

Dissertation Title	Clavicipitoid Fungi in China and Thailand with Focus on Cordycipitaceae
Author	Yu Yang
Degree	Doctor of Philosophy (Biological Science)
Advisor	Assistant Professor Somrudee Nilthong, Ph. D.
Co-Advisor	Adjunct Professor Kevin David Hyde, Ph. D. Yuanpin Xiao, Ph. D.

ABSTRACT

Clavicipitoid fungi (Hypocreales, Ascomycota) constitutes one of the most taxonomically complex and ecologically versatile groups of filamentous fungi. They parasitize a wide spectrum of hosts, including insects, arachnids, fungi, plants, and other substrates, and thereby play critical roles in terrestrial ecosystems as regulators of arthropod populations, mediators of host-pathogen interactions, and contributors to nutrient cycling. Several members are also of substantial applied importance in medicine, agriculture, and biotechnology. Despite this ecological and economic relevance, the taxonomy and evolutionary history of clavicipitoid fungi remain incompletely resolved. Many historically described species lack epitypified material, molecular data are missing for numerous type taxa, and cryptic diversity has been repeatedly uncovered by molecular phylogenetics. As a result, generic concepts and species delimitations remain unstable in several lineages. Addressing these problems requires integrative studies that combine morphology, multilocus phylogeny, divergence-time estimation, and biogeographic reconstruction. This dissertation provides such a framework, with a comprehensive monographic treatment of Cordycipitaceae as the principal focus, supplemented by species-level contributions to Ophiocordycipitaceae, Polycephalomyctaceae, and Clavicipitaceae.

In Cordycipitaceae, the most substantial results of this dissertation are synthesized. A revised taxonomic framework is established through the compilation of a complete checklist of 38 recognized genera, together with diagnostic notes and re-illustrated type species. Morphological synopses are provided for each species treated, emphasizing key diagnostic features. In total, 50 species are documented, including 26 new species, two

newly established genera, 10 new records from China and adjacent regions, and several previously described taxa that are critically re-evaluated. Seven new combinations are also proposed based on molecular evidence. Multilocus phylogenetic analyses based on ITS, LSU, SSU, TEF-1 α , RPB1, and RPB2 resolve generic-level relationships and provide a robust backbone for the family. Divergence-time estimation dates the crown origin of Cordycipitaceae to the early Cretaceous (~140.78 Ma, 95% HPD: 132–149 Ma), coinciding with major radiations of insects and arthropods. Biogeographic reconstructions consistently indicate Asia as the ancestral area and primary dispersal hub, characterized by deep-time conservatism in basal lineages and repeated outward dispersals since the Eocene–Miocene into Europe, Africa, and the Americas, with rarer long-distance dispersals to South America and Oceania. Collectively, these results provide the most comprehensive synthesis of Cordycipitaceae to date, clarifying its taxonomy, evolutionary history, and global distribution.

Complementary investigations across related clavicipitoid families have enriched their known diversity. In Clavicipitaceae we recognize two new species and three new records, including the first Chinese record of *Metarhizium phasmatodeae* and the description of *M. multisynnematum*, which expresses synnematal morphology both in nature and in culture, together with *Moelleriella yusheensis* on scale insects, *Petchia siamensis* on mantid oothecae, and *Yosiokobayasia kusanagiensis*. These findings expand the ecological scope of the family and reinforce the significance of *Metarhizium* as both an entomopathogen and a plant-beneficial endophyte. In Ophiocordycipitaceae we describe 17 new species and four new records, comprising 15 taxa of *Ophiocordyceps*, two of *Paraisaria* and one of *Hirsutella*. These discoveries broaden the host spectrum across Blattodea, Coleoptera, Diptera, Lepidoptera and Arachnida, including rarely reported lineages such as spider and termite parasites, and resolve species complexes where morphology alone has proven insufficient, such as the *O. nutans* group and the Gryllotalpa-associated clade. They highlight both the ecological versatility of Ophiocordycipitaceae and the value of multilocus phylogenies in clarifying cryptic diversity. In Polycephalomycetaceae we introduce four new species of *Pleurocordyceps* (*P. clavisynnema*, *P. multisynnemma*, *P. neoagarica* and *P. sanduensis*) and report three new records, including two in *Pleurocordyceps* and one in *Polycephalomyces*. Phylogenetic analyses based on six loci

confirm their independence as distinct lineages and underscore frequent host switching and repeated evolution of fungicolous lifestyles, suggesting that host identity and niche partitioning are major axes of diversification in this family and that China harbors a still insufficiently documented reservoir of *Pleurocordyceps* diversity. Collectively these results reveal a continued expansion of taxonomic diversity across three clavicipitoid families and emphasize their ecological and evolutionary versatility beyond Cordycipitaceae.

The results provide a comprehensive monographic framework for Cordycipitaceae, clarifying its taxonomy, phylogenetic relationships, divergence time, and biogeographic history, and revealing a dual pattern characterized by long-term conservatism in Asia combined with episodic outward dispersals. In addition, targeted studies of Ophiocordycipitaceae, Polycephalomycetaceae, and Clavicipitaceae contribute new species and records that expand the known diversity of these families and highlight novel host associations. Collectively, this dissertation underscores both the hidden diversity and the taxonomic complexity of clavicipitoid fungi and provides a solid foundation for future studies in fungal systematics, biodiversity, ecology, and applied research.

Keywords: Biogeographic Reconstructions, Checklist, Clavicipitaceae, Phylogeny, Polycephalomycetaceae, Sordariomycetes, Taxonomy