Clinical Characteristics of Pseudomonas Aeruginosa and Aspergillus Species Co-infected Cystic Fibrosis Patients in the UK

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Objectives: Pseudomonas aeruginosa (Pa) and Aspergillus sp.(Asp) are the most common bacterial and fungal organisms to infect the airways of CF patients. Whilst the detrimental effects of Pa infection are well described, less is known about Asp colonisation and the clinical effects of co-infection are not clear. The aim is to examine this in a cross-sectional retrospective cohort study.

Methods: Data from patients registered on the UK CF Registry in 2016 were used. Individuals were grouped into 6 cohorts: 1)no Pa/Asp (clear), 2)Asp without Pa, 3)Intermittent Pa without Asp, 4)Intermittent Pa+Asp, 5)Chronic Pa without Asp, 6)Chronic Pa+Asp. Aspergillus positivity includes Aspergillus fumigatus and non-fumigatus species. The primary outcome measure was best percentage predicted FEV1 (ppFEV1;GLI) for the previous 12 months (<5yrs of age excluded), with a secondary endpoint of requirement for IV antibiotics. Associations between outcome variables and infection stratified cohorts were assessed using linear and logistic regression models.

Results: 9,401 patients were included (294 lung transplant recipients excluded). The median age was 19 years (IQR 8-29), with 53% males and 49% Phe508del homozygous. 4,158 patients (44%) isolated Pa and 1,462 (15%) isolated Asp. CFRD was no more frequent in co-infection vs Pa alone, but was more prevalent in Asp vs clear groups (22% vs 12%, p<0.001). After adjusting for age, sex, Phe508del homozygosity and CFRD, patients with Asp vs no infection had a 6.2% lower ppFEV1 (p<0.001). In patients with Pa, there was no additional impact of Asp co-infection on ppFEV1. However there was a significantly higher probability of co-infected patients receiving IV antibiotics in the preceding 12 months (OR 1.30, p<0.001).

Conclusions: Pa/Asp co-infection is associated with additional use of IV antibiotics despite lung function being unaffected. Causation cannot be ascertained from this cross-sectional data but further longitudinal analyses will explore the impact of co-infection on disease progression.