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MOULDS AND CYSTIC FIBROSIS: WHAT CAN WE LEARN FROM STUDYING LUNG MYCOBIOTA?

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Background and objectives: Given the polymicrobial nature of pulmonary infections in cystic fibrosis (CF) patients and the recent evidence that fungi may be of clinical relevance in the decline of CF lung function, we developed a high-throughput sequencing approach to extensively explore the diversity and dynamics of fungal and prokaryotic populations in CF lower airways.
Methodology and Principal Findings: Since our aim is to address fungal diversity in lung (i.e. lung mycobiota), fungal and bacterial diversity in sputum samples isolated from CF patients was investigated using high-throughput Pyrosequencing (454 FLX).
In a first pilot study, the unveiled microbial community structure was compared to the clinical profile of the CF patients. Pyrosequencing confirmed reported bacterial diversity and observed complex fungal communities, in which more than 60% of the species or genera had not been identified in cultures. Fungal diversity was reported here for the first time, while we validated our 'ITS2-approach'. Strikingly, the diversity and species richness of fungal and bacterial communities was significantly lower in patients with decreased lung function (FEV1, FVC) and poor clinical status (BMI, SK-score).
Secondly, we focused on the role of lung mycobiota in pulmonary exacerbation. Sputum samples from well-documented (with clinical, radiological, and biological data) CF patients with (11) and without (12) pulmonary exacerbation were compared using 454FLX technology plus principal component analysis. More than exacerbation status, bacterial microbiota and mycobiota seem to be linked to spirometry values (especially FEV1). Regarding fungi, *Candida* and *A. fumigatus* are the main species/genus isolated in these studies. Our approach confirms the important role of Streptococcus species in increasing lung microbiota diversity and promoting patient stability (as recently reported by Filkins et al. 2012), and allows us to conceptualize such interactions of the CF lung environment.
To conclude, mycobiota is a dynamic event, part of the overall microbiome (including bacterial microbiota and virome), plus some potential interaction such as resistosome.
Recent data, obtained using deep-sequencing, have demonstrated that the lung microbiota composition contributes to both health and disease such as CF. In light of this recent concept, we analysed the lung mycobiota in CF, and viewed the microbial community as a unique pathogenic entity. We thus interpreted our results to highlight the potential interactions between microorganisms and the role of fungi in the context of improving survival in CF.