

European Respiratory Society Annual Congress 2013

Abstract Number: 6025

Publication Number: OP02

Abstract Group: 1.1. Clinical Problems

Keywords: no keyword selected

Title: LSC 2013 abstract - The role of second-generation sequencing to characterize the fungal microbiota in the adult cystic fibrosis airway, and its correlation with standard culture-based methods and clinical phenotype

Mike Harrison ¹, Kate Twomey ², Yvonne McCarthy ², Oisín O'Connell ¹, Melanie Febrer ³, Mark Alston ³, Robert Ryan ² and Barry Plant ¹. ¹ Cork Adult Cystic Fibrosis Centre, Cork University Hospital/ University College Cork, Cork, Ireland ; ² BIOMERIT Research Centre, Department of Microbiology, Biosciences Institute, University College Cork, Cork, Ireland and ³ Genome Analysis Centre, Norwich Research Park, Norwich, United Kingdom .

Body: Advances in culture-independent methods allow a more extensive characterisation of the fungal community of the CF lung. This study uses a high-throughput sequencing technique to profile the fungal microbiota of the stable CF airway, and correlates this with culture-based methods and clinical phenotype. Clinically stable adult CF patients were prospectively recruited from our Adult CF Centre. Culture-based methods were employed at time of sampling. Fungal DNA was extracted from all samples. High-throughput bar-coded sequencing targeting the internal transcribed spacer (ITS) region was used to profile the fungal microbiota of all sputum samples. Clinical characteristics were recorded by retrospective review of medical notes. 55 clinically stable adult CF patients were recruited. Culture-based methods detected fungus in 15 of the 55 samples. High-throughput bar-coded sequencing identified rich fungal communities in greater than 90% of the samples, with over 82% of the species not detected by culture. A preliminary comparison of patient status with diversity and species richness of fungal microbiota identified that lower fungal diversity associates with decreased lung function. We describe the use of high-throughput sequencing to characterize the fungal microbiota in the largest population of adult patients with CF to date. DNA analysis reveals increased species diversity and richness compared with standard culture-based methods. Preliminary analysis suggests that fungal diversity may contribute to, or be associated with, variability in phenotype seen in CF patients.