Wastewater-Based Surveillance for Antimicrobial Resistance in a Northern California Acute Care Hospital, November 2024 to April 2025

Erika Viana Cardenas¹, Guillermo Rodriguez Nava¹, Alessandro Zulli², Mingjun Jiang², Nida Subhani³, Wajeeha Tariq¹, Eugenia Miranti¹, Alexandria Boehm², Jorge Salinas¹

Background

Antimicrobial resistance poses a global and ever-increasing threat to public health. Wastewater-based surveillance (WBS) offers a novel approach to monitor antimicrobial resistance by capturing pathogens and resistance genes shed by individuals without individual testing. We aimed to monitor the presence of antimicrobial resistance genes relevant to infection prevention and control in hospital wastewater, and compare hospital concentrations to community concentrations.

Methods

We collected 500 ml weekly composite wastewater samples from Tri-Valley Hospital. Samples were processed within 48 hours, with solids separated through centrifugation. Nucleic acids were extracted using column-based kit Zymo R2002. Droplet digital PCR was performed to detect antimicrobial resistance genes (ARGs) previously validated by the WastewaterSCAN program (https://www.wastewaterscan.org/en/pathogens). Community wastewater was "grab sample" from the primary clarifier of Raymond A Boege Alvarado WWTP (Union City, CA), representing composite community wastewater solids. Data was analyzed using the QX Manager Software Version 2.2 (BioRad, #168032), and normalized using Pepper Mild Mottle virus (PMMoV), which is an indicator for the presence of human feces in a wastewater sample.

Results

Clinically relevant ARGs were found in wastewater (Figure 1). We measured 11 targets including Gram-positives (mecA and vanA), Gram-negatives narrow-spectrum/extended-spectrum beta-lactamases (TEM, CTX-M and CMY), and Carbapenems (KPC, NDM, IMP, VIM, OXA-48) (figure 2 and 3). The ARGs VIM, TEM, and KPC were found in high concentration. Among these, VIM exhibited the highest concentration during the observation period. mecA and VanA were found in similar concentration in hospital and community wastewater; while higher levels of VIM, TEM, and KPC were found in hospital wastewater compared to community (Figure 4).

Conclusion

WBS effectively identifies clinically relevant antimicrobial resistance genes in hospital settings. The elevated levels of these resistance genes compared to community wastewater underscore the importance of monitoring AMR in healthcare facilities to inform infection prevention and control strategies.

¹Division of Infectious Diseases & Geographic Medicine, Stanford University School of Medicine, Stanford, CA

²Department Civil and Environmental Engineering, Stanford University, Stanford, CA ³Stanford Health Care Tri-Valley, Pleasanton, CA







