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National outbreaks of *Saprochaete clavata* : A multidisciplinary hunt to discover the source of contamination

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As of 2012, *Saprochaete clavata* was known as a yeast-like ascomycetous species rarely involved in human invasive infection. It suddenly became a national problem when 18 cases occurred within 8 weeks in 10 health care facilities. The majority of these cases were fatal and diagnosed in patients with acute myeloid leukemia. Knowing that the current identification methods misidentified *S. clavata*, we reviewed published reports about grouped-cases of *Geotrichum* spp. infections in Europe. We contacted European colleagues and analysed the available isolates and the collection of the French National Reference Center (NRCMA). We started a collaboration with the French CDC (Santé Publique France), as well as clinicians and hygienists to discover the reservoir of *S. clavata*, determine the risk factors and study the population structure of *S. clavata*. Using whole genome sequencing and animal experiments we determined that the outbreak was due to a clonal cluster, and that translocation from gut to blood occurred, making possible an oral source of contamination. During the following six years, using a new real-time PCR, we followed the various clades without finding the clue. Finally, in 2017 and 2019, new grouped cases of *S. clavata* infections in two hospitals allowed us, with the help of the local teams, to find the source of contamination after sampling the hospitals' environment and discovering that deficient dishwashers were in both hospitals the source of those nosocomial infections. Replacement of the dishwashers stopped the spread of *S. clavata*. This work demonstrates the importance of multidisciplinary approach in outbreak investigation.

Biography

Marie Desnos-Ollivier is research assistant at the National Reference Center of invasive Mycoses & Antifungals (NRCMA) at Institut Pasteur, France. She has completed her PhD in 2012 from University Paris 7, about molecular epidemiology of *Cryptococcus neoformans* complex. She is specialized in yeast identification, antifungal susceptibility, molecular epidemiology using genotyping or whole genome sequencing. She is co-curator of the Institut Pasteur-FungiBank sequences database. She is part of the ISHAM working group Genotyping *C. neoformans/C. gattii*. She has published 58 papers in international peer-reviewed journals and has been serving as a reviewer board member of Frontiers in Cellular Infections.

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