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| **Dissertation Title** | Taxonomy and Phylogeny of Gomphaceae and Other Clavarioid Fungi |
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## ABSTRACT

The clavarioid fungi are very important both economically and ecologically, characterized by coralloid, simple, or branched basidiome. They include 30 genera with about 800 species, distributed in worldwide. In this study, taxonomic and phylogenetic studies were done based on 790 collections of clavarioid fungi, including 666 from China, 88 from Thailand, and 36 collections from other areas. The family containing the largest number of clavarioid fungi is the Gomphaceae.

In the Gomphaceae family, the most representative genus is *Phaeoclavulina*. However, *Phaeoclavulina* species are poorly understood due to insufficient morphological descriptions and a lack of DNA sequence data. In addition, the misidentification of *Phaeoclavulina* specimens has added to the confusion regarding the taxonomy of *Phaeoclavulina* species. In this study, taxonomic and phylogenetic studies were done based on 79 collections of *Phaeoclavulina*, including 50 from China, 6 from Thailand, and 23 collections from other areas. The diversity of *Phaeoclavulina* in China and Thailand was evaluated by employing both morphological and phylogenetic analyses. A multi-locus phylogenetic analysis was performed using the internal transcribed spacer (ITS) region, the mitochondrial rDNA small subunit (mtSSU), partial nuclear ribosomal large subunit (nrLSU), translation elongation factor 1-alpha (*tef*1) and mitochondrial ATPase subunit 6 (ATP6). A total of 461 sequences were used in the phylogenetic analyses, of which 224 were newly generated in this study, including 70 sequences of ITS, 70 sequences of nrLSU, 14 sequences of mtSSU, 26 sequences of ATP6, 44 sequence of *tef*1. Fifteen species of *Phaeoclavulina* were treated in this study, including 6 new species and 9 known taxa. The 6 new *Phaeoclavulina* species found in China are *Phaeoclavulina subabietina, P. qilianensis,* *P. sterigmata, P. jilongensis, P. subcarovinacea and P. subminutispora*. Molecular phylogenies, a summary of species diversity, descriptions and illustrate are provided.

Two new Gomphoid fungi species (*Turbinellus sp1* and *Gloeocantharellus sp1*) and three known species (*Gomphus orientalis*, *Gomphus clavatus* and *Turbinellus szechwanensis*) based on morphology and phylogenetic analysis. 336 sequences derived from three loci (ITS, nrLSU, tef1) were used to reconstruct phylogenetic trees of Gomphoid fungi, including 121 for ITS, 131 for nrLSU and 84 for tef1 representing 41 species from Gomphoid fungi. Newly generated 94 sequences, including 31 for ITS, 36 for nrLSU and 27 for tef1 representing 5 species from Gomphoid fungi. The combined three-gene dataset (ITS+nrLSU+ tef1) included sequences from 146 specimens representing 41 species from Gomphoid fungi.

Nineteen new *Ramaria* species and seven known species based on morphology and phylogenetic analysis. 376 sequences derived from three loci (ITS, nrLSU, mtSSU) were used to reconstruct phylogenetic trees of *Ramaria*, including 273 for ITS, 75 for nrLSU and 28 for mtSSU representing 134 species from *Ramaria*. Newly generated 177 sequences, including 75 for ITS, 75 for nrLSU and 28 for mtSSU representing 26 species from *Ramaria*. The ITS included sequences from 282 specimens representing 134 species from *Ramaria*.

Three new *Clavulinopsis* species, *C. sp1, sp2* and *C. sp3* collected from China and Thailand are described and illustrated, based on morphological characteristics and molecular analyses. A total of 352 sequences were used in the phylogenetic analyses, of which 43 were newly generated in this study, including 23 sequences of ITS, 10 sequences of nrLSU, 10 sequences of ATP6. Twelve species of *Clavulinopsis* were treated in this study, including 2 new species and 10 known taxa. The 2 new *Clavulinopsis* species found in China and Thailand are *C. sp1* nom. prov., *C. sp2* nom. prov.. Molecular phylogenies, a summary of species diversity, descriptions and illustrate are provided.

Two new *Clavariadelphus* species and five known species based on morphology and phylogenetic analysis. 100 sequences derived from two loci (ITS, nrLSU) were used to reconstruct phylogenetic trees of *Clavariadelphus*, including 73 for ITS and 27 for nrLSU representing 26 species from *Clavariadelphus*. Newly generated 54 sequences, including 27 for ITS and 27 for nrLSU representing 7 species from *Clavariadelphus*. The ITS dataset included sequences from 73 specimens representing 26 species from *Clavariadelphus.*

Three known *Lentaria* species based on morphology and phylogenetic analysis. 64 sequences derived from ITS were used to reconstruct phylogenetic trees of *Lentaria*, including 64 for ITS representing 21 species from Lentaria. Newly generated 5 sequences, including 5 for ITS representing 3 species from *Lentaria*. The ITS dataset included sequences from 64 specimens representing 21 species from *Lentaria*

**Keywords:** Fungi, New Fungi Species, Phylogeny, Taxonomy