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Metatranscriptomic analysis to reveal structure and function of microbial managed aquifer recharge (MAR) systems for enhanced trace organic chemical removal

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Introduction

Trace organic chemicals (TOrC) such as household chemicals, pharmaceuticals, personal care products, hormones, industrial chemicals, pesticides and disinfection by-products enter the environment via wastewater discharge[1]. Many of these compounds have been detected in surface water, groundwater and drinking water due to incomplete removal during conventional biological wastewater treatment processes[1]. Managed aquifer recharge (MAR) systems, including riverbank filtration, soil aquifer treatment and artificial recharge and recovery, are natural water treatment processes with the benefit of low-energy demand and no input of chemicals or residual generation[1,2]. Recent studies show that microorganisms play an important role in degradation of dissolved organic carbon (DOC) and TOrC in MAR systems[3]. Results from next-generation sequencing indicate that oxic, oligotrophic conditions with high taxonomic and functional diversity of microorganisms are favourable for co-metabolic degradation of relevant TOrC[3].

Objective

Research objectives include the development and adaptation of new tools to elucidate the key factors for microbial transformation of TOrC in porous media filter systems. Methods for the determination of taxonomic and functional diversity will be established and linked to chemical analyses of TOrC using UHPLC-MS/MS. A major focus lies on the concept of sequential managed aquifer recharge technology (SMART) to combine two MAR systems with an in between aeration step to provide favourable aerobic, carbon limited infiltration in the second system. In addition, removal of TOrC and diversity of microorganisms will be elucidated in other biologically active filters, such as slow sand filtration, activated carbon and quick sand filtration and focuses on the optimization of bank filtration and artificial recharge systems in Berlin for a better attenuation of trace organic chemicals by adopting the SMART approach. To transfer the concept of SMART to recharge sites in Berlin is one major objective of this study. The combination of next-generation sequencing and state-of-the-art analytical tools for micropollutant detection will allow to clarify the role of microbial diversity and functionality to enhance biological transformation.

Material and Methods

Experiments will be conducted within a joint cooperation project with the TU Berlin (TUB), the University of Oldenburg (UO), and the Berliner Wasserbetriebe (BWB). Laboratory-scale column experiments will be set-up in Berlin and Munich to test the SMART concept, further validated by monitoring of full-scale groundwater recharge facility Tegel, Berlin. Columns will be operated at TUM to adopt SMART for enhanced treatment of secondary effluents in the framework of indirect potable reuse. 16S rRNA sequencing, metagenomics and metatranscriptomic analyses will be established in combination with compound and pathway determination by target, suspected target and non-target analytical methods in order to identify composition and function of microbial communities responsible for biodegradation of trace organic compounds.

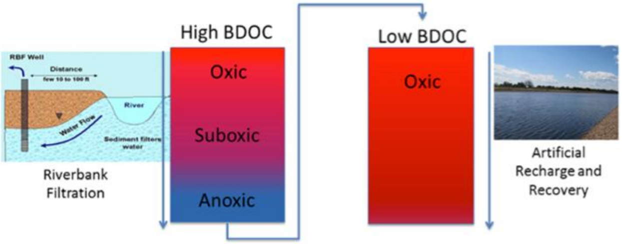

Fig. 1: Principle of sequential MAR technology

References

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[3] *Li, D. et al. 2012, Dissolved Organic Carbon Influences Microbial Community Composition and Diversity in Managed Aquifer Recharge Systems. App. and Envir. Microbiol. 78: 6819-6828.*

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