



Sequential variations of *Rasamsonia* spp. isolate genotypes in cystic fibrosis patients

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Auteur	Matray, Olivier [1], Mouhajir, A. [2], Giraud, Sandrine [3], Gargala, Gilles [4], Zouhair, Rachid [5], Bougnoux, Marie-Elisabeth [6], Bouchara, Jean-Philippe [7], Favennec, Loïc [8]
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Résumé en
anglais

Rasamsonia species have been recently described as emergent pathogens in human and animals. Recent multilocus phylogenetic studies have shown that the genus *Rasamsonia* (R.) includes at least four phylogenetically related species forming the *R. argillacea* complex, *R. argillacea sensu stricto*, *R. piperina*, *R. eburnea* and *R. aegroticola*, which have been mostly reported in the clinical context of chronic granulomatous disease (CGD) and cystic fibrosis (CF). Differences in sensitivity to antifungal therapies which have been noted within the genus *Rasamsonia* underline the importance of early identification of clinical isolates for optimal treatment during the early stages of infection. In this context, the aim of this work was to obtain genotypic characterization of clinical *Rasamsonia* spp. isolates from 26 CF patients and one acutely infected CGD patient using PCR amplification of repetitive DNA sequences (rep-PCR) and to compare species distributions determined by β tubulin sequencing with rep-PCR genotypes/clusters.

One hundred and ten isolates were collected sequentially or simultaneously from 01/09/1998 to 08/2012 from sputum samples of 26 CF patients. One CGD patient (4 isolates) was studied in parallel. Two reference strains (CBS #408.73 (*R. piperina*) and #432.62 (*R. cylindrospora*) were obtained from CBS. After extraction, PCR amplifications of repetitive DNA sequences were realized for each sample using the DiversiLab Fungal kit (bioMérieux). Amplicons were separated by capillary electrophoresis in an Agilent 2100 Bioanalyzer (Massy, France). Single electrophoretic profiles obtained for each isolate were compared using the DiversiLab Healthcare software (version 3.41).

As previously reported in CF patients, beta-tubulin gene sequencing of 110 isolates identified more frequently *R. aegroticola* (72 isolates from 19 CF patients) than *R. argillacea stricto sensu* (30 isolates from 8 CF patients), and *R. piperina* (8 isolates from 5 CF patients), with 15, 6, and 7 distinct profiles, respectively. From the CGD patient, all isolates were identified as *R. argillacea stricto sensu*. Without exception, species identification according to rep-PCR genotypes was entirely consistent with beta-tubulin sequencing results.

Present data provide the first description of sequential *Rasamsonia* spp. variations with time in CF patients. *Rasamsonia argillacea sensu stricto* isolates were found persistent for years in all sequentially sampled CF patients except 1 who presented 4 different successive genotypes. In contrast to *R. argillacea sensu stricto*, sequential detection of *R. aegroticola* and *R. piperina* revealed frequent successive changes in isolate genotypes in most CF patients.

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