

# Impacts of CO<sub>2</sub>-Exposed Microbial Ecology on Reservoir Performance

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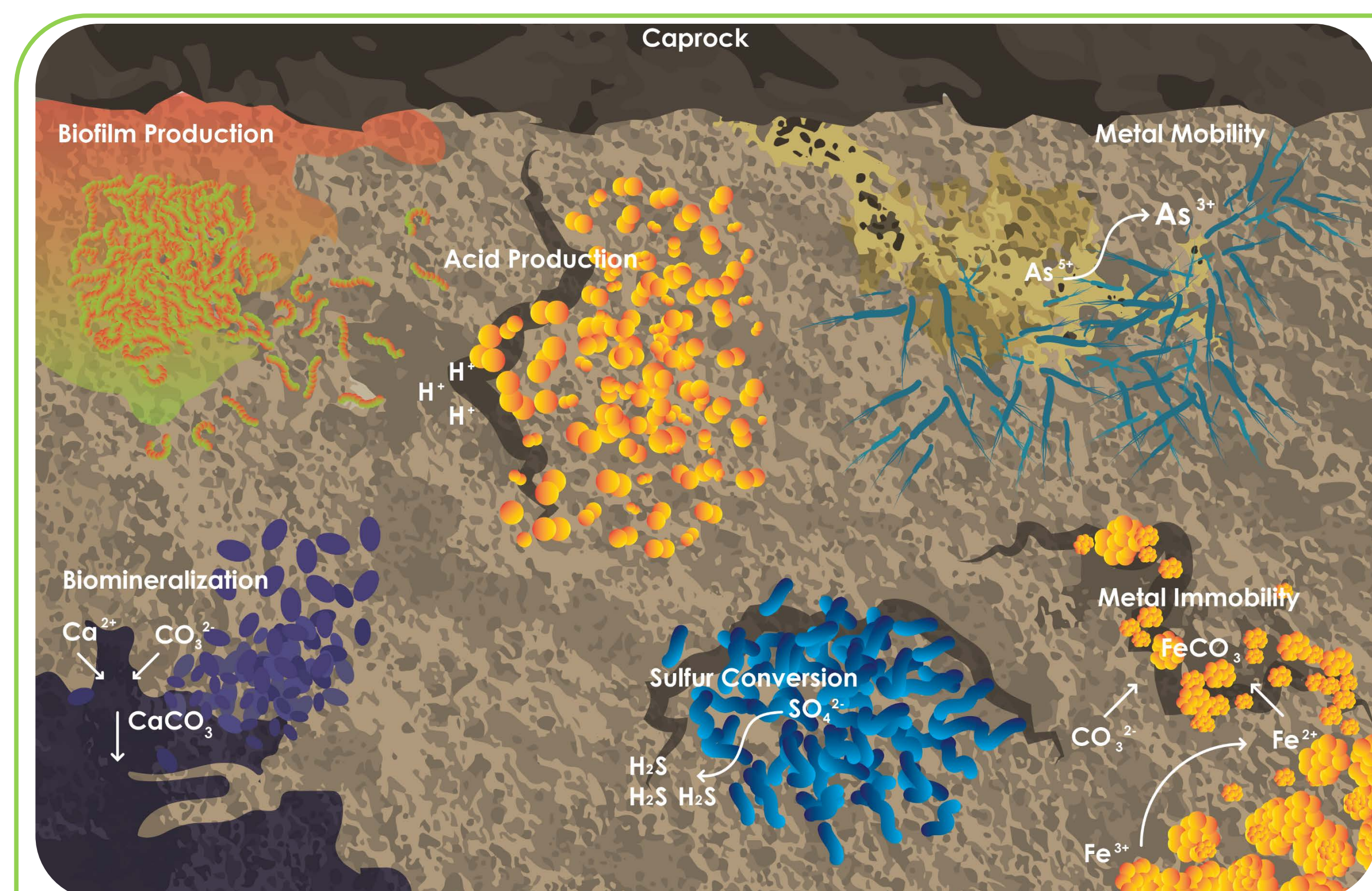
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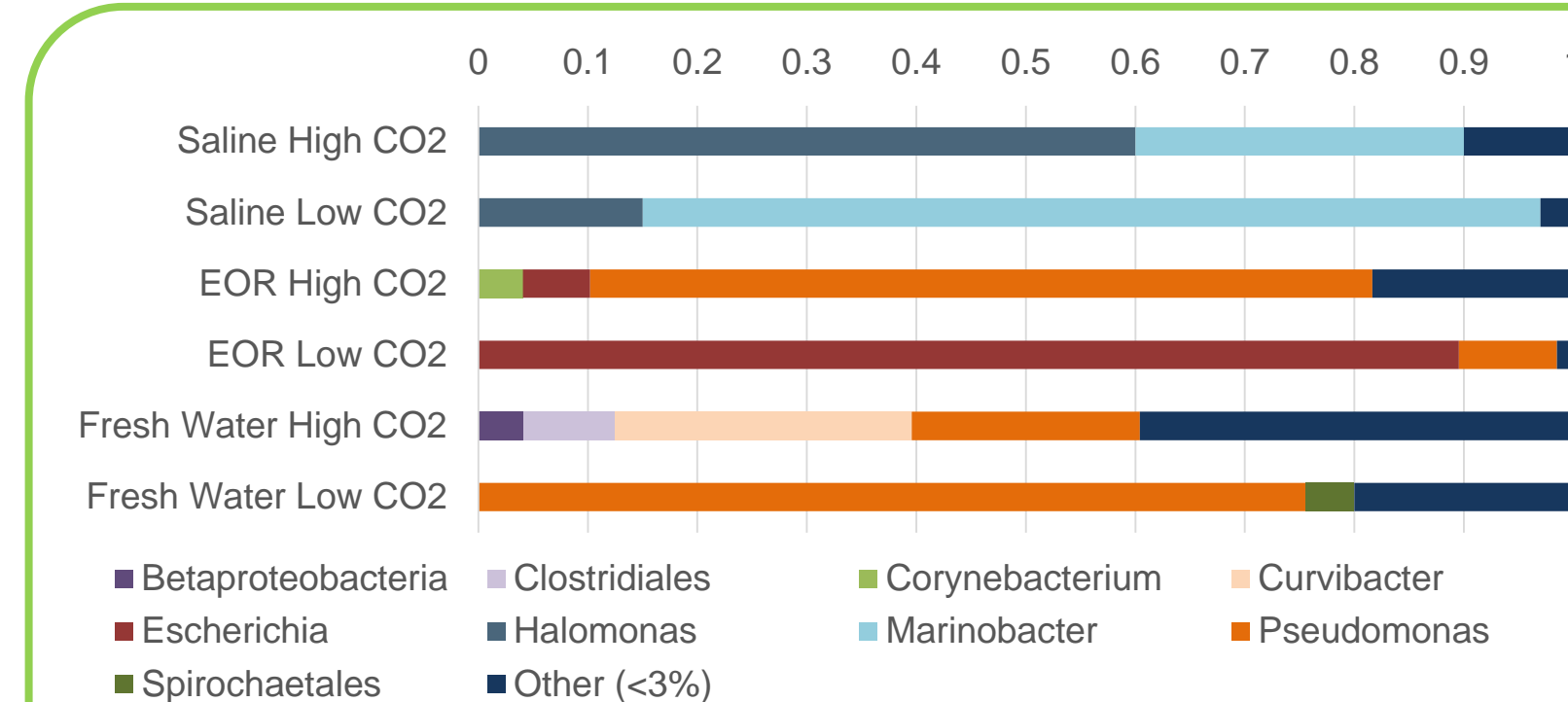
