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The complete mitochondrial genome of the edible Basidiomycete mushroom *Thelephora ganbajun*

Pengfei Wang[a,b], Ying Zhang[a], Tao Sha[a] and Jianping Xu[a,c]

[a]State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, and Key Laboratory for Microbial Resources of the Ministry of Education, Yunnan University, Kunming, Yunnan, Peoples' Republic of China; [b]Department of Key Laboratory, The 2nd Affiliated Hospital of Kunming Medical University, Kunming, Yunnan, Peoples' Republic of China; [c]Department of Biology, McMaster University, Hamilton, Ontario, Canada

ABSTRACT

The complete mitochondrial genome of the edible fungus *Thelephora ganbajun* was determined using Illumina sequencing. This mitogenome is a circular molecule of 52,857 bp in length with a GC content of 25.73%. Gene prediction showed that the mitogenome codes 28 tRNAs, 2 pseudo-tRNAs, and 21 known and 7 hypothetical proteins. The evolutionary relationships between *Th. ganbajun* and other representative species based on the mitogenome are consistent with those based on nuclear genes. The mitogenome information of *Th. ganbajun* should contribute to our understanding of the diversity and evolution of Thelephorales.

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Thelephora species are basidiomycetes and ectomycorrhizal (ECM) fungi (Tedersoo et al. 2014). Members of this genus are distributed globally, contributing significantly to plant health and ecosystem stability (Kõljalg 1995; Martini & Hentic 2005; Yorou & Agerer 2008). In Yunnan province of China, *Thelephora ganbajun* is among the best-known *Thelephora* species, distributes primarily in pine forests and has been heavily harvested as a food delicacy (Zang 1986, 1987; Zhang & Yang 2013). While the nuclear genetic diversity and bioactive compounds of Th. ganbajun have been investigated (Lin & Ji-Kai 2001; Sha et al. 2008; Yang et al. 2004), little is known about its mitochondrial genome. Here we report the complete mitogenome sequence of Th. ganbajun (KY245891) and provide a phylogenetic analysis of its relationships with several representative taxa based on concatenated mitochondrial protein-coding genes.

The mitogenome was extracted from the whole genome sequence of a pure culture of strain P2 (collected in Yunnan province) using the Illumina HiSeq-1TB platform. This strain has been deposited in State Key Laboratory for Conservation and Utilization of Bio-Resources at Yunnan University. To obtain the mitogenome, each fastq file was QC filtered and subsequently assembled using Velvet (Zerbino & Birney 2008). The resulting assembly was used to create a long mate-pair library with insert 3000 ± 300 bp which was further assembled with the original Illumina library using AllPathsLG (Gnerre et al. 2011), to produce a 176.8 × coverage main assembly containing 3 scaffolds. The gaps were filled by separate PCR and sequencing with primers on regions flanking the gaps, resulting in one circular mitochondrial genome. Annotation was performed using MFannot (http://megasun.bch.umontreal.ca/cgi-bin/mfannot/mfannotInterface.pl) and the tRNAs and rRNAs were confirmed using RNAweasel (www.megasun.bch.umontreal.ca/RNAweasel/) and tRNAscan-SE (http://lowelab.ucsc.edu/tRNAscan-SE/) (Schattner et al. 2005). The general representation of the circular mitochondrial genome and the GC skew were prepared using the DNAPlotter software (Carver et al. 2009). The completely annotated mitogenome sequence is available in GenBank (accession KY245891).

The assembled mitochondrial genome was 52,857 bp in length with a GC content of 25.73%, coding for 28 tRNAs, 2 pseudo-tRNAs, 21 known proteins (including one pseudo gene and two overlapped polB2 genes), and 7 hypothetical proteins (or ORFs). The 28 tRNA genes covered 18 standard amino acids but without tRNA genes for Cysteine and Glutamic acid. Introns were found in three genes: nrDNA-LSU (2 group I A introns and 2 group I B introns), NAD5 (1 group I B intron) and COX1 (1 group I A intron and 1 group I B intron). Most introns have an ORF either of unknown function or code for a homing endonuclease.

