Methods Adult patients were recruited from specialist bronchiectasis and Cystic Fibrosis clinics. The gold standard for diagnosing *P. aeruginosa* infection was positive sputum cultures. 72 sputum samples were analysed. A sputum sample was kept in a glass vial with a cap containing septum. The septum was pierced with a solid phase microextraction (SPME) fibre allowing sampling of the headspace for 50 min at 37°C before transferring the fibre into gas chromatography mass spectrometry. AnalyzerPro software (automated peak capture software) and manual identification were used to identify relevant to *P. aeruginosa* specific compounds in the headspace of sputum.

Results 32 samples grew *P. aeruginosa* either on its own or mixed with other species. 2-nonanone was a marker of *P. aeruginosa* in sputum headspace gas with sensitivity of 72% and specificity of 88%. Cyanide was not detected. However, a combination of manually identified 2-nonanone with 17 other volatile compounds as identified by AnalyzerPro, increased sensitivity in detection of *P. aeruginosa* to 91% with specificity of 88%.

Conclusion Optimal sampling and capture protocols still need refinement: we were unable to detect the prior noted biomarker Cyanide. These data however demonstrate the potential for rapid and accurate diagnosis of *P. aeruginosa* infection from sputum samples. In contrast to the 48+ hour turnaround for standard microbiological culture, these results were available within 1–2 h. It also provides a library of compounds as targets to validate in a future study of breath testing.

S22 LUNG CLEARANCE INDEX, FEV1 AND CT FINDINGS IN CYSTIC FIBROSIS: DATA FROM THE UK CF GENE THERAPY CONSORTIUM RUN-IN STUDY

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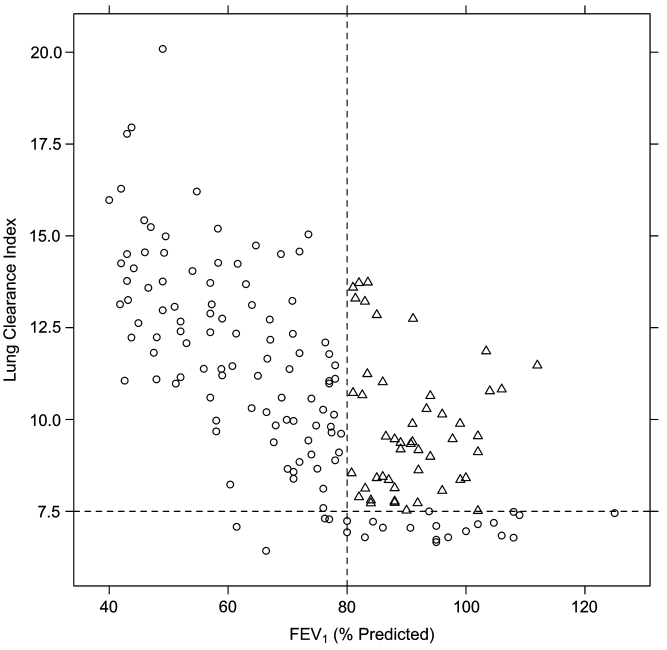
Introduction Lung Clearance Index (LCI) is a measure of lung gas mixing derived from the Multiple Breath Washout (MBW) test. We present LCI, FEV_1 and CT data from the Run-In Study, a longitudinal study in preparation for a multi-dose trial of nebulised gene therapy for CF.

Methods MBW, spirometry and low-dose HRCT chest were performed as part of the first Run-In Study visit. LCI was reported as the mean result from at least two technically acceptable sulphur hexafluoride MBW tests performed using a modified Innocor gas analyser. Spirometry was performed to ERS standards. CT scans were assessed by two independent radiologists for extent and severity of bronchiectasis, wall thickening, presence of small and large airway plugs, and gas trapping.

Results 191 patients attended visit 1, mean (range) age 22.6 (10–59.1) years. Validated LCI, FEV_1 and CT results were available for 167, 191 and 150 patients, respectively. Mean (SD) FEV_1 was 72 (19)% predicted. Mean (SD) LCI was 10.7 (2.7), with mean intravisit coefficient of variation of 4.9%. LCI correlated negatively with FEV_1 ($r=-0.68$, $p<0.001$), but was abnormally elevated in 72% of participants with normal FEV_1 (see Abstract S22 Figure 1; triangles indicate FEV_1 >80% and LCI >7.5). 95% CI for LCI in normal subjects 5.9 to 7.5. Both FEV_1 and LCI correlated with all CT measures ($p<0.001$), most strongly with extent of bronchiectasis. LCI correlated better than FEV_1 with extent of bronchiectasis, $r=0.72$ ($p<0.001$) vs $r=-0.61$ ($p<0.001$), respectively.



Abstract S22 Figure 1

Conclusions Results from this large cohort suggests that LCI is a more sensitive test of early CF lung disease, and correlates better with extent of bronchiectasis seen on CT, than FEV_1. Validation of data from subsequent study visits is in progress and will be reported at a future date.

S23 A COMPARATIVE STUDY OF POLYMICROBIAL DIVERSITY IN CF AND NON-CF BRONCHIECTASIS

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Introduction and Objectives Bronchiectasis is a dilation of the peripheral airways with subsequent mucus hypersecretion. Bronchiectasis can be either genetic, that is cystic fibrosis (CF) or described as non-CF bronchiectasis (eg, idiopathic or post infectious bronchiectasis). Recently, many studies have demonstrated polymicrobial bacterial communities are present in the lower respiratory tract (LRT) of cystic fibrosis (CF) sufferers. These studies have identified complex microbial communities that are affected by many factors including age; CFTR genotype and antibiotic therapy. One prior abstract noted greater diversity in non-CF bronchiectasis as compared to CF (Bilton *et al*, 2009) though the sample size was small. Our aim is to extend prior work by comparing the metabolically active bacterial and fungal communities present in sputum samples from CF patients with those from non-CF bronchiectasis.

Methods Adult CF and non-CF bronchiectasis patients provided spontaneously expectorated sputum samples which were treated with RNA*later*. RNA was extracted from sputum samples and reverse transcribed to cDNA; this was the template for bacterial and fungal community PCR amplification using universal 16S or 28S primer sets. Amplicons were analysed by denaturing gradient gel electrophoresis (DGGE) which separates double stranded DNA based upon bacterial and fungal genomic GC content sequence. Common pathogens were identified such as *Pseudomonas aeruginosa* and *Haemophilus* spp. by comparison to a 16S or 28S standard ladder from pure cultures.