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Reactive transport of dichloromethane in laboratory aquifers: insights from dual-element isotope analysis and biomolecular approaches

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Dichloromethane in aquifers

Dichloromethane (DMC) is one of the most common chlorinated methanes often detected in groundwater as a result of extensive use, inappropriate disposal and accidental spills[1,4].

Why studying water table fluctuations?

> Spreading of pollutants across the saturated and unsaturated zone (e.g., volatile compounds).

> Changes in redox conditions and microbial composition that may further impact pollutant degradation.

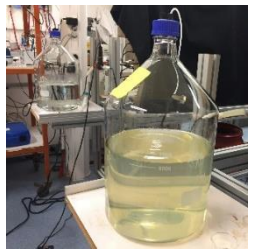
Research questions

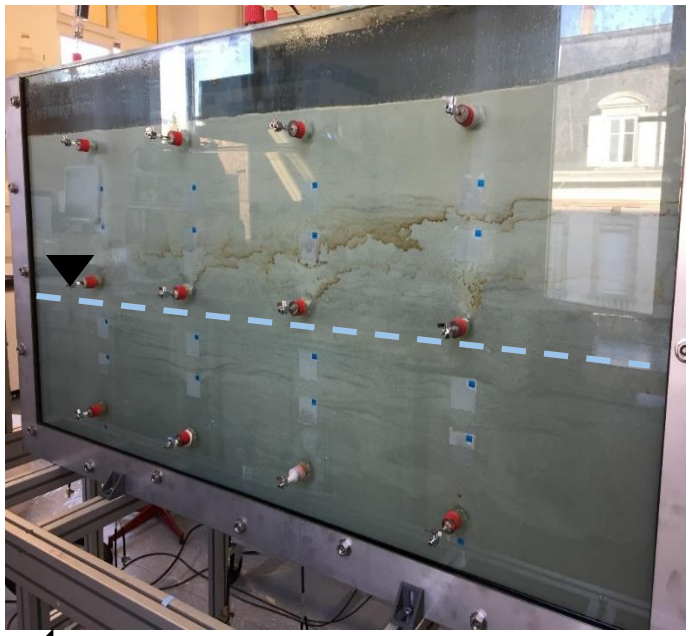
> What is the impact of water table fluctuations on the extent of DCM *in-situ* degradation in aquifers?

> What are the main mechanisms and pathways of DCM dissipation in aquifers?

Dual-element CSIA and high-throughput analysis may help?

