28th ECCMID EUROPEAN CONGRESS OF CLINICAL MICROBIOLOGY AND INFECTIOUS DISEASES
Madrid, Spain
21 – 24 April 2018

P2380 Identification of Malassezia species by MALDI-TOF MS after improvement of database

Prasanna Honnavar*[1 2], Anup Ghosh[1], Saikat Paul[1], Pankaj Singh[1], Sunil Dogra[3], Arunaloke Chakrabarti[1], Shivaprakash M Rudramurthy[1]

[1]Postgraduate Institute of Medical Education & Research, Chandigarh, India, Medical Microbiology, Chandigarh, , [2]Xavier University School of Medicine, Aruba-Dutch Caribbean, Microbiology and Immunology, Oranjestad, Aruba, [3]Postgraduate Institute of Medical Education & Research, Chandigarh, India, Dermatology, Venerology and Leprolog, Chandigarh, India

Background: *Malassezia* species is associated with many dermatological diseases along with blood stream infection. The taxonomy of *Malassezia* species is evolving after introduction of molecular techniques for identification, and difficulty is faced to identify the species by phenotypic methods. Among 15 known *Malassezia* species, the present Bruker Daltonics database could identify only two species (*M. furfur and M. pachydermatis*). The present study was aimed to improve MALDI-TOF MS MSP (Main spectrum profile) database for *Malassezia* species, and evaluate its potential for identification of those species comparing with PCR-RFLP and DNA-sequencing method.

Materials/methods: A total of 88 sequence identified (D1/D2 domain of 28S rDNA and ITS region) *Malassezia* isolates including 11 reference strains were used to improve MALDI-TOF MS in-house database. A second set of PCR-RFLP confirmed 190 strains were subjected to MALDI-TOF MS analysis to validate our in-house database. The clinical isolates were from the skin of patients with seborrhoeic dermatitis, psoriasis and healthy controls, and isolated during our previous epidemiological survey and kept at -80 ºC. We followed our previously standardized on-plate formic acid sample extraction protocol with slight modification. Mass spectrometry analysis was carried out using a MALDI-TOF MS Microflex LT. MALDI Biotyper software was used to create composite correlation Index and MSP dendrogram.

Results: A very good agreement was detected between MALDI-TOF MS and PCR-RFLP with kappa value 0.9, though 10 isolates had log scores <2.0. The updated *Malassezia* database could identify 94.7% and 5.3% strains to the species (with log scores of ≥2.0) and genus level (with log scores of ≥1.7) respectively.

Distribution and number of strains included

***Malassezia* species**	**Strain used**	
	Database generation (DNA sequence)	**Clinical validation (PCR-RFLP)**
M.furfur	30	85
M.globosa	29	49
M.restricta	11	41
M.arunalokei	5	7
M.slooffiae	1	4
M.sympodialis	2	4
M.japonica	6	
M.nana	1	
M.caprae	1	
M.dermatis	1	
M.yamatoensis	1	
Total	**88**	**190**

Conclusions: We standardized, improved MALDI-TOF MS protocol and developed in-house database for the identification of wide range of clinical *Malassezia* species. MALDI-TOF MS could be a possible feasible alternative tool to other molecular method for rapid and accurate identification of *Malassezia* species.