First Draft Genome of Two *Candida haemulonii* Strains from Pediatric Patients with Candidemia in Brazil

Luiza Souza Rodrigues^{1,2}, Rajesh Kumar Gazara³, Hemanoel Passarelli³, Robson Francisco de Souza⁴, Thiago Motta Venancio^{3#} and Libera Maria Dalla Costa^{1#}

¹ Faculdades Pequeno Príncipe e Instituto de Pesquisas Pelé Pequeno Príncipe (FPP/IPPPP), Curitiba-PR, Brazil; ² Centro Universitário Autônomo do Brasil (UniBrasil), Curitiba-PR, Brazil; ³ Lab. de Química e Função de Proteínas e Peptídeos, CBB/UENF, Campos dos Goytacazes-RJ, Brazil; ⁴ Laboratório de Estrutura e Evolução de Proteínas (LEEP)/ICB/USP, São Paulo-SP, Brazil.

Co-Corresponding authors

INTRODUCTION

Members of the *Candida haemulonii* species complex (*C. haemulonii*, *C. duobushaemulonii* and *C. haemulonii* var. *vulnera*) are emerging yeasts associated to bloodstream and other invasive infections. Considered as opportunistic pathogens they are phylogenetically related to *C. auris*, which shares a propensity for multidrug resistance. However, genomic information of *C. haemulonii* remains scarce. We describe the draft genome sequencing of two *C. haemulonii* strains isolated from pediatric patients with candidemia at a tertiary pediatric hospital of South of Brazil.

METHOD

RESULTS

Figure 1. a. *C. haemulonii* has highest number of genes orthologs in *C. pseudohaemulonii*. b-d Functional annotation of *C. haemulonii* predicted proteins for the main ontology domains (GO terms).

The draft genomes comprised 352 and 388 scaffolds, with a N50 of 78,004 bp and 75,117 bp, and largest scaffolds with 393,866 bp and 251,044 bp. Total genome sizes were 13,21 Mb and 13,26 Mb, with an average G+C content of 44%. BUSCO analysis (*Saccharomycetales* dataset as reference, 1,771 genes) indicated that the assemblies are 94.6% and 94.5% complete. Less than 2.0% of the sequences were masked. The complete genomes sequences contain genes for 6 rRNAs, 175 and 173 tRNAs. AUGUSTUS resulted in 5,484 and 5,508 proteins-coding genes and functional annotations were done in Blast2GO resulted in 3,690 and 3,682 sequences with GO terms.

CONCLUSION

The data provided here will constitute a powerful tool for fungal biology and virulence studies, also to better understand of the phylogenetic relationships to other *Candida* species, such as the emerging pathogen *C. auris*.

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