

First Record of the Complete Mitochondrial Genome of a Saprotrophic and Opportunistic Human Pathogenic Fungus, *Scopulariopsis brevicaulis*

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ABSTRACT

Scopulariopsis brevicaulis is a widely distributed soil fungus known as a common saprotroph of biodegradation. It is also an opportunistic human pathogen that can produce various secondary metabolites. Here, we report the first complete mitochondrial genome sequence of *S. brevicaulis* isolated from air in South Korea. Total length of the mitochondrial genome is 28,829 bp and encoded 42 genes (15 protein-coding genes, 2 rRNAs, and 25 tRNAs). Nucleotide sequence of coding region takes over 26.2%, and overall GC content is 27.6%. Phylogenetic trees present that *S. brevicaulis* is clustered with *Lomentospora prolificans* with presenting various mitochondrial genome length.

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Scopulariopsis genus contains 22 fungal species [1] usually isolated from soil, air, plant debris, paper, and moist indoor environments [2,3]. They are soil saprophytes, pathogenic to animals including human [4]. *Scopulariopsis brevicaulis* (teleomorph: *Microascus brevicaulis*), which is one of five human pathogenic *Scopulariopsis* species usually involved in onychomycosis [5–7], can cause various skin problems and onychomycosis [7]. Here, we present a complete mitochondrial genome of *S. brevicaulis* as the first mitochondrial genome in *Scopulariopsis* genus.

A strain of *S. brevicaulis* was collected from mycobiota of air inside and outside the Meju fermentation room in South Korea [8] and its total DNA was extracted by using a DNeasy Plant Mini kit (QIAGEN, Hilden, Germany). In total 2.825 Gbp raw data generated by MiSeq (Table 1) were subject to *de novo* assembly done by Velvet 1.2.10 [9] and gap filling with SOAPGapCloser 1.12 [10] to get complete mitochondrial genome after confirming each bases using BWA 0.7.17 and SAMtools 1.9 [11,12]. Coverage of raw reads against the mitochondrial genome is 3090.52× (Table 1). Geneious R11 v11.0.5 (Biomatters Ltd, Auckland, New Zealand) was used to annotate its mitochondrial genome by comparing with that of *Collectotrichum siamense* strain YT02 (KX885103). ARWEN [13] was used for finding novel tRNAs on the mitochondrial genome. The sample was deposited into

Korean Agricultural Culture Collection (KACC-47468).

The length of *S. brevicaulis* mitochondrial genome (GenBank accession number: MK672942) is 28,829 bp (Table 1). *S. brevicaulis* mitochondrial genome encodes 42 genes consisting of 15 protein-coding genes, 2 rRNAs, and 25 tRNAs (Figure 1). This configuration of *S. brevicaulis* mitochondrial genome is same to those of *C. siamense* used for mitochondrial genome annotation and *Lomentospora prolificans*, which is the nearest species in phylogenetic tree (Figure 2(A)). Nucleotide sequence of coding region takes over 26.2%, and overall GC content is 27.6%. It is different from those of *L. prolificans*: GC ratio of coding region is 25.5% and overall GC content is 26.9%.

Each sequence alignment of conserved 12 genes from 20 *Microascales* mitochondrial genomes by MAFFT 7.450 [14] was concatenated. Annotation of *L. prolificans* mitochondrial genome was also conducted for incorporating into the trees. The bootstrapped neighbor-joining and maximum likelihood phylogenetic trees were constructed using MEGA X [15]. Lengths of nineteen *Microascales* mitochondrial genomes vary, ranging from 23,987 bp (*L. prolificans*) to 2,67,504 bp (*Juglanconis juglandina*; Figure 2(B)). Phylogenetic tree presents that *S. brevicaulis* is clustered with *L. prolificans*, of which lengths are two of the shortest mitochondrial genomes (Figure 2(B)). Interestingly, length of

