Diversity and function of microbial communities in charge of micropollutants degradation analyzed by shotgun and 16S rRNA metagenomic sequencing

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Background

- Several trace organic chemicals (TOrC) are detected in the bank filtrate from the Lake Tegel → degradation of TOrC during managed aquifer recharge (MAR) becomes more important
- Microorganisms play an important role in the degradation of dissolved organic carbon (DOC) and TOrC during MAR [1, 2]
- The most likely mechanism for the TOrC attenuation is the co-metabolism [3]
- A combination of two MAR systems with an in between aeration step leads to the preferred oxic and oligotrophic conditions for an enhanced co-metabolic TOrC removal:
  → sequential managed aquifer recharge technology (SMART):

Lab-scale and field experiments

- Parallel soil column set-up at TU Berlin (Figure 3, Figure 4a):
  - Three systems of two columns:
    - no aeration
    - aeration with air / pure oxygen
    - aeration with ozone
  - Hydraulic retention time (HRT) ~ 6 days (whole system)
  - Biomolecular sampling possibilities at 0 and 100 cm; water sampling is possible at:
    - 0 cm (HRT: 0 h), 25 cm (18 h), 50 cm (36 h), 75 cm (54 h), 100 cm (72 h), 125 cm (90 h), 150 cm (108 h), 175 cm (126 h) and 200 cm (144 h)
- Influent: Lake Tegel Water
- Dissolved oxygen measurements via flow through cells in the influent and effluent of each column

Objectives

- Analytical approach
  - The TOrC analysis is conducted by a Siex LC – Qtrap MS-MS
  - The combination of both methods, next generation sequencing and target analytical methods (LC-MS/MS), can be used for the identification of the microbial community composition and function responsible for TOrC removal.

Literature