

Identification of dermatophyte species causing onychomycosis and tinea pedis by MALDI-TOF mass spectrometry.

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Details



Abstract

Identification of dermatophytes is currently performed based on morphological criteria and is increasingly supported by genomic sequence comparison. The present study evaluates an alternative based on the analysis of clinical fungal isolates by mass spectrometry. Samples originating from skin and nail were characterized morphologically and by sequencing the internal transcribed spacer 1 (ITS1), ITS2 and the 5.8S rDNA regions of the rDNA clusters. In a blind comparative study, samples were analyzed by matrix assisted laser desorption/ionization time-of-flight (MALDI-TOF MS). The mass spectra were compared to a database comprising of the spectral data of reference strains by applying the saramis software package. All fungal isolates belonging to the taxa *Trichophyton rubrum*, *T. interdigitale*, *T. tonsurans*, *Arthroderma benhamiae* and *Microsporum canis* were correctly identified, irrespective of host origin and pathology. To test the robustness of the approach, four isolates were grown on five different media and analyzed. Although the resulting mass spectra varied in detail, a sufficient number of signals were conserved

resulting in data sets exploitable for unequivocal species identification. Taken together, the usually widespread dermatophytes can be identified rapidly and reliably by mass spectrometry. Starting from pure cultures, MALDI-TOF MS analysis uses very simple sample preparation procedures, and a single analysis is performed within minutes. Costs for consumables as well as preparation time are considerably lower than for PCR analysis.

Beteiligte Forschungseinheiten

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