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The complete mitochondrial genome of the Basidiomycete fungus
Pleurotus cornucopiae (Paulet) Rolland

Li-Ming Xu, Damien Daniel Hinsinger and Guo-Feng Jiang

The genus Pleurotus, belonging to the family Pleurotaceae (Agaricales, Agaricomycetes, Basidiomycota), is one of the most diverse group of cultivated mushrooms in the world. The Pleurotus species establish a wide range of interactions with other organisms, and are efficient bioconverters of lignocellulosic residues into human food (Tsuneda and Thorn 1995; Philippoussis 2009). The biodiversity of Pleurotus remains highly investigated and recently, molecular studies have increase our knowledge about intra and inter-specific heterogeneity of the genus Pleurotus using both ribosomal and mitochondrial DNA (Li and Yao 2004; Wang et al. 2008; Yang et al. 2016; Chaudhary and John 2017). The edible fungus Pleurotus cornucopiae is emerging as an important species in the genus, with isolation of medicinal metabolites from the fruiting body (Wang et al. 2012). The genetic diversity and population structure of P. cornucopiae is well known (Iracabal and Labarere 1994; Zervakis et al. 1994; Shnyreva et al. 1996; Zhang et al. 2007; Zhou et al. 2009; Adebayo et al. 2016); however, no complete mitogenome is available to date for the species. Here, we report the complete mitogenome of P. cornucopiae (GenBank accession MG652610) to provide new genetic resources and performed a phylogenetic analysis of related taxa of this species.

The strain SWS_15 of Pleurotus cornucopiae is maintained in the Biology Institute, Guangxi Academy of Sciences (Nanning, Guangxi, PR China). Total genomic DNA was extracted as previously described (Xu et al. 2017). Library construction and sequencing were processed by Novogene (Beijing, China), according to the Illumina HiSeqX-ten manufacturer instructions (Illumina, San Diego, CA). The mitogenome of Pleurotus cornucopiae was de novo assembled using ORG.Asm v0.2.05 (https://pythonhosted.org/ORG.asm/) followed by manual curation in Geneious R9 v9.1.6 (Biomatters Ltd, Auckland, New Zealand) as described previously (Hinsinger and Strijk 2016; Jiang et al. 2016; Xu et al. 2017). Genome annotation and phylogenetic analysis were performed with DOGMA (http://dogma.ccbb.utexas.edu/index.html) and Phyml 3.1 (Guindon et al. 2010), respectively. Maximum-likelihood (ML) tree was constructed including 10 available mitogenomes of Agaricales and Heterobasidion irregulare as an outgroup (Figure 1).

The complete mitogenome of Pleurotus cornucopiae was 72,134 bp in length with a GC content of 26.7%. The mitogenome contained 14 conserved protein coding genes, 2 rRNA genes (rnl and rns), ribosomal protein gene rps3 and 24 tRNA genes. Pleurotus cornucopiae has a similar gene content and gene order of the mitogenome as P. ostreatus and P. eryngii. A phylogenetic analysis based on complete mitogenome in related fungi showed that P. cornucopiae is a member of the order Agaricales, forming a clade with P. ostreatus and P. eryngii, with P. ostreatus as a sister taxa. The mitochondrial genome sequence of P. cornucopiae appeared a promising tool for further studies of the taxonomy and evolution of Pleurotaceae and Agaricales.
result based on ITS data (Shnyreva and Shnyreva 2015; He et al. 2016). The complete mitochondrial genome of P. cornucopiae provides the community a useful bioresource that will help to delineate taxonomic units in Pleurotus, and will be of interest for further applied researches by selecting the most suitable species for biotechnological and nutritional interest.

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Disclosure statement

The authors report no conflicts of interest.

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ORCID

Guo-Feng Jiang http://orcid.org/0000-0002-3221-8608

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Figure 1. ML phylogenetic tree of the 10 available mitogenomes of Agaricales in GenBank, plus the mitogenome of Pleurotus cornucopiae. The tree is rooted with Heterobasidion irregularare. Bootstraps values (1000 replicates) are shown at the nodes. Scale in substitution per site.

