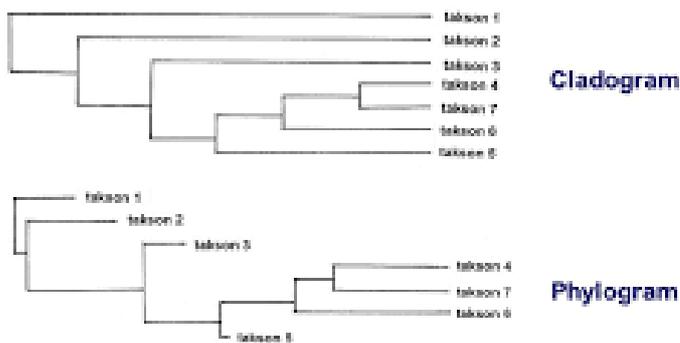
A phylogram is a phylogenetic tree that has branch lengths proportional to the amount of character change. If the tree you are looking at has branches that do not end flush and a scale bar you are most likely dealing with a phylogram. If the branch lengths are multiples of one, it is most parsimonious to assume that the tree is the result of a parsimony analysis. A length of one then means that one character change took place along the branch, two means two, and so on. Diagrams with vertical axis representing the degree of apomorphy are now more appropriately known as phylograms. The earliest well-known example of

such a phylogram is 'Bessey's cactus'. In such diagrams the most primitive groups end near the base and the most advanced reach the farthest distance.



Besseyan cactus or *Opuntia Besseyi* showing the relationship of orders recognized by Bessey

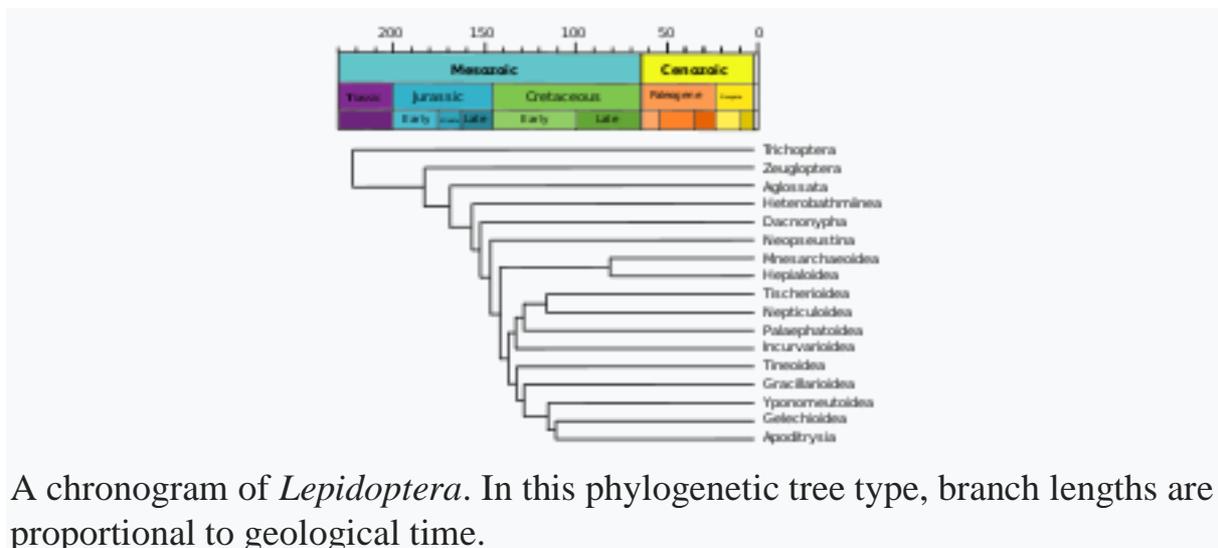
Cladogram / Phylogram



Chronogram

A chronogram is a phylogenetic tree that explicitly represents time through its branch lengths. A chronogram is a phylogenetic tree whose branch lengths are proportional to time. If the tree you are looking at is ultrametric, that is all

branches end flush, and it has a full-length scale bar, you may be dealing with a chronogram.

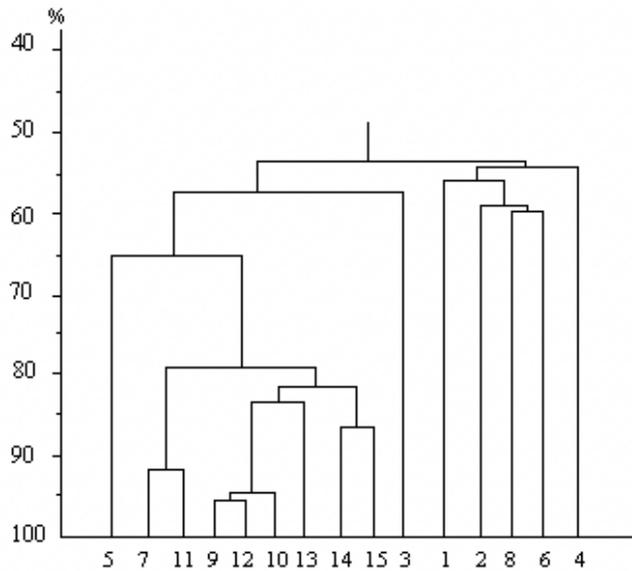


A chronogram of *Lepidoptera*. In this phylogenetic tree type, branch lengths are proportional to geological time.

Phenogram

Phenogram is a diagram constructed on the basis of numerical analysis of phenetic data. Such a diagram is the result of utilization of a large number of characters, usually from all available fields, and involves calculating the similarity between taxa and constructing a diagram through cluster analysis. Such a diagram (Figure 8.20) is very useful, firstly because it is based on a large number of characters, and secondly because a hierarchical classification can be achieved by deciding upon the threshold levels of similarity between taxa assigned to various ranks.

It must be pointed out that the modern phylogenetic methods, which aim at constructing phylogenetic trees, also sometimes use large number of characters for comparison, especially when dealing with morphological data, and there seem to be a lot of similarities in data handling and computation, but are unique in the utilization of evolutionary markers and, consequently, produce slightly different results. With the incorporation of distance methods in the construction of trees, the classical difference between the terms is largely disappearing. Modern cladistic programs develop trees in which branch lengths are indicated, and plotting programs offer the choice to indicate branch lengths (and often called phylograms) or not. In latter case branches may be square (line running vertically and horizontally- and often called phenogram.



Cluster diagram of 15 OTUs based on similarity matrix

Reference links:

<https://www.khanacademy.org/science/high-school-biology/hs-evolution/hs-phylogeny/a/phylogenetic-trees>

<http://phylobotanist.blogspot.com/2016/01/types-of-phylogenetic-tree-diagrams.html>

Plant-systematics-third-edition Gurcharan Singh.pdf

(epdf.pub_plant-systematics-third-edition-an-integrated-appr)