Laboratory aquifers under near-natural settings

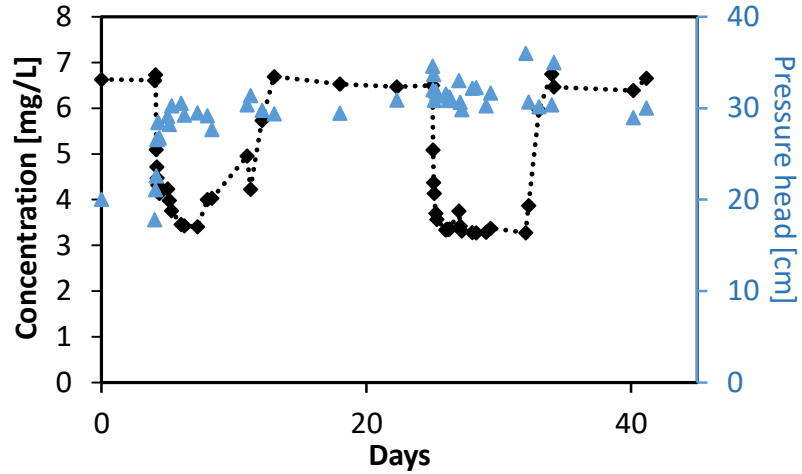


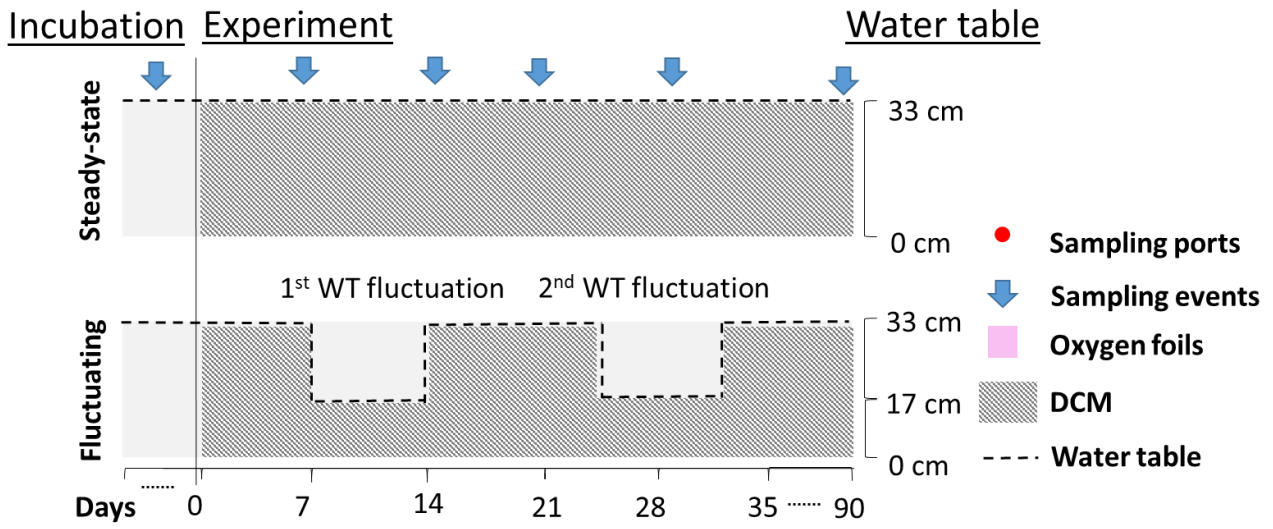


Flow direction

Dimensions: 160 x 80 x 7 cm³
Flow rate: 0.33 mL/min
DCM injection: 0.45 mM/L
Oxygen content: **< 0.3 mg/L**
Residence time: 31 days

Oxygen evolution: transient conditions





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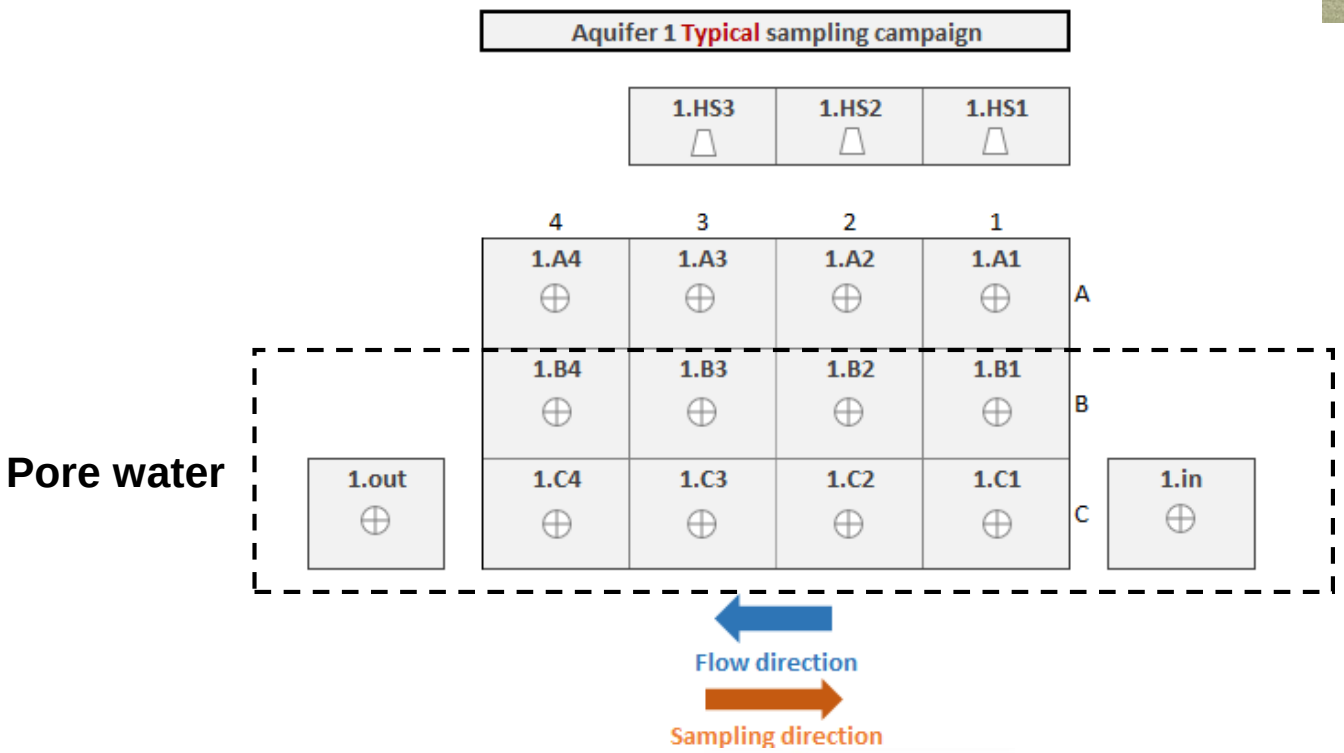
Material and methods

