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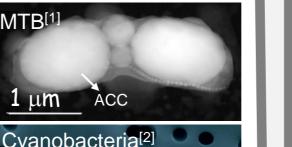
Mineralogical and Geochemical controls on intracellular amorphous calcium carbonate (ACC) formed by magnetotactic bacteria in Lake Pavin, France



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Background

Recently, phylogenetically diverse magnetotactic bacteria (MTB) from Lake Pavin sediments (France) were shown to form intracellular amorphous calcium carbonate (ACC), thereby expanding the taxonomical diversity of iACC-forming bacteria^[1]. The ACC found in MTB (and other bacteria^[4]) remains relatively stable intracellularly, which is surprising as pure abiogenic ACC is highly unstable. The mechanisms underlying such stability are unclear. Moreover, the ACC-forming MTB are proposed as an overlooked player in the geochemical cycle of Ca given their high abundance (>10⁴ cells mL⁻¹) and ability to sequester large quantities of Ca as ACC.



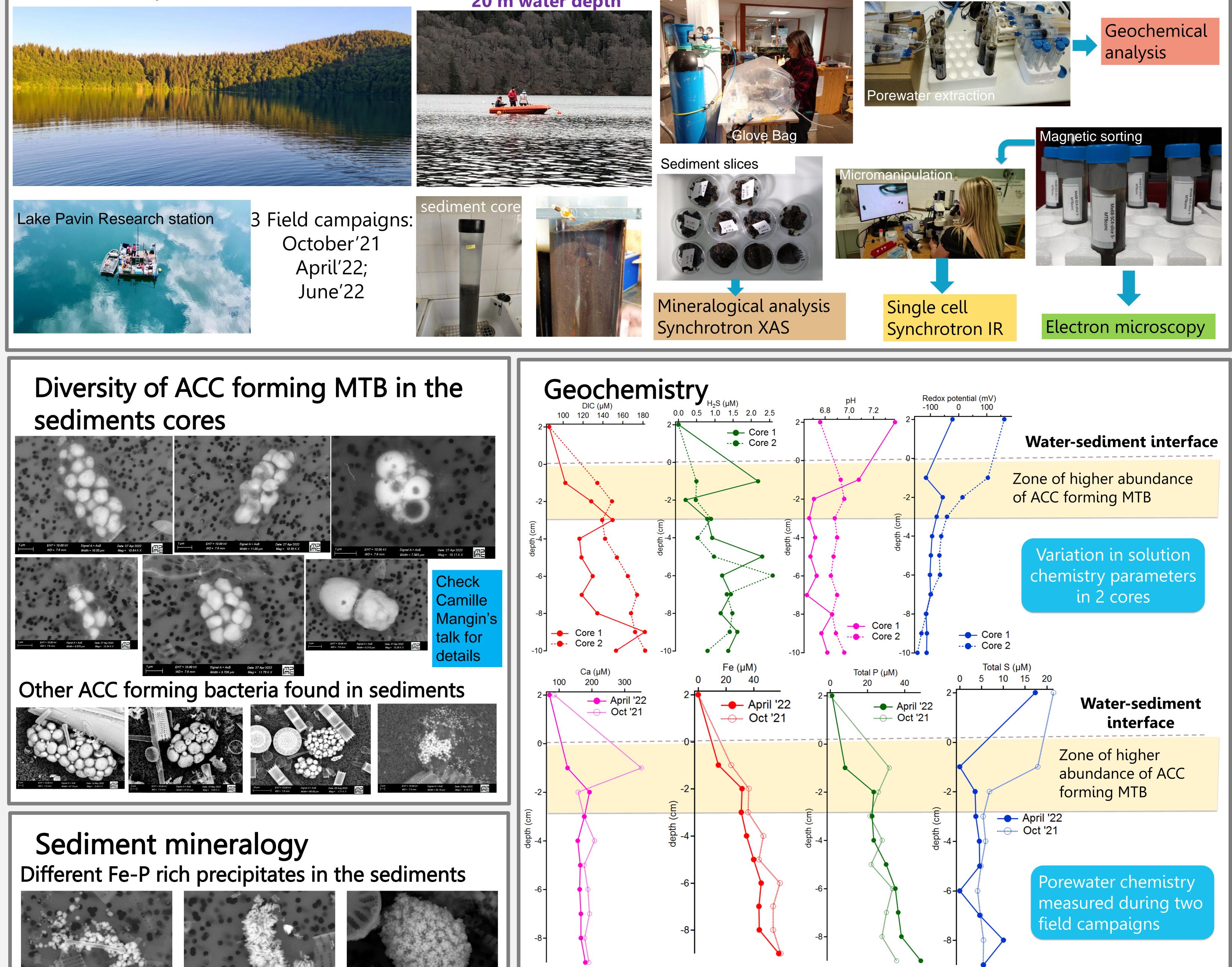
Objective

What <u>biogeochemical factors</u> control the abundance and population structure of ACC forming MTB in the sediments?



What is the <u>fate of intracellular ACC</u> in the sediments and its overall impact on sedimentary <u>geochemical cycle of calcium</u>?

