

Resource Summary Report

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AFTOL

RRID:SCR_004650

Type: Tool

Proper Citation

AFTOL (RRID:SCR_004650)

Resource Information

URL: <http://www.aftol.org/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented Jan 13, 2022; To enhance the understanding of the evolution of the Kingdom Fungi, 1500+ species were sampled for eight gene loci across all major fungal clades, plus a subset of taxa for a suite of morphological and ultrastructural characters with resulting data: AFTOL Molecular Database (generated by WASABI - Web Accessible Sequence Analysis for Biological Inference), Blast search the AFTOL Database (generated by WASABI), AFTOL primers (generated by WASABI), AFTOL primers by species (generated by WASABI), AFTOL alignments, and the AFTOL Structural and Biochemical Database. Users may submit samples to the AFTOL project. AFTOL is a collaboration centered around four universities in the United States: Duke University (Francois Lutzoni and Rytas Vilgalys), Clark University (David Hibbett), Oregon State University (Joey Spatafora), and University of Minnesota (David McLaughlin). Participants throughout the world have donated vouchers, taxon samples, and gene sequences. The aim of the project is to reconstruct the fungal tree of life using all available data for eight loci (nuclear ribosomal DNA: LSU, SSU, ITS (including 5.8s, ITS1 and ITS2); RNA polymerase II: RPB1, RPB2; elongation factor 1-alpha; mitochondrial SSU rDNA, and mitochondrial ATP synthase protein subunit 6). A further objective of this study is to summarize and integrate current knowledge regarding fungal subcellular features within this new phylogenetic framework. The name of the bioinformatic package developed for AFTOL is WASABI which provides an efficient communication platform to facilitate the collection and dissemination of molecular data to (and from) the laboratories and participants. All molecular data can be viewed, downloaded, verified, and corrected by the participants of AFTOL. A central goal of the WASABI interface is to establish an automated analysis framework that includes basecalling of newly generated chromatograms, contig assembly, quality verification of sequences (including a local BLAST), sequence alignment, and congruence test. Gene sequences that pass all tests and are finally verified by their authors will undergo automated phylogenetic analysis on a regular schedule. Although all steps are initially carried out noninteractively, the users can verify and correct the results at any step and

thus initiate the reanalysis of dependent data.

Abbreviations: AFTOL

Synonyms: Assembling the Fungal Tree of Life

Resource Type: storage service resource, service resource, material storage repository, biospecimen repository

Defining Citation: [PMID:17486962](#), [PMID:21652303](#)

Keywords: cytology, morphology, phylogeny, ultrastructure, primer, alignment, blast, sequence, taxonomy, structure, biochemical, subcellular, organism-related portal, data analysis service, culture, sporocarp, dna, pcr product, molecular, molecule, gene sequence

Funding: NSF EF-0228671;
NSF 0090301

Availability: The community can contribute to this resource, THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: AFTOL

Resource ID: SCR_004650

Alternate IDs: nlx_64804

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260731T042701+0000

Ratings and Alerts

No rating or validation information has been found for AFTOL.

No alerts have been found for AFTOL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

He J, et al. (2024) ???Two new species of Ganoderma (Ganodermataceae, Basidiomycota) from Southwest China. MycoKeys, 106, 97.

- Shen H, et al. (2022) Novel Species and Records of Dictyosporiaceae from Freshwater Habitats in China and Thailand. *Journal of fungi* (Basel, Switzerland), 8(11).
- Shen HW, et al. (2021) Two novel species and two new records of *Distoseptispora* from freshwater habitats in China and Thailand. *MycoKeys*, 84, 79.
- Pem D, et al. (2020) Ribosomal and Protein Gene Phylogeny Reveals Novel Saprobiic Fungal Species From *Juglans regia* and *Urtica dioica*. *Frontiers in microbiology*, 11, 1303.
- Garcia-Mazcorro JF, et al. (2019) Descriptive Bacterial and Fungal Characterization of Propolis Using Ultra-High-Throughput Marker Gene Sequencing. *Insects*, 10(11).
- Wang XW, et al. (2019) Phylogenetic re-evaluation of *Thielavia* with the introduction of a new family *Podosporaceae*. *Studies in mycology*, 93, 155.
- Aime MC, et al. (2018) Deconstructing the evolutionary complexity between rust fungi (Pucciniales) and their plant hosts. *Studies in mycology*, 89, 143.
- Phukhamsakda C, et al. (2018) Two novel species of *Neoaquastroma* (Parabambusicolaceae, Pleosporales) with their phoma-like asexual morphs. *MycoKeys*(34), 47.
- Lutzoni F, et al. (2018) Contemporaneous radiations of fungi and plants linked to symbiosis. *Nature communications*, 9(1), 5451.
- Kruse J, et al. (2018) The first smut fungus, *Thecaphoraanthemidis* sp. nov. (Glomosporiaceae), described from *Anthemis* (Asteraceae). *MycoKeys*(41), 39.
- Yarza P, et al. (2017) A phylogenetic framework for the kingdom Fungi based on 18S rRNA gene sequences. *Marine genomics*, 36, 33.
- Wang XW, et al. (2016) Phylogenetic reassessment of the *Chaetomium globosum* species complex. *Persoonia*, 36, 83.
- Taylor DL, et al. (2016) Accurate Estimation of Fungal Diversity and Abundance through Improved Lineage-Specific Primers Optimized for Illumina Amplicon Sequencing. *Applied and environmental microbiology*, 82(24), 7217.
- Rodrigues RR, et al. (2015) Plant Invasions Associated with Change in Root-Zone Microbial Community Structure and Diversity. *PloS one*, 10(10), e0141424.
- Wynns AA, et al. (2015) Convergent evolution of highly reduced fruiting bodies in Pezizomycotina suggests key adaptations to the bee habitat. *BMC evolutionary biology*, 15, 145.
- Yurkov A, et al. (2015) Multigene assessment of the species boundaries and sexual status of the basidiomycetous yeasts *Cryptococcus flavescens* and *C. terrestris* (Tremellales). *PloS one*, 10(3), e0120400.
- Weber CF, et al. (2015) Relative abundance of and composition within fungal orders differ between cheatgrass (*Bromus tectorum*) and sagebrush (*Artemisia tridentata*)-associated soils. *PloS one*, 10(1), e0117026.

Lee WD, et al. (2014) A checklist of the basidiomycetous macrofungi and a record of five new species from mt. Oseo in Korea. *Mycobiology*, 42(2), 132.

Luo J, et al. (2014) Temperate pine barrens and tropical rain forests are both rich in undescribed fungi. *PloS one*, 9(7), e103753.

Urbina H, et al. (2012) Multilocus phylogenetic study of the *Scheffersomyces* yeast clade and characterization of the N-terminal region of xylose reductase gene. *PloS one*, 7(6), e39128.