

Seasonal Dynamics and Genomic Characteristics of ICU Derived Drug-resistant Pathogens: Significance of Phage Therapy

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ABSTRACT Infections caused by drug-resistant pathogens in intensive care units (ICUs) pose a global health threat with 40 to 60 percent mortality rates. This study characterised seasonal patterns and genomic features of ICU-acquired multidrug-resistant organisms through systematic environmental and clinical sampling across four seasons (spring to winter). Whole-genome sequencing (performed on Illumina NovaSeq and Nanopore platforms) revealed significant seasonal variations in resistance gene distribution. Autumn isolates showed 100 percent *bla*CTX-M-3 carriage, strongly associated with increased bed turnover (59.4% rise, $p < 0.001$) and extended disinfection intervals (OR=2.31, 95% CI: 1.47-3.62). Winter demonstrated 75 percent *qacEΔ1*-positive clones with elevated resistance indices (0.82 ± 0.08 versus 0.3 ± 0.2 , $p < 0.001$). These findings support two seasonally-adjusted interventions, that is, antibiotic stewardship during autumn peaks, and enhanced disinfection protocols for *qacEΔ1*-positive clones in winter.