



Developing collaborative works for faster progress on fungal respiratory infections in cystic fibrosis

Submitted by Beatrice Guillaumat on Thu, 08/29/2019 - 10:53

Titre	Developing collaborative works for faster progress on fungal respiratory infections in cystic fibrosis
Type de publication	Article de revue
Auteur	Schwarz, Carsten [1], Vandeputte, Patrick [2], Rougeron, Amandine [3], Giraud, Sandrine [4], Dugé de Bernonville, Thomas [5], Duvaux, Ludovic [6], Gastebois, Amandine [7], Alastruey-Izquierdo, Ana [8], Martin-Gomez, Maria Teresa [9], Martin Mazuelos, Estrella [10], Sole, Amparo [11], Cano, Josep [12], Peman, Javier [13], Quindos, Guillermo [14], Botterel, Françoise [15], Bougnoux, Marie-Elisabeth [16], Chen, Sharon [17], Delhaès, Laurence [18], Favennec, Loïc [19], Ranque, Stéphane [20], Sedlacek, Ludwig [21], Steinmann, Joerg [22], Vazquez, Jose [23], Williams, Craig [24], Meyer, Wieland [25], Le Gal, Solène [26], Nevez, Gilles [27], Fleury, Maxime [28], Papon, Nicolas [29], Symoens, Françoise [30], Bouchara, Jean-Philippe [31]
Organisme	ECMM/ISHAM working group Fungal respiratory infections in Cystic Fibrosis (Fri-CF) [32]
Editeur	OUP
Type	Article scientifique dans une revue à comité de lecture
Année	2018
Langue	Anglais
Date	1er 2018
Numéro	S1
Pagination	S42-S59
Volume	56
Titre de la revue	Medical Mycology
ISSN	1460-2709
Mots-clés	Antifungal Agents [33], Cystic fibrosis [34], Drug Resistance, Multiple, Fungal [35], fungi [36], Genomics [37], Humans [38], Microbiological Techniques [39], Mycoses [40], Respiratory Tract Infections [41], Scedosporium [42]

Cystic fibrosis (CF) is the major genetic inherited disease in Caucasian populations. The respiratory tract of CF patients displays a sticky viscous mucus, which allows for the entrapment of airborne bacteria and fungal spores and provides a suitable environment for growth of microorganisms, including numerous yeast and filamentous fungal species. As a consequence, respiratory infections are the major cause of morbidity and mortality in this clinical context. Although bacteria remain the most common agents of these infections, fungal respiratory infections have emerged as an important cause of disease. Therefore, the International Society for Human and Animal Mycology (ISHAM) has launched a working group on Fungal respiratory infections in Cystic Fibrosis (Fri-CF) in October 2006, which was subsequently approved by the European Confederation of Medical Mycology (ECMM). Meetings of this working group, comprising both clinicians and mycologists involved in the follow-up of CF patients, as well as basic scientists interested in the fungal species involved, provided the opportunity to initiate collaborative works aimed to improve our knowledge on these infections to assist clinicians in patient management. The current review highlights the outcomes of some of these collaborative works in clinical surveillance, pathogenesis and treatment, giving special emphasis to standardization of culture procedures, improvement of species identification methods including the development of nonculture-based diagnostic methods, microbiome studies and identification of new biological markers, and the description of genotyping studies aiming to differentiate transient carriage and chronic colonization of the airways. The review also reports on the breakthrough in sequencing the genomes of the main *Scenedosporium* species as basis for a better understanding of the pathogenic mechanisms of these fungi, and discusses treatment options of infections caused by multidrug resistant microorganisms, such as *Scenedosporium* and *Lomentospora* species and members of the *Rasamsonia argillacea* species complex.

Résumé en anglais

URL de la notice <http://okina.univ-angers.fr/publications/ua20159> [43]

DOI [10.1093/mmy/myx106](https://doi.org/10.1093/mmy/myx106) [44]

Lien vers le document https://academic.oup.com/mmy/article/56/suppl_1/S42/4925969 [45]

Titre abrégé Med. Mycol.

Identifiant (ID) 29538733 [46]

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Liens

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