

RETRACTED ARTICLE: Characterization of the complete mitochondrial genome of an important edible fungus *Auricularia Polytricha*

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ABSTRACT

In the present study, we presented the complete mitochondrial genome of an important edible fungus *Auricularia auricula*. It has a total length of 76,297 bp, with the base composition as follows: A (38.3%), T (40.2%), C (10.2%), and G (11.3%). The mitogenome contains 37 protein-coding genes, 2 ribosomal RNA genes (rRNA), and 25 transfer RNA (tRNA) genes. The taxonomic status of the *A. polytricha* mitogenome was distant from other sequenced mitogenomes from *Agaricomycetes*.

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Auricularia polytricha is an edible jelly fungus, which is often used in Asian cooking, especially Chinese cuisine (Yan et al. 2004). *A. polytricha* is widely distributed in moist-deciduous and wet evergreen forests of the world (Du et al. 2007; Li et al. 2008). Modern pharmacological studies have shown that *A. polytricha* has the functions of antioxidation, anti-cancer, antinociceptive, and lowering blood pressure (Koyama et al. 2002; Song and Du, 2012; Sun et al. 2010). Species of the *Auricularia* genus have been used for several decades in Chinese traditional medicine. *Auricularia polytricha* is widely cultivated in Asia, such as China, Japan, and Korea. To the best of our knowledge, this is the first report on the complete mitochondrial genome of *A. polytricha*, which will provide a reference for understanding the phylogeny and evolution of this important species.

The specimen (*A. polytricha*) was isolated from the decaying stumps in Chengdu, Sichuan, China (106.73E; 30.48N) and was stored in Sichuan Academy of Agricultural Sciences (No. SLZAP6). The total genomic DNA of *A. polytricha* was extracted using Fungal DNA Kit D3390-00 (Omega Bio-Tek, Norcross, GA, USA) and purified through a Gel Extraction Kit (Omega Bio-Tek, Norcross, GA, USA). Purified DNA was stored in the sequencing company (BGI Tech, Shenzhen, China). Sequencing libraries were constructed with purified DNA following the instructions of NEBNext® Ultra™ II DNA Library Prep Kit (NEB, Beijing, China). Whole genomic sequencing was performed by the Illumina HiSeq 2500 Platform (Illumina, San Diego, CA). Multiple steps were used for quality control and de novo assembly of the mitogenome. The complete mitochondrial genome was assembled as implemented by SPAdes 3.9.0 (Bankevich et al. 2012). Gaps among contigs were filled by using MITObim V1.9 (Hahn et al. 2013).

The determined genome was annotated using the MAnnot tool (<http://megasun.bch.umontreal.ca/cgi-bin/mfanno/fannot.html#face.pl>), combined with manual corrections. tRNAs were annotated by tRNAscan-SE (Lowe and Eddy 1997).

The total length of *A. polytricha* circular mitogenome is 76,297 bp. This mitogenome was submitted to the GenBank database under accession No. MK388091. The circular mitogenome contains 37 protein-coding genes, 2 ribosomal RNA genes (*rns* and *rnl*), and 25 transfer RNA (tRNA) genes. The base composition of the genome is as follows: A (38.3%), T (40.2%), C (10.2%), and G (11.3%).

To validate the phylogenetic position of *A. polytricha*, we constructed phylogenetic trees of 26 closely related species from *Agaricomycetes*. Bayesian analysis (BI) was used to construct the phylogenetic trees with the 14 core protein-coding genes and 2 rRNA genes according to Qiang et al. 2018a, 2018b). As shown in the phylogenetic tree (Figure 1), the taxonomic status of the *A. polytricha* based on mitogenome was distant from other *Agaricomycetes* species with sequenced mitogenomes.

Disclosure statement

The authors have declared that no competing interests exist.

