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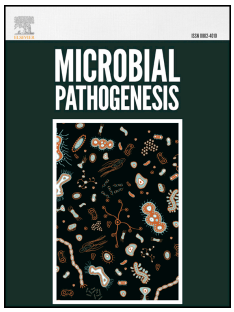

Candida albicans - Biology, molecular characterization, pathogenicity, and advances in diagnosis and control – An update

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ACCEPTED MANUSCRIPT

Candida albicans - biology, molecular characterization, pathogenicity, and advances in diagnosis and control – An Update

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ABSTRACT

Candida albicans is an emerging multidrug-resistant fungal pathogen representing an important source of invasive disease in humans and generating high healthcare costs worldwide. This fungus is frequently found in different anatomical sites of healthy persons and could induce systemic and superficial infections under optimal environmental conditions. Invasive candidiasis (IC) is an important nosocomial infection with high morbidity and mortality rates in hospitalized children. It represents a major source of prolonged infections in intensive care unit (ICU), particularly in immunosuppressed or elderly patients. Clinical diagnosis of candidiasis could be difficult because of the lack of specific symptoms and clinical signs. Although *C. albicans* is the most frequently isolated *Candida* species in IC, non-albicans *Candida* (NAC) species are also commonly detected. Multilocus enzyme electrophoresis (MLEE), fragment length polymorphism (RFLP), electrophoretic karyotyping (EK), and random amplified polymorphic DNA (RAPD), multilocus sequence typing (MLST) are known as an efficient technique used for molecular typing of *Candida* species. The efficacy of antifungal treatment against candidiasis has been

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