microbial community in the COPD lung contributing to the pathogenesis of COPD.

Methods Nine clinically stable COPD patients attending the Freeman Hospital had a bronchoalveolar lavage fluid (BALF) taken. DNA extraction from these samples was performed using an Ultraclean® Microbial DNA Isolation Kit. DNA obtained from these samples was then used as template for conventional PCR. Both primer sets used targeted the universal bacterial and fungal V3 variable regions of the 16S rRNA gene and 28S rRNA gene respectively with attachment of a GC-clamp. Amplicons were then run out for analysis by denaturing gradient gel electrophoresis (DGGE) performed on a DCode System (BIO-RAD). Microbial DNA extracted from all nine BAL samples was then sent for 454 pyrosequencing to perform metagenomic analysis.

Results Molecular fingerprinting of BAL analysis by DGGE produced a distinct number of bands in each sample strongly indicating the presence of a diverse microbial community in the COPD infected lung. This was also seen in culture negative patients. Migration of bands present at the top of the denaturing gradient suggests that the lungs of COPD patients are heavily colonised with bacteria that have a low GC content such as *Haemophilus influenzae*, *Streptoccocus pneumoniae*, and *Moraxella catarrhalis*. Metagenomic analysis of the nine BAL samples by 454 pyrosequencing supports this hypothesis by detecting numerous other bacterial taxa present.

Conclusions This preliminary study shows that the lungs of COPD sufferers are colonised with multiple species of bacteria and demonstrates that a complex microbial community is present. Metagenomic analysis performed demonstrates the key bacterial taxa which may be responsible for inducing the damaging inflammatory response and the differences in bacterial diversity shown in the nine patients studied. Thus a complex microbiota may elicit ongoing inflammation leading to lung function loss and destruction of the lung architecture.

Pulmonary thromboembolism: acute and chronic studies

S20 TIME-RESOLVED CT PULMONARY ANGIOGRAPHY CONTRAST TRANSIT TIME IN PATIENTS WITH PULMONARY EMBOLISM: A NOVEL FUNCTIONAL CT METRIC OF RIGHT HEART STRAIN?

doi:10.1136/thoraxjnl-2011-201054b.20

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Introduction and Objectives Acute right ventricular (RV) failure is known to cause death in patients with pulmonary embolus due to circulatory collapse. CT pulmonary angiogram (CTPA) is now considered the gold standard test for the detection of pulmonary emboli, the technique provides excellent structural detail, however provides limited functional information. This aim of this was to assess time-resolved CTPA contrast transit times (TT) as a potential functional CT marker for the detection of right heart strain in patients with PE.

Methods We retrospectively reviewed consecutive patients who underwent CTPA at our institution over a 2-month period. Scans were performed on a Phillips Brilliance 16-slice scanner with a 4 ml/s OptirayTM 300 pressure injection. TT was defined as the time from the start of the injection to the scan trigger at the threshold of 150 hounsfield units measured from ROI analysis at the main pulmonary artery. Established CT structural imaging metrics were scored for comparison.

Results 56 consecutive patients were identified with evidence of pulmonary embolic disease or normal thoracic CT appearances from CTPA scans. One patient with PE was excluded as the CTPA scan was non-diagnostic. TT, RV septum to free wall distance, RV/LV ratio and PA diameter were all significantly elevated in patients with pulmonary embolus compared to patients with a normal CTPA. On analysis of bivariate correlation, TT had a statistically significant positive correlation with hepatic reflux, PA diameter and RV/LV ratio. Notably, the TT and RV/LV ratio demonstrated a significant direct linear correlation (p=0.001).

Conclusions This study supports previous evidence of existing markers, such as RV/LV ratio, being useful imaging marker in pulmonary embolic disease. It also suggests that TT, could be a new useful functional marker of right heart strain. The importance of further research into this field is highlighted, and particularly into TT as a haemodynamic prognostic indicator in acute pulmonary embolism.

S21 OBJECTIVE AND PATIENT REPORTED OUTCOMES OF LONG TERM MANAGEMENT OF PATIENTS WITH CHRONIC THROMBOEMBOLIC PULMONARY HYPERTENSION (CTEPH): A SINGLE CENTRE EXPERIENCE

doi:10.1136/thoraxjnl-2011-201054b.21

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Objective To determine long-term objective and Patient Reported Outcomes at a single centre in patients with CTEPH (distal or residual post Pulmonary endarterectomy).

Method A retrospective study of all incident patients with CTEPH (2000–2011). Data obtained from the service database—6-minute walk test (6MWT), CAMbridge Pulmonary Hypertension Outcome Review (CAMPHOR) symptom, activity and Quality of Life (QoL) scores, and NTproBNP. Results obtained at baseline (at the time of diagnosis, pre-commencement of first targeted therapy), 3 months,

Abstract S21 Table 1 Summary of change scores over time for CTEPH cohort

	6MWT	CAMPHOR symptoms	CAMPHOR activity	CAMPHOR QoL	NTproBNP
CTEPH	n=98	n=75	n=77	n=76	n=64
3-month change score mean (SD)	30.03 (77.2)†	1.1 (3.8)*	0.7 (3.4)*	1.1 (4.1)†	714.9 (2342.2)†
CTEPH	n=97	n=80	n=79	n=79	n=60
1-yr change score mean (SD)	37.03 (72.69)†	1.8 (4.6)†	0.7(4.3)	1.6 (4.7)†	891.6 (1815.5)†
CTEPH	n=80	n=62	n=61	n=61	n=50
2-yrs change score mean (SD)	35.1 (76.1)†	0.9 (4.4)	0.1 (4.6)	1.1 (5.1)	904.7 (1832.80)†
CTEPH	n=61	n=56	n=56	n=54	n=39
3-yrs change score mean (SD)	40.4 (74.6)†	1.3 (4.6)*	0.1 (5.2)	0.3 (4.3)	1009.4 (2083.9)†
CTEPH	n=44	n=34	n=34	n=34	n=29
4-yrs change score mean (SD)	18.8 (97.2)	0.9 (3.6)	0.3 (4.8)	0.4 (4.9)	780.1 (1695.1)*

Wilcoxon signed rank test * Significant ($p<0.05$), † Highly significant ($p<0.01$).