

# Draft Genome Sequence of the Pathogenic Filamentous Fungus *Aspergillus lentulus* IFM 54703<sup>T</sup>

Yoko Kusuya,<sup>a</sup> Kanae Sakai,<sup>a</sup> Katsuhiko Kamei,<sup>a</sup> Hiroki Takahashi,<sup>a,b</sup> Takashi Yaguchi<sup>a</sup>

Medical Mycology Research Center, Chiba University, Chiba, Japan<sup>a</sup>; Molecular Chirality Research Center, Chiba University, Chiba, Japan<sup>b</sup>

*Aspergillus lentulus*, a sibling species of *Aspergillus fumigatus*, has been reported as a causative agent of aspergillosis, and exhibited low susceptibility to azole. Here, we present the draft genome sequence of *A. lentulus* strain IFM 54703<sup>T</sup> for the first time.

Received 16 November 2015 Accepted 18 November 2015 Published 14 January 2016

**Citation** Kusuya Y, Sakai K, Kamei K, Takahashi H, Yaguchi T. 2016. Draft genome sequence of the pathogenic filamentous fungus *Aspergillus lentulus* IFM 54703<sup>T</sup>. *Genome Announc* 4(1):e01568-15. doi:10.1128/genomeA.01568-15.

**Copyright** © 2016 Kusuya et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](http://creativecommons.org/licenses/by/4.0/).

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

Aspergillosis is a clinically important mycosis that comprises a wide variety of bronchopulmonary infections, such as invasive pulmonary aspergillosis, fungus ball in the lung cavity, and allergic bronchopulmonary aspergillosis (1). The most significant causative agent is *Aspergillus fumigatus*. Recently, it has been reported that cases of aspergillosis are caused by closely related species, phylogenetically distinguished with *A. fumigatus*. *Aspergillus lentulus*, one of these sibling species isolated from clinical specimens in the United States was described as a new species, not able to survive at 48°C, and potentially drug resistant, especially to voriconazole (2, 3). The molecular mechanisms of resistance against azole for *A. lentulus* are dependent on 14- $\alpha$  sterol demethylase (Cyp51A) but are different than what has been described previously for *A. fumigatus* (4). The whole-genome sequence of *A. lentulus* may be useful for elucidating the mechanisms resistant to antifungal agents, developing appropriate therapy in aspergillosis, and addressing the genetic diversity of *Aspergillus* species.

The fungal strain used in this study, *A. lentulus* IFM 54703<sup>T</sup>, was stored and maintained at the Medical Mycology Research Center, Chiba University (IFM strains) in Japan. *A. lentulus* genomic DNA extracted from 1-day-old culture by phenol-chloroform extraction and Nucleobond AXG column (TaKaRa) with Nucleobond buffer set III (TaKaRa). Genome sequencing was performed on a Pacific Biosciences RS II (Pacific Biosciences, Menlo Park, CA, USA) using libraries prepared with the SMRTbell template prep kit 1.0 (Pacific Biosciences). A draft genome of *A. lentulus* was assembled using SMRT Analysis 2.3 (Pacific Biosciences) (5). The sequencing runs and assembly of the libraries were carried out by TaKaRa Bio (Mie, Japan). Eventually, 19 scaffolds were obtained, summing up to 30,956,128 bp with an overall G+C content of 49.45%. The  $N_{50}$  and maximum scaffold were 4,166,724 bp, and 5,062,644 bp, respectively. Gene annotation using AUGUSTUS program 2.5.5 (6) trained with the parameters of the species *Aspergillus fumigatus* resulted in 9,860 genes. 200 tRNAs and 106 rRNAs were predicted by tRNAscan-SE 1.3.1 (7) and RNAmmer 1.2 (8), respectively.

**Nucleotide sequence accession numbers.** The whole-genome sequence of *A. lentulus* has been deposited at NCBI under the accession numbers [BCLY01000001](https://ncbi.nlm.nih.gov/assembly/GCF_01568_01/) to [BCLY01000019](https://ncbi.nlm.nih.gov/assembly/GCF_01568_01/).

## ACKNOWLEDGMENTS

This work was partly supported by MEXT KAKENHI (221S0002) and the Tenure Tracking System Program of MEXT (Y.K.). We are grateful to the National Bioresource Project: Pathogenic Microbes in Japan (<http://www.nbrp.jp/>).

## FUNDING INFORMATION

The Ministry of Education, Culture, Sports, Science, and Technology (MEXT) provided funding to Yoko Kusuya and Hiroki Takahashi under grant number 221S0002.

## REFERENCES

- Bodey GP, Vartivarian S. 1989. Aspergillosis. *Eur J Clin Microbiol Infect Dis* 8:413–437. <http://dx.doi.org/10.1007/BF01964057>.
- Balajee SA, Gribskov JL, Hanley E, Nickle D, Marr KA. 2005. *Aspergillus lentulus* sp. nov., a new sibling species of *A. fumigatus*. *Eukaryot Cell* 4:625–632. <http://dx.doi.org/10.1128/EC.4.3.625-632.2005>.
- Tamiya H, Ochiai E, Kikuchi K, Yahiro M, Toyotome T, Watanabe A, Yaguchi T, Kamei K. 2015. Secondary metabolite profiles and antifungal drug susceptibility of *Aspergillus fumigatus* and closely related species, *Aspergillus lentulus*, *Aspergillus udagawae*, and *Aspergillus viridinutans*. *J Infect Chemother* 21:385–391. <http://dx.doi.org/10.1016/j.jiac.2015.01.005>.
- Mellado E, Alcazar-Fuoli L, Cuenca-Estrella M, Rodriguez-Tudela JL. 2011. Role of *Aspergillus lentulus* 14- $\alpha$  sterol demethylase (Cyp51A) in azole drug susceptibility. *Antimicrob Agents Chemother* 55:5459–5468. <http://dx.doi.org/10.1128/AAC.05178-11>.
- Chin C, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. 2013. Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. *Nat Methods* 10:563–569. <http://dx.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. <http://dx.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. <http://dx.doi.org/10.1093/nar/25.5.0955>.
- Lagesen K, Hallin P, Rødland EA, Staerfeldt H-H, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. *Nucleic Acids Res* 35:3100–3108. <http://dx.doi.org/10.1093/nar/gkm160>.