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THE ROLE AND IMPORTANCE OF MOLECULAR EPIDEMIOLOGY IN THE INTENSIVE CARE UNIT

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Background: Healthcare associated infections (HAIs) remain among the most important challenges in healthcare facilities. Traditional culture-based and phenotypic methods are valuable for identifying pathogens, but may provide limited information on transmission pathways and the genetic relationships between isolates. Molecular epidemiology, particularly whole-genome sequencing (WGS), enables high-resolution characterization of pathogens, antimicrobial resistance determinants, and possible transmission links.

Objective: To demonstrate the role and importance of molecular epidemiology in intensive care unit (ICU) infection surveillance by integrating genomic characterization of environmental isolates with previously collected clinical and environmental isolates.

Methods: Environmental surveillance was conducted at Tbilisi State Medical University Hospital. In November 2024, 30 environmental swabs were collected and 33 potentially clinically relevant bacterial colonies were isolated. In May 2025, 20 additional environmental swabs yielded 20 bacterial colonies from 10 swabs. Isolates were characterized by WGS and compared with clinical and environmental isolates collected at the hospital between 2018 and 2025. Sequence types, genetic relatedness, antimicrobial resistance genes, and selected virulence determinants were assessed.

Results: Genomic analysis demonstrated persistent contamination by both Gram-positive and Gram-negative bacteria and identified important epidemiological relationships. A *Klebsiella pneumoniae* ST-147 isolate recovered from ICU bed rails was highly genetically related to 37 clinical isolates and two previously collected ICU environmental isolates and carried **blaCTX-M-15, blaNDM-1, and blaOXA-48**. Twelve *Acinetobacter baumannii* isolates recovered from ICU-3 belonged to pandemic clone ST-2; 11 were highly genetically related and were recovered from nine different locations, indicating contamination of multiple ICU surfaces. A *Pseudomonas aeruginosa* ST-357 isolate was highly genetically related to three patient isolates, suggesting possible nosocomial transmission. In contrast, another *P. aeruginosa* isolate recovered from an

ICU sink was not closely related to previously collected isolates and carried no antimicrobial resistance genes of interest. An *Enterococcus faecium* ST-80 isolate recovered from an ICU air vent carried the **vanA** operon but was distantly related to previous patient isolates.

Conclusion: Molecular epidemiology provides important additional resolution for ICU surveillance by distinguishing persistent environmental contamination, possible transmission clusters, and genetically unrelated isolates while simultaneously identifying antimicrobial resistance determinants. Integration of WGS with routine infection prevention and control can support more precise identification of transmission pathways, targeted environmental interventions, and improved surveillance of antimicrobial-resistant organisms.

Keywords: Molecular epidemiology; Intensive care unit; Whole-genome sequencing; Healthcare-associated infections; Antimicrobial resistance