Genome Sequence of *Aspergillus aculeatinus* IC_8, Isolated from an Indoor Air Sample of an Urban Housing Complex in Abidjan, Ivory Coast

Shu Zhao,a,b David Kofi,c Jean-Paul Latge,d Karidia Sylla,c John G. Gibbonsa,b,e

aDepartment of Food Science, University of Massachusetts, Amherst, Massachusetts, USA
bMolecular and Cellular Biology Graduate Program, University of Massachusetts, Amherst, Massachusetts, USA
cParasitology and Mycology Department, Institut Pasteur de Côte d’Ivoire, Abidjan, Ivory Coast
dAspergillus Unit, Institut Pasteur, Paris, France
eOrganismic & Evolutionary Biology Graduate Program, University of Massachusetts, Amherst, Massachusetts, USA

**ABSTRACT** *Aspergillus aculeatinus* is an industrially important species of *Aspergillus* section *Nigri* capable of producing bioactive, antibiotic, and antitumor compounds. We sequenced the genome of a strain of *A. aculeatinus* that was isolated from the interior of a housing complex in Abidjan, Ivory Coast.

*Aspergillus* section *Nigri* (the black aspergilli) consists of species that cause food spoilage, cause plant disease, and produce industrially relevant compounds like lipases, amylase, citric acid, and gluconic acid (1). *Aspergillus aculeatinus* is a member of the black aspergilli and closely related to *Aspergillus aculeatus* (2). *A. aculeatinus* has the potential for industrial application, as it produces the bioactive compound neoxaline, the antifungal compound aculeacin, and the antitumor compound paclitaxel (originally named Taxol [Bristol-Myers Squibb]) (2, 3). To date, only one *A. aculeatinus* genome has been sequenced (4).

To provide additional genomic resources for *A. aculeatinus*, we sequenced the genome of *A. aculeatinus* IC_8 after isolating it from an indoor air sample of a 23-story urban housing complex in Abidjan, Ivory Coast; it houses ~2,000 residents. Specifically, petri dishes with Sabouraud chloramphenicol agar were left open for 24 hours and then incubated at 25°C for 3 days. We used the hyphal tipping approach followed by incubation and single spore isolation to retrieve pure culture. DNA extraction was carried out as previously described (5). Briefly, spores were plated onto potato dextrose agar (PDA) and incubated at 37°C for 96 hours. Spores were collected and directly used for DNA extraction using the MasterPure yeast DNA purification kit following the manufacturer’s instructions, with several minor modifications.

Next, 150-bp paired-end libraries were constructed and sequenced on an Illumina NovaSeq 6000 sequencer by Novogene. Raw reads were first deduplicated using Tally v15-065 with the “--with-quality” and “--pair-by-offset” options (6). Trim_Galore v0.4.2 was then used to remove residual adaptor sequences and to trim low-quality sequences using the parameters “--paired,” “--stringency 1,” “--quality 30,” and “--length 50” (http://www.bioinformatics.babraham.ac.uk/projects/trim_galore/) (7). The deduplicated and trimmed data set contained 14,017,719 paired reads with a total of 4.07 billion bp. Next, the data were error corrected, and the genome was assembled de novo using SPAdes v3.13.1 with the “--careful” mode and a k-mer range of 55, 77, and 99 (8).

The assembly consisted of 441 scaffolds, a cumulative assembly size of 36.47 Mb (nearly identical to that of the *A. aculeatinus* CBS 121060 genome [4]), an N_{50} value
of 649,318 bp, and a GC content of 50.48%. Genome completeness was evaluated with BUSCO v3.1.0 using the "ascomycota_odb9" gene set (9). A total of 98.9% of BUSCO genes were recovered from the IC_8 genome, indicating a high-quality genome assembly.

To verify the species of IC_8, we conducted a phylogenetic analysis of IC_8 and 24 genomes from 22 Aspergillus section Nigri species, including A. aculeatinus CBS 121060 (4). For all genomes, we used the Funannotate v1.7.0 (10) pipeline to predict gene models. Next, we used Orthofinder v2.3.3 to identify orthologous genes across the 25 genomes (11). A concatenated amino acid sequence alignment was generated from 4,680 translated genes. FastTree v2.1.10 was used to infer the phylogenetic relationship of isolates from the concatenated sequence alignment, using the MLACC = 3 and nearest-neighbor interchange (NNI) options, with 100 bootstraps (12, 13). IC_8 is monophyletic with A. aculeatinus CBS 121060, and both taxa have short branch lengths (Fig. 1), providing clear evidence that the species identity of IC_8 is A. aculeatinus.

