

OC13 - The airway microbiome in cystic fibrosis: where are we now?

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Patients with cystic fibrosis (CF) can experience periodic episodes of acute pulmonary exacerbation, which are associated with a poor health-related quality of life, disease progression and survival. Only recently scientists began to appreciate the complexity of CF polymicrobial infection and the implications it may have for disease prognosis and response to therapy. New insight into the impact of antibiotic treatment, patient age increasing, and periodic pulmonary exacerbation on CF microbiology has been obtained. Anyway, the analysis of both taxonomic assessment of CF microbiome and its functional potential (ie which genes and pathways are present) have not been investigated yet. Understanding the role of the CF airway microbiota and detecting microbial species associated with the decline in lung function are key challenges for the delivery of new potential biomarkers for bacterial infections managements in CF patients and improving health care treatment. Dr Annamaria Bevivino from ENEA Casaccia Research Centre in Italy will present the state of the art on CF microbiome focusing on her research activity funded by the Italian CF Research Foundation. Bevivino and coll. showed that the airway microbial communities of CF patients change with a severe decline in lung function (Paganin et al. PLoS ONE 2015;10:e0124348; Bacci et al. PLOS ONE 11(6): e0156807). In a recent work [Bacci et al., 2017, International Journal of Molecular Sciences, 18(8)], the research group coordinated by Dr. Bevivino identified a different microbiome gene repertoire in the airways of CF patients with severe lung disease, suggesting that the microbiome of severely affected adults with CF seems to encode different mechanisms for the facilitation of microbial colonization and persistence in the lung, consistent with the characteristics of multidrug-resistant microbial communities that are commonly observed in patients with severe lung disease. aim was to understand and describe the complex interaction networks underlying the host-lung microbiome interaction at taxonomic and functional level. More recently, Bevivino and coll. investigated in a longitudinal study the temporal dynamics of the airway microbiome in CF, paying special attention to the episodes of exacerbation by using by using shotgun metagenomic sequencing that permits targeting the entire genomic repertoire of the microbial community, down to the strain level. Overall, such results suggest the need for future development of personalized therapeutic approaches based on patient-specific airways microbiome. These new insights may alter future clinical management of CF.

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