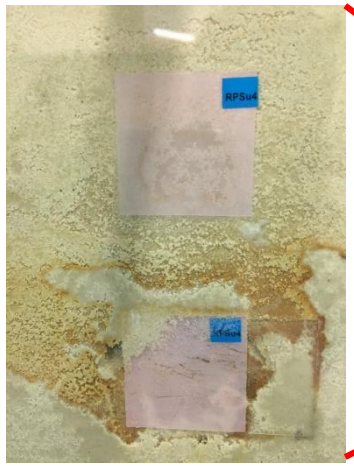
High-resolution sampling:

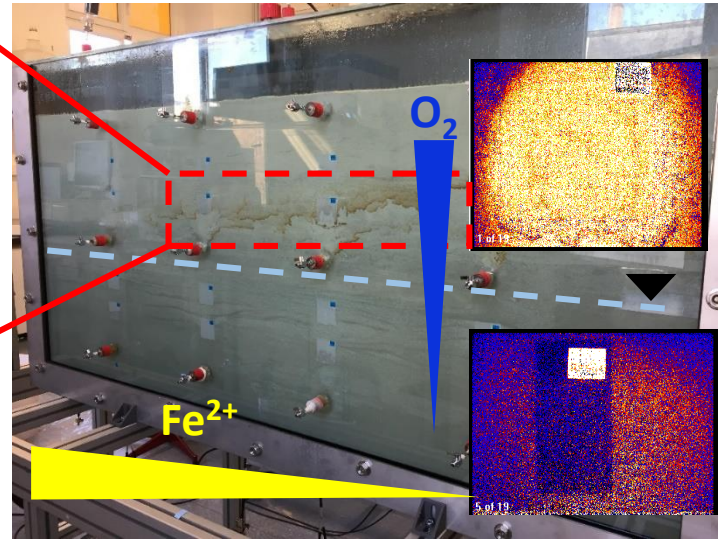
- Quantification of DCM
- Isotope analysis of ^{13}C (GC-IRMS) and ^{37}Cl (GC-MS)
- DNA analysis
- Hydrochemical parameters



