

months increasing by a quarter. The median hospital length of stay in adults was 17 days (IQR 8 to 32). The proportion requiring surgery has remained stable (15.2%), but the proportion of open surgery has fallen. Mortality rates remain approximately 12–14% throughout the study period. Incidence correlates closely with rates of viral influenza ($r=0.60$) and was highest in the children and young adults during the 2010/2011 influenza season.

Conclusion This is the first population level assessment of empyema incidence in this country. Rates of empyema admissions have steadily increased with a seasonal variation that may be related to influenza incidence. Results of linkage of the HES data to Public Health England influenza statistics will be presented at the conference.

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S13 THE MICROBIOLOGY OF PLEURAL INFECTION, AN APPROACH BASED ON 16S rRNA GENE NEXT GENERATION SEQUENCING

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10.1136/thorax-2019-BTSAbstracts2019.19

Background Pleural infection (PI) is a common and complicated disease, bearing a heavy healthcare burden worldwide. Definitive pathogen identification based on current methods occurs in only 40% of cases, mainly due to prior antibiotic administration and special bacterial nutritional culture requirements. To this end PI microbiology knowledge remains incomplete. Novel deep sequencing techniques could increase the rate of reliable pathogen identification and shed light on the complex polymicrobial patterns of PI.

Aim To investigate and further characterise the microbial nature of PI using next generation sequencing (NGS).

Methods Pleural fluid samples from the 'Pleural Infection Longitudinal Outcome Study' (PILOT, ISRCTN50236700, n=243) underwent bacterial DNA extraction followed by 16S rRNA NGS using Illumina MiSeq. Data were analysed with DADA2 and Phyloseq R packages.

Results Bacterial DNA from pleural fluid samples was successfully extracted and sequenced. NGS detected 391 diverse pathogens up to the genus level and analysis showed that PI is a polymicrobial disease. 131 (54%) samples had one pathogen with relative abundance over 50% and 89 (36%) samples had at least 3 pathogens with relative abundance over 10%. *Streptococcus Pneumoniae* was detected in 40 (16%) and *Staphylococcus Aureus* in 20 (8%) samples.

Discussion It is feasible to extract and sequence bacterial DNA from pleural fluid samples from patients with PI. 16S rRNA NGS is a robust method for investigating the total bacteriology of pleural fluid samples.

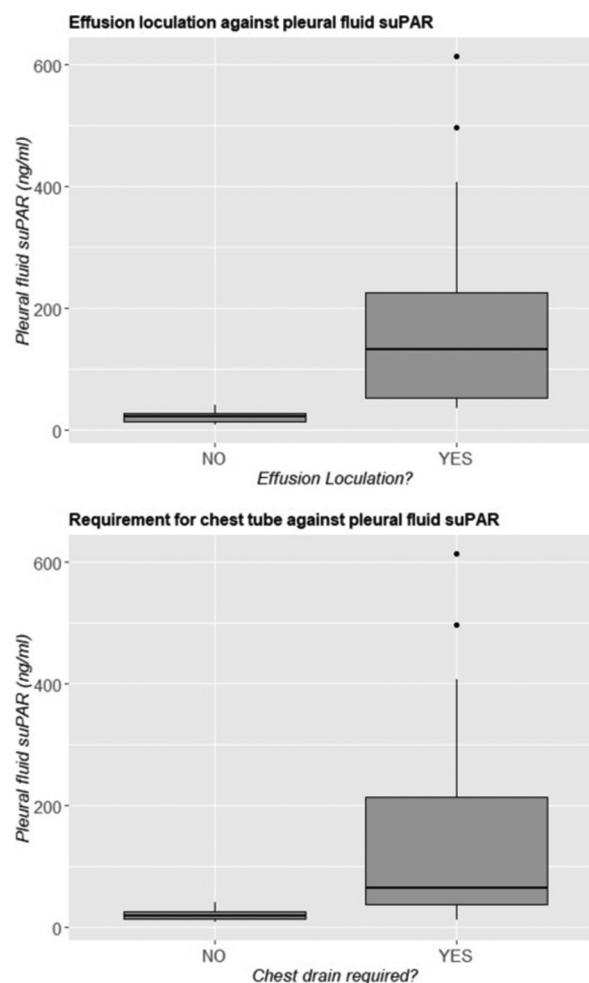
Funding National Institute for Health Research (NIHR) Oxford Biomedical Research Centre (BRC).

S14 THE ROLE OF SOLUBLE UROKINASE PLASMINOGEN ACTIVATING RECEPTOR (SUPAR) IN PARAPNEUMONIC EFFUSIONS

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10.1136/thorax-2019-BTSAbstracts2019.20

Introduction For decades the management of parapneumonic effusions has relied on pleural fluid pH measurement. However, the eventual requirement for fibrinolytics or surgery is more often dictated by the development of loculations. Soluble urokinase Plasminogen Activating Receptor (suPAR) is a novel biomarker released by pleural mesothelial cells in response to infection as part of the fibrinolysis cascade. This study



Abstract S14 Figure 1