

Dissertation Title	Morpho-molecular Characterization of Fungi Associated with Wild Mushrooms and Mushroom Cultivation, with Digital Documentation of Fungicolous Fungi
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ABSTRACT

Fungicolous fungi that grow on or within other fungi represent an ecologically important but poorly understood group within the fungal kingdom. They play diverse ecological roles ranging from parasitism to commensalism and contribute significantly to fungal diversity and ecosystem dynamics. Despite their importance, knowledge of fungicolous fungi, particularly in tropical regions, remains limited. This study (1) identified fungicolous fungi associated with wild mushrooms from northern Thailand and southwest China, (2) investigated fungi associated with mushroom cultivation in northern Thailand and reviewed fungal diseases and competitor molds affecting global mushroom production, and (3) established a comprehensive digital platform to consolidate existing knowledge on fungicolous fungi.

During this study, a total of 32 fungicolous taxa were identified from wild mushrooms collected in northern Thailand and southwest China, representing 11 genera across the *Sordariomycetes*, *Dothideomycetes*, and *Mucoromycetes*. The *Sordariomycetes* genera included *Clonostachys*, *Diaporthe*, *Fusarium*, *Hypomyces*, *Hypoxylon*, *Mariannaea*, *Xenoacremonium*, and *Zarea*; *Lasiodiplodia* and *Neorousoella* represented *Dothideomycetes*, while *Mucor* belonged to *Mucoromycetes*. Among these, four were newly described species (*Hypomyces Chiangraiensis*, *Mucor yunnanensis*, *Zarea boleticola*, and *Z. thailandica*), five were newly proposed combinations (*Hypomyces chalcipori*, *H. laevigatus*, *H. novovarius*,

H. paravirescens, and *H. protrusus*), and 23 were new records (*Clonostachys rogersoniana*, *Diaporthe talong*, *Fusarium fabacearum*, *F. grosnichelii*, *F. mangiferae*, *F. pernambucanum*, *F. proliferatum*, *F. teslae*, *F. verticillioides*, *Hypomyces boletiphagus*, *H. chlorinus*, *H. cornea*, *H. protrusus*, *H. mycophilus*, *H. pseudocorticiicola*, *H. semicircularis*, *Hypoxylon fendleri*, *Lasiodiplodia thailandica*, *Mucor circinelloides*, *M. hiemalis*, *M. nederlandicus*, *Neorousoella entadae*, and *Xenoacremonium allantoideum*). Morphological characterization combined with multi-locus phylogenetic analyses (Maximum Likelihood and Bayesian Inference) was conducted to confirm the identification of all fungal taxa. The presence of rare or unexpected genera such as *Diaporthe*, *Hypoxylon*, and *Lasiodiplodia* indicates ecological versatility and possible host-switching behavior of fungicolous fungi. Moreover, some species identified as fungicolous on wild mushrooms in this study, such as *Hypomyces protrusus*, *H. cornea*, *H. mycophilus*, *H. semicircularis*, and *H. pseudocorticiicola* are previously known mushroom pathogens on cultivated mushrooms, suggesting potential pathogenicity of fungicolous fungi on their living hosts.

During the investigation of fungi associated with mushroom cultivation in northern Thailand, *Daldinia eschscholtzii* and *Scedosporium apiospermum* were identified from oyster mushroom growing substrates. Whereas, *Aspergillus quadrilineatus*, *Fusarium sulawesiense*, and *Mucor irregulari* were isolated from cultivated *Phlebopus spongiosus*, *Hericium coralloides* and *Pleurotus* sp. fruiting bodies, respectively. Identification of these fungal taxa was also based on morphological characteristics and molecular phylogenetic analyses. The occurrence of *Daldinia eschscholtzii* on mushroom growing substrates highlights its potential for artificial cultivation and the large-scale harvesting of bioactive compounds produced by this species.

Fungal contaminations, manifesting as destructive diseases or rapidly spreading competitor molds, pose a major challenge to mushroom cultivation. These contaminants can arise at various stages of the cultivation process, causing growth inhibition, deformation, or decay of fruiting bodies, which leads to significant losses in both yield and quality. Addressing these impacts requires a clear understanding of

the causative agents and effective management strategies. In this study, four major fungal diseases, dry bubble, wet bubble, cobweb, and green mold, along with slippery scar and yellow rot, were comprehensively reviewed. The taxonomic placement of these pathogens was clarified through phylogenetic trees reconstructed from published DNA sequence data, and their morphological characteristics were illustrated. Additionally, nine competitor molds associated with mushroom cultivation were reviewed, with detailed accounts of their causal agents, symptoms, disease cycles, epidemiology, and management strategies compiled from available literature.

This study also compiled knowledge on 150 genera containing fungicolous species, including 108 in *Ascomycota*, 37 in *Basidiomycota*, and five in *Mucoromycota*. These generic notes include morphological, ecological, and host association information, accompanied by illustrations of morphological characters of each genus. A considerable number of these genera remain *incertae sedis*, indicating the need for further morpho-molecular studies to resolve their taxonomic placement. To integrate scattered data on this group of fungi, the fungicolous fungi webpage (<https://www.fungicolousfungi.org/>) was developed, providing an accessible platform for accurate identification, data sharing, and taxonomic updates. This marks a significant advancement in the documentation of fungal biodiversity and will serve as a valuable resource for mycologists, students, and other stakeholders interested in this group of fungi.

Overall, this study expands the current understanding of fungicolous fungal diversity, host associations, and ecological roles. The integrative approach combining morphological, molecular, and digital documentation provides a strong foundation for future research, including studies on host specificity, pathogenicity, evolution, and taxonomy of this remarkable fungal group.

Keywords: Fungicolous Fungi, Mushroom Diseases, Mycoparasites, Taxonomy and Phylogeny, Webpage