

TITLE: GENOTYPES OF CLINICAL AND ENVIRONMENTAL *CRYPTOCOCCUS NEOFORMANS/C. GATTII* SPECIES COMPLEX PREVALENT IN ALAGOAS, BRAZIL

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ABSTRACT:

Cryptococcus neoformans and *C. gattii* species complex is the etiologic agent of cryptococcosis, the second most common life-threatening systemic fungal disease of worldwide occurrence, whose infection is acquired by inhalation of airborne infectious particles from pigeon droppings, tree hollows, and decaying wood. The epidemiological significance of certain genotypes has been noticed, mainly due to the frequent association between the geographic origin and specific genotypes. Considering that genotype data from Alagoas (AL) are nonexistent, the main objective of the current study was to determine the molecular types of 21 strains, of which 12 were clinical and recovered from cerebrospinal fluid (CSF) of 9 patients with suspected meningitis attending the Hospital Escola Dr. Hέλvio Auto, mostly with impaired immunity HIV/AIDS related, and 9 were from environmental sources (pigeon droppings and tree hollows) in Maceiό-Alagoas, Brazil (2013 to 2016). Restriction fragment length polymorphism (RFLP) of *URA5* was performed according to the Rede Brasileira de Criptococose, and the fragment patterns were compared to the eight standard genotypes (VNI-VNIV and VGI-VGIV). Out of 21 isolates, 66,67% (14/21) were assigned to *C. neoformans* VNI, 12 of them (12/14) being recovered from patients with cryptococcal meningitis, and 2 were isolated from a tree hollow (2/14). VNI genotype corresponds to *C. neoformans* var. *grubii* serotype A and is globally prevalent in immunocompromised patients. One isolate from pigeon droppings (1/21) corresponded to *C. neoformans* VNIV, that represents *C. neoformans* var. *neoformans* serotype D which has been reported as frequent in Latin America. Five strains from tree hollows and one from pigeon droppings (6/21) corresponded to *C. gattii* genotype VGII, represented by serotypes B or C, which is the most common environmental type of the species. Additionally, from the 7 strains of a tree hollow, 2 were VNI and 5 VGII. Concluding, *C. neoformans* VNI and VNIV, as also *C. gattii* VGII are present in clinical and environmental sources in Alagoas. The genotypes identified in this study were similar to others taking into account strains from South America and from Northeast Brazil and can provide additional information on the globally ecoepidemiology of *Cryptococcus* spp., contributing to the detection of emergent high virulent strains and to the understanding and development of preventive and effective clinical responses.

Keywords: *Cryptococcus* spp., genotyping, *URA5*, PCR/RFLP

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