Impacts of CO_2 exposed microbial ecology on reservoir performance

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U.S. Department of Energy

National Energy Technology Laboratory

Mastering the Subsurface Through Technology Innovation, Partnerships and Collaboration:
Carbon Storage and Oil and Natural Gas Technologies Review Meeting

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Presentation Outline

- Overview FY17
  - Research Team
  - Task Goals and Structure
- Technical Status
- Lessons Learned
- Project Summary
- Synergistic Opportunities
- Accomplishments to Date

FY2018 Research Team

- Daniel Lipus, ORISE-RIC
- Dan Ross, AECOM-RIC
- James Gardiner, AECOM-NETL
- R. Burt Thomas, AECOM – NETL
- Mengling Stuckman, AECOM-NETL
- Kyle Bibby, University of Notre Dame




Task 15 (FY18): CS Microbiology Goals

Evaluate microbial processes that could 1) decrease storage capacity through pore-plugging pathways such as biofouling and biomineralization, or 2) lead to storage failure through biocorrosion or biomobilization of rock material

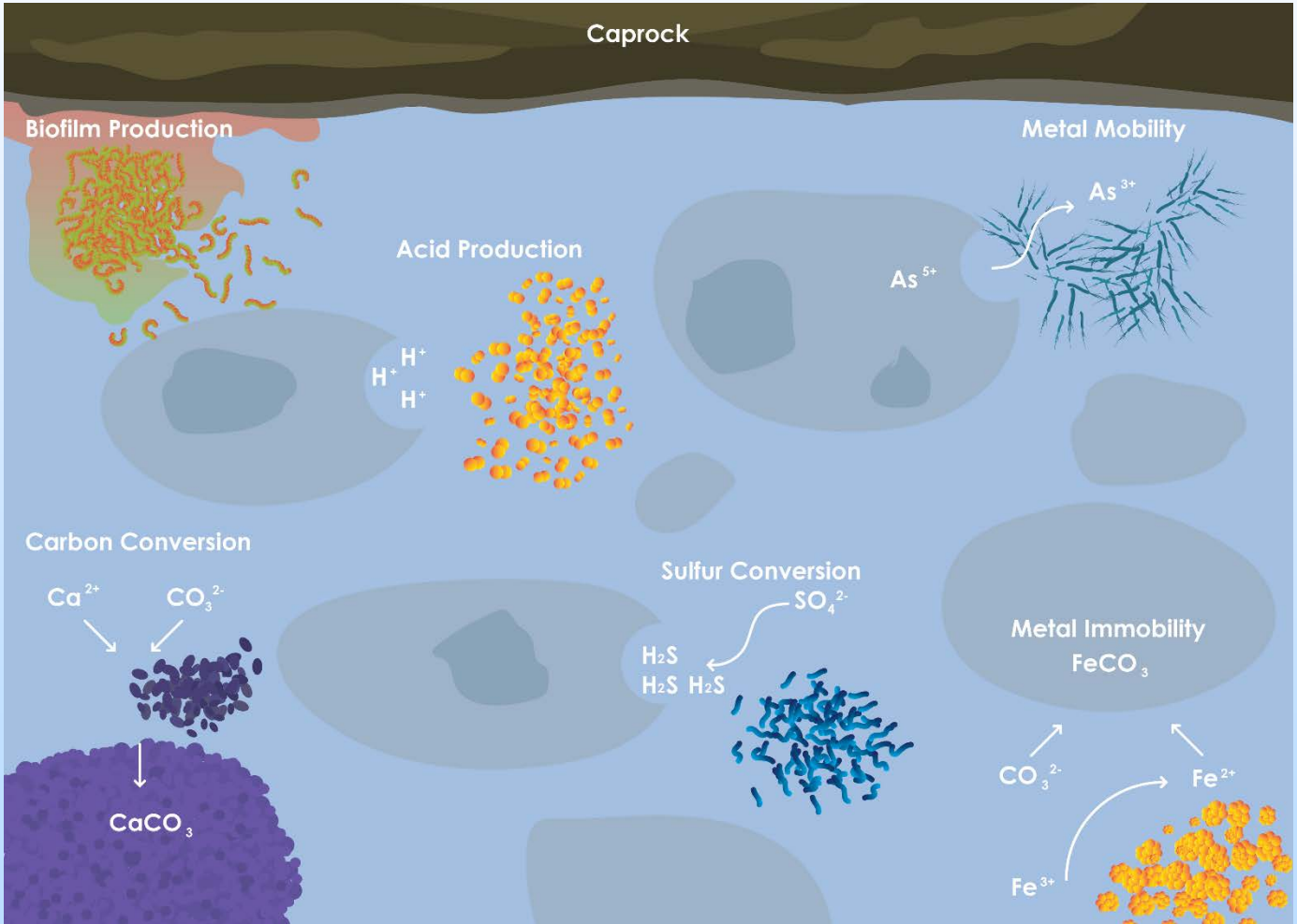


Figure by Jacob Howell at NETL MultiMedia

Task 15 (FY18): CS Microbiology Goals

- **Subtask 15.1: Impacts of CO_2 exposed microbial ecology on reservoir performance**
  - Characterize microbial communities from CO_2 storage site of existing industrial partnerships
- **Use in depth characterizations to develop guidance on the risks of microbial processes and mitigation strategies.**
  - Closely couple with geochemistry to predict reactions

Technical Status

Previous Years: Characterize microbial community structure from CO_2 storage site, EOR site and CO_2 leakage

- Correlated with geochemistry and reservoir conditions
- Compared CO_2 tolerant microorganisms across different sites
- Gulliver, D. M., Lowry, G. V., Gregory, K. B., 2016. "Comparative study of effects of CO_2 concentration and pH on microbial communities from a saline aquifer, a depleted oil reservoir, and a freshwater aquifer", *Environmental Engineering Science*.

FY18: Characterize microbial communities from CO_2 exposed site of existing industrial partnerships

- Completed metagenomic profile of Plant Daniel freshwater aquifer
  - 4 downgradient wells
  - 1 upgradient well
- Gulliver, D. M., Lipus, D., Ross, D. E., Bibby, K. 2018. "Metagenomic insights from a shallow CO2 leakage aquifer demonstrate microbial selection and adaption", *Environmental Microbiology Reports*.

