Abstract 6065

Presence and distribution of fungal species and dermatophytes in nail and skin samples

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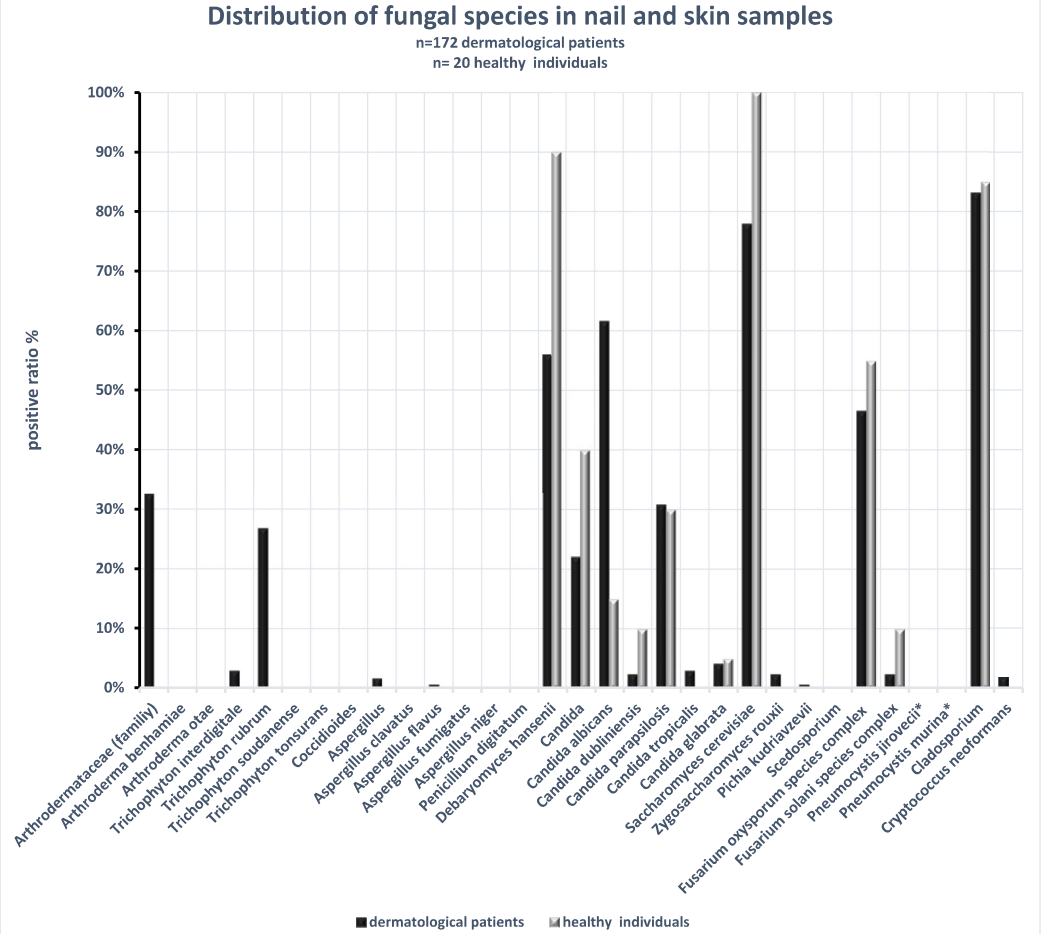
Background: Cube Dx' test *hybcell Fungi DNA xB* detects 6 fungal genera and 33 species by amplifying 28S DNA followed by the proprietary compact sequencing process. The limit of detection of this test is about 20 CFU/sample. This study examines the abundance of other (potential pathogenic) fungal species besides dermatophytes in healthy and patients' skin samples.

Materials/methods: In total 192 skin and nail samples were analysed in this study, thereof 172 clinical dermatological samples from patients and 20 samples from individuals without signs of disease (healthy controls). Samples were lysed and total DNA was isolated using the automated MagnaPure96 system (Roche Diagnostics). All samples have been verified for dermatophytes with a lab-developed test using real-time PCR and melting point analysis (Unilabs AB). The relative frequencies of tested fungal species in patient samples and samples from healthy individuals were calculated and are shown in the illustration below.

Results: Of the clinical samples 34% were positive for dermatophytes by the conventional lab method. In the *hybcell Fungi DNA* positive samples could be identified by Tm peaks > 89°C. Some species were only detected in the patient group: *Trichophyton spp.*, some *Aspergillus* species, *Candida tropicalis*, *Zygosaccharomyces rouxii*, *Pichia kudriavzevii* and *Cryptococcus neoformans*. Most others were found in both groups at similar ratios, but in different combinations for individual samples. Two fungal species exhibited exceptional patterns: *Saccharomyces cerevisiae* was identified in all samples of healthy individuals and in about 80% of patient samples, whereas *Candida albicans* was positive in more than 60% of patient samples but in only about 15% of samples from healthy individuals.

Conclusions: *Trichophyton spp.*, *Aspergillus spp.*, *Candida tropicalis*, *Zygosaccharomyces rouxii*, *Pichia kudriavzevii* and *Cryptococcus neoformans* were only found among the clinical samples, as expected. No difference in abundance was observed for most non-dermatophyte fungal species in nail and skin samples of patients and healthy individuals. These species were detected at individual ratios in all samples and should be regarded as normal flora of human skin and nails. Further investigation and inclusion of more samples is necessary to validate initial results.



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