Our mitogenome is the first submitted Thelephorales mitogenome in the GenBank database. Based on the concatenated protein sequences, our analyses revealed that *Th. ganbajun* was a member of Agaricomycotina and closely related to Polyporales and Russulales (Figure 1), consistent

CONTACT Jianping jpxu@mcmaster.ca Department of Biology, McMaster University, Hamilton, Ontario, L8S 4K1, Canada

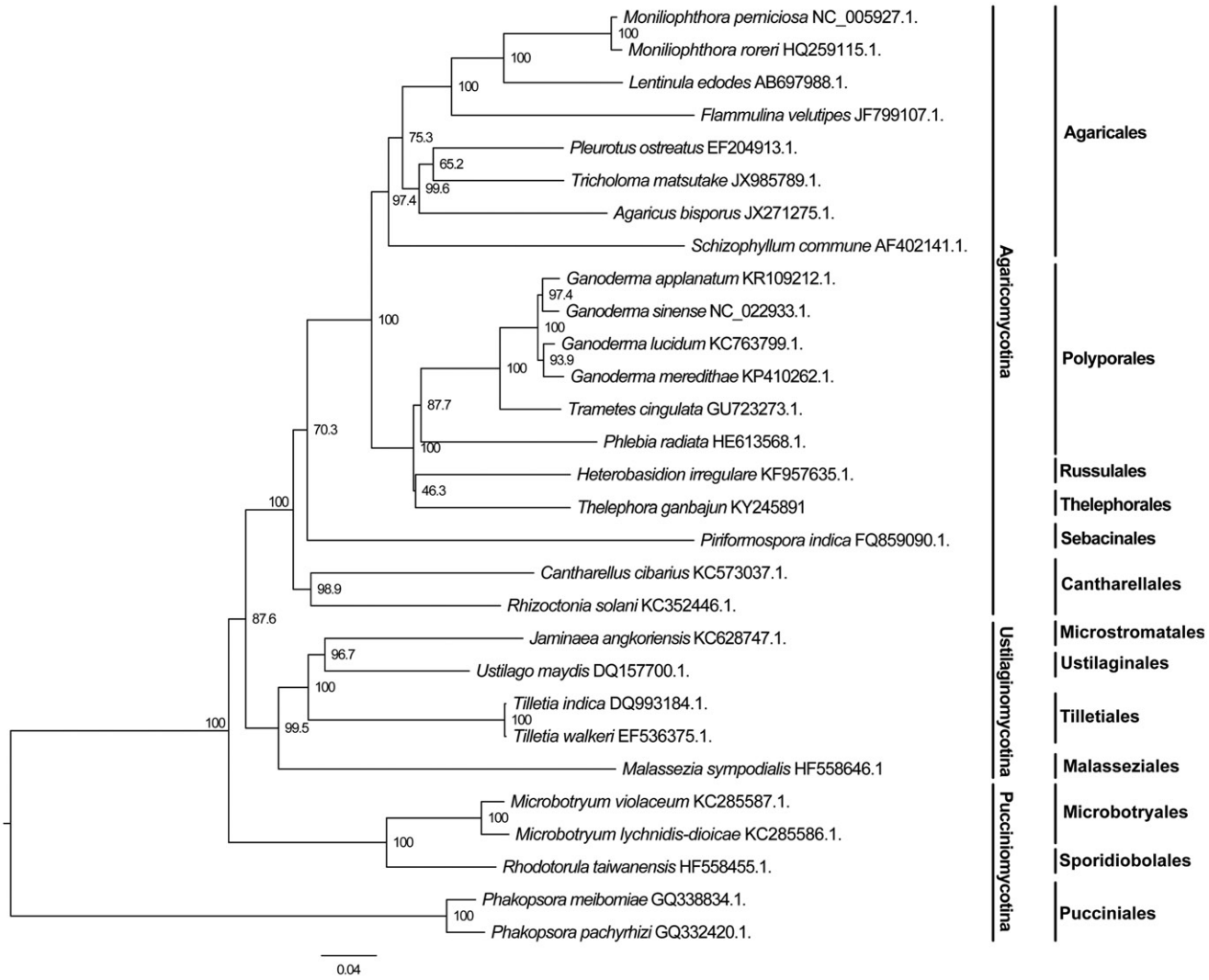

Figure 1. Phylogenetic analysis of 19 species of Agaricomycotina constructed using the Neighbour-Joining method as implemented in MEGA7.0 (Kumar et al. 2016) based on concatenated amino acid sequences of 14 mitochondrial protein-coding genes. The following 14 mitochondrial protein-coding genes were concatenated: atp6, atp8, atp9, cytb, cox1, cox2, cox3, nad1, nad2, nad3, nad4, nad4L, nad5 and nad6. The concatenated amino acid sequences were aligned using Clustal X (Thompson et al. 1997). The percentages of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) were shown next to the branches.

with the results obtained based on nuclear genes (Binder & Hibbett 2002; Garcia-Sandoval et al. 2011; Hibbett et al. 2007).

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the manuscript.

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