Bacterial communities as biosensors in water infrastructure

ABSTRACT
The microbiome in water supply and sewage infrastructure presents a long-overlooked source of information about both infrastructure status and human health. Advances in NextGen DNA sequencing technology have enabled rapid acquisition of tetrabytes of genomic data from water infrastructure, however, adequate methods for sampling, modelling, and data analysis are required to gain insights useful for engineering applications. Here, I will describe our studies using household water meters, a common residential water system component, as a sampling device, and using an ecological community assembly model to predict water bacterial community shifts due to everyday water stagnation. I will also discuss an ongoing effort utilizing the distribution of human-associated bacteria to estimate the number of upstream residents that contribute to a sewage sample, useful as a data normalization tool to advance smart infrastructure and sewage-based health studies. Taken together, these studies show that understanding of generalizable and system-specific determinants to bacterial communities in water will create new ways for water quality assessment and infrastructure design.

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Fangqiong Ling is a postdoc research fellow at the Department of Biological Engineering at MIT. She is interested in understanding the underlying forces shaping the diversity of microbial communities in built environments and exploring microbiome data as a tool to drive innovations in water infrastructure. Prior to postdoctoral training, she studied in Tsinghua University and University of Illinois, Urbana-Champaign. Her current work is supported by the Microbiology of Built Environment Fellowship from the Alfred Sloan Foundation.