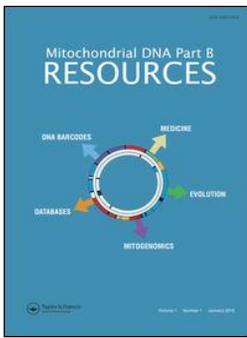


The complete mitochondrial genome sequence of the edible mushroom *Stropharia rugosoannulata* (Strophariaceae, Basidiomycota)

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The complete mitochondrial genome sequence of the edible mushroom *Stropharia rugosoannulata* (Strophariaceae, Basidiomycota)

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ABSTRACT

Stropharia rugosoannulata (Strophariaceae, Basidiomycota) is an edible mushroom distributed in northern temperate zones throughout the world. In this study, the complete mitochondrial genome sequence of *S. rugosoannulata* was determined. This mitochondrial genome is 60,551 bp in length with a GC content of 31.0% and encodes 14 conserved proteins, 2 ribosomal RNAs, 29 transfer RNAs, and 12 further ORFs. Phylogenetic relationships based on the mitochondrial genome between *S. rugosoannulata* and other basidiomycetes are inconsistent with those based on nuclear genes. This is the first report of the mitochondrial genome of mushrooms belonging to the family *Strophariaceae*.

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Stropharia rugosoannulata;
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Stropharia rugosoannulata is an edible mushroom belonging to the family *Strophariaceae*, which is distributed in northern temperate areas. Several studies on functional-food constituents of this mushroom, such as polysaccharides (He et al. 2012) and low-molecular weight compounds (Wu et al. 2011; Wu et al. 2012; Wu et al. 2013a; Wu et al. 2013b) have been reported. Recently, genome sequences of 90 mushrooms including *S. rugosoannulata* were determined and their phylogenetic relationships were analyzed based on all single-copy orthologous genes (Li et al. 2018). Although the mitochondrial genome has been widely used for fungal studies on molecular evolution and phylogenetics (Bullerwell and Lang 2005), little is known about the mitochondrial genome of the family *Strophariaceae* to which *S. rugosoannulata* belongs. In the present study, we determined the complete mitochondrial genome sequence of *S. rugosoannulata* and analyze its phylogenetic relationship with other basidiomycetes based on the mitochondrial genome.

The genomic DNA library of *S. rugosoannulata* strain NBRC 31871 (collected in Shiga, Japan) was constructed using the TruSeq DNA PCR-Free Sample Preparation Kit and sequenced for 301-bp paired-end reads using the MiSeq (Illumina, San Diego, CA). The raw sequence reads were cleaned up using Trimmomatic (Bolger et al. 2014) by trimming adapter sequences and low-quality ends (quality score, <10), and the reads derived from mitochondrial genome were extracted using khmer (Crusoe et al. 2015; Bankevich et al. 2012) with a high k-mer coverage (>100). The resultant 300,102 pair

reads totaling 168.5 Mb were assembled using SPAdes ver. 3.12.0 (Bankevich et al. 2012). The complete mitochondrial genome of this mushroom is a circular DNA of 60,551 bp in length with a GC content of 31.0% (DDBJ/EMBL/GenBank: AP019006).

Gene prediction and annotation of the mitochondrial genome of *S. rugosoannulata* was performed using the MFannot tool (<http://megasun.bch.umontreal.ca/cgi-bin/mfannot/mfannotInterface.pl>) and manually curated. Ribosomal RNA genes were predicted by aligning the mitochondrial genome to that of *Coprinopsis cinerea* (NW_003307477.1) using Mauve (Darling et al. 2004). The mitochondrial genome of *S. rugosoannulata* contained 57 genes including 26 protein-coding genes, two ribosomal RNA genes (*rnl* and *rns*), and 29 tRNA genes (for all 20 standard amino acids). The 26 protein-coding genes encoded 14 conserved mitochondrial proteins (*cox1–3*, *cob*, *nad1–6*, *nad4L*, *atp6*, *atp8*, and *atp9*), 9 endonucleases, a ribosomal protein S3, DNA polymerase, and hypothetical protein.

