



# Draft Genome Sequences of Several Fungal Strains Selected for Exposure to Microgravity at the International Space Station

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**ABSTRACT** The whole-genome sequences of eight fungal strains that were selected for exposure to microgravity at the International Space Station are presented here. These baseline sequences will help to understand the observed production of novel bioactive compounds.

In a screening project of natural products, fungal strains isolated from environments associated with the Chernobyl nuclear power plant (ChNPP) accident (1) have been investigated. The radiation-tolerant microorganisms selected for exposure to microgravity at the International Space Station were known to produce valuable natural products; their genomic sequences coded for secondary metabolism pathways; or they displayed positive radiotropism.

*Aspergillus niger*, an industrially important filamentous fungus, contains a sequence resembling the fumonisin gene cluster, which suggests that the fungus has the genetic potential to produce carcinogenic fumonisins (2). *A. niger* also produces an abundance of naphtho-gamma-pyrone secondary metabolites, which have been shown to have antibacterial, antifungal (3), antitumor (4), and cytotoxic (3, 4) activity.

*Aspergillus terreus* is used to produce organic acids, such as itaconic acid (5), or enzymes, such as xylanases (6, 7). One of the most important secondary metabolites made by *A. terreus* is the cholesterol-lowering molecule lovastatin. Discovery of this potent compound revolutionized the treatment of hypercholesterolemia (8, 9).

*Aureobasidium pullulans* is an important producer of pullulan, a homopolysaccharide of glucose that is widely used in the food, pharmaceutical, and electronics industries (10, 11). The whole-genome sequence of *A. pullulans* revealed significant biotechnological potential but also the presence of virulence factors that cannot be overlooked (12).

*Beauveria bassiana* is an entomopathogenic fungus used to produce biodegradable, nonpoisonous, and cost-efficient bioinsecticides (13). Genomic analysis of *B. bassiana* exhibits its capacity to produce a plethora of secondary metabolites, such as oosporein, bassianin, beauvericin, or oxalic acid (14). Beauvericin possesses antimicrobial, antiviral, antifungal, and antitumor activity (15).

*Cladosporium cladosporioides*, a ubiquitous organism, produces cladosporin and isocladosporin—secondary metabolites known to have antifungal activities. Its genome has not been sequenced yet (16, 17).

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**TABLE 1** Statistical summary for the eight draft fungal genome sequences

| Strain                              | Strain designation | NCBI accession no. | Isolation location <sup>a</sup> | No. of contigs | Genome size (bp) | $N_{50}$ (bp) | G+C content (%) |
|-------------------------------------|--------------------|--------------------|---------------------------------|----------------|------------------|---------------|-----------------|
| <i>Aspergillus niger</i>            | JSC-093350089      | MSJD00000000       | ISS environmental surface       | 223            | 36,080,355       | 543,773       | 49.46           |
| <i>Aspergillus terreus</i>          | IMV 01167          | MSJE00000000       | Soil, Kirovograd region         | 331            | 31,580,414       | 482,632       | 52.24           |
| <i>Aureobasidium pullulans</i>      | IMV 00882          | MSJF00000000       | Wall surface, unit 4, ChNPP     | 879            | 40,984,331       | 98,085        | 51.01           |
| <i>Beauveria bassiana</i>           | IMV 00265          | MSJG00000000       | Wall surface, unit 4, ChNPP     | 735            | 35,190,057       | 138,299       | 51.72           |
| <i>Cladosporium cladosporioides</i> | IMV 00236          | MSJH00000000       | Wall surface, unit 4, ChNPP     | 843            | 47,573,060       | 186,555       | 42.89           |
| <i>Cladosporium sphaerospermum</i>  | IMV 00045          | MSJI00000000       | Wall surface, unit 4, ChNPP     | 959            | 50,156,125       | 72,128        | 53.05           |
| <i>Fusarium solani</i>              | IMV 00293          | MSJJ00000000       | Wall surface, unit 4, ChNPP     | 876            | 51,318,644       | 812,484       | 47.58           |
| <i>Trichoderma virens</i>           | IMV 00454          | MSJK00000000       | Soil, 10-km ChEZ                | 197            | 42,025,033       | 1,319,489     | 48.44           |

<sup>a</sup>ISS, International Space Station; ChNPP, Chernobyl nuclear power plant; ChEZ, Chernobyl exclusion zone.

*Cladosporium sphaerospermum* is a plant endophyte but also an allergen to immunocompromised populations. It has the capacity to produce a variety of allergens, such as enolase, mannitol, dehydrogenase, and aldehyde dehydrogenase (18).

*Fusarium solani* is a plant pathogen that produces multiple phytotoxins, such as marticin, isomarticin, anhydrofusarubin, and javanicin, that cause sudden death syndrome of soybean (19), for example.

*Trichoderma virens* is a common rhizosphere fungus beneficial to plants and reported to induce a defense response of cotton to *Rhizoctonia solani*-incited seedling disease (20, 21).

The whole-genome sequences of these eight fungal strains were obtained by shotgun sequencing performed on an Illumina HiSeq2500 platform with a paired-end module. The NGS QC toolkit version 2.3 (22) was used to filter the data for high-quality vector- and adaptor-free reads for genome assembly (cutoff read length for high quality: 80%; cutoff quality score: 20). High-quality vector-filtered reads were used for assembly with the MaSuRCA genome assembler ( $k$ -mer size = 70) (23). Data from the final assembly of the strains, including number of scaffolds, total size,  $N_{50}$  contig length, G+C content, and GenBank accession numbers, are given in Table 1.

**Accession number(s).** This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession numbers given in Table 1. The versions described in this paper are the second versions.

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