AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

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

Citation Zhao S, Latgé J-P, Gibbons JG. 2019. Genome sequences of two strains of the food spoilage mold *Aspergillus fischeri*. Microbiol Resour Announc 8:e01328-19. https://doi.org/10.1128/MRA.01328-19.

Editor Antonis Rokas, Vanderbilt University

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Received 21 October 2019
Accepted 9 November 2019
Published 12 December 2019

of the assemblies (21). *A. fischeri* IBT 3003 and IBT 3007 were assembled into 1,037 and 1,193 scaffolds, with N_{50} 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.

ACKNOWLEDGMENT

This work was supported by the National Institutes of Health, National Institute of Allergy and Infectious Diseases (1R21AI137485-01).

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