

Study enriches species diversity, phylogeny and evolution regularity of hydnnaceae

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Basidiocarps of new taxa in Hydnaceae. A–B. *Cantharellus laevihymininus* (IFP 019441). C–D. *Cantharellus magnus* (IFP 019443). E. *Cantharellus subminor* (IFP 019445). F. *Craterellus badiogriseus* (IFP 019452). G. *Craterellus croceialbus* (IFP 019454). H. *Craterellus macrosporus* (IFP 019456). I. *Craterellus squamatus* (IFP 019457). J. *Hydnum brevispinum* (IFP 019464). K–L. *Hydnum flabellatum* (IFP 019459). M–N. *Hydnum flavidocanum* (IFP 019460). O. *Hydnum longibasidium* (IFP 019462). P–Q. *Hydnum pallidocroceum* (IFP 019466). R–S. *Hydnum pallidomarginatum* (IFP 019468). T–U. *Hydnum sphaericum* (IFP 019470). V. *Hydnum tangerinum* (IFP 019473). W. *Hydnum tenuistipitum* (IFP 019476). X–Y. *Hydnum ventricosum* (IFP 019478). Scale bars: A, B, E–Y = 1 cm; C, D = 2 cm. Credit: DOI: 10.1016/j.simyco.2021.100121

The family Hydnaceae is a significant group of fungi in Cantharellales. Some genera with lichenicolous or lichenised nutritional modes are also embedded in Hydnaceae, they all play important roles in the material cycle of terrestrial ecosystems.

In recent years, the method of molecular phylogeny has been widely used in taxonomy of [fungi](#). However, a comprehensive phylogeny based on a multiple-marker dataset for the entire Hydnaceae is still lacking and the delimitation, morphology and ecological evolution as well as of the diversity of genera is unclear, the species diversity of this taxa in China need further research.

Dr. Yuan Haisheng and his team from the Institute of Applied Ecology (IAE) of the Chinese Academy of Sciences conducted a systematic study of the Hydnaceae, especially the umbelliform fungi, and they made a phylogenetic overview of Hydnaceae and its new taxa.

The researchers proposed the infrageneric subdivision within the genera *Cantharellus*, *Craterellus* and *Hydnum* based on morphological and [phylogenetic analyses](#).

They integrated the global sequences data of Cantharellales fungi from GenBank database and first inferred five sequence fragment dataset based Maximum Likelihood and Bayesian phylogenies for the Cantharellales and reappraised the taxonomic status of Hydnaceae in the order. Seventeen genera included in Hydnaceae were confirmed according to the phylogenetic relationship.

Then, the phylogenetic status of genera *Cantharellus*, *Craterellus*, Hydnaceae and umbelliform fungi of *Sistotrema* in the family has been clarified. Phylogenetic relationship of taxa within Hydnaceae were further systematically sort out by fitting the morphology, ecology and phylogeny features.

In addition, the evolution of ecological (from saprotrophic, lichenised/lichenicolous to ectomycorrhizal) and morphological (from bulbil-forming/resupinate, coralloid/clavarioid to umbelliform) characteristics of Hydnaceae species was preliminarily speculated.

Furthermore, 29 fungal taxa were published, including eight new subgenera, 17 new species, two synonyms and two newly recorded species.

This study enriches the [species](#) diversity of this group in China. It has important reference value for further exploring the co-evolution of fungi in this group and their hosts as well as the morphological and ecological evolution of fungi in other groups.

The study, titled "A phylogenetic overview of the Hydnaceae with new taxa from China," has been published in *Studies in Mycology*.

More information: Ting Cao et al, A phylogenetic overview of the Hydnaceae (Cantharellales, Basidiomycota) with new taxa from China, *Studies in Mycology* (2021). [DOI: 10.1016/j.simyco.2021.100121](https://doi.org/10.1016/j.simyco.2021.100121).
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