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GENOME SEQUENCES

Draft Genome Sequences of *Aspergillus* and *Penicillium* Species Isolated from the International Space Station and Crew Resupply Vehicle Capsule

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ABSTRACT The draft whole-genome sequences (WGS) of 30 fungal strains isolated from the International Space Station and belonging to the *Penicillium* and *Aspergillus* genera were assembled. The WGS will allow for detailed genomic characterization to determine the possible applications and importance for space and biotechnological industries.

During an ongoing microbial tracking study of the International Space Station (ISS), 30 strains representing seven species belonging to the *Penicillium* (n = 5) and *Aspergillus* (n = 2) genera were isolated (1), and whole-genome sequences (WGS) were generated. The *Penicillium* genus encompasses more than 350 species found worldwide in soil, vegetation, air, indoor environments, and food (2). *Aspergillus* species are saprophytes found in a variety of environmental niches; however, some of them are also opportunistic human pathogens (3, 4). Members of the *Penicillium* and *Aspergillus* genera are of economic and industrial importance, including *Penicillium chrysogenum*, which is used to produce β-lactam antibiotics (5), *Penicillium camemberti*, which is used for maturation of soft cheeses such as Camembert, Brie, and Neufchatel (6), and *Aspergillus niger*, which is a known producer of citric acid (7, 8). Recently, *Penicillium polonicum* has been shown to tolerate and effectively remove lead (Pb) from polluted water, indicating a promising solution for new remediation strategies to purify contaminated water (9). Lastly, *Aspergillus unguis*, *Penicillium dipodomyicola*, and *Penicillium griseoroseum* have been reported to produce novel bioactive compounds (10–13). Considering existing and yet-to-be uncovered, versatile applications of *Penicillium* and *Aspergillus* species, characterization of WGS of these fungi is critical. Additionally, since fungi are excellent models for studying evolution and adaptation, due to their experimental features (14), the ISS-isolated species are of unique significance for investigating how microgravity and irradiation affect them when compared to their ground counterparts.

The procedure for collecting samples and performing consecutive processing steps has been described elsewhere (1). Briefly, surface samples were collected with premoistened polyester wipes and then resuspended in 200 ml of sterile phosphate-buffered saline (PBS) with vigorous shaking. The extracted samples were concentrated using InnovaPrep (Drexel, MO) CP-150 concentrating pipettes. Aliquots (100 μl) of each sample were plated onto potato dextrose agar (PDA) containing 100 μg/ml chloramphenicol and incubated at 25°C for 7 days. A single colony was picked, restreaked onto PDA, and incubated at 25°C for 7 days. About 1 μg of biomass grown overnight was collected and used for DNA extraction with the ZymoBIOMICS DNA MagBead kit (Zymo

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TABLE 1 Summary of the draft WGS of 30 *Aspergillus* and *Penicillium* strains isolated from the ISS

