Abstract KAS

Infection due to antibiotic resistant bacteria is a significant problem for clinicians and patients. Due in part to improper use of antibacterial agents, resistance in microbial populations in the environment, a potential source of such infections, is increasing.

To assess the diversity of microbes found in aquatic environments around Louisville, KY, whole communities of microbes as well as the subset resistant to colistin and vancomycin, two last line antibiotics, were isolated from 48 water sources classified in four categories: agricultural waters, natural waterways, wastewaters, and sink drains in commercial establishments. 16S rRNA libraries were generated from each sample, sequenced using high throughput sequencing, and OTUs, alpha diversity, and beta diversity were assessed.

The most common genus of bacteria, Ochrobactrum – a genus containing several opportunistic pathogens, was found in 78 out of 87 samples with an average abundance of 31% across all samples but appeared to be enriched in antibiotic-treated samples (average 42% vs 19% in control samples). Other common isolates belonged to the genera *Microbacterium*, *Leucobacter*, and *Serratia*. In general, agricultural samples showed a greater diversity than drains, natural water, or wastewater samples, a finding that we hypothesize may be due to increased carbon inputs from plants and animals or carbon-rich drainage. Additionally, there were significant differences in alpha and beta diversity between sites or isolation conditions. Understanding the natural reservoir of antibiotic resistance will lay the groundwork for understanding emerging antibiotic resistant pathogens and possibly inform new policies dictating the usage of antibiotics for non-therapeutic uses.