

Characterization of the complete mitochondrial genome of *Peniophora lycii* (Russulales: Peniophoraceae) with its phylogenetic analysis

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ABSTRACT

Peniophora lycii is a resupinate lichen-like species distributed all over the world. In the present study, we sequenced and assembled the complete mitochondrial genome of *Peniophora lycii*. The size of the mitochondrial genome of *P. lycii* was 38,296 bp, with a GC content of 25.89%. Twenty protein-coding genes, 2 ribosomal RNA genes, and 24 transfer RNA genes were identified in the mitochondrial genome of *P. lycii*. Phylogenetic analysis based on combined mitochondrial gene dataset indicated that the mitochondrial genome of *P. lycii* exhibited a close relationship with that of *Heterobasidion irregulare*.

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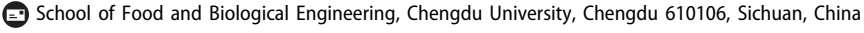
Mitochondrial genome;
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The species *Peniophora lycii* (Pers.) Hohn. & Litsch. 1907 belongs to the Peniophoraceae family of the Russulales order. *P. lycii* is a resupinate lichen-like species that usually colonizes dead branches of deciduous and coniferous trees all over the world (Pontoppidan et al. 2007; Glazunova et al. 2020). The Russulales is a well-known order that contained morphologically diverse mushrooms (Miller et al. 2006). Species from this order have diverse lifestyles, including saprotrophic, ectomycorrhizal, root-parasitic, and insect-symbiotic (Geml et al. 2010; Zhou and Dai 2013). The family Peniophoraceae is primarily saprotrophic fungi. Mitochondrial genome has been widely used to understand the phylogeny, life pattern evolution and genetics of fungal species (Li et al. 2020a, 2020c; Wang et al. 2020a; Wu et al. 2021). However, up to now, no complete mitochondrial genome from the genus *Peniophora* has been reported. The mitochondrial genome of *P. lycii* will promote the understanding of the phylogeny, origin, and taxonomy of this important fungal genus.

The specimen (*P. lycii*) was collected from Sichuan, China (101.23 E; 27.56 N). A specimen was deposited in Collection Center of Chengdu University under the voucher number Ply_s93. The complete mitochondrial genome of *P. lycii* was sequenced and *de novo* assembled according to previous described methods (Li et al. 2019b; Cheng et al. 2021). Briefly, the total genomic DNA of *P. lycii* was extracted using a Fungal DNA Kit (D3390-00, Omega Bio-Tek, Norcross, GA). The extracted genomic DNA was purified using a Gel Extraction Kit (Omega Bio-Tek, Norcross, GA). We stored the purified DNA in Leshan Vocational and Technical College (No. DNA_Ply_s93). Sequencing libraries were constructed for sequencing using a NEBNext® Ultra™ II DNA Library Prep Kit

(NEB, Beijing, China). Whole genomic sequencing (WGS) of *P. lycii* was conducted using Illumina HiSeq 2500 Platform (Illumina, San Diego, CA). Illumina PCR adapter reads and low-quality reads from the paired-end were filtered using custom scripts. About 1.5% of low quality sequences were excluded from downstream analysis. The mitochondrial genome of *P. lycii* was assembled by NOVOPlasty v4.3.1 (Dierckxsens et al. 2017) using the *rns* gene of *Lactarius hatsudake* as the seed sequence (Li et al. 2019a). The average mitochondrial sequence coverage was 1357 ×. We annotated the complete mitochondrial genome of *P. lycii* according to previous described methods (Wang et al. 2020b; Ye et al. 2020). Briefly, the protein-coding genes, rRNA genes, tRNA genes, and introns of the *P. lycii* mitogenome were annotated using MITOS (Bernt et al. 2013) and MFannot (Valach et al. 2014), both based on the genetic code 4. The tRNA genes in the *P. lycii* mitochondrial genome were also predicted using tRNAscan-SE v1.3.1 (Lowe and Chan 2016). Different annotation results were verified and manual corrected according to the annotations of close related mitogenomes (Li et al. 2018).

The complete mitochondrial genome of *P. lycii* is 38,296 bp in length, which is the smallest mitochondrial genome in *Russulales* to date (Li et al. 2018, 2019a). The base composition of the *P. lycii* mitochondrial genome is as follows: A (36.80%), T (37.31%), G (12.87%) and C (13.01%). The complete mitochondrial genome of *P. lycii* contains 20 protein-coding genes, 2 ribosomal RNA genes (*rns* and *rnl*), and 24 transfer RNA genes. No intron was detected in the *P. lycii* mitochondrial genome (Zhang and Zhang 2019). We constructed a phylogenetic tree for 13 Russulales species to investigate the phylogenetic status of *P. lycii*. Bayesian