Phylogenetic analysis based on 9 proteins (*cox1–3*, *cob*, *nad1–3*, and *nad5–6*) conserved in 29 basidiomycetes and 2 ascomycetes was performed using Geneious version 9.1 (Kearse et al. 2012), as reported previously (Tanaka et al. 2017). The concatenated amino acid sequences were aligned using the MAFFT (Katoh et al. 2002) and the phylogenetic tree was constructed by the neighbor-joining method (Saitou and Nei 1987). Phylogenetic analysis based on the mitochondrial genome showed that *S. rugosoannulata* was closely

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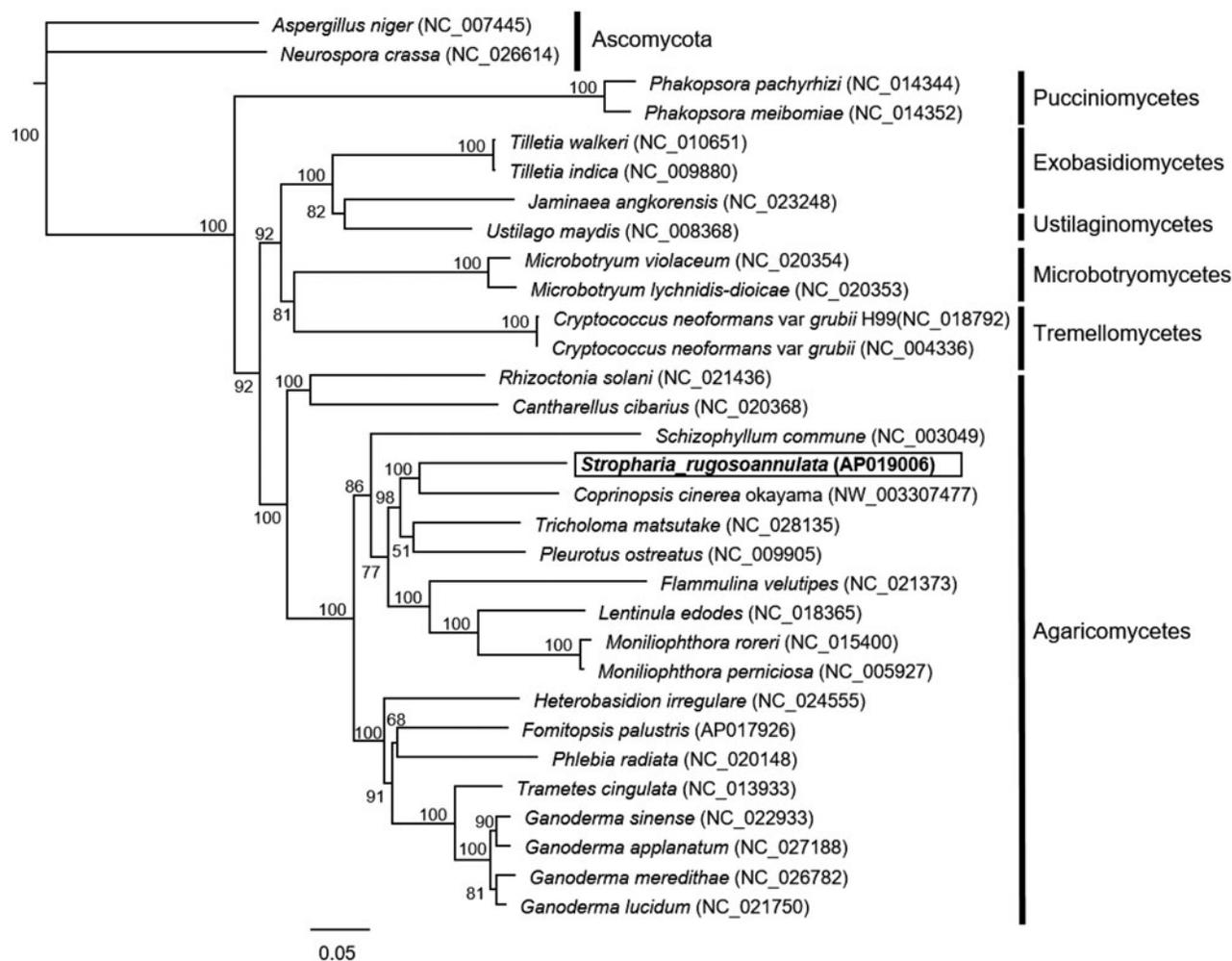


Figure 1. Molecular phylogenetic analysis of 29 basidiomycetes and 2 ascomycetes. The phylogenetic tree was constructed by the neighbor-joining method based on concatenated amino acid sequences of 9 mitochondrial proteins (cox1–3, cob, nad1–3 and nad 5–6). Genbank accession numbers used in this analysis are provided next to each species name. Bootstrap values higher than 50 are shown at the nodes. Scale bar indicates the number of substitutions per site.

related to *C. cinerea* (Figure 1), which is inconsistent with nuclear gene-based phylogenetic relationships reported previously (Li et al. 2018). This is the first report on the mitochondrial genome of the family *Strophariaceae*, which will contribute to future studies on the evolution and classification of mushrooms.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

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