Objectives The aim of the present study was to determine whether adult CF patients with pulmonary NTM infection have worse clinical outcomes, when compared to a matched group of CF patients who have never had NTM isolated. Additionally, the study also aims to determine what proportion of the overall bacterial community is NTM compared to other bacteria.

Method Clinical data were collected from 12 spontaneously expectorating CF patients who cultured *M abscessus* in the sputum since they were first infected with *M abscessus*, and 24 matched controls who have CF, but never been infected with *M abscessus*. Student unpaired t-test was used to compare the mean forced expiratory volume (FEV_1) per year between the two groups.

Results Data from 36 individuals were studied. Cases and controls were well matched. Mean absolute decline in FEV_1 was 100 ml/year (SD±0.19) in cases and 79 ml/year (SD±0.19) in controls. Student unpaired t-test was not significant (0.73). Mean absolute percentage predicted decline in FEV_1 was 3.85% (SD±5.62) in cases and 2.78% (SD±6.58) in controls. Student unpaired t-test was not significant (0.62).

Conclusion These results indicate that there is a small decline in mean FEV_1 per year between the two groups; *M abscessus* and the controls, but the difference is statistically and clinically insignificant.

P166 TEMPORAL DYNAMICS OF POLYMICROBIAL COMMUNITIES IN THE LOWER RESPIRATORY TRACT OF PATIENTS WITH CYSTIC FIBROSIS

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Introduction and Objectives The microbial communities present in CF sputum are polymicrobial and consist of bacteria, viruses and fungi. Although stratified studies have demonstrated a change in the CF bacterial microbiota with increasing age, individual patients have not been followed longitudinally across stable phases and exacerbation episodes period of time. The aim of this study was to follow CF patients who were either homo- or heterozygous for the F508del mutation over a period of up to 20 months to assess how the bacterial and fungal communities fluctuate over this period to determine whether a shift in the microbiota could be linked with acute pulmonary exacerbations.

Methods Adult CF patients were recruited and spontaneously expectorated sputum samples were collected. DNA was extracted from the samples and PCR-DGGE was used to analyse the bacterial and fungal communities using universal primer sets.

Results Routine microbial culture identified a mean of 1.52 bacterial species and 0.62 fungal species, whereas molecular analysis found a mean of 12.24 bacterial species and 1.41 fungal species across the cohort. The composition of the bacterial communities between patients varied significantly according to gender and being culture positive for *P aeruginosa*. Patients homozygous for the F508del mutation had more rich fungal communities than heterozygotes. However, a bacterial or fungal community characteristic for pulmonary exacerbations was not observed.

Conclusions Our data clearly demonstrates that bacterial and fungal communities in the CF lower respiratory tract are more diverse than previously thought. Furthermore, the microbial communities in the lower respiratory tract of CF patients are subject are selected by predisposing factors such as gender but still remain unique to individual patients. Monitoring the microbial communities has found that although they are subject to some fluctuation a characteristic community does not assemble to cause acute pulmonary exacerbations. Furthermore, particular bacterial taxa were present throughout the sampling period, suggesting that current antimicrobial therapies are not adequate at removing these taxa.

P167 SCREENING FOR VIRAL UPPER RESPIRATORY TRACT INFECTION IN PULMONARY EXACERBATIONS IN CYSTIC FIBROSIS

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Introduction and objectives It is unclear if respiratory viruses are important in precipitating pulmonary exacerbations in adults. Respiratory viruses are considered important pathogens in children with cystic fibrosis (CF), as they may be associated with deterioration in lung function and bacterial infection.[1 2] Following the "flu" pandemic in 2009 we have started screening CF patients for viral upper respiratory tract infection for infection control. Our aim was to determine if adult CF patients admitted with a pulmonary exacerbation had positive nasopharyngeal swabs suggesting a viral aetiology.

Methods Retrospective review of admissions to an adult CF unit between May 2009 and May 2011 to identify those who had nasopharyngeal swabs (NPS) for the molecular detection (PCR) of viruses in the nasopharyngeal tract. Data were collected from the hospitals' computer information system. Continuous variables are described as median averages (IQR), and categorical variables as counts.

Results 365 admissions were identified during this period (93 patients). 299 admissions were due to pulmonary exacerbation. A NPS was performed on 211 admissions (174 due to pulmonary exacerbation). Characteristics of patients that had NPS on admission are listed in Abstract P167 table 1. Only 5 (2.9%) NPS detected upper respiratory tract viruses in patients with a pulmonary exacerbation. Influenza A [H1N1] and Parainfluenzae were detected in three and two NPS respectively.

Abstract P167 Table 1 Characteristics of patients at admission—for patients with nasopharyngeal swabs

	Pulmonary exacerbation (n=174)	Non-pulmonary exacerbation (n=37)
Age (years)	22 (6)	21 (5)
FEV_1 (% predicted)	58 (34)	70 (31)
FVC (% predicted)	76 (32)	91 (32)
Length of stay (days)	13 (8)	5 (11)
White cell count ($\times 10^9$/l)	9 (5)	8 (2)
C-reactive protein (mg/l)	14 (28)	5 (11)
Virus NPS positive	5	0

Conclusions Viral infection, detected by NPS, is not common in adult CF patients admitted to our hospital with or without pulmonary exacerbations. Screening all adult patients with CF admitted to hospital for the presence of viruses in the upper respiratory tract has a low yield and is not recommended.

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P168 ERADICATION OF BURKHOLDERIA CEPACIA IN CF: TIME FOR A COORDINATED APPROACH?

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Introduction New infection with *Burkholderia cepacia* complex (Bcc) organisms is a significant event for patients with cystic fibrosis (CF). In addition to potential clinical impact, there are implications for

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