

<b>Dissertation Title</b>	Lignicolous Freshwater Fungi of the Pan Qinghai-xizang Plateau, China
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## ABSTRACT

The Qinghai-Xizang Plateau (Q-X Plateau), often referred to as the “Asia Water Tower,” is a globally significant ecological region characterized by its complex topography, high elevation, and unique freshwater ecosystems. Despite the recognized importance of this region, comprehensive studies on its microbial biodiversity particularly lignicolous freshwater fungi remain scarce. These fungi play essential ecological roles in aquatic environments, contributing to the decomposition of woody debris, nutrient cycling, and energy flow, especially in oligotrophic high-altitude habitats. This dissertation aims to systematically investigate the taxonomic diversity, ecological distribution, and phylogenetic relationships of lignicolous freshwater fungi in the Q-X Plateau, thereby enhancing our understanding of their role in plateau ecosystems and contributing to global fungal taxonomy.

This study is based on an extensive field survey conducted as part of the Second Comprehensive Scientific Expedition to the Tibetan Plateau. Submerged decaying wood was collected from freshwater habitats across seven major ranges, encompassing a wide range of ecological types including alpine desert, alpine steppe, montane forest, plateau lakes, and glacial-fed rivers. A total of 588 fungal strains were isolated using single-spore isolation techniques. 123 collections were selected for detailed morphological observation and molecular analyses. Multilocus phylogenetic analyses (ITS, LSU, SSU, RPB2 and TEF1- $\alpha$ ) were performed to determine taxonomic placement.

Experimental results show that 123 taxa distributed in three classes, 26 orders, 40 families and 58 genera are described and illustrated. Taxa include three new families, five

new genera, 67 new species, and 13 new geographical distribution reports. Three new families are *Acronigrasporaceae* (*Natipusillales*), *Longirostraceae* (*Pleosporales*) and *Xizangmycetaceae* (*Pisorisporiales*); new genera are *Acronigraspora* (*Acronigrasporaceae*, *Natipusillales*), *Catamurium* (*Phaeoseptaceae*, *Pleosporales*), *Hyalambispora* (*Microthyriaceae*, *Microthyriales*), *Longirostrum* (*Longirostraceae*, *Pleosporales*); *Xizangmyces* (*Xizangmycetaceae*, *Pisorisporiales*); new species comprise *Acrodictys altitudinalis*, *Acrogenospora alticampestricola*, *Acronigraspora subsphaerica*, *Acronigraspora zhuomulariensis*, *Aquapteridospora linzhiensis*, *Aquapteridospora submersa*, *Aquapteridospora yadongensis*, *Brachiosphaera radiaticonidiosa*, *Brachysporium nielamuense*, *Catenatimuriformis sporodochialis*, *Chaetopsina motuoensis*, *Chaetosphaeria aseptata*, *Chloridiopsiella septate*, *Cladophialophora biguttulata*, *Cladophialophora kaiduensis*, *Conioscypha brevipioniophora*, *Conioscypha motuoensis*, *Conioscypha reniformis*, *Conioscypha subglobosa*, *Conioscypha xizangensis*, *Cordana linzhiensis*, *Cordana reniformis*, *Cordana tumida*, *Dematiosporium dictyosporum*, *Dematiosporium phaeohyphum*, *Dictyocheirospora luojiensis*, *Gamsomyces namco*, *Gohteikhimycetes dulongjiangensis*, *Hongkongmyces fusiformis*, *Hyalambispora drungiorum*, *Hyalambispora reniformis*, *Junewangia chenyue*, *Kernia xizangensis*, *Kirschsteiniotelia mucosa*, *Lentistoma motuoense*, *Longirostrum aquaticum*, *Neohelicosporium xinjiangense*, *Neomyrmecridium gaoligongense*, *Neomyrmecridium luguense*, *Paramonodictys dispersa*, *Periconia xizangensis*, *Pleopunctum megalosporum*, *Pleopunctum multicellularum*, *Pleopunctum rotundatum*, *Pleurotheciella bambusisiliquosa*, *Pseudoascotaiwania aquatica*, *Pseudostanjeiughesia nielamuensis*, *Ramophialophora ramose*, *Savoryella claviformis*, *Savoryella daemonocula*, *Savoryella submersa*, *Spadicoides hydei*, *Sporidesmiella gezaensis*, *Sporidesmiella yadongensis*, *Sporidesmium bostenicum*, *Sporidesmium fluviale*, *Sporidesmium mucilaginosum*, *Sporidesmium napaense*, *Sporoschisma hyalomucilaginosum*, *Sporoschisma lignicola*, *Sporoschisma verruculose*, *Teichospora xinjiangensis*, *Thysanorea hyaloconidia*, *Thysanorea linzhiensis*, *Wiesneriomyces aquaticus*, *Xizangmyces aquaticus* and *Xylolentia subhyalina*; new geographical records are *Bactrodesmiastrum pyriforme*, *Bactrodesmium diversum*, *Bactrodesmium obovatum*, *Cordana crassa*, *Halosphaeriopsis mediosetigera*, *Jennwenomyces navicularis*,

*Pleurothecium recurvatum*, *Ramophialophora vesiculosa*, *Scedosporium minutisporum*, *Sterigmatobotrys macrocarpus*, *Vanakripa mucosa* and *Vargamyces aquaticus*.

Ecological analysis revealed clear patterns in species richness and distribution. Fungal diversity peaked at mid-elevations (1,500–2,000 m), likely due to optimal microclimatic conditions and substrate availability, and declined at both lower and higher altitudinal extremes. Several taxa, including *Stachybotrys chartarum* and *Vanakripa Chiangmaiense*, were found in extreme environments, from arid lowlands (–103 m) to high-altitude zones (5,277 m), demonstrating the remarkable ecological adaptability of freshwater fungi.

Additionally, we provided comprehensive checklist identifies 605 freshwater fungal species in the Q-X Plateau region, distributed across five major classes: *Dothideomycetes*, *Eurotiomycetes*, *Orbiliomycetes*, *Pezizomycetes*, and *Sordariomycetes*. In conclusion, this dissertation significantly advances the understanding of freshwater fungal diversity in the Q-X Plateau and contributes to broader discussions on fungal biogeography, taxonomy, and ecosystem functioning in extreme environments. The discovery of new taxa and updated classifications provides a critical reference for future biodiversity assessments and conservation planning. Moreover, this work underscores the Q-X Plateau as a reservoir of untapped fungal resources and a key region for future mycological exploration in the context of global environmental change.

**Keywords:** 74 New Taxa, Asexual Morph, Multi-gene, Phylogeny, Sexual Morph, Taxonomy