Draft Genome Sequence of *Fonsecaea nubica* Strain CBS 269.64, Causative Agent of Human Chromoblastomycosis

Flávia F. Costa,a,b Sybren de Hoog,b,c,d Roberto T. Raittz,c Vinicius A. Weiss,c Aniele C. R. Leão,c Amanda Bombassaro,b, Jiufeng Sun,b,d Leandro F. Moreno,b,c,e Emanuel M. Souza,c,f,g Fabio O. Pedrosa,c,f,g Maria Berenice R. Steffens,c,f,g Valter Baura,c Michele Z. Tadra-Sfeir,f Eduardo Balsanelli,f M. Javad Najafzadeh,g Renata R. Gomes,g Maria S. Felipe,h Marcus Teixeira,i,1 Germana D. Santos,b,1 Liyan XJ,h Mauro Antônio Alves de Castro,b,1 Vânia A. Vicente,a,b

Engineering Bioprocess and Biotechnology Post-Graduation Program, Department of Bioprocess Engineering and Biotechnology, Federal University of Pará, Pará, Brazil; b Microbiology, Parasitology and Pathology Post-Graduation Program, Department of Pathology, Federal University of Pará, Pará, Brazil; c Laboratory of Bioinformatics, Professional and Technological Education Sector, Federal University of Pará, Pará, Brazil; d Guangdong Provincial Institute of Public Health, Guangdong Provincial Center for Disease Control and Prevention, Guangdong, China; e CBS-KNAW Fungal Biodiversity Center, Utrecht, The Netherlands; f Department of Biochemistry, Federal University of Pará, Pará, Brazil; g Department of Parasitology and Mycology, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran; h Catholic University of Brasilia UCB, Brasília, Brazil; i Division of Pathogen Genomics, Translational Genomics Research Institute, Flagstaff, Arizona, USA; j Department of Dermatology, Sun Yat-Sen Memorial Hospital, Sun Yat-sen University, Guangzhou, China

On the basis of multilocus phylogenetic data, *Fonsecaea nubica* was described in 2010 as a molecular sibling of *F. monophora*, an established agent of the human skin disease chromoblastomycosis in tropical zones. Genome analysis of these pathogens is mandatory to identify genes involved in the interaction with host and virulence.

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Address correspondence to Vânia A. Vicente, vaniava63@gmail.com, or Mauro Antônio Alves de Castro, mauro.a.castro@gmail.com.

The genus *Fonsecaea* comprises anamorphic members in the *Chaetothyriales*, an ascomycete order of black yeasts and filamentous relatives covering numerous opportunistic pathogens on humans (1–3). *Fonsecaea* is one of the prevalent genera of etiologic agents of chromoblastomycosis (4,5), a chronic, cutaneous, and subcutaneous infection characterized by slowly expanding, polymorphic skin lesions with muriform cells in tissue, provoking a granulomatus immune response (6,7). The disease occurs preferentially in humans, although some cases have been reported in other mammals (8–10). Several *Fonsecaea* species are involved as etiologic agents of the disease, i.e., *F. pedrosoi*, *F. monophora*, *F. nubica*, and *F. pogonactis*, each with different virulence potentials (6,11). *F. nubica* was first described in 2010 with type strain CBS 269.64, isolated from a human patient with chromoblastomycosis in the west Cameroon (6,12). Genome analysis of the pathogenic fungus *F. nubica* is needed to identify genes involved in the interaction with host cells and molecular mechanisms in response to cytotoxic agents (13).

Strain *F. nubica* CBS 269.64 was grown in Sabouraud’s broth, with shaking at 150 rpm at 28°C for 7 days and DNA was extracted by the cetyltrimethylammonium bromide (CTAB) method with phenol-chloroform/isooamyl alcohol. Total DNA was purified with the microbial DNA UltraClean kit. DNA of *F. nubica* was used for library construction using the Ion Plus Fragment library kit (Thermo, FisherScientific) and Nextera XT (Illumina) following the manufacturer’s instructions. The libraries were sequenced on an Ion Proton (Thermo, FisherScientific) for single-end reads and in MiSeq (Illumina) for paired-end reads. The quality of the reads was assessed by means of FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc). The reads were assembled de novo using SPADES v3.6.2 (14). The draft genome comprised 258 contigs and the genome size was 33.7 Mb, with a G+C content of 52.46%. Protein-coding genes were predicted with GeneMark-ES (15). Gap closure was performed with FGAP software (16). Annotation for 11,681 predicted genes was assigned based on similarity searches against the nr database using RAFTS3 (17) and InterProScan (18) comparisons. The genome contained 36 tRNAs identified using ARAGORN (19).

Information about the genome sequence of this black yeast might provide a better understanding of the basic mechanisms of adaptation to requirements of the environmental habitat, and of pathogenicity and virulence.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under accession number LVCI00000000. The version described in this paper is version LVCI01000000.

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