

Genome Sequence of *Spizellomyces punctatus*

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***Spizellomyces punctatus* is a basally branching chytrid fungus that is found in the *Chytridiomycota* phylum. *Spizellomyces* species are common in soil and of importance in terrestrial ecosystems. Here, we report the genome sequence of *S. punctatus*, which will facilitate the study of this group of early diverging fungi.**

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Spizellomyces punctatus is the type species of the fungal genus *Spizellomyces*, which is in the phylum *Chytridiomycota* (1). Like all chytrids, *Spizellomyces* produces unflagellated zoospores during its reproductive cycle, but in contrast to other zoosporic fungi (e.g., *Allomyces*), spizellomycetalean zoospores can be ameoboid while actively swimming, and the flagellar insertion site may move to a lateral position (2). *Spizellomyces* species are exclusively terrestrial (3). They are common in soil and of importance in terrestrial ecosystems—with both beneficial and detrimental impacts—found in association with a range of mycorrhizal fungi, mildews, plants, and soil nematodes (4, 5). In biochemical research, *S. punctatus* has gained attention because of the presence of mitochondrial 5' tRNA editing (6), a form of post-transcriptional RNA processing previously only known from the unrelated ameoboid protist *Acanthamoeba castellanii*. The *S. punctatus* genome was sequenced as part of the Origins of Multicellularity project; in addition to *S. punctatus*, this project sequenced genomes of several primitive eukaryotes to investigate commonalities and differences underlying multicellularity in animals and fungi (7).

To sequence the genome of *S. punctatus*, genomic DNA was extracted from strain DAOM BR117. For genome sequencing, we constructed three libraries, 4 and 10 kb plasmids and 40 kb Fosmids, and generated paired-end reads using Sanger chemistry. The reads were assembled using Arachne (8) Assemblez-Build 20090202 from roughly 11.7-fold sequence coverage; during manual review, gaps were newly introduced to address misassemblies or were closed based on read support.

Based on the assembly, the genome size was estimated to be 24.13 Mb with a G+C content of 47.6%. The assembly was organized in 329 contigs, which are linked by paired end reads into 38 scaffolds. The average base is found in a scaffold of N_{50} size 1.45 Mb and a contig of N_{50} size 155.89 kb. A total of 8,952 protein coding genes and 9,424 transcripts were predicted by combining the output from different annotation methods and RNA-Seq as previously described (9).

S. punctatus is the first member of the order *Spizellomycetales* to be sequenced and an important representative of *Chytridiomy-*

cota, as one of only three species to have annotated genomes released in NCBI. This report is a major step in genomic studies of this basal group of fungi.

Accession number(s). The whole-genome sequence and annotation of *S. punctatus* isolate DAOM BR117 have been deposited at DDBJ/EMBL/GenBank under the accession number [ACOE00000000](https://www.ncbi.nlm.nih.gov/nuccore/ACOE00000000). The version described in this paper is version [ACOE01000000](https://www.ncbi.nlm.nih.gov/nuccore/ACOE01000000).

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