Genome Sequences of Two Strains of the Food Spoilage Mold

Aspergillus fischeri

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ABSTRACT

Aspergillus fischeri is a common food spoilage fungus and a close relative of the opportunistic human pathogen Aspergillus fumigatus. Here, we sequenced the genomes of two isolates of A. fischeri to build resources for comparative genomics and to aid in differentiation between A. fischeri subspecies.

Aspergillus fischeri is a filamentous fungus that is naturally found in soil and other decaying organic matter (1, 2), a common agent of food spoilage (1–3), and a rare opportunistic pathogen in humans (4–6). In contrast, Aspergillus fumigatus is a closely related species but is responsible for hundreds of thousands of infections and deaths each year (7, 8). A. fischeri and A. fumigatus diverged as recently as ~4 million years ago (mya) (9) and share several phenotypic similarities (e.g., thermotolerance, hypoxia tolerance, ascospore formation and morphology, and the production of certain secondary metabolites) (4, 10–12). To date, the genomes of more than 100 A. fumigatus isolates have been fully sequenced (13–17), while only one A. fischeri genome has been sequenced (16).

We sequenced the genomes of A. fischeri IBT 3003 and IBT 3007, which are part of a collection in the Department of Biotechnology at Technical University of Denmark (Lyngby, Denmark) and were originally isolated from soil in Denmark (10). For each isolate, 1 × 10^6 spores were inoculated onto potato dextrose agar (PDA) plates at 37°C for 72 hours. DNA was isolated directly from spores using the MasterPure yeast DNA purification kit following the manufacturer’s instructions, with several minor modifications.

The 150-bp paired-end libraries were constructed and sequenced by Novogene on an Illumina NovaSeq 6000 sequencer. Raw sequence reads were first deduplicated using Tally (version 15-065) with “–with-quality” and “–pair-by-offset” options to remove potential PCR duplicates (18). Next, we used Trim Galore (version 0.4.2; http://www.bioinformatics.babraham.ac.uk/projects/trim_galore/) to remove residual adaptor sequences and trim reads at low-quality sites using the parameters “–paired,” “–stringency 1,” “–quality 30,” and “–length 50.” The preassembly-improved data sets consisted of 14,619,651 and 15,944,684 read pairs for A. fischeri IBT 3003 and IBT 3007, respectively. These data sets were error corrected and assembled using SPAdes (version 3.9.1) with the “–careful” parameter and k-mer sizes of 31, 43, 73, and 93 (19). The cumulative assembly sizes for A. fischeri IBT 3003 and IBT 3007 were 31.61 Mb and 31.25 Mb and the G+C contents were 49.5% and 49.5%, respectively. We extracted the internal transcribed spacer (ITS) region from the A. fischeri IBT 3003 and IBT 3007 genomes, and they were subjected to a BLAST search against the NCBI nonredundant database (20). Both ITS sequences shared 100% sequence identity to the reference A. fischeri NRRL 181 genome (16). We then used QUAST (version 5.0.2) to assess the quality...
of the assemblies (21). A. fischeri IBT 3003 and IBT 3007 were assembled into 1,037 and 1,193 scaffolds, with N₅₀ values of 365 kb and 377 kb, respectively. BUSCO (version 3) was used to evaluate the completeness of the genome assemblies, using the “ascomycota_odb9” gene set (22). Totals of 98.4% and 98.5% of BUSCO genes were recovered from the A. fischeri IBT 3003 and IBT 3007 assemblies, respectively.

**Data availability.** The whole-genome shotgun projects for A. fischeri IBT 3003 and IBT 3007 have been deposited in GenBank under the accession numbers VWYB00000000 and VWYA00000000, respectively. Raw Illumina data have been deposited to the NCBI Sequence Read Archive under the project accession number PRJNA564742.

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**REFERENCES**