

# Phylogenetic characters



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The evolution of organisms over the ages has seen transformations from ancestral to more advanced forms. As much as most of the ancestral traits are retained, gradual modification and supplementation with new traits have led to improved living standards in their current environment. The study of organisms' phylogeny aids in unraveling the differences and similarities among animals, plants and other organisms. The genealogical relationships of organisms can be represented by an enormous tree of evolution known as the 'Tree of life'. This in turn embodies the organism's phylogeny. This is the organism's lineage history that signifies evolution through the ages. Thus, this tree provides a guideline to the vast biological sub-disciplines. The phylogenetic tree provides information on the evolutionary connection between two groups and also the manner in which previously related species advanced separately. Close relationship between two phyla of organisms is determined by their proximity in the phylogenetic tree (Sober 2006). These phyla can be further grouped into class, order, family, genera and species. The more back in time a phylum was divided, the greater the period of time it required to attain divergent evolution. On the other hand, phyla that divided closer to the focal point of the tree represented close relations.

The systematic procedure employed to achieve this include; choosing of the taxa to be classified, selection of the characteristics required to substantiate relationship between organisms, analysis of the characteristics in order to rebuild the connection between the taxa in a tree format, translation of the tree into a formal classification system that is universally accepted by scientists and the utilization of the tree to check the varying hypotheses

about the course of advancement in the phyla. The system may adhere to either phenetic or cladistic principles approach (Knapp 2010).

The utilization of cladistic principles as the approach to diagramming connections between organisms has to consider the primary assumptions associated with this process. Among the assumptions proposed in this method is that members of a phyla share similar evolutionary record. This insinuates that these organisms are closely connected to each other than to other clusters of organisms. The application of these necessities results to varying methods in which the organisms can be grouped. When all the species are organized in monophyletic sets, then a cladogram is recognized to be completely determined. Another assumption to be considered is that species arise basically by divergence of familial pedigree and are determined extinct whenever they crossbreed with other species (Knapp 2010).

However, it is assumed that crossbreeding is uncommon or lacking.

Related clusters of organisms are acknowledged since they share distinctive features. These features may not have existed in the distant ancestors but are distributed proportionally to the majority, if not all of the members within a cluster. The shared features are known as synapomorphies. As a result, cladistic clusters are not determined by the physical traits shared among the members of a group but rather on evolutionary connections. With regard to this, two organisms may have similar characteristics yet still, they are considered to belong to diverse groups since the similarities may be deceptive. Organisms may share similar features as a result of evolutionary connection. This means that the features

were inherited from a common ancestor by both species. These are known as homologous features.

Contrary to this, species with no ancestral connection may also adopt a related lifestyle. In this case, the evolution of body parts may result to the performance of similar duties and resemblance of the parts. This constitutes convergent evolution and the similar features are referred to as being analogous. Due to this, these organisms are not considered to be related in any way. Organisms are said to be related when they solely have homologous similarities known as synapomorphies (Sober 2006).

Considering the above, the utilization of body parts and characters in determining the phylogenetic connections between species is not advocated with regard to either phenetic or cladistic approaches.