

A Framework for Alternative Ways of Looking at Biodiversity

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Abstract

Phylogenetics is the study of the evolutionary relatedness among groups of organisms. Molecular phylogenetics uses sequence data to infer these relationships for both organisms and the genes they maintain. With the large amount of publicly available sequence data, phylogenetic inference has become increasingly important in all fields of biology. In the case of natural product research, phylogenetic relationships are proving to be highly informative in terms of delineating the architecture and function of the genes involved in secondary metabolite biosynthesis.

Polyketide syntheses and non-ribosomal peptide syntheses provide model examples in which individual domain phylogenies display different predictive capacities, resolving features ranging from substrate specificity to structural motifs associated with the final metabolic product. This chapter provides examples in which phylogeny has proven effective in terms of predicting functional or structural aspects of secondary metabolism. The basics of how to build a reliable phylogenetic tree are explained along with information about programs and tools that can be used for this purpose. Furthermore, it introduces the Natural Product Domain Seeker, a recently developed Web tool that employs phylogenetic logic to classify ketosynthase and condensation domains based on established enzyme architecture and biochemical function.

Introduction

The human elbow forms the link between brachium and forearm, controlling length of reach and orientation of the hand, and is one of our most distinctive anatomic regions. An appreciation of elbow phylogeny complements anatomic knowledge in three ways: it demonstrates how the elbow has evolved to facilitate specific functional demands, such as suspensory locomotion and dexterous manipulation; it explains the functional significance of each morphologic feature; and it assists in predicting the consequences of loss of such features through disease, injury, or treatment.

Most of the characteristic features of the human elbow significantly predate the appearance of modern *Homo sapiens*. In fact, current evidence suggests that this morphology can be traced back to the common ancestor of humans and apes, extant approximately 15 to 20 million years ago (mya).

Phylogenies also provide a framework for alternative ways of looking at biodiversity. Most measures of biodiversity use species richness, either in a geographic (either broad or local) or ecologic sense. Other views of diversity may focus on the nature and breadth of adaptation. Such measures unfortunately require a subjective view of the importance of particular adaptations—e.g., the birds might be considered “diverse” because they include so many adaptations for use of the bill. However, phylogeny provides

another perspective on biodiversity that allows an objective way to compare uniqueness and diversity of taxa. Although various specific measures of phylogenetic diversity have been proposed, most share a basic approach by which phylogenetic trees are used to evaluate species richness in concordant groups. It means little to say that “orchids are highly speciose” or “monotremes are species depauperate” unless we have some idea as to the relationships of the two groups being compared. Phylogenetic pattern provides the basis for such comparisons.

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, this is likely to change. 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.

Phylogenetic methods can be used for many purposes, including analysis of morphological and several kinds of molecular data. We concentrate here on the analysis of DNA and protein sequences.

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