Analysis of microbial community diversity and function responsible for transformation of micropollutants in MAR systems using next generation sequencing

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Background

- During managed aquifer recharge (MAR), such as riverbank filtration (RBF), soil aquifer treatment and artificial recharge and recovery, microorganisms play an important role in the biotransformation of dissolved organic carbon (DOC) and trace organic chemicals (TOC) [1, 2].
- The innovative Sequential Managed Aquifer Recharge Technology (SMART) concept combines two MAR systems with an in-between aeration step to provide favorable aerobic and carbon limited conditions during infiltration in the second system.

Fig. 1: Principle of Sequential MAR technology

- Co-metabolism is the most likely mechanism for TOC degradation [3].
- Oxic and oligotrophic conditions (0.5 – 5 mg DOC/L) enhance TOC degradation.
- High-throughput sequencing revealed that the diversity of microbiome in the infiltration layer of the vadose zone of MAR systems is directly influenced by the concentration and composition of DOC. Microbial community diversity increases:
  (i) at low DOC concentration [1].
  (ii) in the present of low biodegradable DOC as primary substrate (BDOC, see Fig. 1) [2].

Fig. 2: Composition of microbial community at phyla level in soil columns receiving higher and lower BDOC concentrations at different depth [2]

Objectives

- Simulate the SMART concept by using two sequential lab-scale column systems with an in-between aeration step
- Transfer the SMART model to recharge sites in Berlin for a better attenuation of TOC like household chemicals, pesticides and disinfection byproducts
- Identification of composition and function of microbial communities responsible for biodegradation of TOC using Metagenomics and Metatranscriptomics in combination with target analytical methods (LC-MS/MS)

Lab-scale and field experiments

- Laboratory scale-column experiments at TUM are conducted to adopt SMART for enhanced treatment of secondary effluents leading to indirect potable reuse.
- 2 set-ups of four columns in series are operated under different feed water conditions.
- Hydraulic retention time (HRT) in each system can be varied from 1 – 10 days.
- The connection of several columns in series enables sampling for biomolecular analyses at the following filter depth: 0, 30, 60 and 90 cm. Samples for chemical analysis are taken at lateral ports at 10 and 20 cm of the first column, at ports between the columns and on the influent and effluent of the column system.
- Dissolved oxygen concentration can be measured at different filter depth by non-invasive optical oxygen probes.
- Field experiments are operated at the groundwater recharge facility in Berlin Tegel

Fig. 3: Laboratory scale soil column experiments

Analytical approach

- Next generation sequencing (NGS) including 16S rRNA gene analysis, metagenomics and metatranscriptomics are used for the identification of the composition, diversity and functionality of microbial communities.
- The combination of NGS with a compound and pathway determination by target, suspected target and non-target analytical methods is used to identify microbial communities responsible for biodegradation of TOC.

Fig. 4: HILIC-RP/HPLC-API-TOF/MS

Cooperation and Funding

Literature