The complete mitochondrial genome of the edible mushroom *Grifola frondosa*

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**ABSTRACT**

The culinary-medicinal mushroom *Grifola frondosa* is widely cultivated in East Asia. In this study, the complete mitochondrial genome of *G. frondosa* was determined using Illumina sequencing. The circular molecule was 197,486 bp in length with a content of 25.01% GC, which was one of the largest mitochondrial genomes in the order Polyporales. A total of 39 known genes encoding 13 common mitochondrial genes, 24 tRNA genes, 1 ribosomal protein s3 gene (rps3), and 1 DNA polymerase gene (dpo) were predicted in this genome. The phylogenetic analysis showed that *G. frondosa* clustered together with *Sparassis crispa*, *Laetiporus sulphureus*, *Wolfiporia cocos*, and *Taiwanofungus camphoratus*. The complete mitochondrial genome reported here may provide new insight into genetic information and evolution for further studies.

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the previous report (Justo et al. 2017). The mitochondrial genome of *G. frondosa* would contribute to the understanding of the phylogeny and evolution of Polyporales.

**Disclosure statement**

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

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**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov/](https://www.ncbi.nlm.nih.gov/) under the accession number MW324678. The associated BioProject, Biosample, and SRA of numbers are PRJNA703746, SAMN18022987, and SRR13759100, respectively. The strain used in this study was deposited at Guangdong Microbial Culture Collection Center (GDMCC, [http://www.gimcc.net/](http://www.gimcc.net/), gdmcc@gdim.cn) under the number GDMCC5.625.

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