Recent papers on microbiology of the built environment: Microbes in pipes

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New papers on microbes in water treatment plants and pipes.

Microbes in pipes

Revealing the microbial community structure of clogging materials in dewatering wells differing in physico-chemical parameters in an open-cast mining area – Juanjuan Wang – Water Research

Iron rich deposits cause clogging the pumps and pipes of dewatering wells in open-cast mines, interfering with their function; however, little is known about either the microbial community structure or their potential role in the formation of these deposits. (…) The overall high abundance of Gallionella suggests that microbes may make major contributions to pipe deposit formation irrespective of the water geochemistry.

Limited dissemination of the wastewater treatment plant core resistome – Christian Munck – Nature Communications

Wastewater treatment plants (WWTPs) are believed to play a central role in the dissemination of antibiotic resistance genes. However, the contribution of the dominant members of the WWTP resistome to resistance in human pathogens remains poorly understood. Here we use a combination of metagenomic functional selections and comprehensive metagenomic sequencing to uncover the dominant genes of the WWTP resistome. We find that this core resistome is unique to the WWTP environment, with <10% of the resistance genes found outside the WWTP environment.

Microbial control of dental unit water: Feedback on different disinfection methods experience – Julie
A water quality study of dental units showed biofilm and opportunistic microorganisms. We report the steps that ultimately allowed us to obtain water quality as water for standard care with no pathogens throughout all dental units. In summary, treatment with continuous disinfection associated with use of sterile water allowed us to restore the water quality at the output of dental care units while ensuring the safety of care.

Bacterial community shift drives antibiotic resistance promotion during drinking water chlorination – Shuyu Jia – Environmental Science & Technology

For comprehensive insights into the effects of chlorination, a widely used disinfection technology, on bacterial community and antibiotic resistome in drinking water, this study applied high-throughput sequencing and metagenomic approaches to investigate the changing patterns of antibiotic resistance genes (ARGs) and bacterial community in a drinking water treatment and distribution system.

Investigation of denitrifying microbial communities within an agricultural drainage system fitted with low-grade weirs – Beth H. Baker – Water Research

This study examined the spatial resolution of microbial communities involved in denitrification in agricultural drainage systems fitted with low-grade weirs. Appropriate sampling scales of microbial communities were investigated using 16S rRNA and denitrification functional genes nosZ, nirS, and nirK. (…) This study provides the basis for additional investigations of these unique environments in the Mississippi Alluvial Valley and a starting point for adaptive management to enhance agricultural drainage systems for microbial communities towards nutrient remediation goals.