



Reliable Identification of Environmental Fungi Requires Multigene-Based Phylogenetic Analyses

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As noted in the letter by Houbraken et al. (4), some of the fungal species identified for the 2017 publication by Singh et al. (1) were miscategorized due to the use of only the internal transcribed spacer (ITS) region for identification. The NCBI bioinformatics team contacted the authors of this publication with updated species identification based on whole-genome analysis in April 2019, and the records in the NCBI GenBank database were subsequently updated (Table 1). Strains identified to the species level by NCBI were confirmed using a whole-proteome analysis using EUKulele v1.0.6 (2).

We appreciate Houbraken et al. for pointing out the problems associated with fungal identification, which is a widespread issue in this area of research. As suggested by Houbraken et al., we have begun to reanalyze these fungal strains not yet identified to the species level (Table 1) using various genus-specific markers, and we will further update the NCBI GenBank database as necessary.

The genus-specific markers for correctly identifying fungal species (from R. A. Samson et al. [3]) are as follows:

1. *Scedosporium* spp.: tubulin and ITS.
2. *Beauveria* spp.: elongation factor, RPB2, and ITS.
3. *Cladosporiaceae* spp.: elongation factor and actin.
4. *Byssochlamys* spp.: The genus name *Byssochlamys* is not accepted and is a synonym of *Paecilomyces*. Tubulin-based phylogenetic analysis and comparison with the whole-genome sequence (WGS) of appropriate type species are needed to finalize the fungal identification.
5. *Trichoderma* spp.: RPB2 and elongation factor.

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This is a response to a letter by Houbraken et al. (<https://doi.org/10.1128/MRA.01074-20>).

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TABLE 1 Statistical summary for the eight draft fungal genome sequences

Original strain identification	Strain designation	Updated strain identification ^a	GenBank accession no.	Isolation location ^b	No. of contigs	Genome size (bp)	N_{50} (bp)	G+C content (%)
<i>Aspergillus niger</i>	JSC-093350089	<i>Aspergillus niger</i>	MSJD000000000	ISS environmental surface	223	36,080,355	543,773	49.46
<i>Aspergillus terreus</i>	IMV 01167	<i>Aspergillus</i> aff. <i>floccosus</i>	MSJE000000000	Soil, Kirovograd Region	331	31,580,414	482,632	52.24
<i>Aureobasidium pullulans</i>	IMV 00882	<i>Scedosporium</i> sp.	MSJF000000000	Wall surface, unit 4, ChNPP	879	40,984,331	98,085	51.01
<i>Beauveria bassiana</i>	IMV 00265	<i>Beauveria</i> sp.	MSJG000000000	Wall surface, unit 4, ChNPP	735	35,190,057	138,299	51.72
<i>Cladosporium cladosporioides</i>	IMV 00236	<i>Cladosporiaceae</i> sp.	MSJH000000000	Wall surface, unit 4, ChNPP	843	47,573,060	186,555	42.89
<i>Cladosporium sphaerospermum</i>	IMV 00045	<i>Byssoschlamys</i> sp.	MSJI000000000	Wall surface, unit 4, ChNPP	959	50,156,125	72,128	53.05
<i>Fusarium solani</i>	IMV 00293	<i>Fusarium oxysporum</i>	MSJJ000000000	Wall surface, unit 4, ChNPP	786	51,318,644	812,484	47.58
<i>Trichoderma virens</i>	IMV 00454	<i>Trichoderma</i> sp.	MSJK000000000	Soil, 10-km ChEZ	197	42,025,033	1,319,489	48.44

^aSpecies identification was based on whole-genome sequence analysis, updated in NCBI GenBank on 9 April 2019, and verified using EUKulele (2).

^bISS, International Space Station; ChNPP, Chernobyl Nuclear Power Plant; ChEZ, Chernobyl Exclusion Zone.

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