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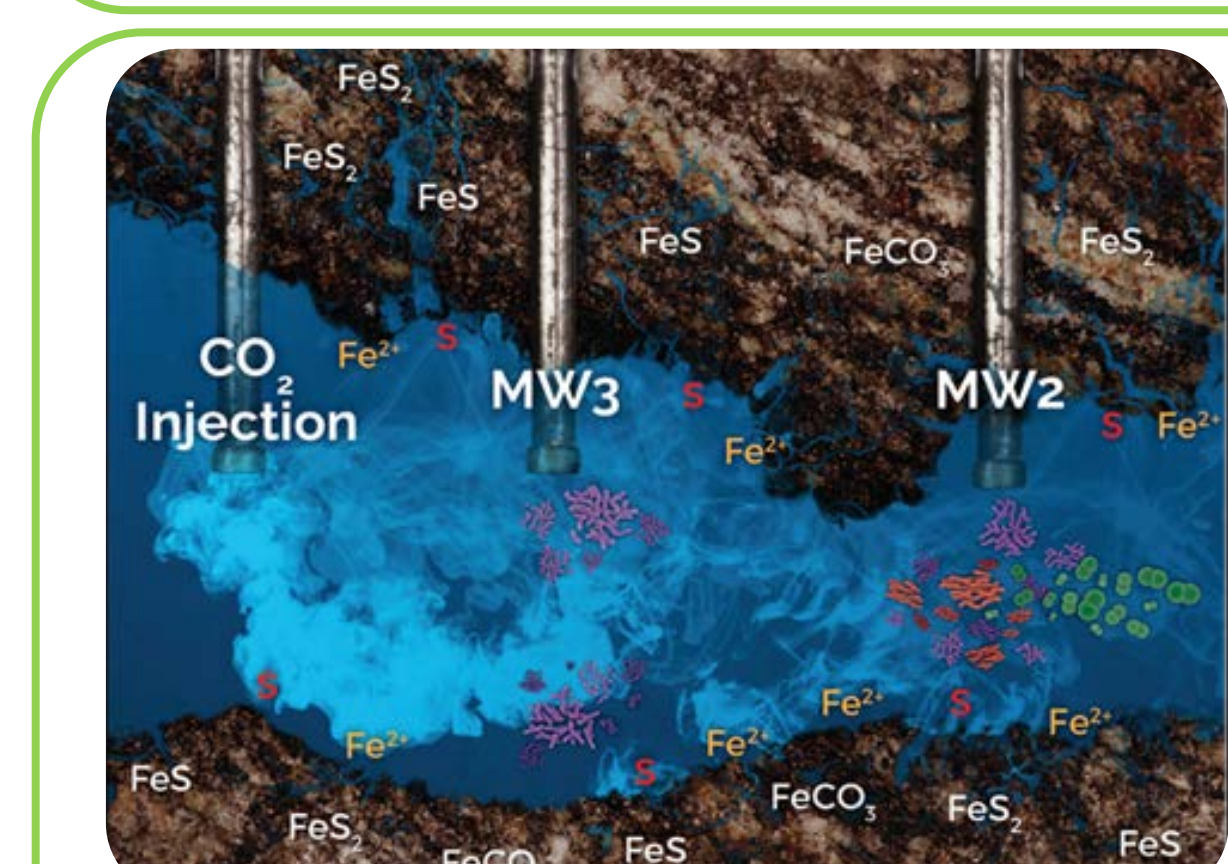
## Previous Work



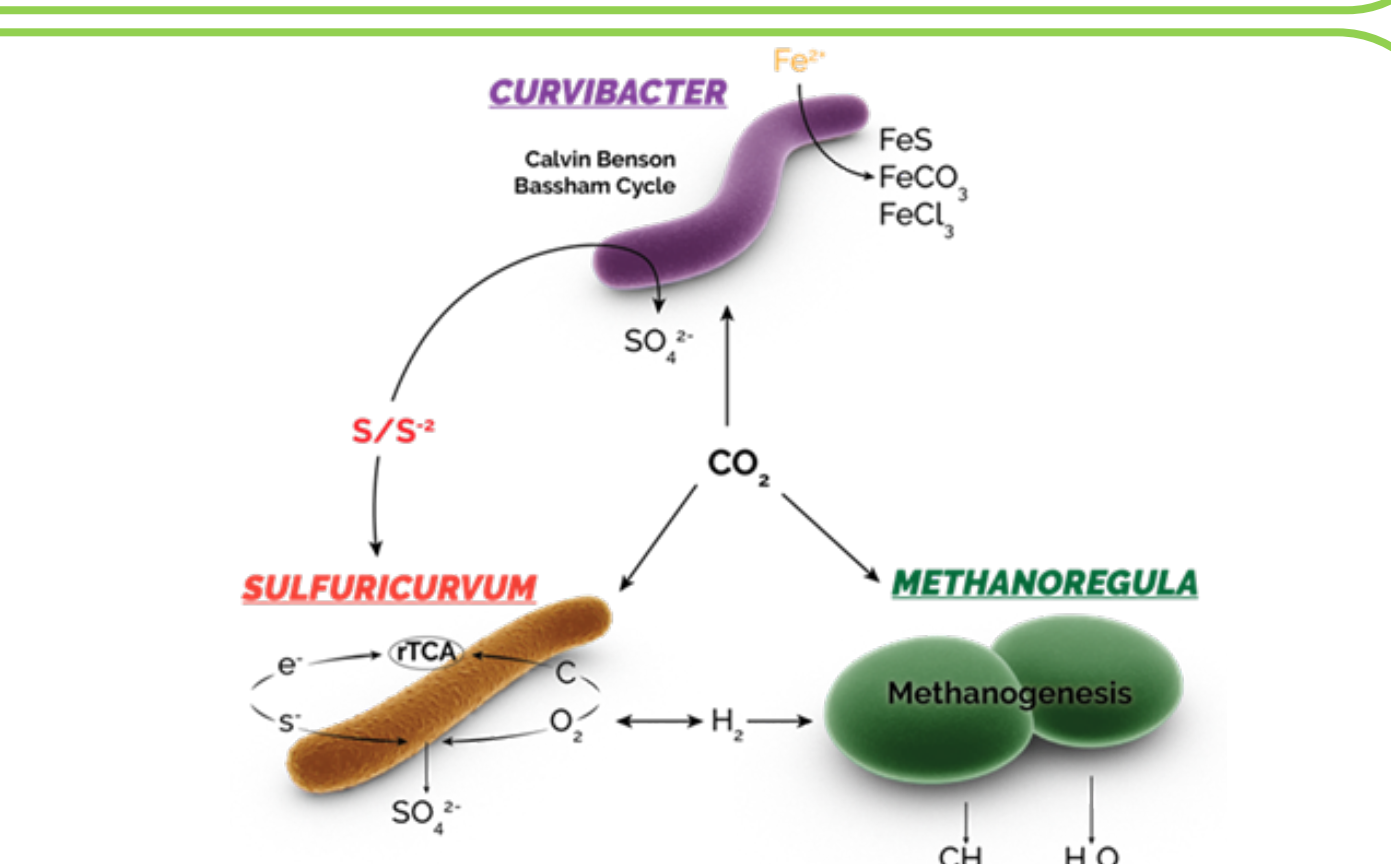
Pore-plugging/dissolution reactions in carbon storage reservoirs will affect the CO<sub>2</sub> storage and wellbore integrity. Evidence indicates that subsurface microbial communities