

The complete mitochondrial genome of the edible mushroom *Pleurotus giganteus* (Agaricales, Pleurotus) and insights into its phylogeny

Zengliang Liu^a , Shengjin Wu^a , Xuefeng Chen^a, Wenlong Zhang^a, Shuangyun Zhou^b and Xiaoguo Wang^a

^aMicrobiology Research Institute, Guangxi Academy of Agricultural Sciences, Nanning, China; ^bHorticulture Research Institute, Guangxi Academy of Agricultural Sciences, Nanning, China

ABSTRACT

Pleurotus giganteus (Berk.) Karunarathna & K.D. Hyde 2011 is one of the largest edible mushrooms integrating medicinal value and edible value. The complete mitochondrial genome of the edible fungus *P. giganteus* was published in this paper. It was determined using Pacbio and Illumina sequencing. The circular molecule is 102,950 bp in length, consisting of 30 protein-coding genes (PCGs), two ribosomal RNA (rRNA) genes, and 24 transfer RNA (tRNA) genes. The base composition of the whole mitogenome is A (37.3%), T (37.7%), G (12.2%), and C (12.8%). The phylogenetic tree shows *P. giganteus* was the basal taxon in *Pleurotus* and closely related to *Pleurotus citrinopileatus* Singer 1990.

ARTICLE HISTORY

Received 31 March 2022
Accepted 18 June 2022

KEYWORDS

Pleurotus giganteus;
mitochondrial genome;
phylogenetic relationship

Pleurotus giganteus (Berk.) Karunarathna & K.D. Hyde 2011, previously reported as *Lentinus giganteus* or *Panus giganteus*, has been used as a culinary mushroom and is increasing in popularity for its medicinal properties and commercial prospects (Baskaran et al. 2017). *P. giganteus* has been recorded in Sri Lanka (Klomklung et al. 2012), Thailand (Klomklung et al. 2012), Laos (Phonemany et al. 2021), China (Bi et al. 1993; Phan et al. 2012), and Oceania (Bi et al. 1993). *P. giganteus* has high contents of magnesium, potassium, amino acids, iron, and calcium which may benefit human health (Phan et al. 2014, 2019). Furthermore, *P. giganteus* has been reported to be containing stimulation of neurite outgrowth (Phan et al. 2012), possessing liver protection properties (Wong et al. 2012), was a healthy dietary supplement for brain and cognitive health (Phan et al. 2013), and inhibition of growth of *Candida* species (Phan et al. 2013).

Mitochondria are presumed to be derived from bacteria through endosymbiosis (Muñoz-Gómez et al. 2017). The mitochondrial genome contributes to systemic evolution, population genetics, and taxonomy (Carpí et al. 2016; Ramos et al. 2018). However, no complete mitogenome is available to date for *P. giganteus*. Here, we report the complete mitogenome of *P. giganteus* using next-generation sequencing, which might provide new insights into genetic structure and differentiation of this species (Figure 1).

The specimen of this study was mushroom and no ethical issues are involved. The study has been granted an exemption from requiring ethical approval by the Committee on the Ethics of Microbiology Research Institute, Guangxi Academy of Agricultural Sciences, Nanning, China. The specimen used in this study was collected from artificial

cultivation in Nanning, Guangxi Province, China (108.24E, 22.84N) with the permission granted by Guangxi Academy of Agricultural Sciences, and it was stored in Guangxi Academy of Agricultural Sciences Herbarium (voucher specimen: MG-GX2020024, Zengliang Liu, zengguang201010@163.com). The specimen was identified as *P. giganteus* by morphology, internal transcribed spacer (ITS) sequence and small subunit ribosomal RNA (rRNA) (rns) sequence. The living culture was deposited at Institute of Microbiology, Guangxi Academy of Agricultural Sciences (no. WZDBX006, Zengliang Liu, zengguang201010@163.com). The mitochondrial genome of *P. giganteus* was obtained by Illumina sequencing technology (Novaseq 6000, San Diego, CA) and assembled in SPAdes v. 3.11.0 (Bankevich et al. 2012). The original annotation of mitochondrial genome was obtained from a sequencing laboratory: Huitong Biotechnology (Shenzhen, China). MITOS (<http://mitos.bioinf.uni-leipzig.de/index.py>) was used for mitochondrial genome annotation (Bernt et al. 2013).

The complete mitochondrial genome of this mushroom is a circular DNA of 102,950 bp in length with a GC content of 25.0% (GenBank: OM681506). The base composition of the *P. giganteus* mitochondrial genome is as follows: A (37.3%), T (37.7%), G (12.2%), and C (12.8%). The mitochondrial genome of *P. giganteus* contained 56 genes including 30 protein-coding genes (PCGs), two rRNA genes (rnl and rns), and 24 transfer RNA (tRNA) genes. The 30 PCGs encoded 14 conserved mitochondrial proteins (cox1-3, cob, nad1-6, nad4L, atp6, atp8, and atp9) and a ribosomal protein S3. There were 15 introns distributed in two PCGs, i.e. cob (three introns) and cox1 (12 introns).

