Finding needles in haystacks: linking scientific names, reference specimens and molecular data for Fungi.


Abstract

DNA phylogenetic comparisons have shown that morphology-based species recognition often underestimates fungal diversity. Therefore, the need for accurate DNA sequence data, tied to both correct taxonomic names and clearly annotated specimen data, has never been greater. Furthermore, the growing number of molecular ecology and microbiome projects using high-throughput sequencing require fast and effective methods for en masse species assignments. In this article, we focus on selecting and re-annotating a set of marker reference sequences that represent each currently accepted order of Fungi. The particular focus is on sequences from the internal transcribed spacer region in the nuclear ribosomal cistron, derived from type specimens and/or ex-type cultures. Re-annotated and verified sequences were deposited in a curated public database at the National Center for Biotechnology Information (NCBI), namely the RefSeq Targeted Loci (RTL) database, and will be visible during routine sequence similarity searches with NR_prefixed accession numbers. A set of standards and protocols is proposed to improve the data quality of new sequences, and we suggest how type and other reference sequences can be used to improve identification of Fungi. Database URL: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA177353.

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