Technical Status

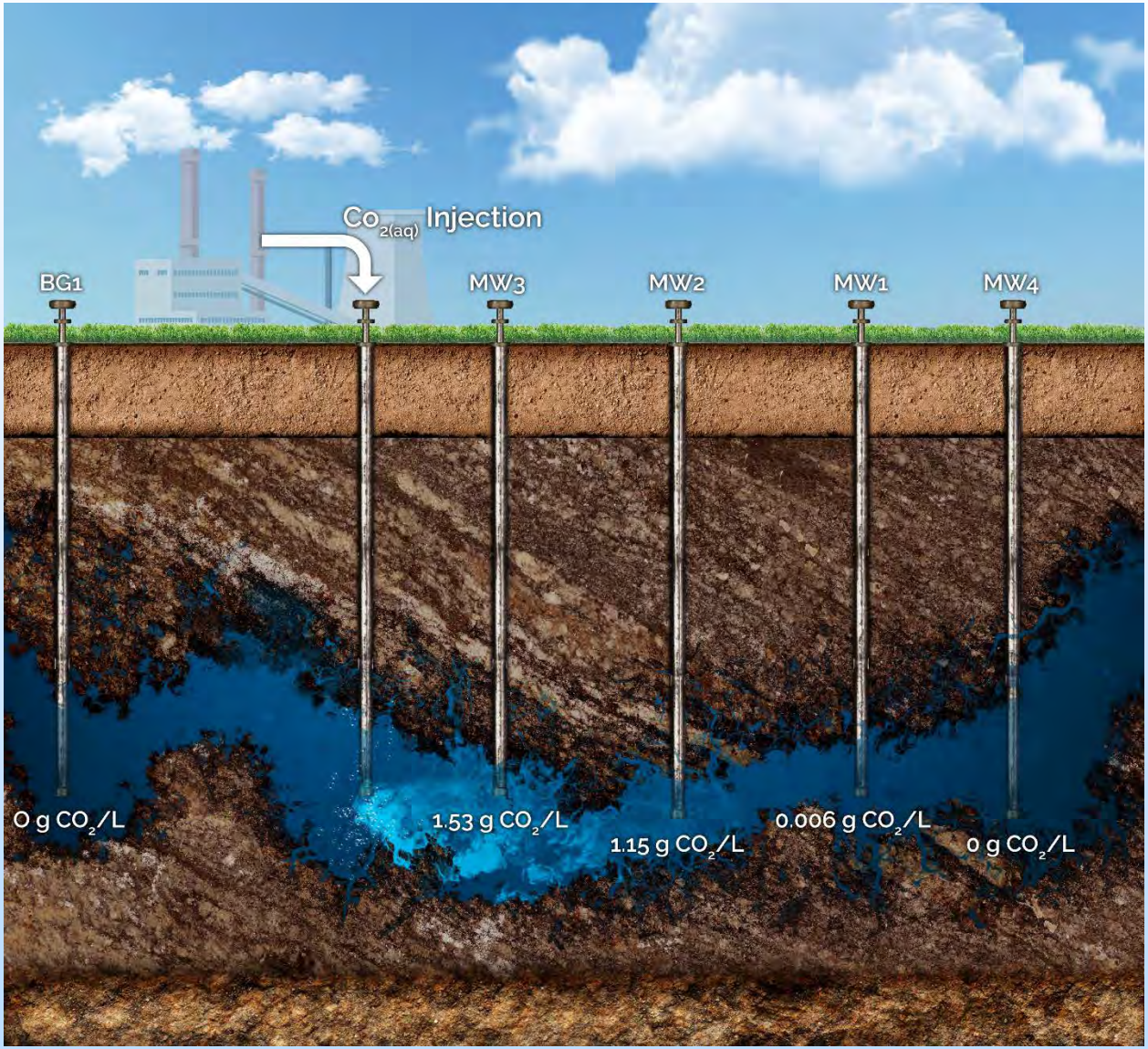