currently catalyze these plugging/dissolution processes through mechanisms such as biomineralization (scaling), acid formation (biocorrosion), and biofilm formation (biofouling). However, it is still widely unknown in the energy industry which of these processes will occur during carbon storage and how to properly mitigate these occurrences. We examined overall shifts in dominant microbial taxa in response to the CO<sub>2</sub> in the subsurface environment.



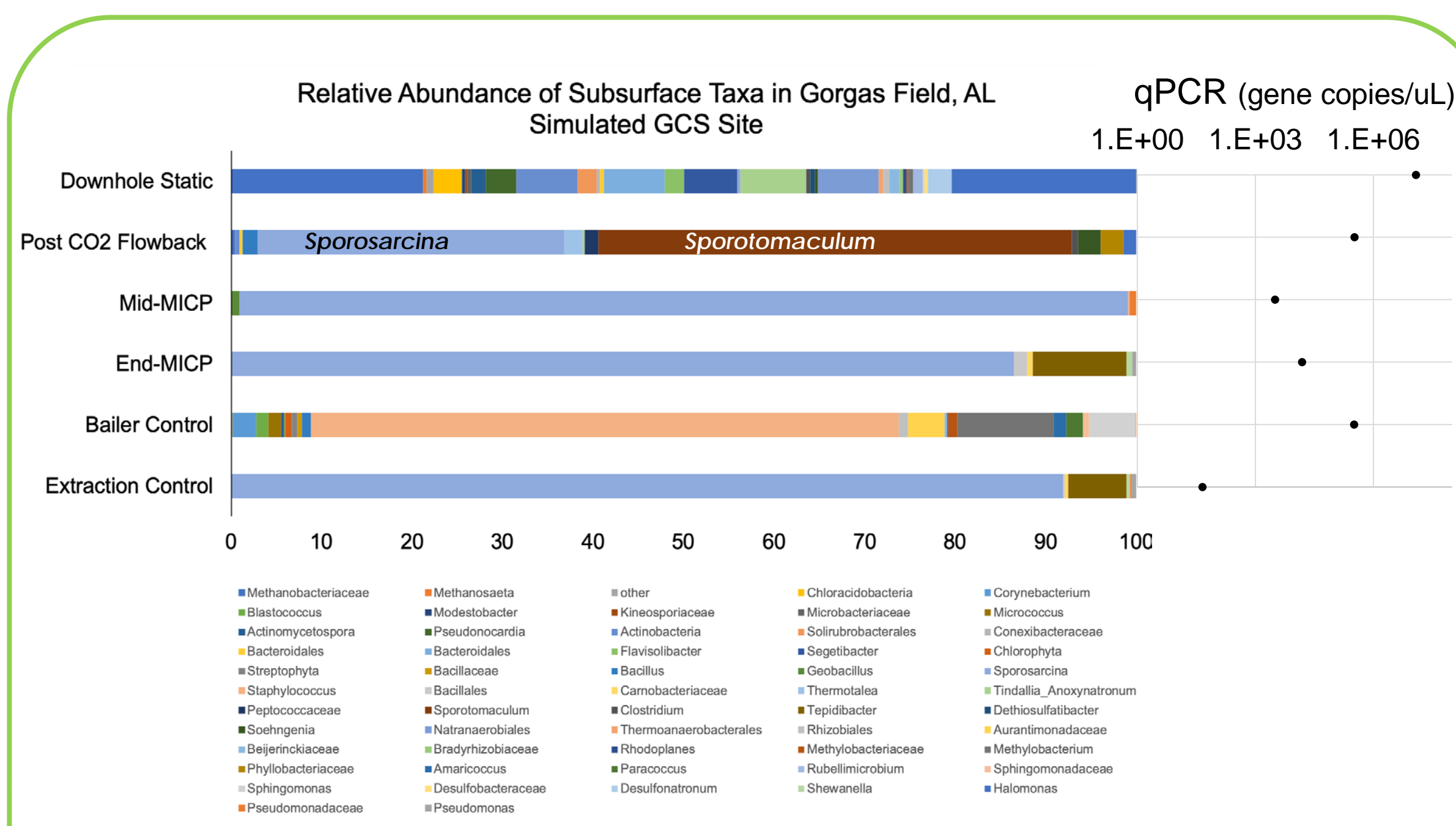
- The dominant species of the saline formation were *Halomonas* and *Marinobacter*.
- The dominant species in the EOR site was *Pseudomonas* and *Escherichia*.
- The dominant species in the CO<sub>2</sub>-impacted fresh water aquifer was *Pseudomonas* and *Curvibacter*.
- Correlation between sites and geochemistry demonstrated the CO<sub>2</sub>-resilient microorganism unique to each system.



