Dissertation Title A Taxonomic Monograph of 19 Familes of Helotiales
Incorporating New Collections
Author Le Luo
Degree Doctor of Philosophy (Biological Science)
Advisor Assistant Professor Kitiphong Khongphinitbunjong, Ph. D.
Co-Advisor Adjunct Professor Kevin David Hyde, Ph. D.
Assistant Professor Thilini Chethana Kandawatte Wedaralalage, Ph. D.

ABSTRACT

Helotiales is one of the largest and most morphologically diverse lineages within Ascomycota, comprising approximately 5,000–6,000 species in more than 40 families and 500 genera. Their ascomata are typically small, cupulate or discoid, less than 2 mm in diameter, with colors ranging from dark brown to bright red, orange, and occasionally blue-green. Members exhibit saprobic, pathogenic, and endophytic lifestyles, and play crucial roles in forest ecosystems. Although Helotiales has been the subject of considerable taxonomic and phylogenetic research, most previous studies have focused on temperate regions of Europe and North America, relying largely on herbarium specimens or limited molecular datasets. Consequently, many genera remain insufficiently revised, family boundaries are still unclear, and only a small fraction of type specimens has been critically re-examined. In contrast, biodiversity hotspots such as southwestern China and northern Thailand—characterized by unique karst and montane ecosystems—have received little systematic investigation. These gaps hinder our understanding of the evolutionary relationships, ecological roles, and distribution patterns of Helotiales in Asia. To address these issues, the present study aims to comprehensively document the diversity of Helotiales in these regions, clarify their phylogenetic relationships using multi-gene analyses, re-evaluate type specimens, and provide an updated taxonomic framework. In this monograph, we review 19 families and 231 genera of Helotiales based on 40 fresh collections from southwestern China and northern Thailand, together with herbarium specimens loaned from worldwide herbaria. By integrating morphological observations with multi-gene phylogenetic analyses (ITS, LSU, *RPB2*, *TEF1-α*), we describe 22 new species, document 18 new records, and expand the geographical distribution of three taxa. In total, requests were sent to 193 herbaria, from which 27 specimens were successfully obtained. Among these, 13 specimens had sufficiently preserved features for detailed morphological examination. Eight type specimens were re-examined through detailed morphological study, including microscopic observations of apothecia, asci, and ascospores, and updated descriptions were prepared. In addition, detailed notes were compiled for 19 families and 137 genera, providing a comprehensive framework for comparative taxonomy. Furthermore, based on the order-level phylogenetic tree reconstructed from multi-gene datasets, several traditionally broad families were redefined, and their monophyly was supported.

In the order-level phylogenetic analyses, DNA sequence data clarified the placements of several of the 94 genera formerly considered as *incertae sedis*. Seventeen of these genera resolved into well-supported clades corresponding to known families, recealing their true phylogenetic affinities. However, most of the remaining genera are still unresolved, largely due to the absence of adequate or incomplete molecular datasets.

This study refines the taxonomic framework of Helotiales, enriches global molecular datasets with newly generated sequences, and highlights Asian montane regions as important centers of fungal diversity. Collectively, these contributions provide a robust foundation for future research on the systematics, ecology, and biogeography of Helotiales, and open new opportunities for applied studies in biotechnology and ecosystem services.

Keywords: Helotiales, Taxonomy, Morphology Diversity, Ecosystem Roles