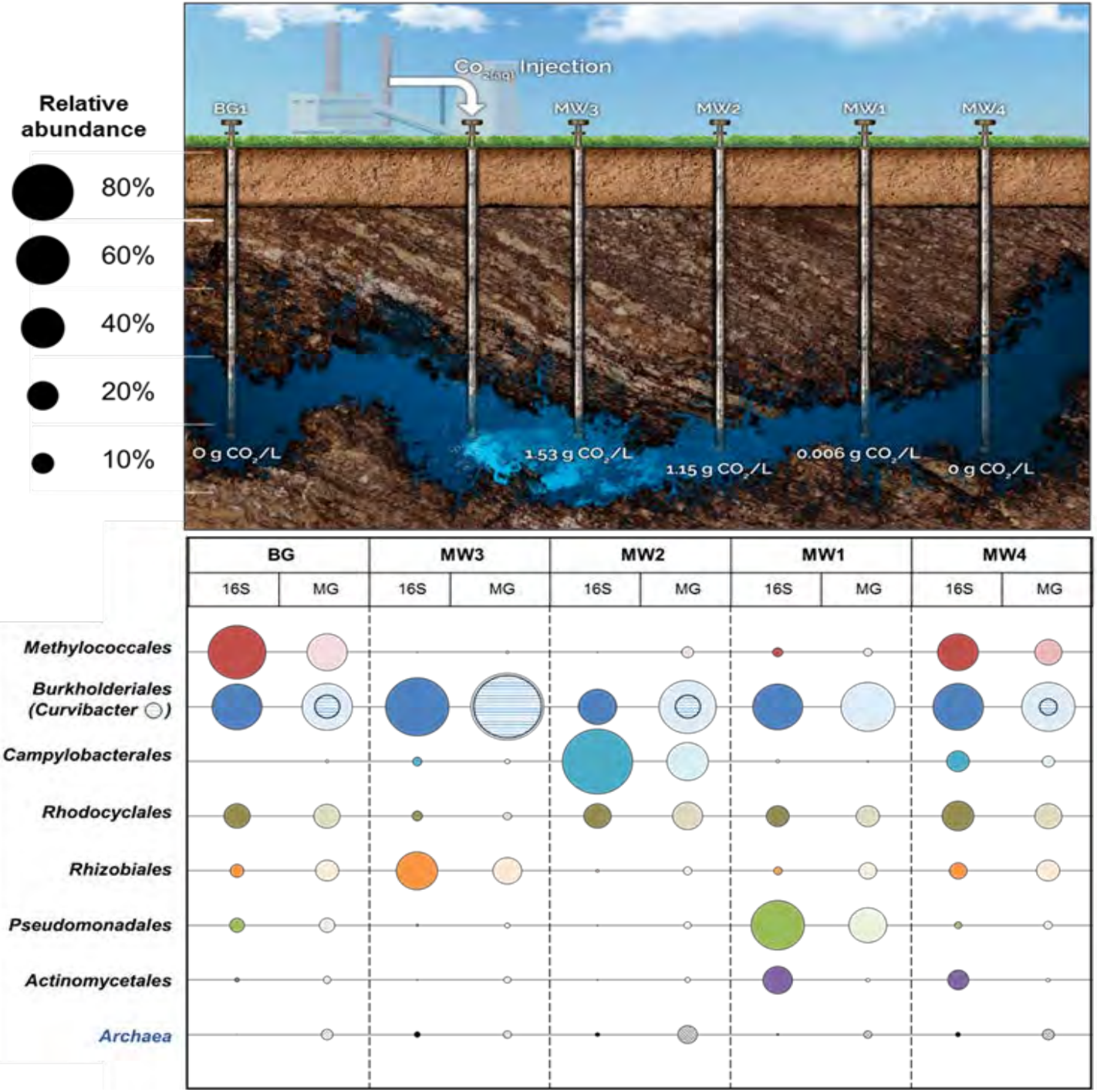