Pore water

Iron-reducing conditions in both aquifers





Core sampling for DNA analysis

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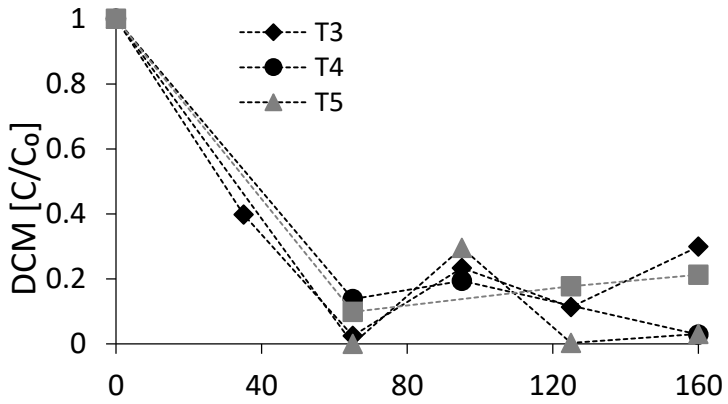
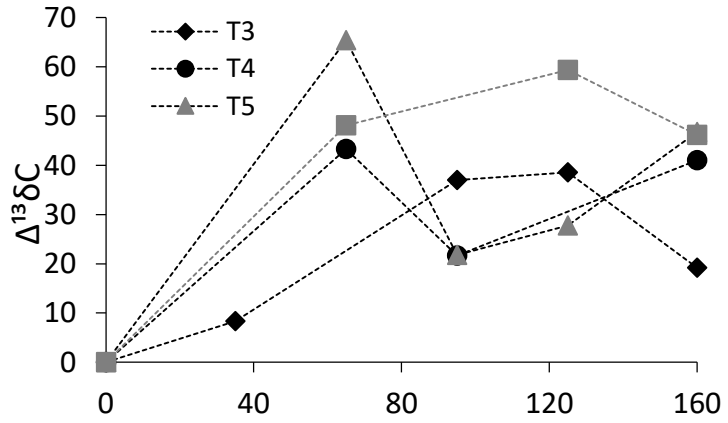
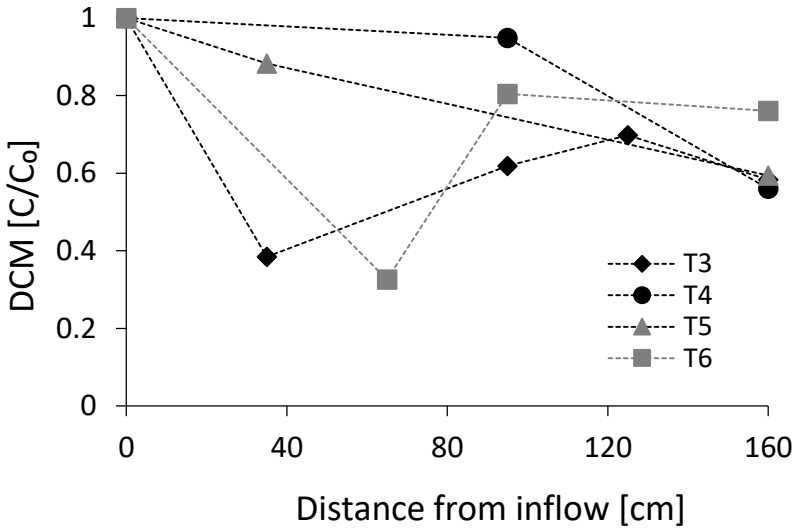
Mass dissipation and carbon isotope composition of DCM