CONTACT Shengjin Wu  gxwusj@126.com; Xuefeng Chen  Xuefeng767@126.com  Institute of Microbiology, Guangxi Academy of Agricultural Sciences, No. 174, Daxue East Road, Nanning, Guangxi 530007, China

© 2022 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

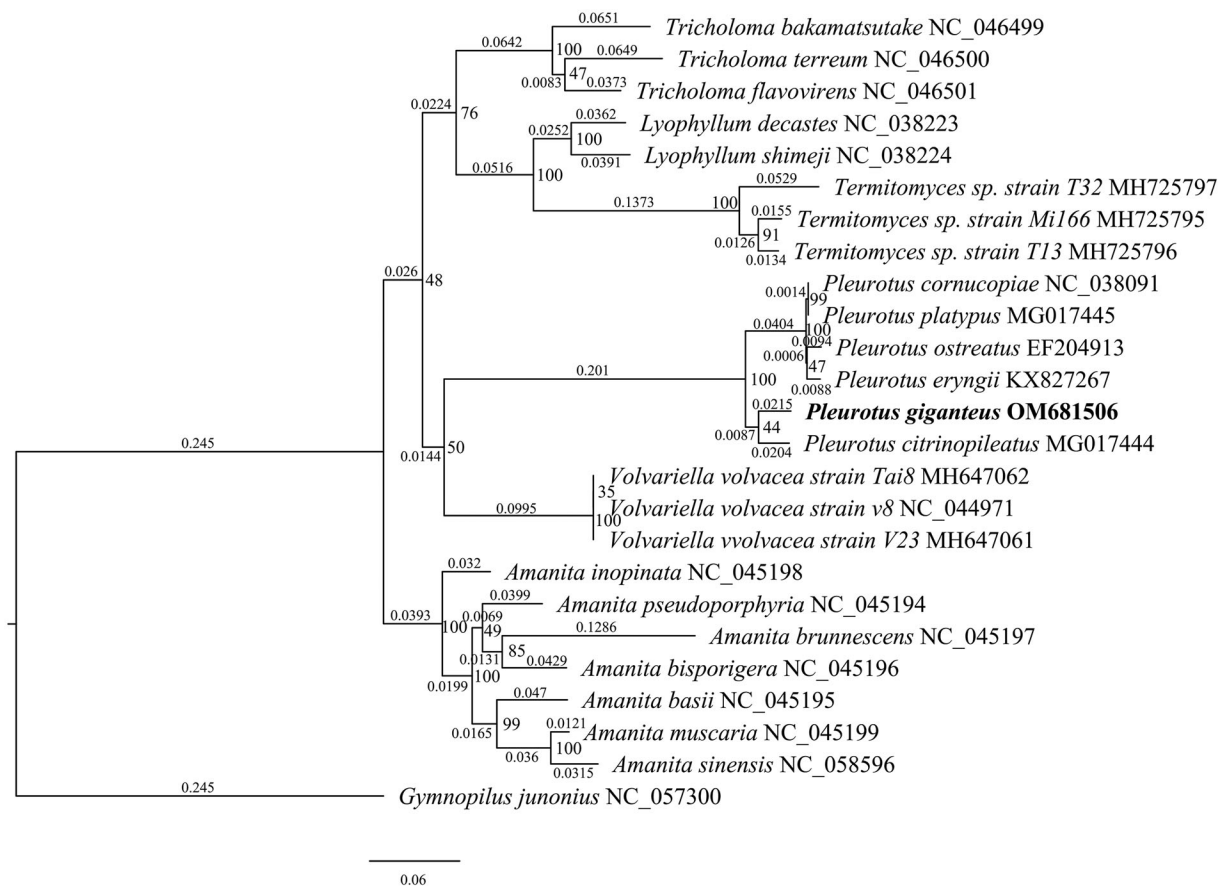


Figure 1. The ML phylogenetic tree of 24 species conducted based on the amino acid dataset of eight mitochondrial protein-coding genes, including *cox1*, *rps3*, *nad6*, *cob*, *atp9*, *cox3*, *nad4L*, and *nad5*.

We used OrthoFinder v2.3.14 (Emms and Kelly 2019) to select eight homologous single-copy PCGs in 24 species with *P. giganteus* from NCBI database, then we aligned them with *P. giganteus* by using muscle v3.8.1551 (Edgar 2004). The best substitution model was tested based on the Bayesian information criterion (BIC) by protest v3.4 (Darriba et al. 2011). The best-fitting model in the analysis was CpREV + I + G + F. Maximum-likelihood analysis was performed in RAxML v.8.2.12 (Stamatakis 2014) with 1000 rapid bootstrap analyses, followed by a search for the best-scoring tree in one single run. *Gymnopilus junonius* was used as outgroup. The analysis confirmed that *P. giganteus* was a member of *Pleurotus* and closely related to *Pleurotus citrinopileatus*. The complete mitochondrial genome sequence of *P. giganteus* will be helpful for further studies on population genetics, taxonomy, or resource protection.

