P380
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