Postdoc Journal
Vol. 3, No. 12, December 2015

Journal of Postdoctoral Research
www.postdocjournal.com

FFC Proceedings 2015

13th Convention of Investigators in Cystic Fibrosis – Italian Cystic Fibrosis Research Foundation (FFC)

Investigating the airway microbiome in cystic fibrosis patients with a severe decline in lung function: an opportunity for a personalized microbiome based therapy

Bevivino A[1], Mengoni A[2], Taccetti G[3], Fiscarelli EV[4], De Alessandri A[5]

[1]ENEA Casaccia Research Center, Rome, Italy; [2]University of Florence, Department of Biology, Florence, Italy; [3]Cystic Fibrosis Center, Meyer Hospital, Florence, Italy; [4]Cystic Fibrosis Center, Gaslini Hospital, Genoa, Italy; [5]Children's Hospital and Research Institute Bambino Gesù, Rome, Italy (Grant No. FFC#10/2014 – FFC#14/2015, New) doi.org/92d

Background. Cystic fibrosis (CF) is characterized by a progressive decline in lung function. Despite antibiotic treatment, patients with CF may show a rapid and severe decline in lung function. In the previous project (FFC#8/2012), we found changes in CF airway microbiota associated with a severe decline in lung function (Paganin, Fiscarelli et al. PLoS ONE 10(4): e0124348). Moreover a large set of metagenomic and metabarcoding data were produced allowing to identify additional novel biomarkers for factors responsible for the seriously decline in lung function.

Hypothesis and objectives. The starting hypothesis is that a number of hidden pathogens/biomarkers from non-culturable bacteria may be present in patient's airways of cystic fibrosis and could be used as predictive markers of severe decline in lung function, allowing earlier intervention and improving health care treatment of CF patients. The main objectives of the study, which follows a pilot project supported by the FFC (FFC#8/2012) are: i) to characterize the airway microbiome of substantial decliners (SD) and stable (S) patients with CF, by bioinformatics analysis of airway metabarcoding and metagenomic sequences obtained in the previous project; ii) to identify additional biomarkers (non-culturable pathogens and gene functions) of the serious decline in lung function; iii) to characterize the changes over time in the composition of the airway microbiome of S and SD patients.

Methods. This is a two steps project: 1. Bioinformatic analysis with ad-hoc pipelines softwares of Next Generation Sequencing (NGS) data (16S rRNA metabarcoding and full-genome shotgun metagenomics analysis) obtained in the previous project (FFC#8/2012). 2. Beginning of a longitudinal metagenomic study where specific individual patients will be followed at regularly scheduled CF clinic visits at 2-months intervals.

Rresults. A sharp difference in the structure and composition of airway microbiota between S and SD patients was found, especially in patients with severe lung disease, where Pseudomonas represented the most abundant genus. A co-occurrence network analysis showed that microbial communities were less complex in SD patients than in S ones. Moreover, an inverse relationship between bacterial community diversity and disease severity was found. Additionally significant differences in antibiotic resistance genes and metabolic pathways of the microbiome between normal/mild and severe lung disease FEV_1 groups were found.

Spin-off for research and clinical purpose. The analysis of the meta-community dynamics can give us a set of tools to unlock the potential of microbiome-based personalized medicine in major disease areas including CF.

Acknowledgment. FFC #10/2014: funded by FFC, supported by Delegazione FFC di Villa D'Almè – Bergamo, Gruppo di Sostegno FFC di Reggello Firenze, Gruppo di Sostegno FFC di Lainate, Delegazione FFC di Verbania e V.C.O