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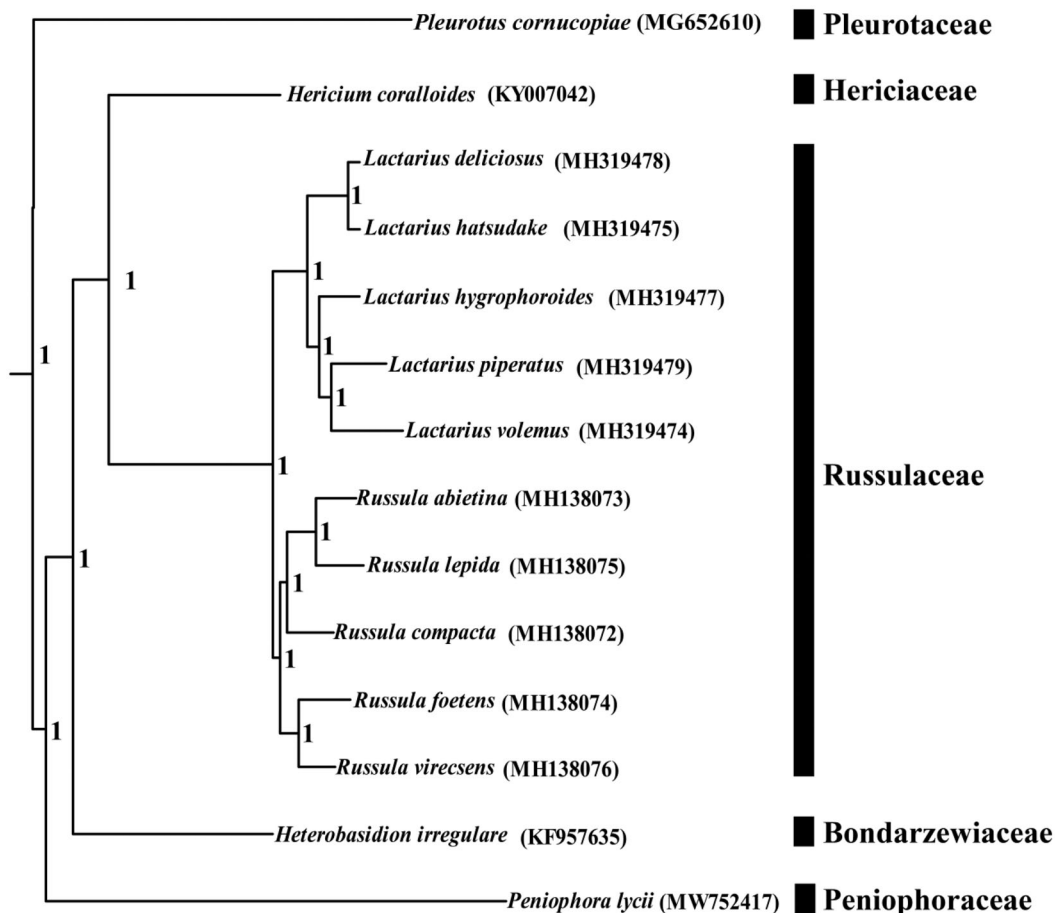


Figure 1. Bayesian phylogenetic analysis of 13 Russulales species. *Pleurotus cornucopiae* from the order Agaricales was set as outgroup. Accession numbers of mitochondrial genomes used in the phylogenetic analysis are listed in brackets.

analysis (BI) method was used to construct phylogenetic tree based on the combined 14 core protein-coding genes and 2 rRNA genes of mitochondrial genomes (*atp6*, *atp8*, *atp9*, *cob*, *cox1*, *cox2*, *cox3*, *nad1*, *nad2*, *nad3*, *nad4*, *nad4L*, *nad5*, *nad6*, *rns*, and *rnl*) according to previous described methods (Li et al. 2019c; 2020b; 2021b). First, we aligned individual protein-coding genes of mitochondrial genomes using MAFFT v7.037 (Kato et al. 2019), and then we concatenated these alignments into a combined gene dataset using SequenceMatrix v1.7.8 (Vaidya et al. 2011). Potential phylogenetic conflicts between different genes were detected by a partition homogeneity test (Li et al. 2021a); PartitionFinder 2.1.1 (Lanfear et al. 2017) was used to determine best-fit models of evolution and partitioning schemes. MrBayes v3.2.0 (Ronquist et al. 2012) was used to perform the BI analysis. *Pleurotus cornucopiae* from the order Agaricales was set as outgroup (Xu et al. 2018). As shown in the phylogenetic tree (Figure 1), the mitochondrial genome of *P. lycii* exhibited a close relationship with that of *Heterobasidion irregulare* (Himmelstrand et al. 2014).

Disclosure statement

The authors have declared that no competing interests exist.

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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/> under the accession no. MW752417. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA724896, SRR14320041, and SAMN18864199, respectively.

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