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Draft Genome Sequence of *Fonsecaea monophora* Strain CBS 269.37, an Agent of Human Chromoblastomycosis

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The black yeast *Fonsecaea monophora* is one of the main etiologic agents of chromoblastomycosis in humans. Its pathogenicity profile is more invasive than that of related *Fonsecaea* species, causing brain infection in addition to (sub)cutaneous infections.

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The black yeasts are heterogeneous organisms responsible for a wide variety of clinical conditions, ranging from superficial to deep and disseminated infections (1, 2). Chromoblastomycosis is a unique disease characterized by lesions of skin and subcutaneous tissue, leading to a warty appearance with ulcerative, tumorous eruptions. Occasionally, the same fungi manifest systemically in internal organs (3). The disease has three main etiological agents, *Fonsecaea pedrosoi*, *Phialophora verrucosa*, and *Cladophialophora carrionii* (4). Recently, different species have been recognized in *Fonsecaea* as agents of disease (4–7). These agents probably have a life cycle in the environment but have a pathogenic potential. The pathogenicity of *F. monophora* is reflected in low environmental occurrence and high frequency in the human host. Chromoblastomycosis appears to be polyphyletic within a single family of fungi, and is caused by different, rather distantly related species (8). The species *F. monophora* presents a virulence profile that differs from that of other *Fonsecaea* agents of the disease, as it causes cutaneous and subcutaneous chromoblastomycosis but frequently also primary brain infection (9, 10). The epidemiology of the disease has not been fully elucidated; questions related to its infection route, prevalent etiologic agents, and virulence have to be clarified. Total genome sequencing will help to elucidate virulence genes and pathogenicity mechanisms of the agents. Functional analysis of these genes will contribute to finding novel targets for drug development to improve therapy, and will provide further understanding of relevant genes expressed during infection (11).

Fonsecaea monophora CBS 269.37, a type strain of the species, was isolated in South America in 1936, redescribed by de Hoog et al. (4), and used in this study. The strain 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 using phenol-chloroform/isoamyl alcohol. Total DNA was purified with the Microbial DNA ultra-clean kit. Two libraries were constructed using the kit Nextera XT for construction of the paired end library (2 × 300) and library prep kit for Ion Torrent (Thermo, Fisher Scientific) generating over 6 million readings. Genomic sequence reads were generated on the Illumina platform MiSeq (Life Technology) and Ion Torrent PGM platform (Thermo, Fisher Scientific). The reads were assembled *de novo* using SPADES v3.5.0 (12). The draft comprised 324 contigs, with a N_{50} of 268,916 bp and the genome size was 35.22 Mb, with a G+C content of 52.22%. Gap closure was performed with FGAP software (13). Protein-coding genes were predicted with GeneMark-ES (14). Annotation for 11,984 predicted genes were assigned based on similarity searches against the nr database using RAFTS3 (15) and InterProScan (16) comparisons. The genome contained 37 tRNAs identified using ARAGORN (17).

The information generated via this genome sequence might provide better understanding of the basic mechanisms of adaptation to its natural habitat, as well as of its pathogenicity and virulence.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. LVKK00000000. The version described in this paper is version LVKK01000000.

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