

Poster 9

Assessment of antimicrobial resistance throughout a wastewater treatment plant

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Abstract

Background: As one of the leading worldwide causes of death, infections caused by antimicrobial resistant (AMR) pathogens, represent a global health crisis that can be tackled under the One Health approach [1]. Wastewater treatment plants (WWTP) have long been considered hotspots for transmission and selection of AMR genes and, as such, surveillance of AMR in WWTP is crucial [2, 3]. Objective: In this study we aimed to isolate AMR bacteria from different sites along a WWTP, and subsequently assess their phenotypic antimicrobial susceptibility profiles, and search for different AMR genetic determinants. Methods: Wastewater samples were collected from four sites within a WWTP for the isolation of Enterobacteriaceae, Staphylococcus spp., and Enterococcus spp. and inoculated on MacConkey Agar (MCA), Mannitol Salt Agar (MSA), and Slanetz Bartley Agar (SBA), with and without supplementation with antibiotics: imipenem or ciprofloxacin in MCA, while vancomycin in MSA and SBA. Isolate's phenotypic antimicrobial susceptibility profiles were determined by disk diffusion assay for several antibiotics (representative of different classes), according to CLSI guidelines [4]. Presence of integrons and resistance genes was assessed through PCR amplification. Results: A total of 50 bacterial isolates were obtained, of which 25 were affiliated with the genus Enterococcus. Ten isolates were affiliated with Enterobacteriaceae, and no isolate affiliated with Staphylococcus spp. were retrieved. Other isolates were affiliated with clinically relevant species such as Pseudomonas aeruginosa or Aeromonas media. Phenotypic resistances were observed in isolates from all wastewater samples, being the most common to tetracycline and ampicillin. Three isolates were resistant to three distinct classes of antimicrobials. Preliminary PCR screening results showed presence of tet(M) and class 1 integrons. Conclusions: This study reflects the importance of monitoring WWTP for presence of AMR genes, since AMR strains are found from the raw influent of the WWTP to the final effluent discharged into the environment.

Keywords: antimicrobial resistance; wastewater; One Health

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