Candida albicans bloodstream isolates in a German university hospital are genetically heterogenous and susceptible to commonly used antifungals.

Huyke J, Martin R, Walther G, Weber M, Kaerger K, Bougnoux ME, Elias J, Kurzai O (2015) Candida albicans bloodstream isolates in a German university hospital are genetically heterogenous and susceptible to commonly used antifungals. *Int J Med Microbiol* 305(7), 742-747.

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Abstract

From an eight-year-span, 99 Candida bloodstream isolates were collected at the University Hospital Wuerzburg, Germany. In this study, all strains were analyzed using molecular and phenotypic typing methods. Confirmatory species identification revealed three isolates that were initially diagnosed as C. albicans to be actually C. dubliniensis. Two isolates contained a mixed culture of C. albicans and C. glabrata, in one of the specimens both species could be separated while it was not possible to recover C. albicans in the other sample. The remaining 95 C. albicans isolates were profiled by multilocus sequence typing (MLST). Phylogenetic analyses showed a highly heterogenous collection of strains, associated with many different clades and constituting a set of new diploid sequence types (DST). For all strains with identical DST, patient data were reviewed for potential nosocomial transmission. In addition, all isolates were tested for their susceptibility to amphotericin B, caspofungin, fluconazole, itraconazole, posaconazole and

voriconazole. No clinically relevant resistance could be detected. Furthermore, these data underline that correlation between minimal inhibitory concentrations for caspofungin and anidulafungin is low.

Involved units

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Leibniz-HKI-Authors



Johanna Huyke

Details



Kerstin Kaerger

Details



Oliver Kurzai

Details



Ronny Martin

Details



Grit Walther

Details



Michael Weber

Details

Identifier

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