Concordance between upper and lower airway microbiota in children with Cystic Fibrosis

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Introduction

Cystic fibrosis (CF) is characterized by repeated pulmonary infections and chronic inflammation leading to pulmonary exacerbation (PE). The “Mucoviscidose, Virus Respiratoires and Intracellular Bacteria” MUCOVIB project aims to address the impact of respiratory viruses respiratory bacterial diversity changes overtime. This sub-study of the MUCOVIB project aims to compare the upper and lower respiratory tract bacterial biodiversity.

Methods

- Prospective, longitudinal, multicenter cohort study of children with CF included from April 2016 to June 2018 during their follow-up visits or an episode of pulmonary exacerbation (PE)
- Bacterial biodiversity was measured by 16S rRNA amplicon PCR metagenomics from paired lower (expectoration) and upper respiratory tracts (throat smears)
- Paired-read were assembled with PANDAseq and clustered into operational taxonomic units (OTUs) using vsearch and assigned to taxonomical ranks using Qime and the EzBioCloud database.
- Standard descriptive and comparative statistics were performed on categorical variables and non-metric multidimensional scaling, ANOVA and PERMANOVA were used to analyze the bacterial diversity in upper and lower respiratory niches

Results

Preliminary analyses of 10 patients, 20 visits, 40 samples

- Diversity indexes are statistically not different between upper and lower respiratory tract samples
- Group variance is similar in expectorations and throat smears from the same patient but different between patients

Conclusions

- Throat smears can be used as proximal samples to investigate changes over time of the microbial diversity in pediatric CF patients.