Results Out of 907 patients with lung cancer, 183 (20%) did not have a histological diagnosis. Based on TNM staging, 10% had stage I, 5% stage II, 19% stage III and 50% stage IV disease. Co-morbidities were significant in this group—57% had severe COPD, 12% had IHD and 11% had had a previous CVA. Of the 183 patients identified, 49 (27%) had at least one attempt at obtaining histology that proved to be non-diagnostic, either bronchoscopy (46 pts) or other procedure (3 pts). 41 (22%) were actively treated—6 (15%) had radical treatment, 5 (12%) had palliative chemotherapy and 29 (70%) had palliative radiotherapy. Performance status (PS) and co-morbidities were the main factors affecting decision to obtain histology. As the Abstract P163 table 1 suggests, patients without histology tended to be older ($p<0.0008$) and a greater proportion had a PS of three or more.

Abstract P163 Table 1

Characteristic	Histology (N=724)	No histology (N=183)
Mean age (SD)	72 (11)	75 (10)
Men	52%	53%
1 yr mortality	60%	75%
PS of 3 or more	210 (29%)	115 (63%)
Stage 3–4	484 (67%)	126 (69%)

Conclusion These data suggest that patients who do not ultimately receive histological confirmation of a diagnosis of lung cancer are a heterogenous population. In most cases the factors that influenced the failure to obtain histology were poor performance status and co-morbidities. We conclude that the percentage of lung patients without histological confirmation of diagnosis may ultimately reflect the overall health of the local population rather than the specific quality of a lung cancer unit's clinical practice. As such we would advocate caution when interpreting differences in this parameter between units.

P164 EGFR MUTATION PREVALENCE IN PATIENTS WITH NON-SMALL CELL LUNG CANCER: AN AUDIT OF TESTING WITHIN THE NORTH OF ENGLAND CANCER NETWORK

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In July 2010, NICE published a technology appraisal relating to the use of a Tyrosine Kinase Inhibitor (TKI) as first line treatment for patients with locally advanced or metastatic non-small cell lung cancer (NSCLC) in whom an epidermal growth factor receptor (EGFR) mutation was found. Subsequently, the North of England Cancer Network implemented region wide testing for EGFR mutations in all patients with a pathological confirmation of NSCLC. A retrospective audit was undertaken to assess the quality of EGFR mutation testing, and to obtain data regarding those patients who had tested positive in order to improve local policy.

Methods Lung cancer MDT lead clinicians from every NHS trust in the region were contacted and asked to provide information about every patient with a confirmed diagnosis of NSCLC for whom specimens had been sent for EFGR mutation testing between October 2010 and February 2011.

Results The 9 trusts identified 314 patients in whom specimens had been sent for EGFR mutation testing; 161 (51%) males; average age 69 years (34–91); 60% were WHO performance status 0–1; 95% were current or ex-smokers; 47% (149) had stage 4 disease. 60 (19%) were female with adenocarcinoma. In 22 (7%) patients an EGFR mutation was found, 16 (73%) were female, 17 (77%) were current or ex smokers, 73% had stage 4 disease. 13 were female with adenocarcinoma, therefore prevalence in this group was 22% (cf 7% for whole local population). 14 (64% of EGFR mutation positive patients, and 4% of all patients tested) were treated with a TKI as first line, (23% had best supportive care, 13% surgery). EGFR mutation testing failed in 29 (9%) patients. The total cost of testing for this period is over £47 000.

Conclusions Local prevalence of EGFR mutations in all patients with NSCLC is 7%, but 22% for female patients with a diagnosis of adenocarcinoma. Prior to this audit, specimens were sent for testing by the pathologist on confirmation of a diagnosis of NSCLC. Local policy has changed as a result of this audit. Specimens are now sent for testing after discussion at the MDM, at the point of referral to Oncology.

Abstract P164 Table 1 EGFR mutation positive patients

	Sex	Age	PS	Cell type	Histology/ cytology	Stage	1 therapy	Smoking status
1	Female	32	0	Adeno	Histology	T4N2M1b	TKI	Never
2	Female	57	0	Adeno	Histology	T3N0M1b	TKI	Current
3	Female	48	0	Adeno	Histology	T1aN3M1a	TKI	Current
4	Female	63	0	Adeno	Cytology	T3N2M0	TKI	Ex
5	Female	65	0	Adeno	Histology	T4N2M1b	TKI	Current
6	Female	62	1	Adeno	Histology	T3N3M1b	TKI	Ex
7	Female	66	1	Adeno	Histology	T2N0M0	Surgery	Current
8	Female	84	1	Adeno	Histology	T3N0M0	TKI	Never
9	Female	56	1	Adeno	Cytology	T2bN2M1a	TKI	Ex
10	Female	73	2	Adeno	Cytology	T2aNxM1b	TKI	Never
11	Female	64	2	Adeno	Histology	T2aN2M1b	TKI	Ex
12	Female	62	3	Adeno	Histology	T1N0M1b	Best supportive	Ex
13	Female	69	3	Adeno	Cytology	T3N3Mx	Best supportive	Ex
14	Female	40	1	Large cell	Cytology	T2aN2M1a	Surgery	Never
15	Female	62	1	Large cell	Cytology	T4N2M1a	Best supportive	Ex
16	Female	69	2	Large cell	Cytology	T2aN0M1a	Best supportive	Current
17	Male	55	0	Adeno	Histology	T2N3M1a	TKI	Current
18	Male	91	0	Adeno	Cytology	T2N0M0	Best supportive	Ex
19	Male	71	1	Adeno	Cytology	T4N2M1b	TKI	Never
20	Male	69	3	Adeno	Histology	T1bN2M1b	TKI	Ex
21	Male	77	1	Squamous	Histology	T4N3M1b	TKI	Ex
22	Male	57	1	Squamous	Histology	T2bN0M0	Surgery	Ex

Infections: from vaccination to treatments

P165 NON-TUBERCULOSIS MYCOBACTERIUM INFECTION IN CYSTIC FIBROSIS LUNG DISEASE; EFFECTS ON BACTERIAL COMMUNITY

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Background Species of Non-Tuberculosis Mycobacterium (NTM), mainly *Mycobacterium abscessus* (*M abscessus*) is of increasing concern in Cystic Fibrosis (CF). *M abscessus* are present in the CF lungs as part of the complex microbiological community. The mode of growth of *M abscessus* in vitro is in biofilms; this maybe a contributing factor for the resistance to antimicrobial agents. Lung infections with *M abscessus* is a major concern in CF patients, as it is difficult to treat them. It has been described that, fatal infections are likely to occur after lung transplantations; therefore pre-transplant colonisation with *M abscessus* has become a relative contraindication to lung transplantation. NTM are recognised pathogens in the CF airways, but associations with clinical outcomes still remains unclear.

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