

Molecular typing of clinical isolates of *Cryptococcus neoformans*/*Cryptococcus gattii* species complex from Northeast Mexico

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Abstract

Cryptococcosis is caused by members of the *Cryptococcus neoformans*/*Cryptococcus gattii* species complex. Based on molecular identification, these two species have been further differentiated into molecular types. The aim of this work was to characterize clinical cryptococcal isolates recovered from six hospitals in Northeast Mexico from 1995 to 2011. One hundred and sixty-six isolates, which were characterized by biochemical tests and in vitro susceptibility to amphotericin B, fluconazole, and voriconazole, and M13 PCR fingerprinting, were included in this study. Utilizing phenotypic tests, 153 isolates (92.16 %) were identified as *C. neoformans* and 13 (7.83 %) as *C. gattii*. All isolates were susceptible to all antifungals tested. Employing M13 PCR fingerprinting, eight molecular types were detected. VNI was the most common genotype (124 cases; 74.6 %), followed by VNII (15 cases; 9 %), VNIII (8 cases; 4.8 %), VNIV (6 cases; 3.6 %), VGI (6 cases; 3.6 %), VGII (3 cases; 1.8 %), and VGIII and VGIV (2 cases, 1.2 % each). We confirm the presence of *C. gattii* in clinical isolates in Northeast Mexico, and a high clonal diversity in the studied strains of *C. neoformans*/*C. gattii* species complex.

Keywords

Fluconazole Clinical Isolate Itraconazole Voriconazole Molecular Type

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Notes

Conflict of interest

The authors declare that they have no competing interests.

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