O099
Oral Session
Microbiome and microbiota: new "M's" in microbiology

AIRWAY MICROBIOTA IN CYSTIC FIBROSIS PATIENTS WITH A SEVERE DECLINE IN LUNG FUNCTION

E. Fiscarelli[1], P. Paganin[2], V. Tuccio[1], M. Chiancianesi[3], G. Taccetti[4], V. Lucidi[5], A. De Alessandri[6], A. Mengoni[3], A. Bevivino[2]

[1]Laboratory, Children's Hospital and Research Institute Bambino Gesu', Rome, Italy ; [2]T.U. for Sustainable Develop. and Innovation System, ENEA Casaccia Research Center, Rome, Italy ; [3]Evolutionary Biology, University of Florence, Florence, Italy ; [4]Pediatrics Cystic Fibrosis Centre, Children's Hospital Meyer, Florence, Italy ; [5]Pediatrics Cystic Fibrosis Centre, Children's Hospital and Research Institute Bambino Gesu', Rome, Italy ; [6]Pediatrics Cystic Fibrosis Centre, G. Gaslini Institute, Genoa, Italy

Objectives

Cystic fibrosis (CF) is characterized by defective mucociliary clearance and chronic airway infection by a complex microbiota. Infection, persistent inflammation and periodic episodes of acute pulmonary exacerbation contribute to a progressive loss of CF lung function. Aim of our study was to assess the composition of airway microbiota in CF patients showing a rapid and severe decline of pulmonary function.

Methods

Culture-based methods, including anaerobic cultivation, and culture-independent methods as Terminal-Restriction Fragments Length Polymorphism (T-RFLP) analysis, have been used to comprehensively examine the airway microbiota of 78 patients attending three large CF Centres, in Italy. Based on forced expiratory volume in 1 second (FEV1), the enrolled patients were categorized in stable (S) and not-responding (NR) groups. They were also subdivided into three categories (mild, moderate, severe) on the basis of their pulmonary disease seriousness.

Results

Overall, our findings confirm that CF airway bacterial communities are highly complex structures. The microbiological results from culture-based methods revealed, as discriminatory bacterial species associated with a worse lung function, *Pseudomonas aeruginosa*, *Rothia mucilaginosa*, *Streptococcus pneumoniae* and *pseudopneumoniae, Prevotella melaninogenica* and *Candida albicans.* Molecular analysis showed a greater bacterial diversity within sputum samples than that detected by culture-based methods. Discriminatory T-RFs classified as *Proteobacteria, Actinobacteria, Bacteroidetes,* and *Firmicutes* resulted more abundant in NR groups. Importantly, there is evidence that decreased evennes rather than richness of community diversity is associated with decreased lung function in CF. In particular, new reassembles and/or unbalance of bacterial communities are observed in CF patients classified as clinically moderate, before detection of lung function decline.

Conclusions

Our findings confirm that combining culture-dependent and culture-independent approaches provides a more comprehensive perspective of CF microbiology than only one approach. The ongoing analysis of the microbiota community composition using 16S rRNA gene amplicon Roche 454 pyrosequencing and metagenomic Illumina massive sequencing will permit to better understand the new and/or emerging pathogens associated with a rapid rate of decline in lung function. We believe that our data may contribute to a better understanding of those factors which could have significant implications for future therapeutic intervention strategies aimed at preserving lung function.

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