Lake Pavin, France



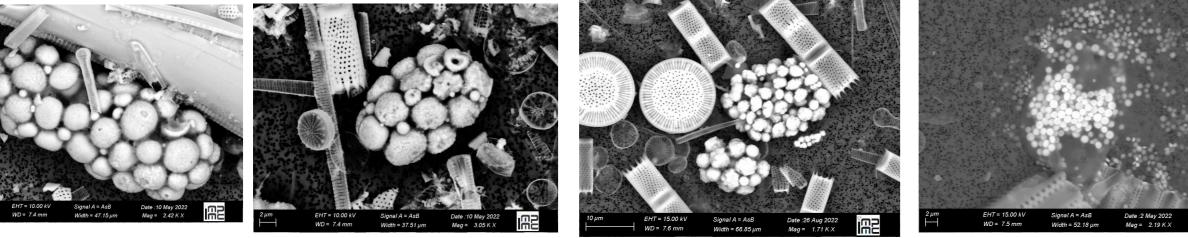
Sediment core collection at

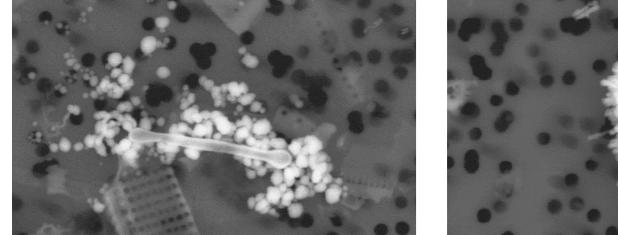
Anoxic sectioning of sediment core (1 cm section)

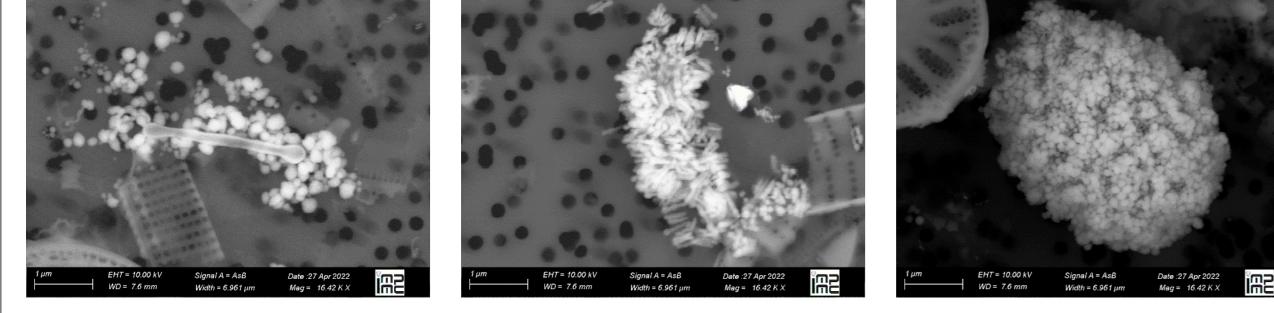




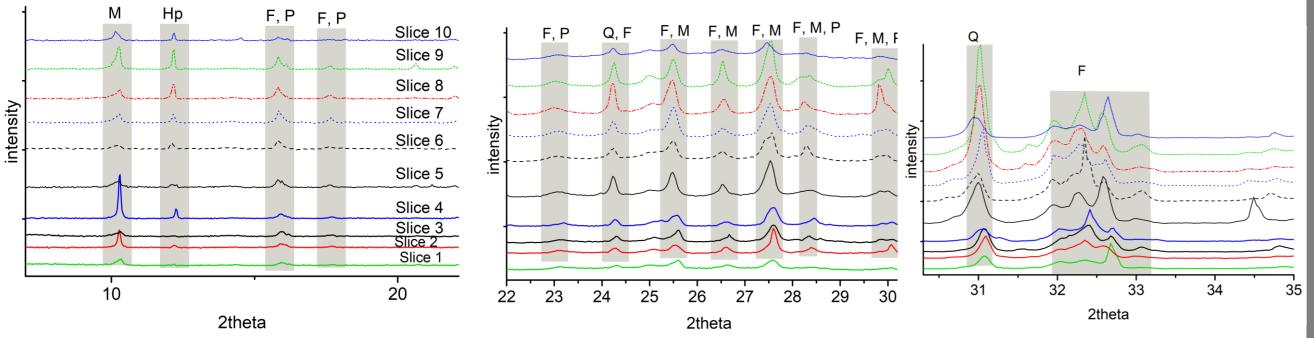








XRD analysis of sediments



Major phases identified in sediments:

- Mica (M), Ca-hydroxyapatite (Hp), Feldspar (F), Pyroxenes (P), Quartz (Q)
- Nature of major host matrix of Ca in the sediments remain unclear \rightarrow Future work will utilize XAS to better constrain sedimentary Ca speciation

Ongoing work

- Sedimentary microbial diversity assessment using metabarcoding
- Mineralogical analysis of sediments using SEM-EDX and multivariate statistics
- MTB-ACC characterization using synchrotron nano IR spectroscopy
- Ca K-edge XAS analysis to quantify impact of ACC forming MTB on Ca cycle

References

[1] Monteil et al., 2021, ISME, 10.1038/s41396-020-00747-3 [2] Couradeau et al, 2012, Science, 10.1126/science.1216171 [3] Benzerara et al, 2020, Geobiology, 10.1111/gbi.12424

[4] Benzerara et al. 2022, Genome Biology and Evolution, 10.1093/gbe/evac026





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