# IDENTIFICATION OF PLEURAL INFECTION BACTERIAL PATTERNS. THE OXFORD PLEURAL INFECTION METAGENOMICS STUDY

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Background Pleural infection (PI) is a common and complicated disease. Empirical antibiotic usage has been correlated to poor clinical outcomes. Although the identification of the pathogen is essential for successful treatment, conventional culture-based pathogen detection techniques fail in approximately 40% of cases. Therefore, the bacteriology of PI remains incomplete. Next generation sequencing (NGS) is a molecularbased methodology which could be applied to metagenomics studies and improve pathogen recognition. Aim To investigate and characterise the bacterial patterns of PI. Methods Pleural fluid specimens from the 'Pleural Infection Longitudinal Outcome Study' 1 (PILOT, n=243) were subjected to bacterial DNA extraction followed by 16S rRNA NGS. The DADA2 and Phyloseq R packages were used for the analysis of the data. Results We identified 363 distinct species of bacteria, with various abundances among the samples. Diverse patterns between monomicrobial and polymicrobial PI were detected. 131 (54%) samples had one pathogen with abundance over 50% and 89 (36%) samples had at least three pathogens with relative abundance over 10%, suggesting a polymicrobial infection. Discussion We developed a methodology to extract bacterial DNA from pleural fluid specimens derived from patients with PI and the quality was satisfactory to be used for NGS. 16S rRNA gene NGS has the potential to detect the total microbiome of pleural fluid samples1 from complex PI. Funding National Institute for Health Research (NIHR) Oxford Biomedical Research Centre (BRC).
REFERENCE 1. Corcoran, J.P., et al. Prospective validation of the RAPID clinical risk prediction score in adult patients with pleural infection: the PILOT study. Eur Respir J (2020).