CO<sub>2</sub>-saturated groundwater was injected into a freshwater aquifer and after two months, CO<sub>2(aq)</sub> was measured in four downgradient wells. Samples were collected on filters and the microbial community from each downgradient well and one upgradient well were analyzed using molecular, DNA-based techniques. Abundant microorganisms were found to be capable of converting CO<sub>2</sub> into biomass (biofouling) and capable of biocatalyzing iron and sulfate precipitation (biomineralization)



## New Results

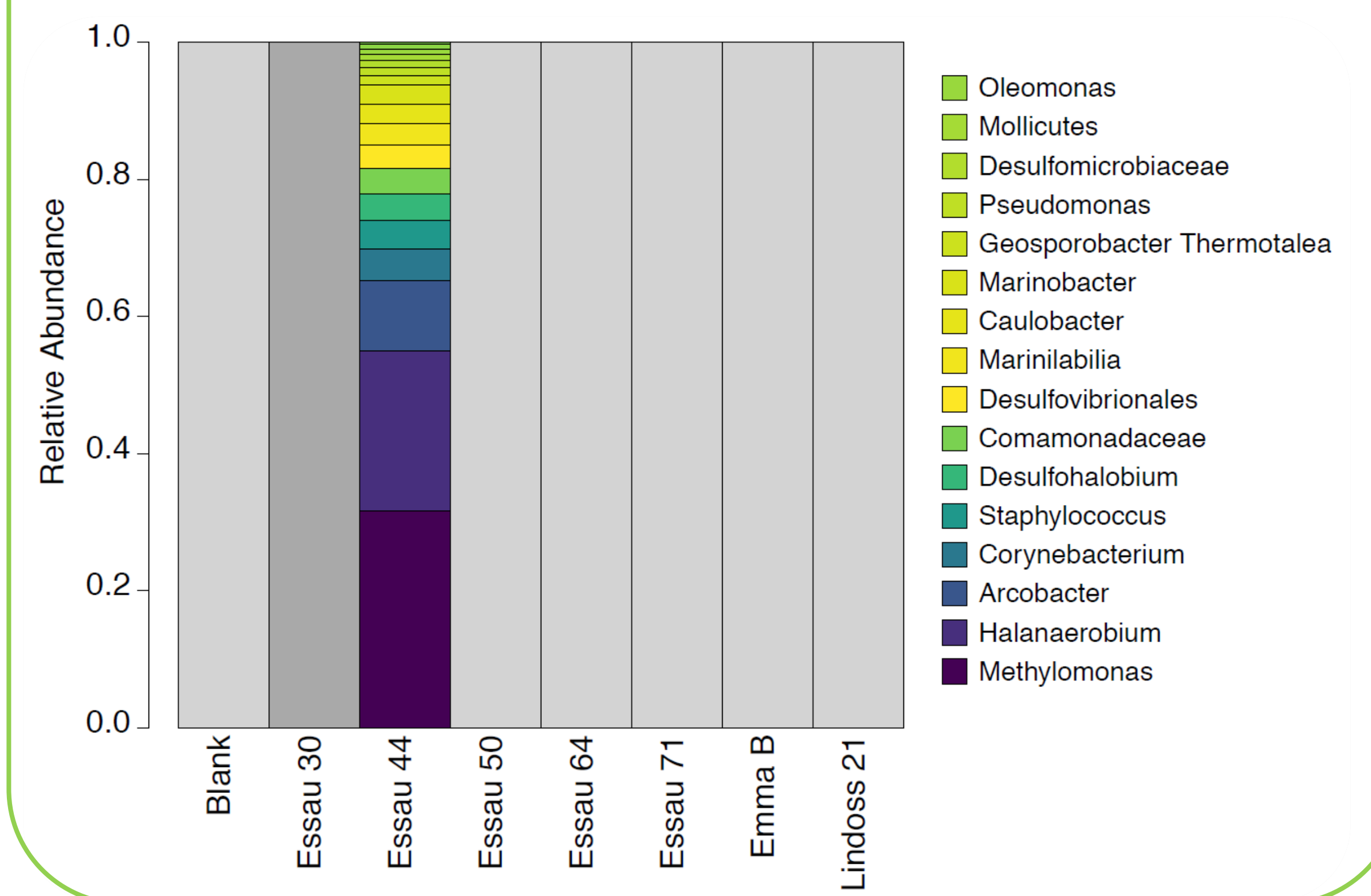


Samples were taken by Montana State University (MSU) at the Gorgas Field site in Jasper, Alabama. After CO<sub>2</sub> exposure, wells were injected with *Sporosarcina* for induced