Prevalence of the sibling species of the Scedosporium apiospermum complex in cystic fibrosis context

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Objectives:
Cystic fibrosis is the most common genetic inherited disease in the European Caucasian population (frequency 1 out of 2500 births). Disease causes are mutations in the CFTR (cystic fibrosis transmembrane conductance regulator) gene, which encodes a chloride channel in the plasma membrane of several epithelial cells. However, prognosis essentially depends on the severity of the lesions in the lungs. The defective mucociliary clearance and the thickening of the bronchial mucus resulting from these mutations facilitate the entrapment of airborne microbes. Patients with such chronic pulmonary defect are at high risk for colonizations/infections by fungi, including the emergent pathogens of the *Scedoporium apiospermum* complex. This species complex ranks the second among the filamentous fungi colonizing the airways of CF patients.
Recent molecular studies supported by morphological, physiological and genetic observations showed that the *S. apiospermum* complex comprises at least five distinct species. Antifungal susceptibility profiles and virulence of these sibling species showed differences. This study aims to determine the prevalence of the different species of *S. apiospermum* complex in the CF context and to analyze the chronic trait of these infections.
Methods:
A set of 50 epidemiologically unrelated isolates was analyzed to estimate the prevalence, all isolates having been recovered from distinct patients with CF followed up in different university hospitals from France and initially identified as belonging to the *S. apiospermum* complex. The internal transcribed spacer (ITS) regions 1 and 2 of the ribosomal RNA gene, a fragment of the nuclear gene calmodulin (CAL) and two regions (BT2 and TUB) within the ß-tubulin gene were amplified and sequenced as described by Gilgado et al.
Additionally, sequential (from successive sputum samples from the same patient) and multiple (from the same clinical sample) isolates were genotyped by random amplification of polymorphic DNA (RAPD) using primers GC70, UBC-701 and UBC-703.
Results and conclusion:
Pseudallescheria boydii was the most common specie encountered (62% of the isolates) in the CF context, followed by *S. apiospermum sensu stricto* (24%) and *S. aurantiacum*
(10%). These results contrast with the natural occurrence of these species in the environment, reinforcing the need for further studies aiming to elucidate the pathogenic mechanisms of these fungi. As reported by Kalsteis et al., S. apiospermum sensu stricto is the most prevalent specie in the environment, accounting for 58.7–77.7% of the isolates (depending on the habitat studied), while low prevalence were found for *S. aurantiacum* and *P. boydii*, which represented 4.8 (industrial areas) to 7.7% (parks and playgrounds) and 1.9–2.3% of the isolates, respectively. Likewise, *Scedosporium dehoogii*, which represented about 13.8–28.8% of the isolates from environmental samples, has not been described in a clinical context as yet.
Moreover, our results suggest a clustering according to the geographic origin of the isolates: CF patients from the West of France were predominantly colonized by *P. boydii*.
Events of chronic colonization were observed for each specie of *S. apiospermum* complex encountered in CF context. The RAPD genotyping demonstrated also that two different species could concomitantly colonize the same patient.

Résumé en anglais

Notes

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