

Characterization of the complete mitochondrial genome of biocontrol yeast *Sporobolomyces* sp. (Sporidiobolales: Sporidiobolaceae) with phylogenetic analysis

Jingwei Huang^{a,b}, Huijuan Qu^c and Xueshan Shen^c

^aCollege of Medicine (School of Nursing), Chengdu University, Chengdu, P.R. China; ^bKey Laboratory of Coarse Cereal Processing, Ministry of Agriculture and Rural Affairs, Chengdu University, Chengdu, P.R. China; ^cSichuan Academy of Agricultural Sciences, Chengdu, P.R. China

ABSTRACT

In this study, we obtained the complete mitochondrial genome of *Sporobolomyces* sp. using next-generation sequencing. The complete mitochondrial genome of *Sporobolomyces* sp. contained 15 protein-coding genes (PCG), two ribosomal RNA (rRNA) genes, and 25 transfer RNA (tRNA) genes. The total length of the *Sporobolomyces* sp. mitochondrial genome is 26,430 bp, and the GC content of the mitochondrial genome is 39.32%. Phylogenetic analysis based on combined mitochondrial gene dataset indicated that the mitochondrial genome of *Sporobolomyces* sp. exhibited a close relationship with that of *Rhodotorula mucilaginosa*.

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Yeast; mitochondrial genome; phylogenetic analysis; evolution

The genus *Sporobolomyces* is a group of ballistoconidium-forming yeast. Dozens of species have been described in this genus (Sato and Makimura 2008; Lorenzini et al. 2019). *Sporobolomyces* species are distributed in various habitats, such as on plant phylloides, on the surface area of soils, and also in the fermentation system (Barahona et al. 2016; Arrigoni et al. 2018; Li, Yuan, et al. 2020). Limited morphological characteristics make it difficult to identify *Sporobolomyces* species accurately only by morphology (Hamamoto and Nakase 2000; Barahona et al. 2016; Lorenzini et al. 2019). Mitochondrial genome has been widely used in the phylogenetic analysis of species (Wang et al. 2020; Li, He, et al. 2020). However, up to now, no mitochondrial genome from the genus *Sporobolomyces* has been reported. The mitochondrial genome of *Sporobolomyces* sp. will promote the understanding of the phylogeny, evolution, and taxonomy of this important yeast.

The specimen (*Sporobolomyces* sp.) was collected from Jilin, China (129.32 E; 42.53 N). The specimen was stored in the Culture Collection Center of Chengdu University (No. Spo_ns1). The complete mitochondrial genome of *Sporobolomyces* sp. was sequenced and assembled according to previously described methods (Li, Liao, et al. 2018; Li, Xiang, et al. 2019; Wang et al. 2020). Briefly, the total genomic DNA of *Sporobolomyces* sp. was extracted using a Fungal DNA Kit D3390-00 (Omega Bio-Tek, Norcross, GA, USA). The extracted genomic DNA was purified using a Gel Extraction Kit (Omega Bio-Tek, Norcross, GA, USA). The purified DNA was stored in Chengdu University (No. DNA_Spo_ns1). We constructed sequencing libraries with the

purified genomic DNA using a NEBNext[®] Ultra[™] II DNA Library Prep Kit (NEB, Beijing, China). Whole genomic sequencing (WGS) of *Sporobolomyces* sp. was conducted using the Illumina HiSeq 2500 Platform (Illumina, San Diego, CA). We *de novo* assembled the mitochondrial genome of *Sporobolomyces* sp. using SPAdes 3.9.0 (Bankevich et al. 2012; Li, Ren, et al. 2020). The complete mitochondrial genome of *Sporobolomyces* sp. was annotated according to previously described methods (Li, Chen, et al. 2018; Li, Wang, et al. 2018).