biomineralization. Strong selection for Post-CO<sub>2</sub> Flowback demonstrate a strong selection for *Sporotomaculum*. Notable qualities of this bacteria are:

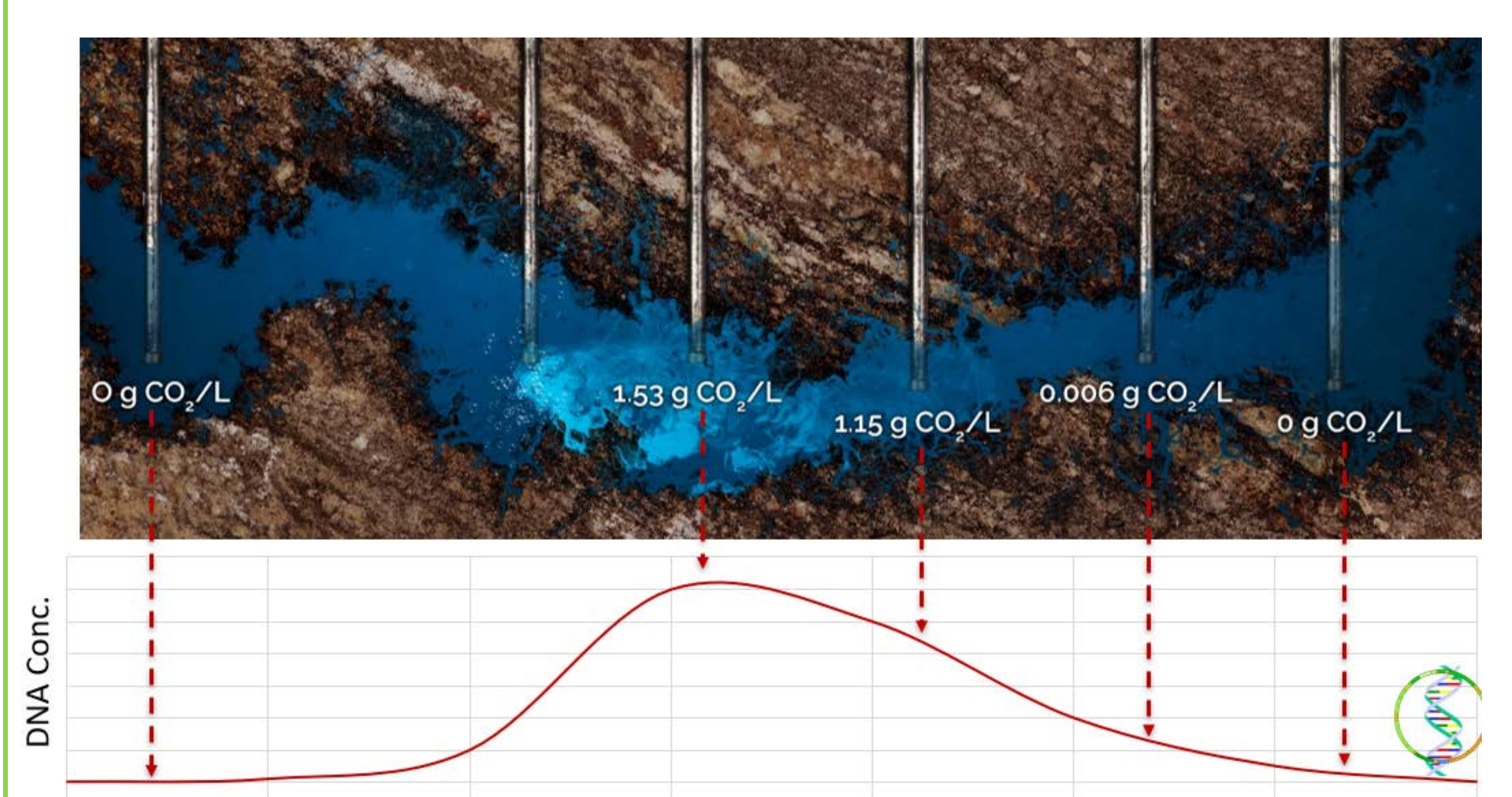
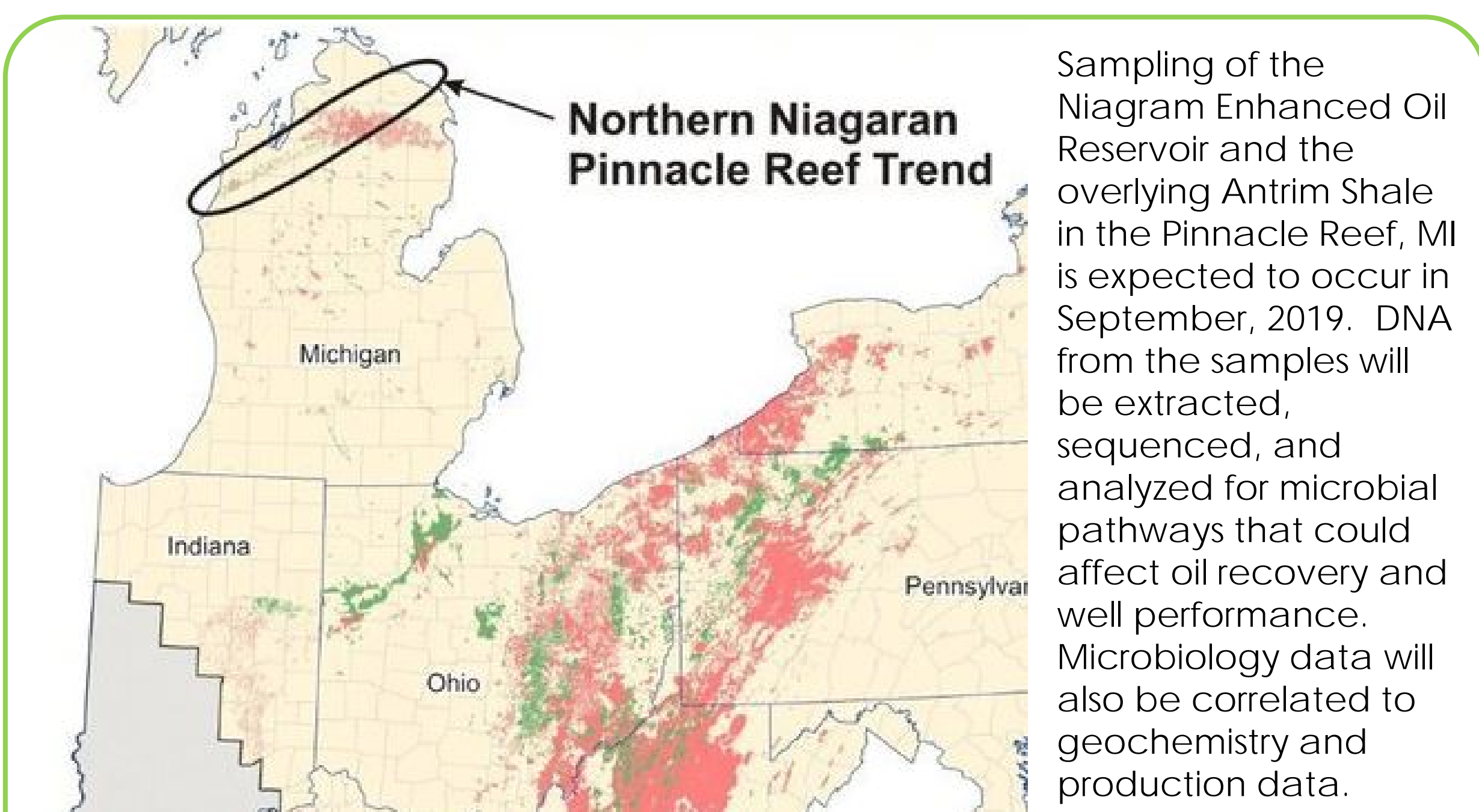
- Non-motile
- Strict anaerobe
- Benzene-degrading bacteria
- Two known bacteria in this genus: *Sporotomaculum hydroxybenzoicum* and *Sporotomaculum syntrophicum*



Seven wells from the Seminole EOR site and Emma EOR site in West Texas were sampled in April, 2018. The wells all had H<sub>2</sub>S concentrations above 10,000 mg/L, and were found to mostly contain low biomass, with the exception of well Essau 44. This well had a high abundance of *Methylomonas* (methane-to-CO<sub>2</sub> converters), *Halanaerobium* (a thiosulfate reducer), and *Arcobacter* (a sulfate oxidizer).



## Future Work



Metagenomic sequencing on a CO<sub>2</sub> impacted freshwater aquifer demonstrates an increase in concentration of genes related to CO<sub>2</sub> fixation. The natural microbial community is expected to be sensitive to the environmental stress of CO<sub>2</sub> exposure, and concentration measurement of DNA related to CO<sub>2</sub> fixation could be a highly sensitive plume migration tracer. Additional metagenomic profiles of CO<sub>2</sub>-impacted environments could help further define the key DNA sequences and help develop a universal DNA signature to utilize as a natural tracer.

## Acknowledgements

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