Airway microbiota resistome in CF - impact on clinical management

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Cystic Fibrosis is a deadly genetic disease mainly due to chronic bacterial colonization and recurrent bacterial infections of the lungs. It has often been documented that once a certain microbial species such as Pseudomonas aeruginosa establishes, the health of the patient rapidly deteriorates in most cases. Although the microbial community associated with this disease has been characterized at a limited resolution using culture-based as well as culture-independent techniques, these methods failed to give an overview of the functional microbial community with its antimicrobial resistance present in the lungs. In a pilot study, we could demonstrate the feasibility of using high-throughput sequencing (metagenomics) on the total DNA collected from sputum samples of CF patients to characterize the microbial community and to identify the genes present in the upper respiratory tract metagenome of the patients. The comprehensive gene profiles also include the pan-microbial resistance genome (resistome) and virulence-related genes. This method can be used to prepare time- or sample specific functional profiles, which can be used to track changes over time to develop a better understanding of the complex lung ecology and improve effective antimicrobial treatment. The objective of this study is perform a whole genome, non-amplified deep sequencing of DNA samples collected from the sputum of CF-individuals with the aim to characterize the composition and the changes of the lung microbiome with its resistome over a 12-month period.

**keywords**

Cystic Fibrosis, microbiota, metagenome, deep sequencing, bacterial exacerbation, resistome

**type of project**

fundamental research

**status**

ongoing - follow up

**start of project**

2014

**end of project**

2016

**project manager**

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