

Characterization and phylogenetic analysis of the complete mitochondrial genome of *Clavulina* sp. (Cantharellales: Clavulinaceae)

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ABSTRACT

In this study, the complete mitochondrial genome of *Clavulina* sp. was sequenced and assembled. The complete mitochondrial genome of *Clavulina* sp. contains 20 protein-coding (PCG) genes, 2 ribosomal RNA (rRNA) genes, and 25 transfer RNA (tRNA) genes. The total size of the *Clavulina* sp. complete mitochondrial genome is 31,816 bp, with the GC content of 27.72%. Phylogenetic analysis indicated that the mitochondrial genome of *Clavulina* sp. exhibited a close relationship with that of the genus *Cantharellus*.

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Ectomycorrhiza; mitochondrial genome; phylogenetic analysis; evolution; taxonomy

The genus *Clavulina* is an ectomycorrhizal fungal group distributed in many countries (Olariaga et al. 2009; Henkel et al. 2011). Most of species from the *Clavulina* genus are edible, and some species also show medicinal values (Khaund and Joshi 2014; Deo et al. 2019). Dozens of species have been described in genus *Clavulina* (Thacker and Henkel 2004; Uehling et al. 2012a, 2012b). Limited and varied morphological characteristics make it difficult to identify and classify *Clavulina* species accurately only by morphology (Thacker and Henkel 2004; Olariaga et al. 2009; Uehling et al. 2012a, 2012b). Mitochondrial genome is widely used to analyze the evolution and phylogeny of species (Li, He, et al. 2020; Wang et al. 2020; Li et al. 2020). However, up to now, no mitochondrial genome of *Clavulina* species has been published. The mitochondrial genome of *Clavulina* sp. will promote the understanding of the evolution, phylogeny, and taxonomy of this important ectomycorrhizal fungal group.

The specimen (*Clavulina* sp.) was collected from a mountain in Chuxiong, Yunnan, China (101.41 E; 25.12 N). The specimen was stored in Culture Collection Center of Chengdu University (No. Clasp08). The complete mitochondrial genome of *Clavulina* sp. was assembled according to previously described methods (Li, Xiang, et al. 2019; Wang et al. 2020). The total genomic DNA of *Clavulina* sp. was extracted using a Fungal DNA Kit D3390-00 (Omega Bio-Tek, Norcross, GA). A Gel Extraction Kit (Omega Bio-Tek, Norcross, GA) was used to purify the extracted total DNA. We stored the purified DNA

in Chengdu University (No. DNA_ Clasp08). Sequencing libraries were constructed with the purified genomic DNA using a NEBNext® Ultra™ II DNA Library Prep Kit (NEB, Beijing, China). We conducted whole genomic sequencing (WGS) of *Clavulina* sp. using the Illumina HiSeq 2500 Platform (Illumina, San Diego, CA). The mitochondrial genome of *Clavulina* sp. was *de novo* assembled using SPAdes version 3.9.0 (Bankevich et al. 2012). We obtained the complete mitochondrial genome of *Clavulina* sp., and then annotated it according to the methods described by Li, Chen, et al. (2018), Li, Ren, et al. (2019), and Li, Wang, et al. (2018).

The complete mitochondrial genome of *Clavulina* sp. is 31,816 bp in length, with the base composition as follows: A (34.94%), T (37.32%), G (14.38%), and C (13.35%). The complete mitochondrial genome of *Clavulina* sp. contains 20 protein-coding genes, 2 ribosomal RNA genes (*rns* and *rnl*), and 25 transfer RNA (tRNA) genes. To investigate the phylogenetic positions of *Clavulina* sp., we constructed a phylogenetic tree for 20 species. The phylogenetic tree was constructed using the Bayesian analysis (BI) method based on the combined 14 core protein-coding genes according to methods described by Li, Wang, Jin, Chen, Xiong, Li, Liu, et al. (2019), Li, Wang, Jin, Chen, Xiong, Li, Zhao, et al. (2019) and Li, Yang, et al. (2020). As shown in the phylogenetic tree (Figure 1), the mitochondrial genome of *Clavulina* sp. exhibited a close relationship with that of the genus *Cantharellus* (Li, Liao, et al. 2018).

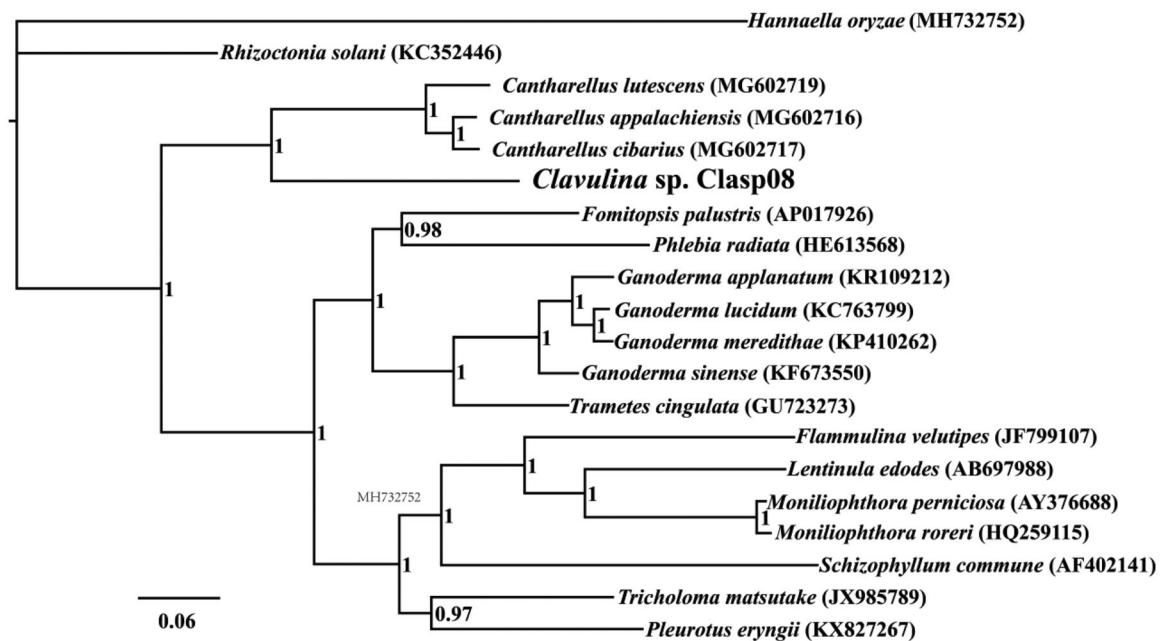


Figure 1. Bayesian phylogenetic analysis of 20 species based on the combined 14 core protein-coding genes. Accession numbers of mitochondrial sequences used in the phylogenetic analysis are listed in brackets after species.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Data availability statement

This mitogenome of *Clavulina* sp. was submitted to GenBank under the accession number of MT649302 (<https://www.ncbi.nlm.nih.gov/nucleotide/MT649302>).

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