



Draft Genome Sequence of the Nonmotile *Tremellomyces* Yeast *Naganishia albida*, Isolated from Aircraft

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ABSTRACT The *Basidiomycota* yeast *Naganishia albida* strain 5307AI was isolated from an aircraft polymer-coated surface. The genome size is 20,642,279 bp, with a G+C content of 53.99%. The genome contains fatty acid transporters, cutinases, hydroxylases, and lipases that are likely used for survival on polymer coatings on aircraft.

Here, we describe the draft genome sequence of the yeast *Naganishia albida* strain 5307AI, which was isolated from the polymer-coated surface of an aircraft. This microorganism was sequenced to understand the taxonomy and enzymatic functions underlying biodegradation and bioremediation on polymer coatings (1).

Naganishia albida strain 5307AI cells were isolated from samples collected inside an aircraft (2). Cultures were recovered from glycerol freezer stocks by streaking on potato dextrose agar (PDA). An isolated colony was resuspended in tryptic soy broth (TSB) and grown overnight at 27°C on a rotary wheel. A 1-mL aliquot of overnight culture was harvested, and the pellet was used for DNA extractions. Genomic DNA was extracted using the Qiagen PowerMicrobiome kit according to the manufacturer's instructions, and the DNA was quantified using the Qubit double-stranded DNA (dsDNA) assay (Life Technologies). Sequencing libraries were prepared using the Nextera DNA Flex library preparation kit (Illumina, San Diego, CA) following the manufacturer's instructions and sequenced using 150-bp paired-end sequencing on an Illumina NextSeq 550 system.

Sequence data processing steps used default parameters unless otherwise specified. Sequencing yielded 46,840,215 raw paired-end reads, which were trimmed with Trimmomatic v.0.39 (3) and quality filtered using FastQC v.0.11.9 (4). The 45,580,726 trimmed and filtered paired-end reads were assembled using SPAdes v.3.15.2 (5), yielding an average coverage of 340.4×, 176 contigs, a G+C content of 53.99%, an N_{50} value of 491,455 bp, an L_{50} value of 15, and a genome size of 20,642,279 bp calculated by QUAST v.5.0.2 (6). Genome completeness was estimated as 85.8% using BUSCO v.5.2.1 (7) with the *Basidiomycota* reference database (*basidiomycota_odb10*) and 51.8% with the *Tremellomyces* database (*tremellomyces_odb10*). A related species, *Naganishia liquefaciens* (8), had an estimated completeness of 51.2% with the same *Tremellomyces* database. We masked the assembled genome using RepeatMasker with the Dfam database v.3.3 (9). Gene prediction was completed using BRAKER v.2.1.6 (10) with *Naganishia albida* JCM2334 as a reference. BRAKER predicted 6,830 putative genes. Functional annotation was completed using InterProScan v.5.51-85.0 (11, 12), using the InterPro database v.86.0. We compared the 18S rRNA gene, internal transcribed spacer (ITS), 28S rRNA gene, actin, and β -tubulin sequences to those from *Naganishia albida* JCM2334. Whereas the 18S rRNA and ITS1 sequences were 100% identical, *Naganishia albida* JCM2334 did not contain complete sequences for the 28S rRNA gene, actin, or β -tubulin. We

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found that the ITS2 and 28S rRNA sequences were predicted to be chimeric using ITSx v.1.1.3 (13), but chimeric ribosomal regions have been observed in other fungi (14, 15).

Based on KEGG analyses using GhostKOALA v.2.2 (16) with default settings, we identified enzymes and pathways putatively involved in polymer degradation. We identified two putative cutinases, enzymes known to biodegrade polymers (17, 18). This genome should contribute to understanding how polymers are potentially degraded by microbial communities for bioremediation applications.

Data availability. The raw sequencing reads and draft genome with annotation have been deposited in GenBank under BioProject accession number [PRJNA811524](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA811524). The Sequence Read Archive (SRA) accession number for the raw sequencing reads is [SRR18183339](https://www.ncbi.nlm.nih.gov/sra/SRR18183339). The draft annotated genome assembly accession number is [JAMKMX000000000](https://www.ncbi.nlm.nih.gov/assembly/JAMKMX000000000).

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