

The complete mitochondrial genome of the widely cultivated edible fungus *Lentinula edodes*

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ABSTRACT

The complete mitochondrial genome of the widely cultivated edible fungus *Lentinula edodes* was determined using the next-generation sequencing technology. The circular molecule is 116,819 bp in length with a GC content of 30.75%. Conserved genes including 13 putative protein-coding genes and 24 tRNAs were located on the same strand. We detected 14 introns invading 4 genes, including *cob*, *cox1*, *nad1*, and *nad5*. The phylogenetic analysis confirmed that *L. edodes* was a member of Agaricales. This mitochondrial genome may open new avenues for understanding the phylogeny and evolution of Omphalotaceae and Agaricales.

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The mushroom *Lentinula edodes* (Berk.) Pegler, named as Xianggu in China, is one of the most important and popular edible mushrooms all over the world, especially in East Asia (Chang 1999). It was reported that the cultivation of *L. edodes* was originated from China, and spread to Japan and other Far East Asian countries (Chang 1999). Several studies have focused on genetic diversities and relationships between strains originated from different regions (Hibbett & Donoghue 1996; Gong et al. 2016, Li et al. 2008). Here, a complete mitogenome of wild *L. edodes* in China was reported, which might provide new insights into genetic structure and differentiation of this fungus.

The monokaryon strain of wild *L. edodes* was isolated from dikaryon strain collected from Guizhou Province (China) using protoplast isolation method published previously (Chang et al. 1985). The living culture was deposited at the Guangdong Microbiology Culture Center (GDMCC 5.566). The whole-genome sequencing was conducted using Hiseq sequencing. A total of 7000 M high-quality reads was generated from 350 insert-size library and assembled using A5-miseq 2.0 (New South Wales, Australia, Coil et al. 2014). All the assembled contigs were mapped to the database of fungal mitogenomes to extract contigs belonging to the mitogenome of *L. edodes*. The completed mitogenome was annotated using MFannot (<http://megasun.bch.umontreal.ca/cgi-bin/mfannot/mfannotInterface.pl>). The phylogenetic analysis of 18 other species belonged to Agaricomycotina conducted based on the neighbour-joining

method using the software MEGA 7.0 (Tokyo, Japan, Kumar et al. 2016) (Figure 1).

The circus mitogenome was 116,819 bp in length with a GC content of 30.75%, which was one of the most largest mitogenome in Agaricales (135 kbp in *Agaricus bisporus*, Férandon et al. 2013). Gene prediction showed 37 putative protein-coding genes and 23 tRNAs were determined in the genome. However, no large or small rRNA subunits (*rnl* or *rns*) were detected in this genome. The 13 conserved protein-coding genes encoded the 6 subunits of NAD dehydrogenase (*nad1*, *nad3–6* and *nad4L* genes), 3 cytochrome oxidases (*cox1–3*), apocytochrome b (*cob*) and 3 ATP synthases (*atp6*, *atp8* and *atp9*). The set of 23 tRNA genes could code for all 20 standard amino acids. 11 group I introns, 1 group II and 3 unclassified intron were distributed in 4 genes *cob* (3 introns), *cox1* (5 introns), *nad1* (5 introns) and *nad5* (1 introns).

Phylogenetic relationship based on concatenated protein sequences confirmed that *L. edodes* was clustered together with *Moniliophthora roreri* and *M. perniciosa* belong to the family Marasmiaceae (Matheny et al. 2006), all of which were belong to Agaricales (Figure 1). At the class level, the evolutionarily relationship among Agaricales, Russulales, Polyporales, Cantharellales and Sebaciales was in agreement with the result of our other study on mitogenomes (Yang et al. 2016) (Figure 1). The mitogenome of *L. edodes* would contribute to the understanding of the phylogeny and evolution of Omphalotaceae and Agaricales.

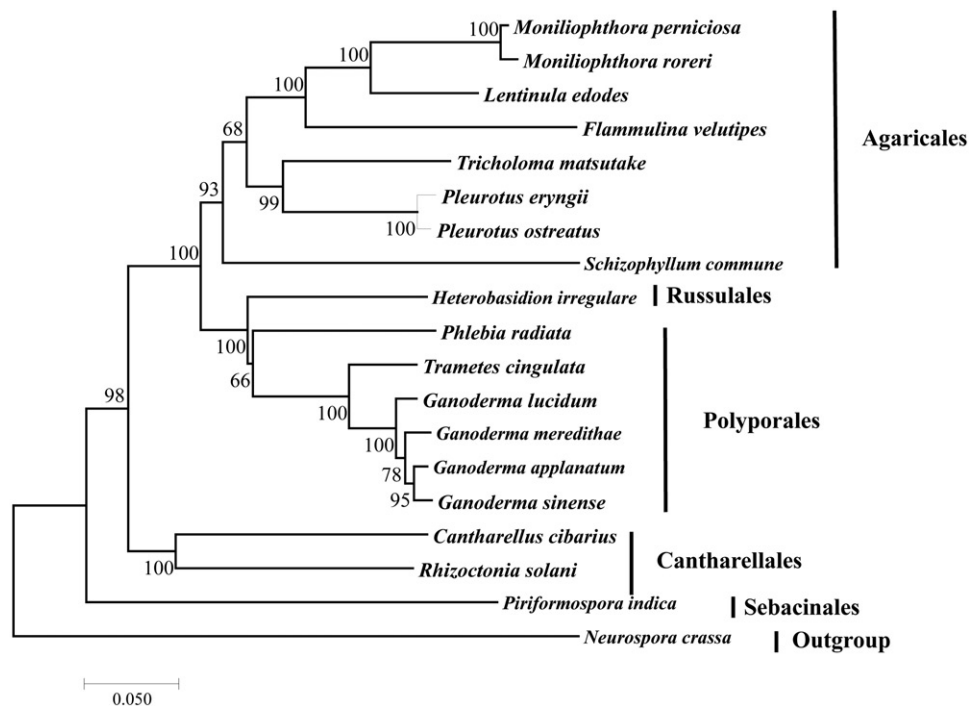


Figure 1. Phylogenetic analysis of 18 species of Agaricomycotina (including *L. edodes*) conducted based on the NJ method implemented in MEGA 7.0 (Kumar et al. 2016). A total of 11 amino acid sequences were used, including *atp8*, *atp9*, *cob*, *cox1*, *cox2*, *cox3*, *nad1*, *nad3*, *nad4L*, *nad5*, and *nad6*. The concatenated sequences were aligned using Clustal (Thompson et al. 2010). All the sequences could be currently available in the GenBank database: *Cantharellus cibarius* (NC_020368), *Flammulina velutipes* (NC_021373), *Ganoderma applanatum* (NC_027188), *Ganoderma lucidum* (NC_021750), *Ganoderma meredithae* (NC_026782), *Ganoderma sinense* (NC_022933), *Heterobasidion irregulare* (NC_024555), *Moniliophthora pernicioso* (NC_005927), *Moniliophthora roreri* (NC_015400), *Phlebia radiata* (NC_020148), *Pleurotus eryngii* (KX827267), *Pleurotus ostreatus* (NC_009905), *Rhizoctonia solani* (HF546977), *Schizophyllum commune* (NC_003049), *Serendipita indica* (FQ859090), *Trametes cingulata* (NC_013933), and *Tricholoma matsutake* (NC_028135). *Neurospora crassa* (NC_026614) was served as an outgroup. The percentages of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the manuscript. The sequence has been submitted to NCBI under the accession number of KY217797.

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