

Tracing Patterns of Evolution through the Tree of Life: Introduction

One and half centuries ago, Charles Darwin (1859) presented overwhelming evidence and argued that all life on the earth shared common descent, and “from so simple a beginning endless forms most beautiful and most wonderful have been, and are being evolved”. Ernst Haeckel (1886) and several of his contemporaries attempted to trace the pattern of descent among all extant and extinct forms in what Darwin referred to as “the great Tree of Life”. Ever since then, systematists and evolutionary biologists have been exploring morphological, cytogenetic, chemical, developmental and molecular characters, and actively developing theories and methods to infer phylogenetic relationships among organisms from these characters. This endeavor has been especially stimulated by the rise of molecular biology and the emergence of computer science over the past 50 years. At the beginning of the 21st century, we are presented with an unprecedented opportunity to reconstruct the entire Tree of Life, and further, to study evolutionary processes and mechanisms in the context of a robust phylogenetic framework.

Over the past decade, research on reconstructing the Tree of Life has been remarkably active, and knowledge is expanding exponentially (Cracraft & Donoghue, 2004; see also Pennisi, 2003). On June 3–7, 2007, an international symposium on the Tree of Life was held in Beijing, China. It brought together some 40 leading speakers from Canada, China, Germany, Japan, New Zealand, Sweden, the UK, and the USA, and nearly 250 participants from within China. This special issue of the *Journal of Systematics and Evolution* consists of 16 of the papers that were presented at the symposium. They represent a broad spectrum of research in systematics and evolutionary biology, ranging from exploration of theoretical issues, such as the effects of taxon and character sampling on phylogenetic analyses, to empirical studies and reviews of the use of multigene and whole genome analyses to infer the phylogeny of prokaryotes, protists, fungi, animals, and plants. These contributions also feature examples of the uses of phylogenetic approaches in studying historical biogeography, character evolution, and the evolutionary history of genes controlling chromosomal structural dynamics and development in eukaryotes. These papers provide an excellent sample of what can be expected in the future, as phylogenetic research becomes increasingly integrated with emerging fields in evolutionary biology, such as evolutionary developmental biology, evolutionary genomics, and evolutionary ecology. We have so much more to learn about how to harness the power of the phylogenetic knowledge that is materializing so rapidly, and we are excited about the prospects of developing a truly integrative phylogenetic biology over the coming decades.

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