Poster: Analyses of hospital microbiomes revealed a diverse range of critical pathogens associated with HAIs

Author	Licence
Julio Cesar Ortega Cambara	CC BY 4.0

New Vistas

Volume 12, Issue 1, 2026, UWL Annual Doctoral Students' Conference 2025

Abstract

Background
Fomite-mediated and airborne transmission can lead to hospital-acquired infections (HAIs), making strict infection control measures essential. We developed a rapid and efficient metagenomic pipeline and demonstrated its power for rapid detection of pathogens, genetic signatures (antimicrobial resistance (AMR) and virulence factors (VFs)), and characterisation of the wider microbiome (including those that are unculturable and resistant), critical for monitoring HAI pathogens.

Methods
Air and surface samples were collected from multiple clinical and non-clinical areas in three multi?storey healthcare units in a UK hospital, including from a haematology/oncology ward that had experienced outbreaks. Samples were subjected to DNA extraction, enrichment (air samples), and amplification and were sequenced using long-read, real-time MinION platform. Data were analysed using an in-house developed bioinformatics pipeline.

Results
868 distinct taxa were identified. Among these, 73.73% were unique to surface samples, 18.08% to air samples, and 7.95% were shared. The analysis of antibiotic resistance genes (ARGs) revealed a concerning threat, as nine critical and emerging pathogens (Pseudomonas aeruginosa, Enterococcus faecium, Staphylococcus aureus, Rahnella aquatilis, Enterobacter hormaechei, Escherichia coli, Acinetobacter lwoffii, Acinetobacter baumanni, and Klebsiella pneumoniae) were identified across 22 hospital locations. These pathogens were associated
with 29 different ARGs, including various blaOXA subtypes, vanA genes cluster, and efflux pumps conferring resistance to eight important classes of antibiotics, such as carbapenems, cephalosporins, penams, and vancomycin. Furthermore, the presence of VFs such as the type IV pili system, the Type VI Secretion System (T6SS), bacterial flagella, alginate, pyoverdine (PvdS) production, and the Type II Secretion System (T2SS) in these pathogens indicates a significant risk of severe infections. Interestingly, eight plasmid replicon families (Col, Col440II, rep14a, rep18b, rep11a, rep2, rep10, and rep21) were also present, which often carry ARGs and VFs raising the possibility of HGT of these
genetic elements.

Conclusions
Our findings highlight that not only the critical pathogens described here are of significant concern but also numerous other taxa that harbour ARGs, VFs, and mobile genetic elements, which could potentially lead to the emergence of new AMR pathogens if genetic elements are exchanged, increasing antibiotic-treatment failure with HAIs

Keywords

Hospital microbiomes, Hospital acquired infection