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ISHAM INTERNATIONAL SOCIETY FOR HUMAN AND ANIMAL MYCOLOGY

Medical Mycology, 2015, 53, 896–897
doi: 10.1093/mmy/myv031
Letter to the Editors

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Matrix-assisted laser desorption ionization-time of flight identification of *Schizophyllum commune*: perspectives on the review by Chowdhary *et al.*

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Received 23 January 2015; Revised 27 March 2015; Accepted 6 April 2015

SIR: The excellent review of Chowdhary *et al.*[1] emphasizes the significance of filamentous basidiomycetes (FBM) in human pathology. This review raises the challenge of conventional identification of *Schizophyllum commune* and other FBM. Due to the absence of asexual reproduction, monokaryotic isolates usually grow as nonsporulating molds (NSM) lacking characteristic morphological features.[2,3] In dikaryotic strains, those features (clamp connections or spicules) can be lacking or take several weeks to appear. Moreover they are insufficient to identify the species. Induction of characteristic fruiting bodies is inconstant and usually requires 3 weeks.[4] FBM identification is therefore based on molecular analysis.[5] Since the introduction of molecular identification in medical mycology, the number of documented cases involving *S. commune* and other FBM has dramatically increased.[1,6] In a retrospective molecular analysis of 52 NSM strains isolated from respiratory tract specimens,[4] FBM represented 96% of the isolates including *S. commune* (52%). Despite their important contribution, molecular techniques have several limitations. They are time consuming and expensive and interpretation could be difficult.[7] We would like to complete these two identification approaches presented by Chowdhary et al. by matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS).

MALDI-TOF MS is a revolutionary tool in clinical microbiology. It is a soft-ionization mass spectrometry technic based on co-crystallization of the sample with an absorbent matrix allowing acquisition of protein mass spectra "fingerprints." Comparison of the mass spectral profiles

(MSP) to a database allows a quick and easy identification of microorganisms. The equipment is expensive, but identification of a strain is particularly rapid and cost-effective (less than $1 by identification[8]). This technique is increasingly used in routine to identify bacteria and yeasts at species level in a few minutes.[9,10] More and more studies focus on identification of filamentous fungi.[11–13] Therefore, MALDI-TOF MS presents a great potential for identification of strains without fructifications, especially NSM identification. Identification of environmental FBM from rotten wood by MALDI-TOF MS has been described in 2005.[14] More recently, identification of several FBM strains isolated from clinical samples by MALDI-TOF MS has been reported.[13,15]

In our lab, we systematically analyze with MALDI-TOF MS, every NSM isolated from clinical samples. We have recently identified a strain of *S. commune* isolated from a sinusitis case [A. Huguenin, unpublished results]. In our laboratory, it is the first time we identify a strain of *S. commune* isolated from a clinical sample. MALDI-TOF MS has permitted identification at species level of this strain 9 days before we could observe characteristic features of FBM (spicules and clamp-connections). Although there is currently a lack of published reports on this subject, similar results have been observed in other clinical laboratories [J. Michel, personal communication; B. Sendid, personal communication].

MALDI TOF is however limited by the lack of diversity among MSP in the provider's MALDI TOF library: for example *S. commune* is the only species of FBM represented in the Bruker Fungi Library V1.0. The NIH library including 11 MSP of FBM, has permitted to identify only 12 (32%) of 37 FBM clinical isolates.[15] Many species considered as nonpathogenic, are not represented in the library. This issue could be addressed by the development of an in-house library for MSP. Moreover, the quality of MSP could be an important issue. Phenotypic state (conidia, basidiocarp) may be a variability source of measured spectra, making essential to define standardized conditions for the production of MSP and the implementation of the spectral data base.

In conclusion, *S. commune* and other FBM are emerging agents in human diseases. MALDI-TOF MS has an important potential for a fast and inexpensive identification of *S. commune* and other FBM. It could contribute to improve epidemiological data of these infections. For this purpose, improvement in reference spectra library, both in diversity and quality, is a must.

We thank Dr. P.L. Toubas for kindly reviewing the manuscript and Dr. L Brasme for his help with the MALDI-TOF analysis technics.

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