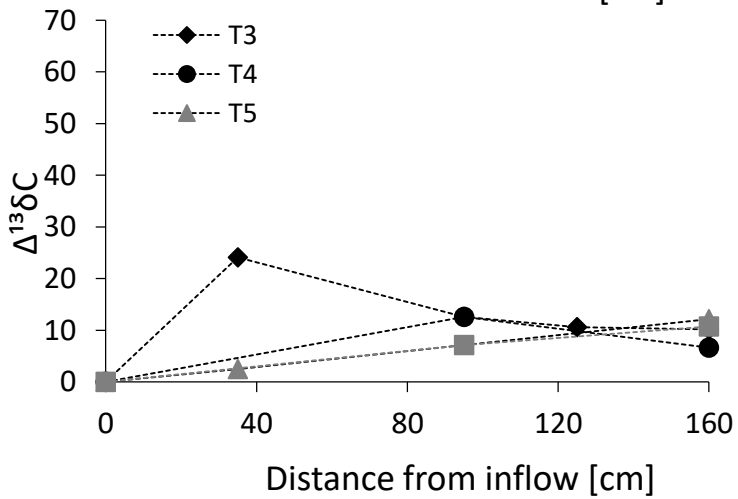
Fluctuating condition





Steady-state condition





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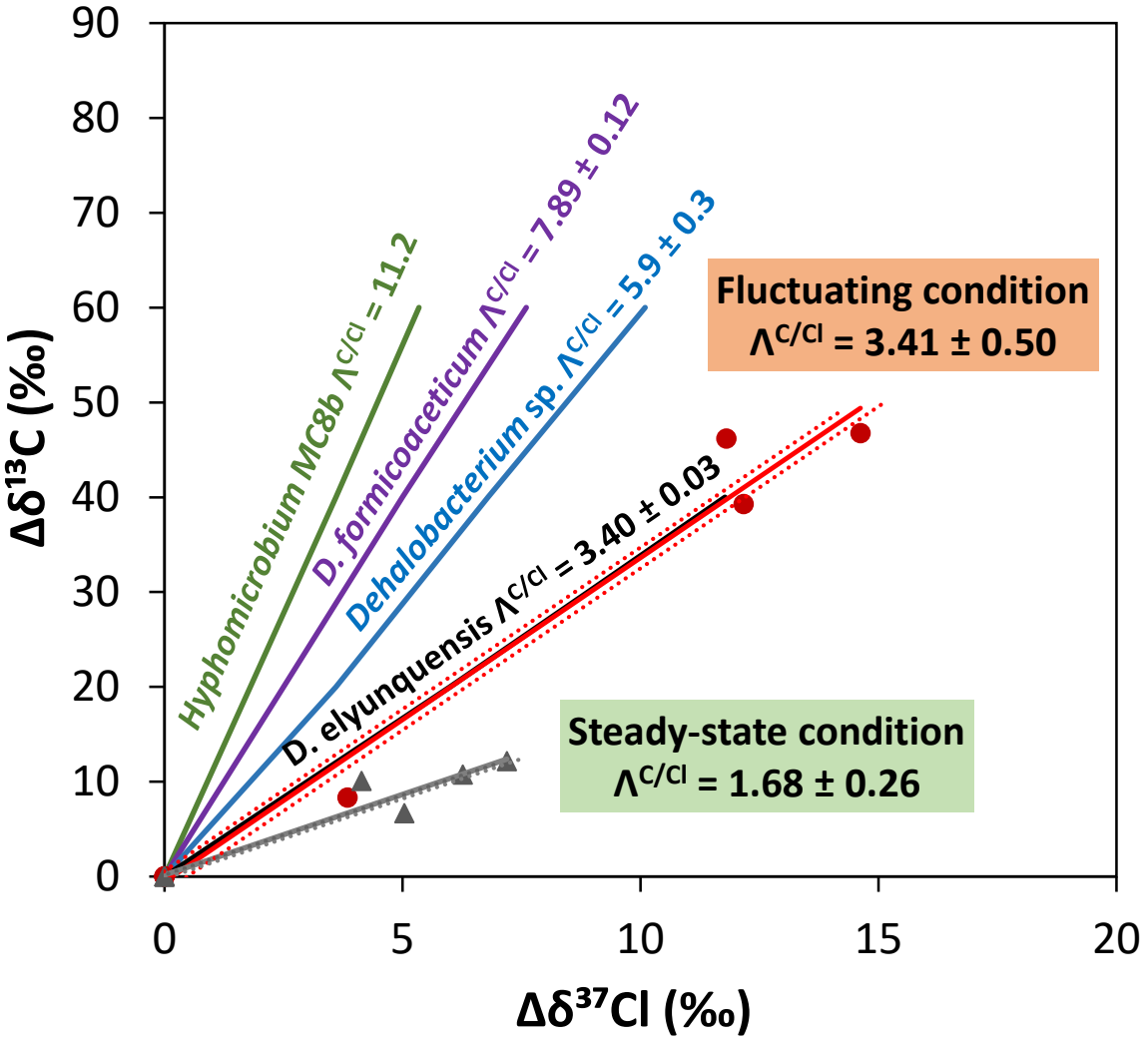
Dual-element CSIA: mechanisms of DCM degradation

