I did not find a lot of recent papers on indoor microbiology, but quite a couple on the microbiology of drinking and wastewater, and some on ballast, pharmacy, and oil-platform water. Since this blog is all about water, I am playing The Waterboys – The Whole Of The Moon in the background.

**Free with registration:** Acute Gastrointestinal Illness Risks in North Carolina Community Water Systems: A Methodological Comparison – Nicholas B. DeFelice – Environmental Science & Technology

The magnitude and spatial variability of acute gastrointestinal illness (AGI) cases attributable to microbial contamination of US community drinking water systems are not well characterized. We compared three approaches (drinking water attributable risk, quantitative microbial risk assessment, and population intervention model) to estimate the annual number of emergency department visits for AGI attributable to microorganisms in North Carolina (NC) community water systems. ... The differences in results between the drinking water attributable risk method, which has been the main basis for previous national risk estimates, and the other two approaches highlights the need to improve methods for estimating endemic waterborne disease risks, in order to prioritize investments to improve community drinking water systems.

**Open Access:** A New Perspective on Microbiome and Resource Management in Wastewater Systems – Veera Gnaneswar Gude – Biotechnology & Biomaterials

With wastewater treatment systems being increasingly recognized as resource (energy, nutrients and water) recovery facilities, the role of microbiome and resource management is crucial for sustainable process development. ... This mini-review focuses on the use of meta-omic
tools to understand wastewater microbiology and potential integrated approaches for simultaneous and simple yet reliable analysis of the microbial systems in anaerobic digestion and microbial fuel cell systems which share several common features including the ability to produce energy and other valuable chemical and energy products under anaerobic conditions with complex microbial ecology.

*Paid access: Detecting nuisance species using NGST: Methodology shortcomings and possible application in ballast water monitoring – Anastasija Zaiko – Marine Environmental Research*

Detecting the presence of potential invasive species in ballast water is a priority for preventing their spread into new environments. … Here we apply high throughput sequencing from DNA extracted from ballast water (BW) samples employing two different platforms, Ion Torrent and 454, and compare the putative species catalogues from the resulting Operational Taxonomic Units (OTU). … Some putative species detected from the two platforms increased in frequency during the *Polarstern* travel, which suggests they were alive and therefore tolerant to adverse conditions. OTU assigned to the highly invasive red alga *Polysiphonia* have been detected at low but increasing frequency from the two platforms. Although in this moment NGST could not replace current methods of sampling, sorting and individual taxonomic identification of BW biota, it has potential as an exploratory methodology especially for detecting scarce species.

*Paid access: Microbial community distribution and genetic analysis in a sludge active treatment for a complex industrial wastewater: a study using microbiological and molecular analysis and principal component analysis – Giulio Moretti – Annals of Microbiology*

In the present work, a microbiological and genetic analysis was performed for the biological pool of an industrial wastewater treatment plant located in Civita Castellana (Viterbo, Italy). … For this study, Biolog community level physiological profiling (CLPP) on EcoPlates and PCR-amplified 16S rRNA denaturing gradient gel electrophoresis (DGGE) were used in comparison and combined as ecological techniques to characterize an anthropic closed ecosystem. Biolog CLPP provides the potential metabolic pattern and DGGE analyses helps to explain the structure and complexity of the microbial community. The results suggest that these techniques could be predictive and more useful when used together than alone.

*Paid Access: Using amplicon sequencing to characterize and monitor bacterial diversity in drinking water distribution systems – Jennifer L. A. Shaw – Applied and Environmental Microbiology*

Here, amplicon sequencing of the 16S rRNA gene region was performed
alongside traditional water quality measures to assess the health, quality, and efficiency of two distinct, full-scale DWDSs. ... In both DWDSs bacterial communities differed significantly after disinfection, demonstrating the effectiveness of both treatment regimes. However, bacterial repopulation occurred further along the DWDSs, and some end-user samples were more similar to the source water than the post-disinfection water. ... From this study, we conclude that metagenomic amplicon sequencing is an informative method to support current compliance-based methods, and can be used to reveal bacterial community interactions with the chemical and physical properties of DWDSs.

Paid Access: Characterization of the microbial community structure and the physicochemical properties of produced water and seawater from the Hibernia oil production platform – C. William Yeung – Environmental Science and Pollution Research

Hibernia is Canada’s largest offshore oil platform. Produced water is the major waste byproduct discharged into the ocean. ... The objectives were to characterize the microbial communities and the chemical composition in the produced water and to characterize changes in the seawater bacterial community around the platform. The results from chemical, physicochemical, and microbial analyses revealed that the discharge did not have a detectable effect on the surrounding seawater. ... Unique microorganisms like Thermoanaerobacter were found in the produced water. Thermoanaerobacter-specific q-PCR and nested-PCR primers were designed, and both methods demonstrated that Thermoanaerobacter was present in seawater up to 1000 m from the platform. These methods could be used to track the dispersion of produced water into the surrounding ocean.


Biological treatment processes offer the ideal conditions in which a high diversity of microorganisms can grow and develop. The wastewater produced during these processes is contaminated with antibiotics and, as such, they provide the ideal setting for the acquisition and proliferation of antibiotic resistance genes (ARGs). This research investigated the occurrence and variation in the ARGs found during the one-year operation of the anaerobic sequencing batch reactors (SBRs) used to treat pharmaceutical wastewater that contained combinations of sulfamethoxazole-tetracycline-erythromycin (STE) and sulfamethoxazole-tetracycline (ST). ... Due to the limited availability of primers to detect ARGs, Illumina sequencing was also performed on the sludge and effluent of the STE and ST reactors. ... According to the expression of genes results, microorganisms achieve tetracycline and erythromycin resistance through a combination of three mechanisms: efflux pumping protein, modification of the antibiotic target and modifying enzymes.