MALDI-TOF MS Identification of Clinically Significant Yeasts and Moulds in a Global Antifungal Surveillance Program

ABSTRACT

Background: The identification of fungi is a critical issue in clinical microbiology. While DNA sequencing methods has become the standard method for identification, MALDI-TOF MS has proven to be an accurate and rapid technique for yeast identification. We aimed at investigating how well MALDI-TOF MS can identify clinically significant yeasts and moulds.

Materials and Methods: A total of 416 clinical isolates were included in this study. Of these, 216 were yeasts and 200 were moulds. Isolates were identified by MALDI-TOF MS, and DNA sequencing to evaluate discordances using 28S and ITS regions. MALDI-TOF MS was used to generate a species level ID for each isolate.

Results: Overall, 318/416 (76.4%) fungi (154/216 yeasts and 164/200 moulds) were concordantly identified to species level by MALDI-TOF MS and DNA sequencing. The most common discordances were due to the inability of MALDI-TOF MS to identify less common fungal species.

Conclusions: MALDI-TOF MS is a powerful tool for the identification of fungi, with great potential for use in clinical microbiology laboratories. However, further studies are needed to understand the limitations of MALDI-TOF MS in the identification of less common fungal species.

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REFERENCES

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