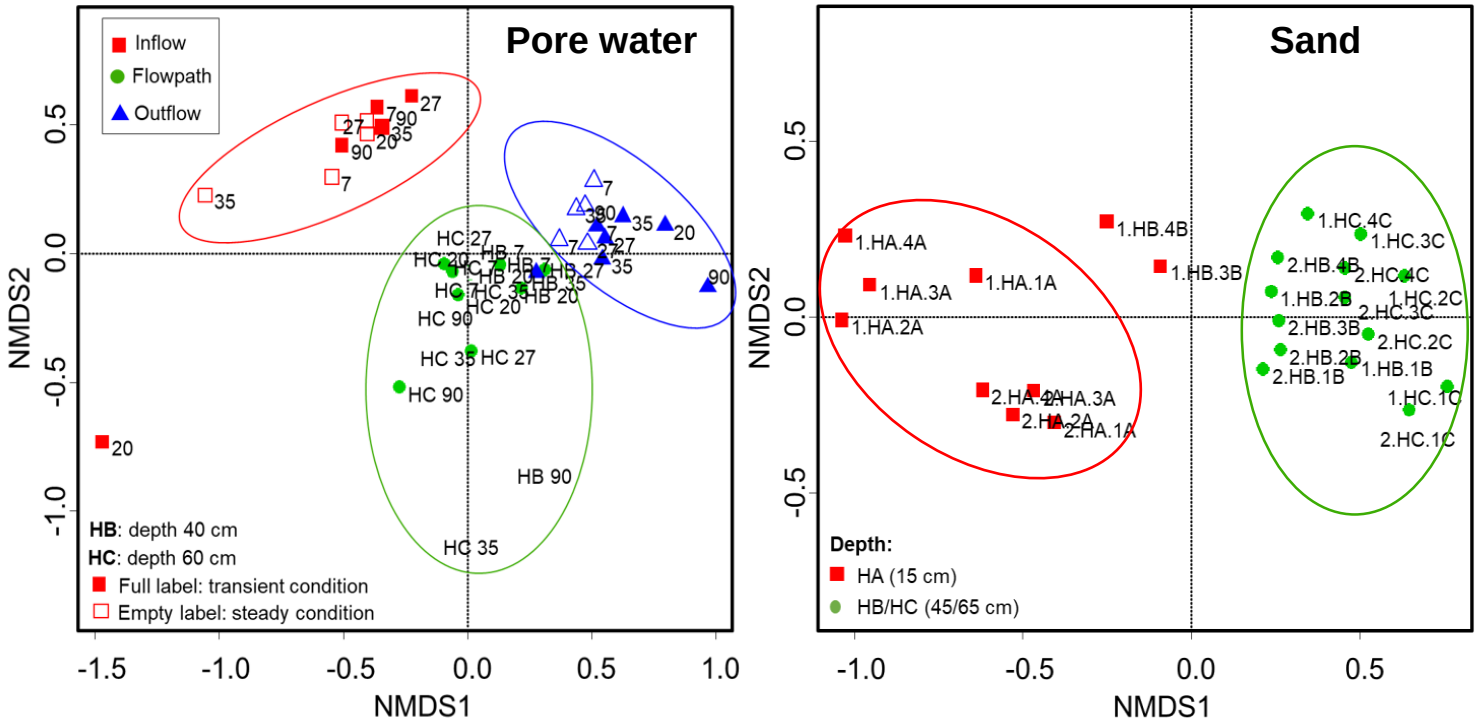


- Dual C-Cl isotope plot of DCM degradation under transient (red dots) and steady-state (gray triangles) conditions.
- Reported mechanisms by *Hyphomicrobium MC8b*[2], *D. formicoaceticum*[3], Ca. Dichloromethamonas elyunquensis[3,6] and *Dehalobacterium* sp.[4] have been added for comparison.