**FIG 1** Phylogenetic relationship of 25 Aspergillus section Nigri genomes, including IC_8. The phylogeny was inferred by the approximately maximum-likelihood approach in FastTree (8) from a concatenated protein alignment of 4,680 sequences. All bootstrap branch support values were 100%. IC_8 is monophyletic with A. aculeatinus CBS 121060, and both taxa have short branch lengths, indicating that the species identity of IC_8 is A. aculeatinus. The species used are as follows (with their GenBank accession numbers for the whole-genome sequences): A. aculeatinus (PSTE00000000), A. aculeatus (GC00000000), A. brumneoviolaceus (PSTC00000000), A. costaricaensis (PSTI00000000), A. ellipticus (PSTI00000000), A. eucalypticola (MSFU00000000), A. fijensis (PSTG00000000), A. heteromorphus (MSFL00000000), A. homomorphus (PSTI00000000), A. ibericus (PSTI00000000), A. inflectoviolaceus (PSTB00000000), A. japonicus (PSTF00000000), A. lacticoffeatus (MSFR00000000), A. neoniger (MSFK00000000), A. niger ATCC 13157 (A. phoenicis) (QQUR00000000), A. niger ATCC 13496 (QQZP00000000), A. piperis (PSTD00000000), A. saccharolyticus (MSFQ00000000), A. sclerotiorubus (PSTZ00000000), A. scirerotoniger (MSFK00000000), A. uvarum (MSFQ00000000), A. vadinis (MSF50000000), A. violaceofuscus (PSTA00000000), and A. welwitschiae (QQZZ00000000).

Data availability. The whole-genome shotgun project for A. aculeatinus IC_8 has been deposited in GenBank under the accession number JADPID00000000. Raw Illumina data have been deposited to the NCBI Sequence Read Archive under the BioProject accession number PRJNA675076.

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REFERENCES

1. Varga J, Frisvad JC, Kocsbéd S, Brankovics B, Tóth B, Szigeti G, Samson RA. 2011. New and revisited species in Aspergillus section Nigri. Stud Mycol 69:1–17. https://doi.org/10.3114/sim.2011.69.01.

2. Noonim P, Mahakarnchanakul W, Varga J, Frisvad JC, Samson RA. 2008. Two novel species of Aspergillus section Nigri from Thai coffee beans. Int J Syst Evol Microbiol 58:1727–1734. https://doi.org/10.1099/ijs.0.65694-0.

3. Qiao W, Tang T, Ling F. 2020. Comparative transcriptome analysis of a taxol-producing endophytic fungus, Aspergillus aculeatinus Tax-6, and its mutant strain. Sci Rep 10:10558. https://doi.org/10.1038/s41598-020-67614-1.

4. Vesth TC, Nybo JL, Theobald S, Frisvad JC, Larsen TO, NielsenKF, Hoof JB, Brandl J, Salamov A, Riley R, Gladden JM, Phatala P, Nielsen MT, Lyhne EK, Kogle ME, Strasser K, McDonnell E, Barry K, Clum A, Chen C, LaButti K, Haridas S, Nolan M, Sandor L, Kuo A, Lipzen A, Hainault M, Drula E, Tsang A, Magnuson JK, Henrissat B, Wiebenga A, Simmons BA, Mäkelä MR, de Vries RP, Grigoriev IV, Mortensen UH, Baker SE, Andersen MR. 2018. Investigation of inter- and intraspecies variation through genome sequencing of Aspergillus section Nigri. Nat Genet 50:1688–1695. https://doi.org/10.1038/s41588-018-0246-1.

5. Zhao S, Latgé JP, 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.

6. Davis MP, van Dongen S, Abreu-Goedde C, Bartonicek N, Enright AJ. 2013. Kraken: a set of tools for quality control and analysis of high-throughput sequence data. Methods 63:41–49. https://doi.org/10.1016/j.ymeth.2013.06.027.

7. Martin M. 2011. Cutadapt removes adapter sequences from high-throughput sequencing reads. EMBnet J 17:10–12. https://doi.org/10.14806/ej.17.1.200.

8. Bankowich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prijibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.

9. Seppey M, Manni M, Zdobnov EM. 2019. BUSCO: assessing genome assembly and annotation completeness. Methods Mol Biol 1962:227–245. https://doi.org/10.1007/978-1-4939-9173-0_14.

10. Palmer J, Stajich J. 2017. Funannotate: eukaryotic genome annotation pipeline. Zenodo. https://doi.org/10.5281/zenodo.3548120.

11. Price MN, Dehal PS, Arkin AP. 2010. FastTree 2—approximately maximum-likelihood trees for large alignments. PLoS One 5:e9490. https://doi.org/10.1371/journal.pone.0009490.

12. Emms DM, Kelly S. 2015. OrthoFinder: solving fundamental biases in whole genome comparisons dramatically improves orthogroup inference accuracy. Genome Biol 16:157. https://doi.org/10.1186/s13059-015-0721-2.

13. Emms DM, Kelly S. 2019. OrthoFinder: phylogenetic orthology inference for comparative genomics. Genome Biol 20:238. https://doi.org/10.1186/s13059-019-1852-y.