We found the complete mitochondrial genome of *Sporobolomyces* sp. is 26,430 bp in length, with the base composition as follows: A (30.82%), T (29.84%), G (20.35%), and C (18.97%). The complete mitochondrial genome of *Sporobolomyces* sp. contains 15 protein-coding genes, two ribosomal RNA genes (*rns* and *rnl*), and 25 transfer RNA (tRNA) genes. To investigate the phylogenetic positions of *Sporobolomyces* sp., we constructed a phylogenetic tree for 18 Basidiomycota species. *Rhizopogon salebrosus* from the Boletales order was set as the outgroup (Li, Ren, et al. 2019). The phylogenetic tree was constructed using the Bayesian analysis (BI) method based on the combined 14 core protein-coding genes according to previously described methods (Li, Wang, Jin, Chen, Xiong, Li, Liu, et al. 2019; Li, Wang, Jin, Chen, Xiong, Li, Zhao, et al. 2019; Li, Yang, et al. 2020). As shown in the phylogenetic tree (Figure 1), the mitochondrial genome of *Sporobolomyces* sp. exhibited a close relationship with that of *Rhodotorula mucilaginosa* (Gan et al. 2017).

CONTACT Xueshan Shen  shenxueshan@126.com  Sichuan Academy of Agricultural Sciences, 20# Jingjusi Rd, Chengdu 610066 Sichuan, China

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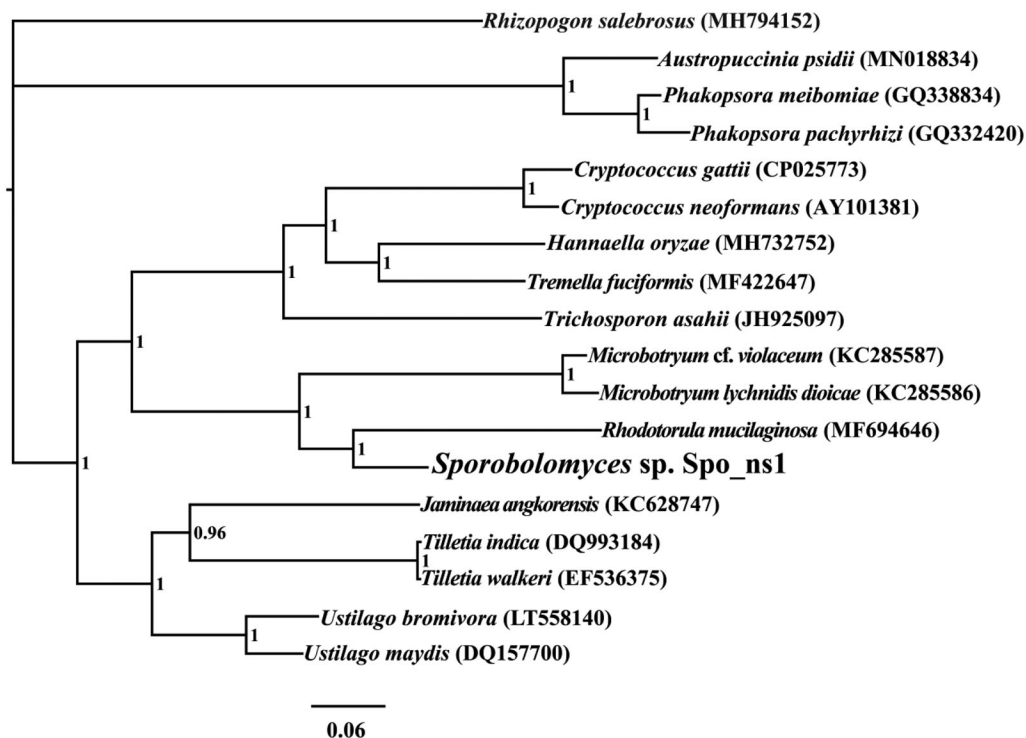


Figure 1. Bayesian phylogenetic analysis of 18 species based on the combined 14 core protein-coding genes. Accession numbers of mitochondrial sequences used in the phylogenetic analysis are listed in brackets after species.

Disclosure statement

The authors have declared that no competing interests exist.

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Data availability statement

This mitogenome of *Sporobolomyces* sp. was submitted to GenBank under the accession number of MT663151. (<https://www.ncbi.nlm.nih.gov/nuccore/MT663151>).

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