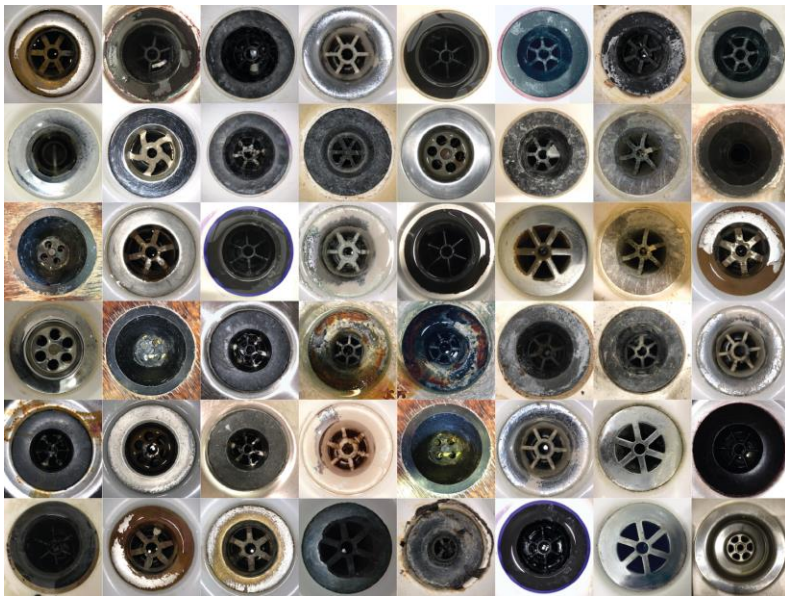# Understanding microbial community dynamics and resilience in communal sink drains

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Sink drains: What's lurking in these drains? Why and how do they persist? How resilient are they? What would be the impact of depositing pathogens or antibiotic resistance genes into the drain, and how long will they persist?

Aim: We will address significant knowledge gaps in the ecology and evolution of sink microbiome, and how it is influenced by sink usage/practice with a key aim to study the resilience and persistence of the communities and species.

Background: There is greater interest than ever in studying microorganisms in the built environment motivated by the fact that people in the developed world spend approximately 90% of their times in buildings [1]. Recent evidence suggests that the majority of microorganisms that we come across in our lifetime are those that occupy the built environment [2]. Due to the increasing trend towards an indoor lifestyle, and the significant roles the indoor microorganisms may play on human health, it is imperative that we develop a greater understanding of the factors that shape microbial communities in the built environment. Despite the interest and increasing amount of knowledge being acquired in microbial communities in buildings [3], very little is known about microorganisms that occupy sink drains and pipes, especially those in communal or public areas. This is possibly due to the general perception that sinks constitute a one-way traffic of waste, i.e. what goes into sink drains and pipes cannot "crawl" back out. A recent study conducted by collaborators of the supervisory team has, however, shown that not only can microorganisms grow out from the bottom of a sink pipe to the top of a drain at an

alarming rate of one inch per day, they have shown that bacteria, having reached the top of the drain, can be dispersed out of the sink and travel up to a metre by the physical mechanistic action of the running water from the tap [4]. While a number of studies have suggested that sinks are an ideal niche for human pathogens to grow and exchange genes such as antimicrobial resistance [5], it has been challenging to identify preventative measures so far. Disturbingly, in hospitals the use of bleach or even replacing the plumbing has been shown to have minimal long term effects on the microbiome and resistance genes, which can regrow and colonise within days. This has significant implications in terms of how sinks in communal areas may play a role in disseminating pathogens and resistance genes.

Key methodology:
This project will feature extensive molecular techniques to study the hidden world of microbes (bacteria and fungi). We will combine both traditional culture-based methods and modern high-throughput DNA sequencing for characterisation of microbial communities (including both short and long-read sequencing technologies). We will also undertake various manipulated studies to understand how the sink drain microbial community shifts under a set of varying environmental conditions, and with the aim of identifying preventative measures.

Specific objectives:
(1) We will characterise microbial communities in communal sink drains and pipes
(2) Evaluate the ecological and evolutionary processes and factors that drive their community dynamics
(3) Investigate the effect sink usage/practices have on resilience of the community (e.g. the use of antibacterial soap, cleaning agents).

Training opportunities:
The student will (1) receive specialist training and mentoring in environmental sampling of microbes. Effective design of experimentation with a clear view on sound statistical principles together with efficient data collection and management will feature heavily in student training; (2) learn advanced molecular techniques in microbial ecology and lab skills in the laboratories at Reading University; (3) acquire bioinformatics and statistics skills through organised courses and mini-projects designed by the supervisory team. Moreover, the student will be exposed to in-depth bioinformatics and statistical knowledge and expertise from the supervisory team who have developed world-class informatic tools for analysing next generation sequencing data.

Student profile:
An ideal candidate would have a strong and passionate enthusiasm for scientific research, both in the field and lab, as well as willingness to learn new skills in both wetlab and bioinformatics. They must have good interpersonal skills for working within a lab environment, but also be able to work responsibly on his/her own initiative in the field. Ideally, the candidate will have strong numerical literacy. Desirable attributes would be skills/knowledge in ecology, molecular biology and computational skills (preferably in bioinformatics).

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[1] Klepeis et al (2001), J. Expo. Anal. Environ. Epidemiol, 11, p231
[2] Dunn et al (2013), PLoS One, 8(5): e64133
[3] Flores et al (2011), PLoS One, 6(11):e28132
[4] Kotay et al (2017), Appl. Environ.Microbiol., 83:8
[5] Brooks et al (2017), Nat. Comm., 8:1814