SMRT-based mitochondrial genome of the edible mushroom Morchella conica

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ABSTRACT

Morchella conica Pers. is a highly-prized mushroom for its edible and medical values. In this study, we determined the complete mitochondrial genome of M. conica combining both PacBio and Illumina sequencing technologies. The complete mitochondrial genome is 280,763 bp in length with a GC content of 39.88%. We identified a total of 14 core conserved protein-coding genes, 127 non-conserved open reading frames (ncORFs) and 30 tRNA genes in the M. conica mitogenome. However, no large or small rRNA subunits (rnl or rns) were identified in this mitogenome. In addition, we detected two mitochondrial RNase P (rnpB) genes and one ribosomal protein genes (rps3). Phylogenetic analysis was performed among M. conica and 18 other representative fungi from Ascomycota, Basidiomycota and Mucoromycota. Our results showed that M. conica was most closely related to M. importuna. The availability of the M. conica mitochondrial genome will form the basis of genetic breeding program and enhance our understanding of the evolution of this species.

Wild mushrooms have increasingly become an important part of human diet for centuries owing to its pleasant taste and nutritional value (Kalac 2009), among which morels were the most highly-prized for their immense economic and scientific values, widely consumed as food and medicine (Elmastas et al. 2007; Genççelep et al. 2009; Wong and Chye 2009). Morchella conica Pers. is an edible mushroom belonging to the Ascomycota phylum (Masaphy and Zabari 2013). However, large-scale cultivation of M. conica has not been successful, and excessive harvesting without replenishment has led to a reduced effective population size, resulting in a global shortage and soaring market prices (Turkoglu et al. 2009). The whole mitogenome sequence data reported here has been deposited in the Genome Warehouse in National Genomics Data Center (BIG Data Center Members 2020), Beijing Institute of Genomics (China National Center for Bioinformation), the Chinese Academy of Sciences, under accession number GWHANVR01000000 that is publicly accessible at https://bigd.big.ac.cn/gwh.

The mitogenome of M. conica was 280,763 bp in length with a GC content of 39.88%. Fourteen conserved protein-coding genes encoded 3 ATP synthases (atp6, apt8 and apt9), 3 cytochrome oxidases (cox1, cox2 and cox3), apocytochrome b (cob) and 7 subunits of NAD dehydrogenase (nad1, nad2, nad3, nad4, nad5, nad6 and nad4L). Two mitochondrial RNase P (rnpB) genes and one ribosomal protein genes (rps3) were identified in the mitochondrial genome. Besides, 127 non-conserved open reading frames (ncORFs) were identified to be uniformly dispersed in the M. conica mitogenome. We also detected 30 tRNA genes, but no rRNA genes were found in the genome.

To investigate the phylogenetic position of M. conica we aligned 14 conserved protein-coding genes using MAFFT v7.305 (Katoh and Standley 2013). A maximum likelihood (ML) tree was constructed using Mega 6.0 (Tamura et al. 2013) with 1,000 bootstrap replicates. Our results showed
that *M. conica* is closely related to *M. importuna* in the genus *Morchella* (Figure 1).

**Disclosure statement**

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

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**Data availability statement**

The data that support the findings of this study are openly available in the Genome Warehouse Database at [https://bigd.big.ac.cn/gwh](https://bigd.big.ac.cn/gwh), accession number GWHANVR01000000.

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![Figure 1. Maximum-likelihood (ML) phylogenetic tree of *M. conica* and related fungal species. The ML-tree is based on 14 conserved core mitochondrial proteins. Bootstraps values (1,000 replicates) are shown at the nodes. All the sequences are currently available in the GenBank database: *Botrytis cinerea* (KC832409), *Epidermophyton floccosum* (NC_007394), *Fusarium oxysporum* (NC_017930), *F. verticillioides* (NC_016687), *Lentinula edodes* (NC_018365), *M. importuna* (NC_045397), *Zymoseptoria tritici* (NC_010222), *Penicillium solitum* (NC_016187), *Phaeosphaeria nodorum* (NC_007947), *Phlebia radiata* (NC_020148), *Pyronema omphalodes* (NC_029745), *Rhizoctonia solani* (NC_021436), *Rhynchosporium agropyri* (NC_023125), *Sclerotinia borealis* (NC_025200), *Trametes cinngulata* (NC_013933), *Verticillium dahliae* (NC_008248) and *V. nonalfalai* (NC_029238). *Rhizopus oryzae* (NC_006836) was served as an outgroup.](image-url)