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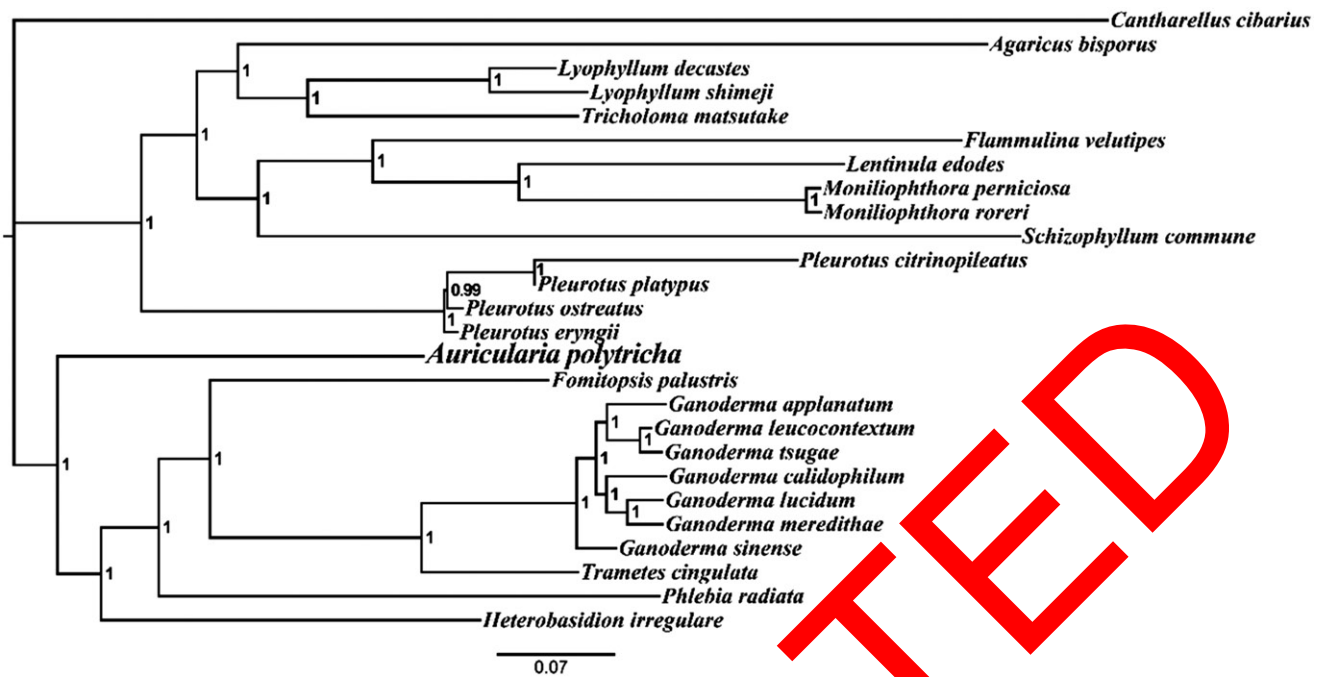


Figure 1. Molecular phylogenies of 26 species based on Bayesian inference analysis of the combined mitochondrial gene set (14 core protein-coding genes + two rRNA genes). Node support values are Bayesian posterior probabilities (BPP). Mitochondrial genome accession numbers used in this phylogeny analysis: *Agaricus bisporus* (JX271275), *Tricholoma matsutake* (JX985789), *Flammulina velutipes* (JF791107), *Lentinula edodes* (AB697988), *Moniliophthora perniciosa* (AY376688), *Moniliophthora roreri* (HQ259115), *Schizophyllum commune* (AF402141), *Pleurotus citrinopileatus* (MG011444), *Pleurotus platypus* (MG017445), *Pleurotus ostreatus* (EF204913), *Pleurotus eryngii* (KX827267), *Fomitopsis palustris* (AP017926), *Ganoderma applanatum* (KR101112), *Ganoderma lucidum* (KC763799), *Ganoderma meridithae* (KP410262), *Ganoderma sinense* (KF673550), *Trametes cingulata* (GU723273), *Phlebia radiata* (HF03568), *Heterobasidion irregulare* (KF957635), *Cantharellus cibarius* (KC573037), *Ganoderma tsugae* (MH252533), *Ganoderma leucocontextum* (MH252534), *Ganoderma calidophilum* (MH252535), *Lyophyllum decastes* (MH447974), *Lyophyllum shimeji* (MH447975).

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