

# Assembling the Fungal Tree of Life (AFTOL)

## Project Summary

Fungi make up one of the major clades of life. There are roughly 80,000 described species of Fungi, but the actual diversity in the group has been estimated to be about 1.5 million species. Fungi play crucial ecological roles as decayers, mutualistic symbionts, and pathogens, including pathogens of humans. The economic significance of fungi is almost incalculable; they perform vital "ecological services" and they impact diverse applied disciplines, including agriculture, medicine, and drug discovery, to name just a few. A comprehensive phylogenetic hypothesis of the Fungi is necessary to understand the history of life and the evolution of ecosystems. A phylogenetic database for Fungi will facilitate the creation of diagnostic tools, and will enable the discovery of the many fungal species that remain undescribed.

Mycologists have made great strides toward resolving fungal phylogeny through studies of subcellular characters and molecular data, especially sequences of genes encoding ribosomal RNA. The majority of this work has been done by individual investigators, concentrating on restricted groups of taxa. Thus, while considerable progress has been made, not all groups of Fungi have been equally well studied, many of the existing datasets are not combinable (because they are drawn from different molecular regions), and there are conspicuous gaps in the sampling of subcellular data.

We propose a collaborative project, titled Assembling the Fungal Tree of Life (AFTOL), to contribute toward a comprehensive phylogenetic hypothesis of the Fungi. AFTOL will develop broad datasets of molecular and subcellular characters, which will be accessible via the world-wide web, in continuously updated databases. Seven molecular regions will be sampled (nuc-ssu rDNA, nuc-lsu rDNA, RPB2, RPB1, EF-1 $\alpha$ , ATP6, and ITS) in approximately 1500 species in all major groups of Fungi. Diverse phylogenetic analyses of these data will be performed, including analyses that incorporate evidence from subcellular characters. This project will be based in five laboratories at four universities. Four laboratories will focus on acquisition and analysis of molecular data from the major groups of Fungi, and one laboratory will focus on generation of subcellular data across all groups of fungi. The Vilgalys and Lutzoni laboratories at Duke University will provide a central facility for high-throughput DNA sequencing and bioinformatics. Core responsibilities of the participating laboratories are outlined below:

- Hibbett (Clark University): Collection of molecular data from Basidiomycota.
- Lutzoni (Duke University): Collection of molecular data from Ascomycota; bioinformatics.
- McLaughlin (University of Minnesota): Collection and databasing of subcellular characters.
- Spatafora (Oregon State University): Collection of molecular data from Ascomycota.
- Vilgalys (Duke University): Collection of molecular data from Chytridiomycota and Zygomycota.

Community participation will be an essential component of the proposed research, and this will be greatly facilitated by the ongoing Deep Hypha Research Coordination Network. AFTOL will involve the fungal systematics community at all stages of the project. The preliminary list of 1500 species to be studied has been developed in consultation with taxonomic experts, many of whom have agreed to provide samples. It will be the policy of AFTOL that all data will be released via the web as soon as they have been generated, and all participants who contribute materials will be invited to coauthor publications that report new data derived from those materials. Already, 113 fungal systematists in 23 countries have indicated that they will participate in AFTOL.

Training and outreach activities are an important aspect of AFTOL and will take several forms:

- Graduate and post-doctoral training: Each of the participating laboratories will support one resident graduate student and one post-doctoral fellow, who will contribute to the data-collection goals of the project. The Lutzoni lab will support a sixth post-doctoral fellow, who will be involved with bioinformatics efforts.
- Support for visiting graduate students: Visiting graduate students, including foreign students, will be supported for 3-12 month visits to the participating laboratories, during which they will receive training, and contribute to the data-collection goals of the project.
- Undergraduate training: Each laboratory will seek REU supplements to involve undergraduates.
- Outreach to K-12 educators: Each laboratory will offer a two-day workshop every summer for high school science teachers on fungal biology and phylogeny. In addition, a "Fungal K-12" web site will be developed with resources about fungal biology for K-12 educators.