Impact of MALDI-TOF MS in Clinical Mycology: Progress and Barriers in Diagnostics

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MALDI-TOF MS has been used as an important component in the polyphasic identification of clinical fungi, and a rapid diagnostic tool for routine clinical fungal identifications (1). However, there are some important limitations to MALDI-TOF MS particularly in relation to the identification of closely related fungal taxa, such as the dimorphic fungi with mycelial- to yeast-phase transitions or highly encapsulated yeasts. Commercial data bases of MALDI-TOF MS spectra have also limitations in their coverage of taxa, although this has expanded recently (2,3). Commercial databases are based on the different protocols used by the main MALDI-TOF MS manufacturers and are widely available. In some cases, sample preparation protocols have been changed over the time and the information kept and amalgamated in the same database. In contrast, others impose a very restricted protocol and quality control to add a new entry. Commercial databases for clinical fungi are less well-established and comprehensive than for bacteria. For fungal identifications by MALDI-TOF MS some commercial databases are built with software that uses a point system based on the peak list with mass signals weighted according to their specificity. Similarity between individual spectra is expressed as the relative or absolute number of mass signals matching after subjecting the data to a single link agglomerative clustering algorithm analysis. A large number of publications contain different (a) growth conditions for fungi, (b) protocols for protein extraction, (c) matrices for MALDI-TOF MS analysis and (d) data acquisition settings. These can affect negatively the spectral quality and thus fungal identification with potentially serious shortfalls in diagnoses. The sources of variation are protein extraction, matrices, growth conditions and databases without even considering the natural intraspecific variation of fungal strains. This conference will focus on the impact of MALDI-TOF MS in Clinical Mycology taking into consideration the progress and barriers faced on fungal diagnostic.

References:
(1) Santos, C. et al. (2010) J. Appl. Microbiol. 108: 375-385. (2) Lohmann, C. et al. (2013) J. Clin. Microbiol. 51: 1231-1236.; (3) Mancini, N. et al. (2013) J. Clin. Microbiol. 51: 2453-2457.

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MALDI-TOF
and TANDEM MS
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Towards Mass Analyser

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