Complete mitochondrial genome of Tolypocladium sp. YFCC 1805002 isolated from Ophiocordyceps sinensis in Baima Snow Mountain, Southwestern China

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ABSTRACT
Tolypocladium sp. YFCC 1805002, an undescribed species isolated from natural Ophiocordyceps sinensis in Baima Snow Mountain, Deqin County of Yunnan in Southwestern China, was sequenced on the Illumina sequencing platform. The complete mitochondrial genome of this fungus is a circular molecule of 46,466 bp in length, and this value is higher than its two relatives T. inflatum and T. ophioglossoides. The circular mitogenome contains 15 protein-coding genes (PCGs), a set of 25 transfer RNA (tRNA) genes, and 2 ribosomal RNA (rns and rnl) genes. The 15 protein-coding genes are atp6, 8–9, cob, cox1–3, nad1–6, nad4L and rps3. The lengths of 25 transfer RNA (tRNA) genes are ranging from 71 to 87 bp, and the sizes of rns and rnl are 1554 bp and 5931 bp, respectively. The overall base composition is 38.3% A, 35.6% T, 11.6% C, 14.5% G, with a low GC content of 26.1%. Phylogenetic analysis inferred from concatenated protein-coding genes of 51 taxa shows that the new species Tolypocladium sp. YFCC 1805002 is closely related to T. inflatum in the family Ophiocordycipitaceae with high credible support by Bayesian inference posterior probabilities (BI-PP = 100%). This study would facilitate the future research of genetics, evolution and medicine of cordycipitoid fungi.

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The cordycipitoid genus Tolypocladium (Ophiocordycipitaceae, Hypocreales) was erected by the type species T. inflatum. Several species of Tolypocladium are medicinally and economically important due to the production of Cyclosporin A with antifungal activity and as immunosuppressant drug (Samson and Soares 1984; Li 1988; Bushley et al. 2013; Quandt et al. 2015; Rocha et al. 2015; Yang et al. 2018; Zhang et al. 2018). Due to the importance of Tolypocladium for mycology, medicine and ecology, more research is necessary to obtain genomic information of this lineage. Based on morphological and nuclear gene phylogenetic evidence, a fungal strain YFCC 1805002 isolated from the natural Ophiocordyceps sinensis specimen was identified as a new species of Tolypocladium and would be described elsewhere. This study aims to report the complete mitochondrial genome (mitogenome) of Tolypocladium sp. YFCC 1805002 and to decipher its phylogenetic relationship to other cordycepid fungi.

Tolypocladium sp. YFCC 1805002 was isolated from the natural fresh O. sinensis specimen collected from Baima Snow Mountain, Deqin County of Yunnan in Southwestern China (28°26′02″N, 99°01′33″E, alt. 4902 m). The strain was deposited at the Yunnan Fungal Culture Collection (YFCC), Yunnan University. Mycelia cultured on PDA at 20°C for 25 days without light condition were prepared to extract total genomic DNA using DNeasy Plant Genomic DNA Purification Mini Kit (QIAGEN). The whole-genome sequencing was carried out by Novogene Co., Ltd. (Beijing, China) on the Illumina sequencing platform (HiSeq-PE150). The software SPAdes v. 3.11.0 was used to assemble mitogenome of Tolypocladium sp. YFCC 1805002 (Bankevich et al. 2012). Mitogenome was annotated using MFannot tool and ARWEN web server, combined with artificial correction technology. To draw the mitogenomic circular map, the Organellar Genome DRAW tool was employed (Lohse et al. 2007).

The annotated mitogenome was submitted to GenBank under accession No. MN 583265. The total length of this circular mitogenome is 46,466 bp, which is higher than those of its two relatives, namely 25,328 bp of T. inflatum and 35,159 bp of T. ophioglossoides. The circular mitogenome contains 15 protein-coding genes (PCGs), a set of 25 transfer RNA (tRNA) genes and 2 ribosomal RNA (rns and rnl) genes. The 15 PCGs are atp6, 8–9, cob, cox1–3, nad1–6, nad4L and rps3. The lengths of 25 tRNA genes are ranging from 71 to 87 bp, and the sizes of rns genes and rnl are 1554 bp and 5931 bp, respectively. The overall base composition is as...
follows: 38.3% A, 35.6% T, 11.6% C, 14.5% G, with a low GC content of 26.1%.

To determine the phylogenetic relationship of *Tolypocladium* sp. YFCC 1805002 and its allies, fourteen concatenated mitochondrial PCGs in total of 12,972 bp were employed for phylogenetic analysis. Sequence alignment and phylogenetic analysis were conducted as described by Wang et al. (2018). Phylogenetic tree showed that the new species *Tolypocladium* sp. YFCC 1805002 is clustered together with *T.* *inflatum* in the family Ophiocordycipitaceae with high credible support by Bayesian inference (BI-PP = 100%), but showing the two has distant genetic distance (Figure 1).

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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