What can be learned from phenotyping and genotyping analyses of Scedosporium prolificans isolates from diverse origins?

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Résumé en anglais	**Introduction:** *Scedosporium prolificans* is a filamentous fungus considered as an emerging opportunistic member of the order Microascaceae. This fungus has a broad clinical spectrum and can cause different types of infections: localized colonization in immunocompetent hosts or disseminated mycosis in immunocompromised patients. Moreover, *S. prolificans* resistance to most antifungal agents has been reported. Compared to the well characterized *Scedosporium* / *Pseudallescheria* complex, little is known about the fundamental aspects of S. prolificans biology, pathogenicity and epidemiology. **Aim of the study:** Our goal was to characterize a large population of S. prolificans strains, isolated from animals, human, or environment samples in different countries (European, USA and Australia). **Results & methods:** All strains were prospectively collected, and grown at 30# C on Sabouraud's agar medium with kanamycin for 1 week. DNA was extracted from subcultures using UltraClean Fecal# DNA kit (MoBio, France). To improve the knowledge of this species at the phylogenetic level, we combined phenotypic criteria such as macroscopic and microscopic morphology features, antifungal susceptibilities based on E-test# method, and genotypic characterization using multi-loci approaches (superoxide dismutase, beta-tubulin and internal transcript spacer genes). Phylogenetic trees were constructed with unambiguously CLUSTALW aligned sequences using the neighbour-joining method with Kimura-2 parameter as substitution model and maximum parsimony analysis, using the BioEdit version 7.0.0 and Phylip version 2.0 softwares. **Discussion:** Among our collection composed of 59 isolates, we identified three macroscopically different morphotypes of S. prolificans and some genetic polymorphisms (1.8–2.2% difference between the analyzed sequences). These low sequence polymorphisms reflected intra-specific genetic variations. Therefore, we hypothesized that S. prolificans might be stable in space, and apparently insensitive to xenical or environmental factors. No correlation between clinical-biological characteristics and genotypic or phenotypic criteria of *S. prolificans* strains was found. In conclusion, our results supported the current perception of *S. prolificans* as a unique species and an emerging opportunistic pathogen.
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