

Dissertation Abstract

R. Henrik Nilsson (2007). Fungal taxonomy and systematics in the digital era, with an outlook on the cantharelloid clade (*Basidiomycota*).

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Fungi form a large and ubiquitous group of organisms where species identification and delimitation on morphological grounds often fall short. DNA sequences have proved an invaluable information source for these pursuits and are now routinely used in most mycological laboratories. Newly generated DNA sequences are typically compared with the entries of the large INSD sequence database for inference of taxonomic affiliations and other properties using the sequence similarity search tool BLAST. This thesis highlights some practical difficulties in using BLAST for these purposes – it is for example very sensitive to the length of the sequences - and shows that improper use of BLAST appears to have had considerable repercussion on the general level of taxonomic reliability of the fungal sequences in INSD, more than 10% of which may be incorrectly identified to species level.

An initiative to build a new DNA sequence database for taxonomically reliable DNA-based identification of mycorrhizal (plant-mutualistic) fungi is described. The database differs from similar initiatives in that its entries are determined to species level by pertinent experts; it allows for integrative sequence annotations, including photos and morphological descriptions; and it employs new, phylogeny-based tools for sequence identification to alleviate the concerns with simplistic, similarity-based tools as arbiters of taxonomic affiliation. That phylogenetic analyses can be beneficial also to classification and nomenclatural projects is shown in the *mor* enterprise, which is a weekly automaton of *Agaricomycetes* (mushroom-forming fungi) phylogeny. All fungal sequences from the nuclear ribosomal large subunit gene are assembled on a weekly basis; automated phylogenetic analyses are undertaken; and the resulting phylogenetic trees are displayed and analyzed for changes in clade topology and inclusiveness.

The enigmatic cantharelloid clade of the *Agaricomycetes* is studied using a four-gene phylogenetic approach. While this heterogeneous assembly of mushroom-like, resupinate, clavarioid, and lichen-forming fungi defies any morphological attempt at indicating a close relatedness for its species, the results from the molecular analyses show that there is indeed strong evidence to support that these fungi form a monophyletic group; a restrictive circumscription of the clade to include the genera *Botryobasidium*, *Sistotrema*, *Multiclavula*, *Membranomyces*, *Hydnum*, *Clavulina*, *Cantharellus*, and *Craterellus* is advocated. Sticher basidia, and to a lesser extent parentheses ultrastructure, are found to be characteristic of the clade, and the previously reported divergent rates of evolution for the genera *Cantharellus* and *Craterellus* are shown to be limited to the nuclear ribosomal genes. The largely resupinate, and purportedly wood-decaying, genus *Sistotrema* is demonstrated to hold mycorrhizal lineages, and the molecular evidence to consider the genus polyphyletic is found to be very convincing.

Key words: cantharelloid clade, ectomycorrhiza, *Agaricomycetes*, phyloinformatics, barcoding

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