Environmental Science Graduate Program Seminar Series

Antibiotic Resistance in the Scioto River Watershed: The Role of Aquatic Microbiomes in Environmental Antibiotic Resistance

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Smith Laboratory, Room 3150

Abstract

A contaminant of growing concern in rivers is antibiotic resistant genes (ARGs), which can spread between neighboring bacteria and increase the potential for transmission of AR bacteria to animals and humans. In order to identify the matrices of most concern for AR in natural waterways, we compared ARG burdens and microbial community structure between sample types from the Scioto River Watershed, Ohio, United States from 2017-2018. Five environmental matrices (water, sediment, periphyton, detritus, and fish) were collected from 26 river sites. Due to our focus on clinically relevant ARGs, three carbapenem resistance genes (*bla*$_{KPC}$, *bla*$_{NDM}$, and *bla*$_{OXA-48}$) were determined via DropletDigital™ PCR. At a subset of nine urbanized sites, we conducted16S rRNA gene sequencing and functional gene predictions. Carbapenem resistance genes were quantified from all matrices, with *bla*$_{KPC}$ being the most detected (88% of samples), followed by *bla*$_{NDM}$ (64%), and *bla*$_{OXA-48}$ (23%). Fish gut samples showed higher concentrations of *bla*$_{KPC}$ and *bla*$_{NDM}$ than any other matrix, indicating potential bioaccumulation of ARGs, and risk of broader dissemination through aquatic and nearshore food webs. Periphyton carried higher concentrations of *bla*$_{NDM}$ than water, sediment, or detritus. Microbial community analysis identified differences by sample type in community diversity and structure. Sediment samples had the most diverse microbial communities, and detritus, the least. Spearman correlations did not reveal significant relationships between the concentrations of the monitored ARGs and microbial community diversity. However, several differentially abundant taxa were identified by sample type that are definitive of these matrices' roles in the river ecosystem and habitat type. In summary, the fish gut and periphyton are a concern as AR reservoirs due to their relatively high concentration of carbapenem resistance genes, diverse microbial communities, and natural functions that promote AR in the environment.

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