

Dissertation Title	Aquatic Fungi: Biodiversity, Classification, and Online Databases
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ABSTRACT

Our knowledge on aquatic fungi has expanded exponentially for almost century and a half of research. The classification system has been updated by using molecular phylogenetics coupled with morphology, following the one fungus=one name ruling. In addition to barcoding of nuclear ribosomal regions (ITS, LSU, SSU), protein-coding genes were added for a better resolution of the phylogenetic tree and resolving the evolutionary relationships of closely related taxa. These resulted in a well-defined classification scheme for aquatic fungi that is unceasingly changing as the continuous exploration of various aquatic habitats in tropical and temperate countries lead to the discovery of novel aquatic fungal taxa and recollection of taxa wherein phylogenetic placement is unknown. Despite all this published information, our knowledge of aquatic fungi is still limited and mostly neglected by many researchers. The exploration of aquatic habitats in Thailand in the present work resulted in discoveries of novel fungi from Dothideomycetes (six species under Pleosporales) [*Halobyssothecium bambusicola* (Lentitheciaceae), *Camposporium dulciaquae* (Melanommataceae), *Brunneofusispora hyalina* (Occultibambusaceae), *Wicklowsia phuketensis* (Wicklowsiaceae)], Sordariomycetes (one genus *Neoxylomyces*, three species) [*Rattania aquatica* (Chaetosphaeriaceae), *Neoxylomyces multiseptatus*

(Phyllachorales genera *incertae sedis*), *Phaeoacremonium thailandense* (Togninia-
ceae), and Ascomycota genera *incertae sedis* (one species *Mycoenterolobium*
aquadictyosporium). The sequence data for *Mycoenterolobium* was obtained and their
closed affinity with Testudinaceae was elucidated. Since the morphology of
Mycoenterolobium and taxa under Testudinaceae are vastly different, we placed the
latter in Pleosporales *incertae sedis* until further taxon sampling is undertaken. The
collection of plant substates from aquatic habitats in Thailand, the UK, and Sweden
resulted in the isolation of novel Lentitheciaceae species wherein two genera,
Halobyssothecium and *Lentithecium*, were assessed and revised. Three novel
Halobyssothecium species were introduced (*H. bambusicola*, *H. phragmitis*, *H.*
versicolor), and transfer of *L. cangshanense*, *L. carbonneanum*, *L. kunmingense*, *L.*
unicellulare, and *L. voraginesporum* to *Halobyssothecium*. Collection of an asexual
morph of *L. lineare* and phylogenetic analysis confirmed its taxonomic placement in
Keissleriella.

In the present work, the taxonomic outline of salt marsh fungi is provided with
486 taxa listed in this ecosystem. Ascomycota dominates the taxa from salt marsh
ecosystems accounting for 95.27% (463 taxa), followed by Basidiomycota (19 taxa),
and Mucoromycota with four taxa. *Juncus roemerianus* has been extensively studied
for its associates with 162 documented taxa, followed by *Phragmites australis* (137
taxa) and *Spartina alterniflora* (79 taxa). The highest number of salt marsh fungi have
been recorded from Atlantic Ocean countries, wherein the USA had the highest
number of species recorded (232 taxa), while China (165 taxa) and India (16 taxa) had
the highest number of salt marsh fungi in the Pacific Ocean and the Indian Ocean,
respectively.

The classification of basal and higher freshwater fungi has been updated, and
numbers were provided based on the scattered taxonomic papers and biodiversity
studies. Freshwater fungal taxa listed in this study total to 3,870 species with
representatives from 13 phyla: Ascomycota (2,968 species, 1,018 genera), Chytridio-

mycota (333 species, 97 genera), Rozellomycota (221 species, 105 genera), Basidiomycota (218 species, 100 genera), Blastocladiomycota (47 species, ten genera), Monoblepharomycota (29 species, six genera), Mucoromycota (19 species, ten genera), Aphelidiomycota (15 species, three genera), Entomophthoromycota (six species, four genera), Mortierellomycota (five species, three genera), Olpidiomycota (four species, one genus), Zoopagomycota (three species, two genera), and Sanchytriomycota (two species, two genera).

The website <https://freshwaterfungi.org/> is developed in the present work to amass scattered published information of freshwater fungi in one online platform and provide up-to-date information for all taxa. Furthermore, the author, together with other curators, also periodically updates the classification of marine fungi on the website <https://marinefungi.org/>. Though it is not included in the succeeding chapters, these open access websites contain essential information on the updated accounts of aquatic fungal classifications.

Keywords: Aquatic fungi websites, Freshwater fungi, Marine fungi, Phylogenetic analysis, Salt marsh fungi, Taxonomy