

Draft Genome Sequences of Two *Aspergillus fumigatus* Strains, Isolated from the International Space Station

Nitin Kumar Singh,^a Adriana Blachowicz,^a Aleksandra Checinska,^a Clay Wang,^{b,c}  Kasthuri Venkateswaran^a

Biotechnology and Planetary Protection Group, Jet Propulsion Laboratory, California Institute of Technology, Pasadena, California, USA^a; Department of Pharmacology and Pharmaceutical Sciences, University of Southern California, Los Angeles, California, USA^b; Dornsife College of Letters, Arts and Sciences, University of Southern California, Los Angeles, California, USA^c

Draft genome sequences of *Aspergillus fumigatus* strains (ISSFT-021 and IF1SW-F4), opportunistic pathogens isolated from the International Space Station (ISS), were assembled to facilitate investigations of the nature of the virulence characteristics of the ISS strains to other clinical strains isolated on Earth.

Received 2 May 2016 Accepted 25 May 2016 Published 14 July 2016

Citation Singh NK, Blachowicz A, Checinska A, Wang C, Venkateswaran K. 2016. Draft genome sequences of two *Aspergillus fumigatus* strains, isolated from the International Space Station. *Genome Announc* 4(4):e00553-16. doi:10.1128/genomeA.00553-16.

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Address correspondence to Kasthuri Venkateswaran, kjvenkat@jpl.nasa.gov.

Fungi are a source of natural products that are useful to human-kind. A variety of bioactive compounds produced by fungi are used in pharmaceutical and food industries, agriculture, and beyond. However, some fungi are plant, animal, and human pathogens. Fungal pathogens could cause serious health complications in immunocompromised populations. Pathogenic fungi can produce a range of secondary metabolites (SMs) that influence their virulence (melanins, siderophores, species-specific toxins) and immunologic potential.

Aspergillus fumigatus is a saprophytic, filamentous fungus that is ubiquitous outdoors (soil, decaying vegetation) and indoors (hospitals, simulated closed habitats, etc.). *Aspergillus fumigatus* can adapt to various environmental conditions and form airborne conidia that are the inoculum for a variety of diseases (e.g., non-invasive and invasive pulmonary infections, allergic bronchopulmonary aspergillosis, etc.) in immunocompromised hosts.

In on-going microbial observatory experiments on the International Space Station (ISS), molecular phylogeny and radiation resistance of several fungal isolates were characterized. Two *Aspergillus fumigatus* strains, ISSFT-021 and IF1SW-F4, were isolated from a HEPA filter (1) and cupola wall (unpublished) of the ISS. Because *A. fumigatus* is an opportunistic pathogen causing pathologies ranging from allergic asthma to invasive aspergillosis, we assessed several pathogenic characteristics of the ISS isolates in comparison to two experimentally established clinical isolates, Af293 (2) and CEA10 (3). Virulence assessment in a larval zebrafish model of invasive aspergillosis revealed both ISSFT-021 and IF1SW-F4 as significantly more lethal compared to both clinical isolates (Af293 and CEA10) (4). In addition, the ISS strains ISSFT-021 and IF1SW-F4 exhibited significantly greater resistance to UV254 doses when compared to clinical isolates (4, 5). The genomics of these ISS isolates might reveal the molecular mechanisms of the increased virulence. Subsequently, if the enhanced virulence is attributed to the microgravity, NASA potentially should consider developing countermeasures to protect the

health of astronauts, whose immune systems are reported to be compromised under microgravity (6).

In this study, we determined the draft genome sequences of *A. fumigatus* strains ISSFT-021 and IF1SW-F4. Whole-genome shotgun sequencing was performed on an Illumina HiSeq2500 instrument with a paired-end module. A total of 27,987,752 and 10,752,032 paired-end reads of 101-nucleotides were collected for ISSFT-021 and IF1SW-F4. The NGS QC Toolkit v2.3 (7) was used to filter the data for high-quality (HQ) vector- and adaptor-free reads for genome assembly (cutoff read length for HQ, 80%; cutoff quality score, 20). A total of 25,515,334 (~230× coverage) for ISSFT-021 and 8,466,430 (~75× coverage) for IF1SW-F4 high-quality vector-filtered reads were used for assembly with MaSuRCA (8) genome assembler (k-mer size = 70). The final assembly of the strain ISSFT-021 contains 301 scaffolds with a total size of 28,526,023 bp and an N_{50} contig length of 275.468 kb; the largest contigs assembled measures 813.103 kb and the G+C% was 49.41. Similarly, the final assembly of the IF1SW-F4 strain contains 208 scaffolds with a total size of 28,240,437 bp and an N_{50} contig length of 367.421 kb; the largest contig assembled measures 900.278 kb and the G+C content was 49.45%.

Nucleotide sequence accession numbers. The whole-genome sequences of both the strains were deposited at DDBL/EMBL/GenBank under the accession numbers [LWRT000000000](https://www.ncbi.nlm.nih.gov/nuccore/LWRT000000000) and [LWRU000000000](https://www.ncbi.nlm.nih.gov/nuccore/LWRU000000000). The versions described in this paper are LWRT01000000 and LWRU01000000. These *A. fumigatus* strains were also deposited in the USDA Agricultural Research Station and DSMZ public culture collections.

ACKNOWLEDGMENTS

Part of the research described in this publication was carried out at the Jet Propulsion Laboratory, California Institute of Technology, under a contract with NASA. This research was funded by 2012 Space Biology NNN12ZTT001N grant 19-12829-26 under task order NNN13D111T awarded to K.V., which also funded post-doctoral fellowships for N.K.S.

and A.C., a graduate fellowship to A.B., and a JPL subcontract 1511581 to C.W.

We thank Jay Perry, Marshall Space Flight Center, for providing the HEPA filter and the implementation team of the Microbial Observatory (Microbial Tracking) project at NASA Ames Research Center.

FUNDING INFORMATION

This work, including the efforts of Kasthuri Venkateswaran, was funded by National Aeronautics and Space Administration (NASA) (19-12829-26).

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