

A Short Commentary on Molecular Phylogenetics

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Commentary

Phylogenetic is a part of systematics that addresses the inference of the evolutionary history and relationships among or within groups of organisms. These relationships are hypothesized by phylogenetic inference methods that evaluate observed heritable traits, such as DNA sequences, protein amino acid sequences, often under a specified model of evolution of these traits. The result of such an analysis is a phylogeny also known as a phylogenetic tree, a diagrammatic hypothesis of relationships that reflects the evolutionary history of a group of organisms. The tips of a phylogenetic tree can be living taxa or fossils, and represent the 'end', or the present, in an evolutionary lineage.

Phylogenies are important for addressing various biological questions such as relationships among species or genes, the origin and spread of viral infection and the demographic changes and migration patterns of species. The advancement of sequencing technologies has taken phylogenetic analysis to a new height. Phylogenies have permeated nearly every branch of biology, and the plethora of phylogenetic methods and software packages that are now available may seem daunting to an experimental biologist. Phylogenies also provide a framework for alternative ways of looking at biodiversity. Most measures of biodiversity use species richness either in a geographic or ecologic sense. Other views of diversity may focus on the nature and breadth of adaptation. Such measures unfortunately require a view of the importance of particular adaptations.

Currently, the use of phylogenetic diversity measures is largely limited to theoretical discussions and there have been few efforts to actually apply such measures to conservation. This is partly due to the relative paucity of high-quality phylogenies that are available across broad groups of taxa and partly because of a distinctly ecological bias in most studies of biodiversity. As molecular data sources provide better and more complete phylogenies for use by other workers. It is probable that in the near future measures of phylogenetic diversity will become standard components, in combination with more traditional measures

of ecologic uniqueness, species richness, and sensitivity, in the formulae that are used to evaluate conservation priorities for areas and endangered species.

More specialized phylogenetic methods have been developed now to meet specific needs such as species and molecular phylogenetic tests, biogeographic hypotheses, testing for evaluating amino acids of extinct or extant proteins, establish disease epidemiology and evolution, and even in forensic studies.

Phylogenetic methods are instrumental to the identification and classification of bacteria. Here, we examine the utility and effectiveness of traditional alignment-based phylogenies for reconstructing the evolutionary relationships among bacterial species, but also consider the more recently developed whole-genome approaches. We addition, illustrate the power of phylogenetic approaches to identify co-evolutionary interactions and cases of Horizontal Gene Transfer (HGT) between bacteria, and between microbes and other organisms. Phylogenetic techniques have been used in conjunction with proteomic and biochemical information to identify functional subgroups within large gene super-families. Ultimately, the versatility and utility of phylogenetic techniques have permitted the in-depth exploration of fundamental questions in evolutionary biology.

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