

dermatophytes. The aim of this study was to evaluate the discriminatory power of a phylogenetic tool based on concatenated sequences of three genomic regions including *Tef-1 α* , *ITS* (*ITS1* to *ITS2*) and *beta-tubulin* to differentiate: 1/ the anthropophilic *Trichophyton interdigitale* species from the zoophilic *Trichophyton mentagrophytes* 2/ the two closely related African anthropophilic species *Trichophyton violaceum* from *Trichophyton soudanense*.

Methods: 26 well characterized strains of *T. interdigitale/mentagrophytes* have been selected including 3 IHEM reference strains; 30 well characterized strains of *T. soudanense/T.violaceum* including 2 IHEM reference strains were also included. All strains were submitted to *ITS*, *beta-tubulin* and *Tef-1 α* PCR/sequencing. Moreover, identification was completed by real time PCR DermaGenius® (PathoNostics). Alignments were performed using MUSCLE in Seaview. The alignments for each of the three genes were then concatenated together based on the name of the sample and gaps were added between genes. Phylogenies were then inferred on the concatenated alignment using PhyML.

Results: After generation of the phylogenetic tree by concatenation of the three sequence genes, the differentiation between *T. interdigitale* and *T. mentagrophytes* was clear. The 16 strains of *T. interdigitale* were well classified into one distinct group on the dendrogram. The 10 strains of zoophilic *T. mentagrophytes* were well distinct of the anthropophilic group and defined by another clade on the dendrogram. Reference strains were correctly classified into the two previously defined groups. Regarding the differentiation between *T. soudanense* and *T. violaceum*, the concatenation permitted to define two well distinct clades on the dendrogram. One clade containing the 10 *T. violaceum* tested and the other containing the 20 *T. soudanense* included in the study. Reference strains were correctly classified into each corresponding clade.

Conclusion: The concatenation of *ITS*, *beta-tubulin* and *Tef-1 α* genes sequences allows the generation of a discriminating dendrogram between the zoophilic *T. mentagrophytes* and the anthropophilic *T. interdigitale* and between the two closely related African anthropophilic species *T. violaceum* and *T. soudanense*. These species are not clearly well defined by *ITS* analysis only. This multilocus phylogenetic approach allows to better define the species boundaries between these dermatophytes species and facilitates the molecular characterization of these species in routine diagnostic.

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Pulmonary mycobiome of patients with suspicion of respiratory fungal infection – an exploratory study

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Objectives: This pilot study aimed to characterize the pulmonary mycobiome of patients with suspicion of fungal infection of the respiratory tract as well as to identify potentially pathogenic fungi colonizing/infecting their lungs.

Methods: A cohort of 10 patients was analyzed, including HIV+ patients and patients with active infection caused by *Mycobacterium* species. Their respiratory samples (bronchoalveolar lavage fluid/ bronchial secretions) were pre-treated with lyticase and proteinase K; DNA was extracted using the High Pure PCR Template Preparation kit following the manufacturer's instructions. The internal transcribed spacer region 1 (*ITS1*) and calmodulin gene were amplified by PCR and the resulting amplicons were sequenced using the Illumina MiSeq platform with pair-end reads of 150 bp. The obtained results were analyzed using the PIPITS pipeline as described by Gweon *et al.* [1]. Operational taxonomic units (OTU) to which less than 0.1% of the total reads attributed were disregarded.

Results: Thirty-seven different OTU were identified from which two belonged to the *Plantae* kingdom, 11 had less than the 0.1% threshold of the total reads and were therefore disregarded. The remaining 24 different OTU (grouped in 17 phylotypes), were considered as part of the pulmonary