Author contributions

Study conception and design: Zengliang Liu and Shengjin Wu; data collection: Xuefeng Chen; analysis and interpretation of results: Wenlong Zhang and Shuangyun Zhou; draft manuscript preparation: Zengliang Liu and Xiaoguo Wang; revising it critically for intellectual content: Xiaoguo Wang and Shengjin Wu. All authors reviewed the results and approved the final version of the manuscript. All authors agree to be accountable for all aspects of the work.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This study was supported by Guangxi Innovation Team of National Modern Agricultural Industrial System [Grant No. nycytxgxcxd-2021-07-02], Science and Technology Base and Talent Project of Guangxi [Grant No. Guike AA21196003], Experimental Station of Characteristic Crops in Guangxi Quanzhou County [Grant No. TS202115], and China Agriculture Research System [CARS-20].

ORCID

Zengliang Liu  <http://orcid.org/0000-0003-0217-2503>
Shengjin Wu  <http://orcid.org/0000-0003-2116-5878>

Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI (<https://www.ncbi.nlm.nih.gov/>) under the accession number OM681506. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA818472, SRR18426954, and SAMN26863501, respectively.

References

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, et al. 2012. SPAdes: a

- new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol.* 19(5):455–477.
- Baskaran A, Chua KH, Sabaratnam V, Ram MR, Kuppusamy UR. 2017. *Pleurotus giganteus* (Berk. Karun & Hyde), the giant oyster mushroom inhibits NO production in LPS/H₂O₂ stimulated RAW 264.7 cells via STAT 3 and COX-2 pathways. *BMC Complement Altern Med.* 17(1):1–10.
- Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. *Mol Phylogenet Evol.* 69(2): 313–319.
- Bi Z, Zheng G, Li T. 1993. The macrofungus flora of China's Guangdong Province. Hong Kong: The Chinese University Press.
- Carpi G, Kitchen A, Kim HL, Ratan A, Drautz-Moses DI, McGraw JJ, Kazimirova M, Rizzoli A, Schuster SC. 2016. Mitogenomes reveal diversity of the European *Lyme borreliosis* vector *Ixodes ricinus* in Italy. *Mol Phylogenet Evol.* 101:194–202.
- Darriba D, Taboada GL, Doallo R, Posada D. 2011. ProtTest 3: fast selection of best-fit models of protein evolution. *Bioinformatics.* 27(8): 1164–1165.
- Edgar RC. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.* 32(5):1792–1797.
- Emms DM, Kelly S. 2019. OrthoFinder: phylogenetic orthology inference for comparative genomics. *Genome Biol.* 20(1):238.
- Klomklung N, Karunarathna SC, Chukeatirote E, Hyde KD. 2012. Domestication of wild strain of *Pleurotus giganteus*. *Sydowia.* 64(1): 39–53.
- Muñoz-Gómez SA, Wideman JG, Roger AJ, Slamovits CH. 2017. The origin of mitochondrial Cristae from Alphaproteobacteria. *Mol Biol Evol.* 34(4):943–956.
- Phan CW, David P, Naidu M, Wong KH, Sabaratnam V. 2013. Neurite outgrowth stimulatory effects of culinary-medicinal mushrooms and their toxicity assessment using differentiating Neuro-2a and embryonic fibroblast BALB/3 T3. *BMC Complement Altern Med.* 13:261.
- Phan CW, David P, Tan YS, Naidu M, Wong KH, Kuppusamy UR, Sabaratnam V. 2014. Intrastrain comparison of the chemical composition and antioxidant activity of an edible mushroom, *Pleurotus giganteus*, and its potent neurotogenic properties. *Sci World J.* 2014(1):1–10.
- Phan CW, Wong WL, David P, Naidu M, Sabaratnam V. 2012. *Pleurotus giganteus* (Berk.) Karunarathna & K.D. Hyde: nutritional value and in vitro neurite outgrowth activity in rat pheochromocytoma cells. *BMC Complement Altern Med.* 12(1):102–112.
- Phan C-W, Wang J-K, Tan EY-Y, Tan Y-S, Sathiya Seelan JS, Cheah S-C, Vikineswary S. 2019. Giant oyster mushroom, *Pleurotus giganteus* (Agaricomycetes): current status of the cultivation methods, chemical composition, biological and health-promoting properties. *Food Rev Int.* 35(4):324–341.
- Phonemany M, Raspé O, Sysouphanthong P, Niego AG, Niego T, Thongklang N, Chuankid B, Hyde K. 2021. Two *Pleurotus* species (Pleurotaceae) from Lao People's Democratic Republic. *Chiang Mai J Sci.* 48(5):1224–1235.
- Ramos B, González-Acuña D, Loyola DE, Johnson WE, Parker PG, Massaro M, Dantas GPM, Miranda MD, Vianna JA. 2018. Landscape genomics: natural selection drives the evolution of mitogenome in penguins. *BMC Genomics.* 19(1):1–17.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.* 30(9): 1312–1313.
- Wong WL, Abdulla MA, Chua KH, Kuppusamy UR, Tan YS, Sabaratnam V. 2012. Hepatoprotective effects of *Panus giganteus* (Berk.) corner against thioacetamide- (TAA)-induced liver injury in rats. *Evid Based Complement Alternat Med.* 2012:170303.