

RATES OF EVOLUTION AND FOSSILS IN PHYLOGENETIC ANALYSIS: A COMPUTER SIMULATION APPROACH

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Whereas many studies have examined the performance of various character-data sets in phylogenetic analysis, little work has been done on the effect that various classes of taxa have on phylogenetic reconstruction. In particular, the "fossil versus living taxa" debate has concentrated mainly on the effects of fossils in reconstructing vertebrate and plant relationships. While this work has contributed to the understanding of the role that fossils play in systematics, a computer model clarifies the relationship among the main determinants of the fossil-taxa problem. In addition, simulations of phylogenies over a wide spectrum of evolutionary rates clarify the relative efficiencies of various tree-estimation procedures.

In this study, computer generated phylogenies were used to examine the relationship between the temporal position and completeness of additional taxa in a phylogenetic analysis and the rate of evolution or, equivalently, the temporal scope of the phylogenetic problem. In the simulations, four fossil taxa of varying temporal position and completeness were added to an analysis that included four living taxa. Additional taxa varied in completeness (25%, 50%, 75%, and 100% completeness) and in temporal position (0%, 33%, 66%, and 100% of the distance from the ancestor to the living time plane). Fifty trees were generated each for low, low intermediate, high intermediate, and high rates of evolution or temporal scope. Because additional taxa that are 100% complete and 100% of the distance to the living time plane are equivalent to the addition of living taxa, this study directly compares the effects of addition of living versus fossil taxa in phylogenetic analysis.

The importance of fossil taxa varied depending on their completeness and temporal position and on the rate of evolution under which the phylogeny was generated. In general, high completeness and temporal position near the ancestor of a clade improved phylogenetic resolution as measured by the percentage of the tree-length distribution that contains the real tree. Furthermore, the conditions of completeness and temporal position under which fossil taxa improved phylogenetic resolution over living taxa became less restrictive as the rate of evolution or the temporal scope of the tree increased.