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| Dissertation Title | Taxonomy and Phylogeny of Pathogenic Ascomycete Genera Associated with Mangroves |
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ABSTRACT

In this study, the taxonomy of mangrove and other fungi are investigated using a dual taxonomic approach including morphological and molecular analyses. Fungal specimens associated with various hosts in terrestrial habitats were collected from Italy, Russia, Taiwan, and Thailand. The collections were morphologically examined and their DNA sequence data from rDNA loci and protein coding genes (ITS, LSU, SSU, *ef1- α* , *β -tubulin*, *act*, *endoPG*, *gapdh*, *rpb2*, *Alta1*, OPA10-2) were analysed to verify their identities and phylogenetic affinities to better assess their natural placement. The backbone tree reflects a more natural classification for all the fungal groups considered in this study. Descriptions, illustrations, and rationales for these novelties are provided for each taxon. Morphological differences and analysis of datasets of single genes and combined sequences support the validity of the species in this study and their placement. Forty-one species are accommodated in ten genera (*Alternaria*, *Cytospora*, *Hercospora*, *Lamproconium*, *Melomastia*, *Neopestalotiopsis*, *Pestalotiopsis*, *Phyllosticta*, *Pseudopestalotiopsis*, *Seimatosporium*), six families (Botryosphaeriaceae, Cytosporaceae, Lamproconiaceae, Pleosporaceae, Pleurotremaceae, Sporocadaceae). Novel fungal taxa that described include one new family (Lamproconiaceae), 32 new species (*Cytospora ampulliformis*, *C. curvata*, *C. donetzica*, *C. erumpens*, *C. longiostiolata*, *C. lumnitzericola*, *C. melnikii*, *C. parakantschavelii*, *C. paratranslucens*, *C. rusanovii*, *C. salicacearum*, *C. salicina*, *C. sorbi*, *C. sorbicola*, *C. thailandica*, *C. ulmi*, *C. xylocarpi*, *Melomastia italica*, *Neopestalotiopsis acrostichi*, *N. brachiate*, *N. petila*, *N. rhizophorae*,

N. sonneratae, *N. thailandica*, *Pestalotiopsis rhizophorae*, *P. thailandica*, *Pseudopestalotiopsis avucenniae*, *Ps. curvatispora*, *Ps. rhizophorae*, *Ps. thailandica*, *Phyllosticta rhizophorae*, *Seimatosporium physocarpi*), one designed epitype (*Seimatosporium rosae*), two reference specimens (*Lamproconium desmazieresii*, *S. lichenicola*), a recombined species (*Melomastia maolanensis*), new host records for four species (*Alternaria gaisen*, *C. nivea*, *C. parasitica*, *C. salicicola*), and a studied herbarium specimens (*Hercospora tiliae*).

Two complex genera, *Diaporthe* and *Phyllosticta* are revisited with morphological evidence coupled with support from multi-gene phylogeny of single gene trees and combined sequence data. Herein, we assembled a comprehensive dataset and for *Diaporthe* with ITS, *efl* α , β -*tubulin*, *cal* and *his3* sequence data. Thirteen workable species complexes for *Diaporthe* were introduced, including the *D. arecae*, *D. biconispora*, *D. carpini*, *D. decedens*, *D. eres*, *D. oncostoma*, *D. pustulata*, *D. rudis*, *D. scobina*, *D. sojiae*, *D. toxica*, *D. varians*, and *D. vawdreyi* species complexes. Nine species were kept as singletons (*D. acerina*, *D. acutispora*, *D. crataegi*, *D. multiguttulata*, *D. ocoteae*, *D. perjuncta*, *D. pseudoalnea*, *D. spartinicola*, *D. undulata*). Two genera of Diaporthaceae, are synonymized under genus *Diaporthe*, *D. cyatheae* (\equiv *Ophiodiaporthe cyatheae*) and *D. pseudobauhiniae* (\equiv *Chiangraiomyces bauhiniae*).

Six workable species complexes of *Phyllosticta* were introduced to assemble a comprehensive ITS, LSU, *efl* α , *actin*, and *gapdh* dataset and reconstruct phylogenetic trees with combined sequence data. From this study, we synonymize two strains of *P. capitalensis* under the *P. rhizophorae*. Six strains are mentioned as unnamed species and probably represent new species. The phylogenetic relationships of *Phyllosticta* species will be reevaluated and provide guidance for future work.

The phylogeny of *Diaporthe* (Diaporthaceae) and *Phyllosticta* (Phyllostictaceae) received new assessments and suggestions for future work. All data presented herein are based on morphological examination of specimens, coupled with

phylogenetic sequence data to better integrate taxa into appropriate taxonomic ranks and infer their evolutionary relationships. The current study provided complete descriptions and illustrations for all the taxa introduced.

Keywords: Ascomycota, Dothideomycetes, Endophytic, Fungal Diversity, New species, Pathogenic, Phylogeny, Saprobic, Sordariomycetes, Taxonomy

