

CHARACTERIZATION, ABUNDANCE, AND DIVERSITY OF ANTIMICROBIAL RESISTANT PATHOGENS IN WASTEWATER TREATMENT TRAINS

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Wastewater treatment facilities (WWTFs) utilize secondary and tertiary treatments that are designed to remove chemical and biological pollutants, but the harsh conditions that they create may select for antimicrobial resistance (AMR). The spread of AMR from reclaimed water and sludge into receiving environmental microbiomes can lead to the propagation and retention of AMR-conferring genes throughout the natural environment, reducing the potency of antimicrobials which these genes confer resistance against and threatening the efficacy of their common uses, such as in food production and the prevention and treatment of microbial infections. This presentation examines the composition of antimicrobial resistant pathogens throughout various WWTF treatment trains. Samples were taken from each of the treatment stages in a municipal WWTF and a university WWTF in north central Florida. The identity and relative abundance of pathogenic species present in each sample were found using biochemical tests performed on colony dilutions and DNA extraction and sequencing. Through observing changes in the occurrence and abundance of pathogenic species in each stage of the facility, the effect of the corresponding secondary or tertiary treatment on AMR selection can be determined. This information can contribute to the development of more effective treatments and management strategies that target the removal of antimicrobial resistant pathogens from wastewater.

PRESENTER BIO: Karen Sem is a student at the University of Florida pursuing a bachelor's degree in Environmental Engineering Sciences. She is interested in investigating the efficacy of waste management and treatment methods in safeguarding public health.