a. Similar mechanims as *Ca.* Dichloromethamonas elyunquensis.
b. Combination of different mechanisms (apparent).

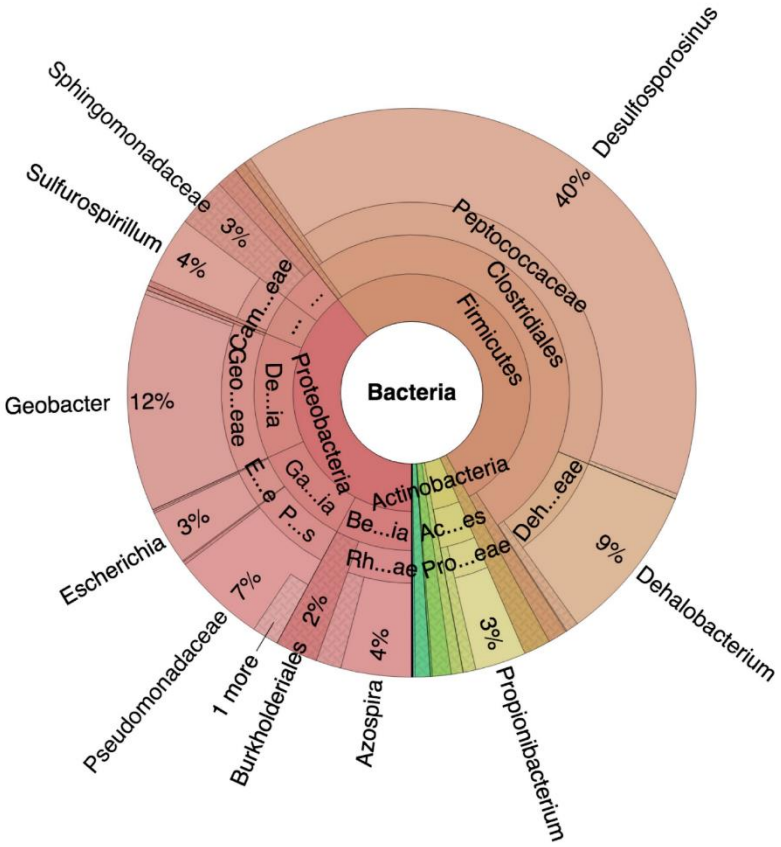
Unknown mechanism under strictly anoxic conditions.

Bacterial community analysis



- NMDS ordination of bacterial communities in pore water and sand compartment. Depth in cm from surface to bottom.

Evidence of anaerobic DCM degraders: Dehalobacterium[4], Geobacter[5], Desulfosporosinus[6,7].



- Representation of relative abundance of taxa from phylum to genus level in pore water.

Highlights

- Pronounced carbon isotope fractionation of DCM associated with large DCM mass removal under fluctuating conditions (>90%) compared to steady-state conditions (mass removal of 35%).

- Distinct DCM degradation pathways under steady and fluctuating conditions:

=> mechanistically distinct C-Cl bond cleavage reactions subjected to microbial adaptations during dynamic hydrogeological conditions?

- Occurrence of anaerobic DCM degraders under both steady and fluctuating conditions:

  => supports DCM degradation under iron-reducing prevailing conditions.

Water table fluctuations enhance DCM biodegradation and influence DCM degradation pathways compared to steady-state conditions.

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THANK YOU!

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