Complete mitochondrial genome of the important entomopathogenic fungus *Cordyceps tenuipes* (Hypocreales, Cordycipitaceae)

Dandan Li, Guodong Zhang, Luodong Huang, Yuanbing Wang and Hong Yu

**CONTACT**

Yuanbing Wang, wangyb001@126.com

Hong Yu, hongyu@ynu.edu.cn

**ARTICLE HISTORY**

Received 11 February 2019
Accepted 13 March 2019

**KEYWORDS**

Cordyceps tenuipes; mitochondrial genome; phylogenetic analyses

**ABSTRACT**

*Cordyceps tenuipes* is a worldwide entomopathogenic fungus and is famous as the edible and medical value in East Asian nations. In the present study, the high-quality whole-genome of *C. tenuipes* was sequenced on the Illumina sequencing platform. The complete mitochondrial genome of this fungus was assembled as a single circular dsDNA of 31386 bp, including 15 protein-coding genes, 2 ribosomal RNA genes and 22 transfer RNA genes. The overall base composition of *C. tenuipes* is 36.6% A, 36.4% T, 11.8% C, 15.2% G, with a CG content of 27%. Phylogenetic analyses based on concatenated protein sequences from 27 taxa of five families within the order Hypocreales were conducted using Maximum likelihood (ML) and Bayesian inference (BI) methods. It is revealed that *C. tenuipes* is more closely related to *C. militaris* in the family Cordycipitaceae. This study would facilitate the future investigation of genetics, evolution and function of cordycipitoid fungi.

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annotated mitogenome of *C. tenuipes* was submitted to GenBank under accession no. MK234910. The total length of this circular mitogenome is 31,386 bp, containing 15 protein-coding genes (PCGs), 2 ribosomal RNA (rRNA) genes and 22 transfer RNA (tRNA) genes. The overall base composition is as follows: 36.6% A, 36.4% T, 11.8% C, 15.2% G, with a CG content of 27%.

To validate the phylogenetic position of *C. tenuipes*, mitogenomic sequences of its 26 allied taxa were downloaded from NCBI. Mitogenomic sequences of *C. tenuipes* and its allies were aligned using the programme HomBlocks (Bi et al. 2018). Phylogenetic analyses of the concatenated protein sequences from 27 taxa were conducted using Bayesian inference (BI) and maximum-likelihood (ML) methods, employing MrBayes v.3.1.2 (Ronquist and Huelsenbeck 2003) and RaxML7.0.3 (Stamatakis 2006), respectively. The BI analysis was run on MrBayes v.3.1.2 for five million generations using the GTR + G + I model. The GTR + I model was selected as the optimal model for ML analysis, and the concatenated protein sequences were performed with 500 rapid bootstrap replicates. BI analysis is consistent with that of ML analysis from 27 taxa of the order Hypocreales. Phylogenetic tree reveals the topological structure of 27 taxa within Hypocreales and is composed of five families, namely Nectriaceae, Hypocreaceae, Ophiocordycipitaceae, Clavicipitaceae, and Cordycipitaceae (Figure 1). *Cordyceps tenuipes* is clustered in the genus *Cordyceps* of Cordycipitaceae and is more closely related to *C. militaris*, the type species of this genus.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

**Funding**

This work was jointly funded by China Postdoctoral Science Foundation [2017M613017], National Natural Science Foundation of China [31760011 and 31870017], and Department of Science and Technology of Yunnan Province [KC1810172, 2018FY001-006]].

**ORCID**

Luodong Huang [http://orcid.org/0000-0001-6788-6158](http://orcid.org/0000-0001-6788-6158)

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