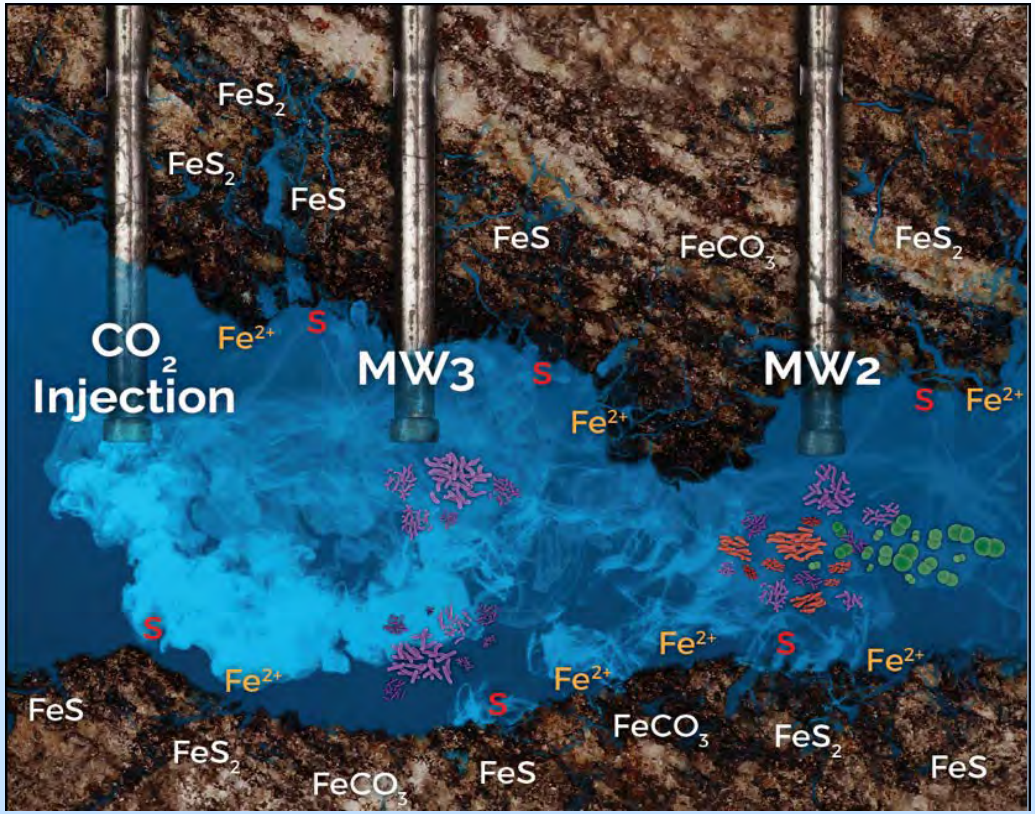


