Molecular typing and antifungal susceptibility of Exophiala isolates from patients with cystic fibrosis

Titre	Molecular typing and antifungal susceptibility of Exophiala isolates from patients with cystic fibrosis
Type de publication	Article de revue
Auteur	Packeu, A. [1], Lebecque, P. [2], Rodriguez-Villalobos, H. [3], Boeras, A. [4], Hendrickx, Marijke [5], Bouchara, Jean-Philippe [6], Symoens, Françoise [7]
Editeur	Society for General Microbiology
Type	Article scientifique dans une revue à comité de lecture
Année	2012
Langue	Anglais
Date	2012/09/01
Numéro	Pt9
Pagination	1226 - 1233
Volume	61
Titre de la revue	Journal of Medical Microbiology
ISSN	1473-5644
Résumé en anglais	The black yeast Exophiala dermatitidis is a frequent agent of colonization of the lungs of patients with cystic fibrosis (CF). A total of 71 clinical isolates of Exophiala from 13 patients were identified at the species level by sequencing the internal transcribed spacer (ITS) regions 1 and 2 of the rDNA genes and typed by random amplification of polymorphic DNA (RAPD), using two different primers, BG-2 and ERIC-1. In vitro susceptibility of these isolates to some systemic antifungal drugs was investigated using the CLSI method. Almost all the isolates were identified as E. dermatitidis, but long-term colonization with the closely related species E. phaeomuriformis was observed in one patient. No clustering was found according to the geographical origin of the isolates, the isolation date or the antifungal susceptibility. Variations were seen in the susceptibility of studied isolates to antifungals but most of them exhibited low susceptibility to amphotericin B and although some patients were successively colonized by two distinct genotypes, most of the isolates were distributed in patient-specific clusters. This phenomenon may be due to genomic variations of E. dermatitidis in the lung environment of CF patients. These results are typical of colonization of the airways of patients by a poorly distributed environmental fungus, which occupies particular reservoirs that need to be defined.
URL de la notice	http://okina.univ-angers.fr/publications/ua4951 [8]
DOI	10.1099/jmm.0.042317-0 [9]
Lien vers le document	http://dx.doi.org/10.1099/jmm.0.042317-0 [9]

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