Title: THE DRAFT GENOME OF *Fonsecaea nubica* CBS 125.198

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Abstract: The black yeasts are agents capable of inhabiting a wide range of soil niches, tree barks, thorns, fruits, plants. There are also reports of acting as pathogens in fish, animals and humans. These fungi can develop a condition called chromoblastomycosis, which is characterized by the slow development of polymorphic skin lesions, often accompanied, in the initial stage, of erythematous papules, which gradually increase in size, with different morphological structures with nodes, warts, plates and scar tissue. The higher incidence of the disease in Latin America takes place in Brazil in the state of Maranhão and has been linked to traumatic infection caused by plants associated with *Fonsecaea pedrosoi*. Elsewhere in the world, the disease is caused by other three species (*F. pedrosoi*, *F. monophora* and *F. nubica*) and have different virulence potential. The *Fonsecaea* genus species, called *F. nubica* was first described in 2010 and molecular tools identified as being *Fonsecaea* genus, also composed by *F. pedrosoi* and *F. monophora*, with the *F. nubica* being more related to chromoblastomycosis. Pathogenic fungus *F. nubica* transcriptome analysis identified genes involved in the interaction with host cells and molecules in response to cytotoxic agents. 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 3 million of reads. The Celera Assembler was used to assemble the draft genome of *F. nubica* CBS 125.198 in 68028 supercontigs with a G+C content of 54% and ~30 Mb. The gap closure was performed with Fgap software and overlap searches using Blast. The genomes of *F. pedrosoi* CBS 271.37, *F. erecta* CBS 125.763 and *F. monophora* CBS 269.37 were used as reference for genome comparisons.

Keywords: chromoblastomycosis, *Fonsecaea nubica*, genome

Development agency: CAPES