EC Journals.ASM.org

GENOME ANNOUNCEMENT

Sequencing of *Cladosporium sphaerospermum*, a Dematiaceous Fungus Isolated from Blood Culture

Kee Peng Ng,[a] Su Mei Yew,[a] Chai Ling Chan,[a] Tuck Soon Soo-Hoo,[a] Shiang Ling Na,[a] Hamimah Hassan,[a] Yun Fong Ngeow,[a] Chee-Choong Hoh,[b] Kok-Wei Lee,[b] and Wai-Yan Yee[b]

Department of Medical Microbiology, Faculty of Medicine, University of Malaya, Kuala Lumpur, Malaysia,[a] and Codon Genomics SB, Jalan Bandar Lapan Belas, Pusat Bandar Puchong, Selangor Darul Ehsan, Malaysia[b]

***Cladosporium sphaerospermum* is one of the most widely distributed allergens causing serious problems in patients with respiratory tract disease. We report the 26,644,473-bp draft genome sequence and gene annotation of *C. sphaerospermum* UM843. Analysis of the genome sequence led to the finding of genes associated with *C. sphaerospermum*'s melanin biosynthesis, allergens, and antifungal drug resistance.**

Cladosporium spp. are dematiaceous fungi usually identified as common airborne contaminants occupying a wide variety of habitats (9). This allergenic fungus has been reported to cause subcutaneous phaeohyphomycosis and intrabronchial lesions in immunocompetent individuals (6, 8). Patients with allergic respiratory tract disease are highly sensitive to *Cladosporium* spores. Despite their clinical importance, *Cladosporium* spp. have been poorly described and no reference genome sequence is currently available. Here, we report a draft genome sequence of *Cladosporium sphaerospermum* UM843 isolated from blood culture. This isolate was identified by macro- and microscopic characteristics and confirmed by internal transcribed spacer (ITS)-based PCR amplification.

The *C. sphaerospermum* UM843 genomic DNA was sequenced to a 50-fold depth of coverage using the Illumina HiSeq 2000 by employing the whole-genome shotgun strategy on a 500-bp DNA insert size library. The genome size was estimated to be 31.92 Mb. All genomic sequencing reads were assembled using the SOAPdenovo assembler, version 1.05 (5). The 129,747 contigs generated were arranged into 340 scaffolds (≥1,000 bp) with an N_{50} size of 257 kb. The total length of the scaffold sequences is 26,644,473 bp, with G+C content of 55.73%. A total of 10,020 genes, with 9,466 (94%) being longer than 100 amino acids, was predicted using GeneMark-ES version 2.3 (7). The predicted gene model has an exon frequency of 2.26 exons per gene. The functional annotation of the gene models was carried out via BLAST searches against the Swiss-Prot protein sequence database, which yielded a total of 6,352 (63.39%) gene matches.

The key enzymes tetrahydroxynaphthalene reductase, scytalone dehydratase, trihydroxynaphthalene reductase, laccase, and precursor malonyl-coenzyme A (CoA) genes were detected in the UM843 genome sequences, indicating the production of melanin via the dihydroxynaphthalene (DHN)-melanin biosynthesis pathway. The fungal melanin function has been postulated to protect against UV irradiation, enzymatic lysis, oxidant attack, and fungal infectivity (2, 4). Genes associated with potent human allergens, such as enolase (Cla h 6), aldehyde dehydrogenase (Cla h 3), and mannitol dehydrogenase (Cla h 8), commonly produced by *Cladosporium* species (1, 3), were also detected. The identification of these allergen gene sequences would further improve future diagnosis and allergen immunotherapy treatments. Several genes associated with resistance to the antifungal drugs fluconazole, quinidine, and fluorocytosine were also revealed. These observations offer tremendous opportunities to study drug resistance mechanisms in *Cladosporium* species.

The draft genome of *C. sphaerospermum* UM843 is the first reported genome sequence from a *Cladosporium* species isolated from a patient's blood culture. The genomic information derived from *C. sphaerospermum* genome sequences provides a crucial reference to improve future allergenic, antifungal, and fungal diagnosis studies, as well as genomic comparison studies between related fungal genera.

Nucleotide sequence accession number. The nucleotide sequence of the *C. sphaerospermum* UM843 genome is deposited in DDBJ/EMBL/GenBank with accession number AIIA00000000.

ACKNOWLEDGMENTS

This study was supported by a research grant UM.C/625/1/HIR/004 from the University of Malaya.

K.P.N., Y.F.N., and H.H. conceived the project and contributed to the writing and editing of the manuscript. K.P.N., T.S.S.-H., C.L.C., and S.L.N. were responsible for the isolation, identification and DNA extraction. S.M.Y., C.-C.H., K.-W.L., and W.-Y.Y. performed the genome sequencing and bioinformatics analysis.

REFERENCES

1. **Bowyer P, Denning DW.** 2007. Genomic analysis of allergen genes in *Aspergillus* spp: the relevance of genomics to everyday research. Med. Mycol. **45**:17–26.
2. **Finch J, Arenas R, Baran R.** 16 January 2012. Fungal melanonychia. J. Am. Acad. Dermatol.
3. **Knutsen AP, et al.** 2012. Fungi and allergic lower respiratory tract diseases. J. Allergy Clin. Immunol. **129**:280–291.

Received 10 March 2012 **Accepted** 13 March 2012

Address correspondence to Kee Peng Ng, kpng@um.edu.my.

doi:10.1128/EC.00081-12

4. **Langfelder K, Streibel M, Jahn B, Haase G, Brakhage AA.** 2003. Biosynthesis of fungal melanins and their importance for human pathogenic fungi. Fungal Genet. Biol. **38**:143–158.
5. **Li R, Kristiansen K, Wang J.** 2008. SOAP: Short Oligonucleotide Alignment Program. Bioinformatics **24**:713–714.
6. **Qiu-Xia C, et al.** 2008. Subcutaneous phaeohyphomycosis caused by *Cladosporium sphaerospermum*. Mycoses **51**:79–80.
7. **Ter-Hovhannisyan V, Lomsadze A, Chernoff Y, Borodovsky M.** 2008. Gene prediction in novel fungal genomes using an ab initio algorithm with unsupervised training. Genome Res. **18**:1979–1990.
8. **Yano S, Koyabashi K, Kato K.** 2003. Intrabronchial lesion due to *Cladosporium sphaerospermum* in a healthy, non-asthmatic woman. Mycoses **46**:330–332.
9. **Zalar P, et al.** 2007. Phylogeny and ecology of the ubiquitous saprobe *Cladosporium sphaerospermum*, with descriptions of seven new species from hypersaline environments. Stud. Mycol. **58**:157–183.