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Title: Fungi communities detected by metagenomic tools in sputum in patients with cystic fibrosis

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Body: Introduction: Cystic fibrosis (CF) is the disease in which respiratory infections are the main cause of morbidity and mortality. Although bacterias are important microorganisms which usually colonize the respiratory tract, recently has been described that some uncultivable fungi may appear in these patients without knowing the long-term impact on disease progression. Aim. Describe the fungal microbiota in CF and assess the clinical aspects related with this microbiota. Method. 50 CF patients were included. Clinical, functional data and sputum sample to study the microbiota were collected in all cases. The microbiological study was performed with a metagenomic approach that allows us to amplify the specific gene by fungal ITS polymerase chain reaction nested type and subsequent direct sequencing for isolated populations or cloning in case of obtaining more than one fungus. Results. Metagenomics techniques detected 37 cases with some isolation of fungi, while by conventional cultivation were only 10 cases. Most were Candida sp. (64.9%) followed by Aspergillus sp. (13.5%). The use of inhaled corticosteroids was associated with the presence of fungi in sputum (51,4% vs 19,4%; p=0,011), without differences between fluticasone and budesonide. There were no differences obstruction degree, and the degree of radiographic involvement by TAC, or with chronic or intermittent colonization of various germs. Conclusions. The colonization of fungi in the airway measured by metagenomic techniques provides information on the prevalence and factors associated with this colonization. This technique enables the detection of unknown fungi and uncultivable which currently play an unknown pathophysiological role.