Strain[a]	Species identified based on ITS gene	Species identified based on calmodulin gene	Species identified based on β-tubulin gene	GenBank accession no.	SRA accession no.	Isolation location[b]	No. of scaffolds	Genome size (bp)	N_{50} (bp)	Median coverage (×)	G+C content (%)	No. of filtered reads used for assembly (million)
F3-1F3-F	*Aspergillus niger*	*Aspergillus niger*	*Aspergillus niger*	JADBHA000000000	SRR12819683	Cupola	75	35,865,776	1,033,225	55	49.46	22.16
F3-4F1-F	*Aspergillus niger*	*Aspergillus welwitschiae*	*Aspergillus welwitschiae*	JADBHC000000000	SRR12819679	Dining table	342	37,533,732	885,952	64	49.25	25.45
F3-4F2-F	*Aspergillus niger*	*Aspergillus welwitschiae*	*Aspergillus welwitschiae*	JADBHD000000000	SRR12819678	Dining table	361	37,317,966	948,069	51	49.41	21.20
IIF6SW-F2	*Aspergillus unguis*	*Aspergillus unguis*	*Aspergillus unguis*	JADBGV000000000	SRR12819688	PMM	20	25,892,012	2,741,393	93	50.3	26.47
IF2SW-F1	*Penicillium camemberti*	*Penicillium biforme*	*Penicillium biforme*	JACSPF000000000	SRR12825356	WHC	834	35,011,981	266,841	56	47.69	23.59
IIF8SW-F2	*Penicillium camemberti*	*Penicillium biforme*	*Penicillium biforme*	JACSOP000000000	SRR12825359	Crew quarters	846	35,011,981	262,211	55	47.7	22.46
IIF8SW-F3	*Penicillium camemberti*	*Penicillium biforme*	*Penicillium biforme*	JACSOO000000000	SRR12825358	Crew quarters	828	35,011,981	256,141	53	47.69	22.37
F3-3F1-F	*Penicillium camemberti*	*Penicillium biforme*	*Penicillium biforme*	JADBHB000000000	SRR12819682	ARED	1,098	36,854,083	303,871	56	47.69	22.97
IF1SG-B2	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JADBGS000000000	SRR12819681	Outside CRV capsule	676	33,342,700	1,054,379	71	48.81	26.71
IF1SW-F3	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JACSPG000000000	SRR12825368	Cupola	764	32,524,241	638,283	57	48.92	21.32
IF2SG-B2	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JADBGT000000000	SRR12819680	Outside CRV capsule	648	33,347,836	931,557	93	48.81	34.88
IF2SW-F4	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JACSPE000000000	SRR12825355	WHC	1,277	32,524,241	640,412	41	48.76	16.80
IF2SW-F5	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JACSPD000000000	SRR12825354	WHC	445	32,524,241	718,663	82	48.96	28.82
IF3SW-F3	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JACSPB000000000	SRR12825352	ARED	843	32,524,241	497,770	42	48.94	15.73
IF4SG-B1	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JADBGU000000000	SRR12819689	Inside CRV capsule	651	33,345,064	939,642	76	48.81	28.76
IF4SW-F1	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JACSPA000000000	SRR12825351	Dining table	481	32,524,241	947,115	54	48.96	18.77
IF7SW-F1	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JACSOZ000000000	SRR12825350	LAB	485	32,524,241	782,807	72	48.96	25.44
IIF2*SW-F2	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium harmonense*	JADBGW000000000	SRR12819687	WHC	460	32,073,134	709,694	64	48.99	22.76
IIF3SW-F2	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JACSOU000000000	SRR12825364	ARED	1,276	32,524,241	643,620	48	48.76	19.83
IIF8SW-F4	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JACSON000000000	SRR12825357	Crew quarters	434	32,524,241	1,028,283	74	48.96	26.01
F3-2F3-F	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium harmonense*	JADBGX000000000	SRR12819686	WHC	353	31,592,617	579,954	77	48.84	26.27
F3-2F4-F	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JADBGY000000000	SRR12819685	WHC	568	32,430,262	701,540	99	48.94	34.71
F3-2F5-F	*Penicillium chrysogenum*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JADBGZ000000000	SRR12819684	WHC	486	32,607,577	1,028,360	66	48.84	23.62
IF7SW-F3	*Penicillium dipodomyicola*	*Penicillium chrysogenum*	*Penicillium tardochrysogenum*	JACSOY000000000	SRR12825349	LAB	1,372	32,524,241	578,872	45	48.81	17.99
IIF7SW-F2	*Penicillium dipodomyicola*	*Penicillium chrysogenum*	*Penicillium harmonense*	JACSOR000000000	SRR12825361	LAB	431	32,524,241	842,068	76	48.99	27.38
IIF7SW-F4	*Penicillium dipodomyicola*	*Penicillium chrysogenum*	*Penicillium harmonense*	JACSOQ000000000	SRR12825360	LAB	455	32,524,241	585,026	71	48.99	25.46
IF3SW-F1	*Penicillium griseoroseum*	*Penicillium chrysogenum*	*Penicillium harmonense*	JACSPC000000000	SRR12825353	ARED	559	32,524,241	577,257	61	48.99	24.14
IF7SW-F5	*Penicillium griseoroseum*	*Penicillium chrysogenum*	*Penicillium harmonense*	JACSOW000000000	SRR12825366	LAB	361	32,524,241	492,361	39	48.85	17.39
IIF4SW-F4	*Penicillium griseoroseum*	*Penicillium chrysogenum*	*Penicillium harmonense*	JACSOT000000000	SRR12825362	Dining table	348	32,524,241	481,150	80	48.85	28.75
IIF1SW-F3	*Penicillium polonicum*		*Penicillium tardochrysogenum*	JACSOV000000000	SRR12825365	Cupola	464	32,524,241	1,262,860	72	48.96	25.30

[a] F1, flight 1; F2, flight 2; F3, flight 3; F4, flight 4; F5, flight 5; SG, surface from CRV; SW, surface wipes from ISS environment. F and B at the end are strain numbers.

[b] PMM, permanent multipurpose module; WHC, waste and hygiene compartment; ARED, advanced resistive exercise device; CRV, crew resupply vehicle; LAB, panel near portable water dispenser.

Corp., Irvine, CA). To acquire the WGS, shotgun libraries were prepared following the Illumina Nextera Flex protocol (15), and paired-end sequencing of 30 strains was performed on a NovaSeq 6000 S4 flow cell paired-end 2 × 150-bp platform. The quality of the raw reads obtained was confirmed with FastQC (v0.11.7) (16). Assessment of the quality filtering steps and adapter removal were performed using fastp (v0.20.0) (17). The cleaned sequences were assembled with SPAdes using the automatic coverage cutoff value (v3.11.1) (18). Assembly quality, number of contigs, N_{50} values, and genome size were calculated using QUAST (v5.0.2). Default parameters were used for all software. The species were identified based on the internal transcribed spacer (ITS), calmodulin, and β-tubulin sequences extracted from the assembled genomes. The details of the final assemblies and phylogenetic identification are summarized in Table 1.

Data availability. The WGS and raw data have been deposited in GenBank under the BioProject accession numbers PRJNA659567 and PRJNA667181. This project has also been deposited in the NASA GeneLab system (https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-350/). The versions described in this paper are the first versions.

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