

## Commentary

# Cladistics Taxonomy of Molecular Phylogenetics and Evolution

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A phylogeny is a pattern of historical evolutionary relationships between species and higher level taxa that is commonly represented as a tree diagram or phylogenetic tree. The study of such relationships is commonly referred to as phylogenetics. Historically, phylogenetic trees were frequently created through indirect methods that were not reproducible. Classifications frequently had little to no direct relationship to phylogeny. Cladistic methods are used in modern phylogenetics to build phylogenetic trees directly from morphological and molecular data. Cladistics, as opposed to phylogenetics, refers only to the methods used to generate branching patterns (e.g., parsimony or maximum likelihood), whereas phylogenetics refers to the interpretation of such diagrams as historical patterns. This is an important distinction to make because cladistic methods are unaffected by the type of data and the interpretations they produce, and they can be applied to nonphylogenetic problems. On the scale of species and higher level taxa, phylogenies are analogous to genealogies (e.g., genera and families). Phylogenies are typically represented as tree-like branching diagrams, with taxa on the same branch thought to be more closely related to each other than taxa on different branches. Interpreting such diagrams as historical patterns necessitates a basic understanding of hierarchy, and phylogenetic trees are frequently incorrectly assumed to support specific historical suppositions that the results do not support. Measures of phylogenetic diversity, which can be used to make conservation and habitat preservation decisions, are another application of phylogenetic information.

Cladistics only recognises monophyletic groups of organisms based on synapomorphies. The only groups that can be defined by objective boundaries are monophyletic ones. In terms of evolution, monophyletic groups include the most recent common ancestor and all of its descendants. Monophy-

letic groups include Amniota, Tetrapoda, Osteichthyes, and Gnathostomata. There are two other types of “groups” that are sometimes mentioned, but they are not the same as monophyletic groups. Paraphyletic “groups” are based on symplesiomorphy; their members are linked by common ancestry, but one or more descendants of the most recent common ancestor are excluded. Pisces (fishes) is a paraphyletic group. Many taxa that have been thought to be ancestral, such as fishes, reptiles, and green algae, are paraphyletic. Polyphyletic “groups” are based on homoplasy, or convergently derived characters that cannot be inferred to have been present in the most recent common ancestor of the included taxa. A polyphyletic group would include the dogfish and the turkey (perhaps based on the observation that both lay eggs surrounded by a shell, though no one would claim such a homology). Attempts to deduce the phylogeny of groups of organisms can be traced back to the use of allozymes (enzymes encoded by different alleles of the same locus), followed by the use of targeted genes in mitochondrial morphological criteria and nuclear genomes, and finally to the current phase of phylogenomics, in which multiple gene loci and even entire genomes can be searched for their application in phylogenetic reconstruction. At each stage of this process, there has been a challenge of incongruence between different markers in statistically resolved phylogenetic patterns, between morphological and molecular characters, and between genetic loci. This chapter discusses these issues with reference to both fossil and living oysters, describes the proposed phylogenies, and discusses the role of phylogenetic analysis in understanding their evolution.

## Acknowledgment

None

## Conflict of Interest

None