

**TITLE:** GENETIC DIVERSITY IN *Cryptococcus laurentii* ISOLATED FROM PUBLIC PLACES IN THE STATE OF MARANHÃO, BRAZIL.

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**ABSTRACT:**

Cryptococcosis is a disease that mainly affects the lungs, with high chances of spreading to the central nervous system. Excreta of pigeons and eucalyptus are environmental sources of infection where *Cryptococcus neoformans* and *Cryptococcus gattii* can be easily isolated. However, *Cryptococcus laurentii* an emerging human pathogen, formerly considered saprophytic and non-pathogenic, is currently associated with several infections, especially in immunocompromised patients, being associated with new cases of human diseases through contact with fungal propagules in the soil. The use of molecular markers becomes a tool of great relevance, since it allows to evaluate the genetic variability, as well as to estimate the divergence between the same species. In this context, we evaluated genetic diversity in *Cryptococcus laurentii* isolated from public places in the State of Maranhão. *C. laurentii* was isolated from squares as João Lisboa (1, 2 and 3), Nauro Machado (4, 5 and 6) Maria Aragão (7, 8 and 9) in the municipality of São Luís; and Balaiada's belvedere in the municipality of Caxias (10). PCR-fingerprint with (GACA)<sub>4</sub> oligo was carried out to investigate polymorphisms in the regions of Inter Simple Sequence Repeats (ISSR). Dendrogram generated by UPGMA analysis of Jaccard similarity (NTSYS, v. 2.10m) displayed two main clusters and a simplicifolious. The first cluster was composed by 1, 3, 4 and 5 isolates that displayed similarities between 55% and 32%. In the second cluster, the number 6 isolate presented 71% similarity with isolates that had identical band patterns (2, 7, 8 and 9). The simplicifolious (10) had the lowest similarity (6%) with the others. The genetic diversity assessment of environmental fungi is important to give strength the microbial biogeography studies, so that eventual cases of mycoses may be monitored.

**Keywords:** *Cryptococcus laurentii*, ISSR, genetic diversity, environmental fungi, mycose.

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