MALDI Applications in Mycology

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Learning Points

- Recognise the key approaches on the identification of clinical fungal isolates
- Understand the limitations on the fungal identification process
- Understand the contribution of MALDI-TOF MS for fungal characterisation and identification
- Integrate knowledge and critical thinking on solving fungal identification problems

The standard method for identifying and classifying fungi remains morphology (e.g. colour, shape, size and ornamentation of conidia and the length of the conidiophores) due, in general, to filamentous fungi having more distinctive morphologies than, for example, single-celled bacteria and yeasts. However, the literature provides extensive examples of problems. Unreliable morphological minutia to describe new species and variability within the morphological characters of accepted species are constant issues. The use of physiological and biochemical characters have also been attempted (e.g. colony colour, growth rates, secondary metabolites production) although these are also variable in many cases. With the introduction of molecular biological methods, mycology has experienced a great renaissance with over 40 whole genome sequences available. This in turn has given comparative fungal genomics a new incentive which is now being actively explored. However, the commonly used ITS rDNA sequences as gold standard for fungal identification[1] do not have the discriminative power to resolve some taxa and three or more housekeeping genes are required for a multilocus sequencing analysis (MLSA). Some of the above constraints have led to increasing interest in Matrix-Assisted Laser Desorption/Ionisation Time-of-Flight Mass Spectrometry (MALDI-TOF MS) for rapid and reliable fungal identification[2] and recent results for *Aspergillus* spp.[3], *Candida* spp.[4], and dermatophytes (*Trichophyton rubrum*[5]) show considerable promise. Furthermore, the technique is rapid, reliable and inexpensive in terms of labour and consumables when compared with other molecular biological techniques. The rapid identification, in pure culture or in complex matrices, of uncommon fungal species that are emerging as human pathogens may be accurately achieved provided that a complete and quality database is available. However, the full impact of this approach will only be appreciated when more diverse species and different conditions are studied in detail. As a matter of consequence, MALDI-TOF MS can be suitable as point-of-care diagnostic for clinical mycology.

References

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