Title: THE DRAFT GENOME OF *Fonsecaea monophora*

Authors: Bombassaro, A.[1], Gomes, R.R.[1], Weiss, V. A. [2], Leão, A. C. R.[2], Costa, F. F.[3], Vicente, V.A.[1]

Institution: 1 UFPR - Federal University of Paraná - Program Post Graduate in Microbiology, Parasitology and Pathology. 2 UFPR - Federal University of Paraná - Program Post Graduate in Bioinformatics. 3 UFPR - Federal University of Paraná - Program Post Graduate in Bioprocess Engineering and Biotechnology - Curitiba / PR - CEP: 81540-970.

Abstract:

The black yeasts are heterogeneous organisms responsible for a wide variety of clinical conditions, ranging from surface infections, skin and subcutaneous tissue, and allergies to disseminated infections. Chromoblastomycosis is characterized by lesions of skin and subcutaneous, warty appearance may emerge as ulcerative eruptions tumor aspect, which can also manifest in systemic and widespread in internal organs. This disease occurs mainly in rural areas of tropical and subtropical regions, with endemic areas in Brazil, the Amazon region and Maranhão. A study of molecular epidemiology of the disease revealed as main etiological agents, *Fonsecaea, Phialophora* and *Cladophialophora*. The *Fonsecaea* genus was recently rewritten, where different species have been reported associated with human, animal and environmental sources hosts whose ecology seems to direct the evolution of the clinical manifestations of the disease. These agents appear to have a life cycle compound and pathogenic potential, thus justifying the low environmental occurrence and frequency of infection in host animals. This potential infection appears to be polifiletic and therefore differs among species. Among these, the species *F. monophora* presents a different virulence profile and can be the cause of most cases of brain infections in human patients. In order to elucidated the questions adressed, performing the genetic sequecing of the *F. monophora* CBS 269.37, aiming to assemble and order the largest number of contigs. The genome sequencing was performed by the Illumina platform (GA technology IIx) MiSeq. It was used the NEXTERA XT kit for paired-end library construction (2x300), generating more than 6 million of reads. The Celera Assembler was used to assemble the draft genome in 1540 supercontigs with a G+C content of 52% and ~34,5Mb. The gap closure was performed with Fgap software and overlap searches using Blast. The GeneMark-ES identified 12628 ORFs and the automatic annotation was obtained with sequence similarity search using SILA software and the NR database. The genomes of *F.*

pedrosoi CBS 271.37 and *F. erecta* CBS 125.763 were used as reference for genome comparisons. More runs are needed to improve the quality of data.

Keywords: chromoblastomycosis, *Fonsecaea monophora*, genome

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