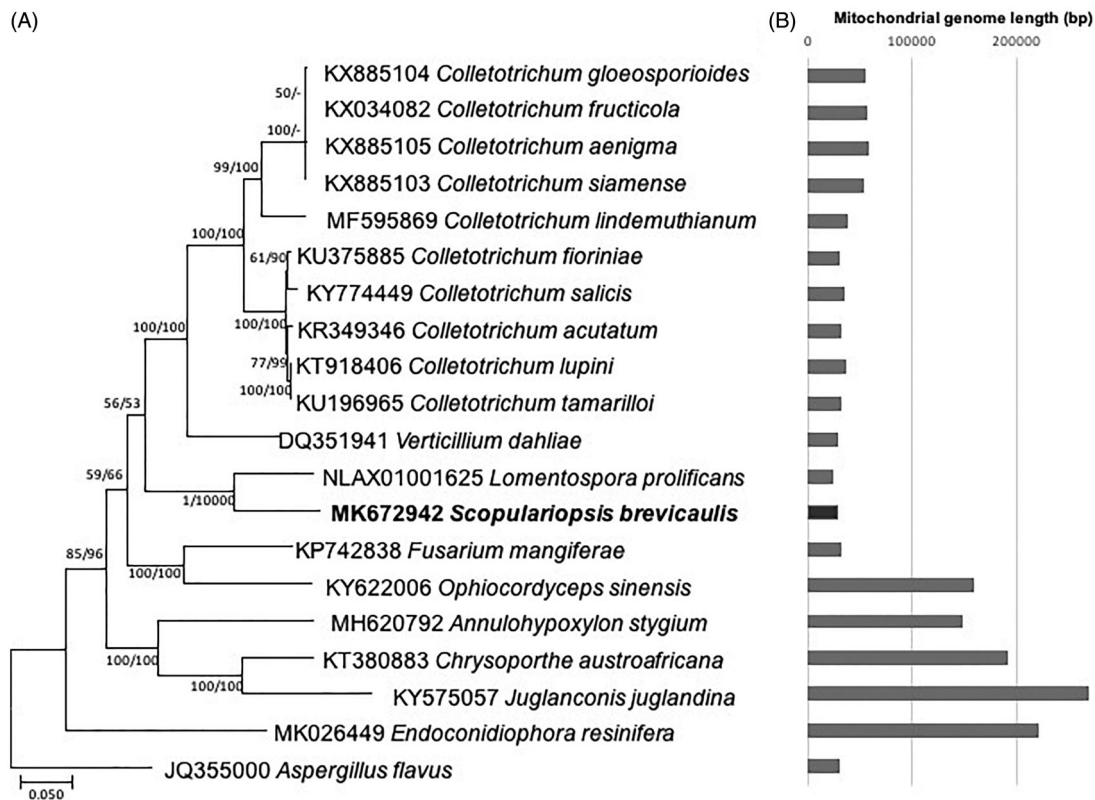


Figure 2. (A) Maximum likelihood (bootstrap repeat is 1,000) and neighbor joining (bootstrap repeat is 10,000) phylogenetic trees of twenty Microascales mitochondrial genomes including that of *Scopulariopsis brevicaulis* and *Aspergillus* mitochondrial genomes as an outgroup: *Scopulariopsis brevicaulis* (MK672942 in this study) *Lomentospora prolificans* (NLAX01001625), *Ophiocordyceps sinensis* (KY622006), *Fusarium mangiferae* (KP742838), *Annulohyphoxylon stygium* (MH620792), *Juglanconis juglandina* (KY575057), *Chrysosporthe austroafricana* (KT380883), *Verticillium dahliae* (DQ351941), *Colletotrichum lupini* (KT918406), *Colletotrichum tamarilloi* (KU196965), *Colletotrichum acutatum* (KR349346), *Colletotrichum fioriniae* (KU375885), *Colletotrichum salicis* (KY774449), *Colletotrichum lindemuthianum* (MF595869), *Colletotrichum gloeosporioides* (KX885104), *Colletotrichum siamense* (KX885103), *Colletotrichum aenigma* (KX885105), and *Colletotrichum fruticola* (KX034082), *Endoconidiophora resinifera* (MK026449), and *Aspergillus flavus* (JQ355000). Phylogenetic tree was drawn based on maximum likelihood phylogenetic tree. The numbers above branches indicate bootstrap support values of maximum likelihood and neighbor joining methods, respectively. (B) Gray graph displays length of twenty mitochondrial genomes.

mitochondrial activity could be involved in its pathogenic properties.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

Mitochondrial genome sequence can be accessed via accession number MK672942 in NCBI GenBank.

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