




Draft Genome Sequence of *Aspergillus awamori* IFM 58123^{NT}

Masaaki Shimizu,^a Yoko Kusuya,^b Yikelamu Alimu,^b Cai Bian,^b  Hiroki Takahashi,^{b,c} Takashi Yaguchi^b

^aFaculty of Science, Chiba University, Chiba, Japan

^bMedical Mycology Research Center, Chiba University, Chiba, Japan

^cMolecular Chirality Research Center, Chiba University, Chiba, Japan

ABSTRACT Species of the *Aspergillus* section *Nigri* are taxonomically very complex. The taxonomic assignment of *Aspergillus awamori* is unclear. Here, we present the draft genome sequence of *A. awamori* strain IFM 58123^{NT}.

Aspergillus awamori belongs to the *Aspergillus* section *Nigri*, which is composed of *Aspergillus niger* and related black aspergilli (1). These species are the second most common isolates from clinical specimens next to those of *Aspergillus fumigatus* and are also known as common food spoilage fungi (2). On the other hand, they are used for the production of enzymes and organic substances by fermentation (2, 3). Despite the vast diversity among these species, the morphological and molecular similarities prevent accurate classification among them (4). The taxonomy of *Aspergillus* section *Nigri* has been revised several times based on molecular phylogenetic methods. Most of the strains previously classified as *A. awamori* have been reclassified as *Aspergillus wel-witschiae* (5). One cause of this misidentification problem is the poor resolution of molecular classification based on the limited number of genes. Thus, the whole-genome sequence of *A. awamori* strain IFM 58123^{NT} should help discern the phylogenetic complexity of the *Aspergillus* section *Nigri* species and develop industrial applications and accurate measures of food contamination.

A. awamori IFM 58123^{NT}, stored at the Medical Mycology Research Center at Chiba University (IFM strains) in Japan, was used in this study. No living type material of *A. awamori* exists, and Al-Musallam (6) revised the taxonomy of black *Aspergillus* spp. using cluster analysis involving all available morphological and cultural parameters; as a result, strain NRRL 4948 (= CBS 557.65) was designated the neotype strain of *A. awamori* (6). The nucleic acid sequence containing the calmodulin gene of strain IFM 58123^{NT} was 100% (543/543 bp) identical to that of NRRL 4948 (= CBS 557.65, GenBank accession number [KF288119](https://www.ncbi.nlm.nih.gov/nuccore/KF288119)). Therefore, the taxonomic position of IFM 58123^{NT} was confirmed. Following incubation in potato dextrose broth (PDB) at 37°C for 1 day, the genomic DNA of *A. awamori* IFM 58123^{NT} was extracted by phenol-chloroform extraction and using a NucleoBond AXG column (Macherey-Nagel, Düren, Germany) with NucleoBond buffer set III (Macherey-Nagel). The DNA libraries were prepared with the SMRTbell template prep kit 1.0 (Pacific Biosciences, Menlo Park, CA, USA), and genome sequencing was performed using a Pacific Biosciences RS II system. After filtering the reads by PreAssembler Filter version 1 (minimum subread length, 500 bp; minimum polymerase read quality, 0.80; minimum polymerase read length, 100 bp) in SMRT Analysis (version 2.3; Pacific Biosciences), we obtained a total of 622,132 reads summing 6,693,972,385 bp. The draft genome of *A. awamori* IFM 58123^{NT} was assembled with RS_HGAP_Assembly.3 protocol in SMRT Analysis (7) by Takara Bio (Mie, Japan). The draft genome contains 33 scaffolds, with a total size of 38,597,812 bp (49.35% G+C content). The N_{50} value and the maximum scaffold size were 4,298,649 bp and 6,450,824 bp, respectively. Prediction of protein-coding genes was performed using AUGUSTUS (version 2.5.5) with the option “–species=*aspergillus_oryzae*” (8), and a

Citation Shimizu M, Kusuya Y, Alimu Y, Bian C, Takahashi H, Yaguchi T. 2019. Draft genome sequence of *Aspergillus awamori* IFM 58123^{NT}. *Microbiol Resour Announc* 8:e01453-18. <https://doi.org/10.1128/MRA.01453-18>.

Editor Christina Cuomo, Broad Institute of MIT and Harvard University

Copyright © 2019 Shimizu et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Hiroki Takahashi, hiroki.takahashi@chiba-u.jp, or Takashi Yaguchi, yaguchi@chiba-u.jp.

M.S. and Y.K. contributed equally to this work.

Received 7 November 2018

Accepted 19 December 2018

Published 24 January 2019

total of 11,224 genes were observed. The 310 tRNAs and 135 rRNAs were predicted by tRNAscan-SE (version 1.3.1) (9) and RNAmmer (version 1.2) (10), respectively.

Data availability. The whole-genome sequences of *A. awamori* IFM 58123^{NT} have been deposited at DDBJ/EMBL/GenBank under the accession numbers [BDHI01000001](#) to [BDHI01000033](#). The raw sequencing reads have been submitted to the SRA under the accession number [DRA007470](#).

ACKNOWLEDGMENTS

We thank Masashi Murakami for helpful discussions and Ryoko Mori for technical assistance.

This work was partly conducted at the Joint Usage/Research Center on Tropical Disease, Institute of Tropical Medicine, Nagasaki University (2018-Kyoten-1).

REFERENCES

- Varga J, Frisvad JC, Kocsu b S, Brankovics B, T th 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>.
- Abarca ML, Accensi F, Cano J, Caba es FJ. 2004. Taxonomy and significance of black aspergilli. *Antonie Van Leeuwenhoek* 86:33–49. <https://doi.org/10.1023/B:ANTO.0000024907.85688.05>.
- Varga J, Kevei F, Hamari Z, T th B, T ren J, Croft JH, Kozakiewicz Z. 2000. Genotypic and phenotypic variability among black aspergilli, p 397–411. *In* Samson RA, Pitt JI (ed), *Integration of modern taxonomic methods for Penicillium and Aspergillus classification*. Harwood Academic Publishers, Amsterdam, the Netherlands.
- Samson RA, Noonim P, Meijer M, Houbraken J, Frisvad JC, Varga J. 2007. Diagnostic tools to identify black aspergilli. *Stud Mycol* 59:129–145. <https://doi.org/10.3114/sim.2007.59.13>.
- Hong SH, Lee M, Kim DH, Varga J, Frisvad JC, Perrone G, Gomi K, Yamada O, Machida M, Houbraken J, Samson RA. 2013. *Aspergillus luchuensis*, an industrially important black *Aspergillus* in East Asia. *PLoS One* 8:e63769. <https://doi.org/10.1371/journal.pone.0063769>.
- Hong SB, Yamada O, Samson RA. 2014. Taxonomic re-evaluation of black koji molds. *Appl Microbiol Biotechnol* 98:555–561. <https://doi.org/10.1007/s00253-013-5332-9>.
- Chin CS, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. 2013. Non-hybrid, finished microbial genome assemblies from long-read SMRT sequencing data. *Nat Methods* 10:563–569. <https://doi.org/10.1038/nmeth.2474>.
- Stanke M, Morgenstern B. 2005. AUGUSTUS: a Web server for gene prediction in eukaryotes that allows user-defined constraints. *Nucleic Acids Res* 33:W465–W467. <https://doi.org/10.1093/nar/gki458>.
- Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res* 25:955–964. <https://doi.org/10.1093/nar/25.5.955>.
- Lagesen K, Hallin P, R dland EA, Staerfeldt HH, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. *Nucleic Acids Res* 35:3100–3108. <https://doi.org/10.1093/nar/gkm160>.