Figure by Jason Guinan at NETL MultiMedia


Relative abundance
80%
60%
40%
20%
10%
$Co_{2(aq)}$ Injection
BG1
MW3
MW2
MW1
MW4
0 g CO_2/L
1.53 g CO_2/L
1.15 g CO_2/L
0.006 g CO_2/L
0 g CO_2/L
BG
MW3
MW2
MW1
MW4
16S
MG
Methylococcales
Burkholderiales (Curvibacter ○)
Campylobacterales
Rhodocyclales
Rhizobiales
Pseudomonadales
Actinomycetales
Archaea

Technical Status



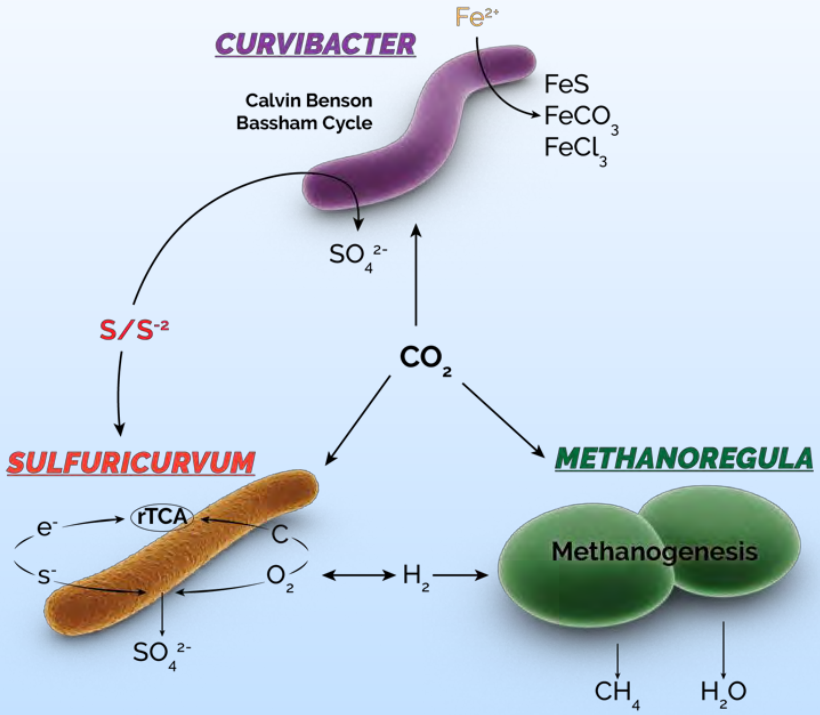
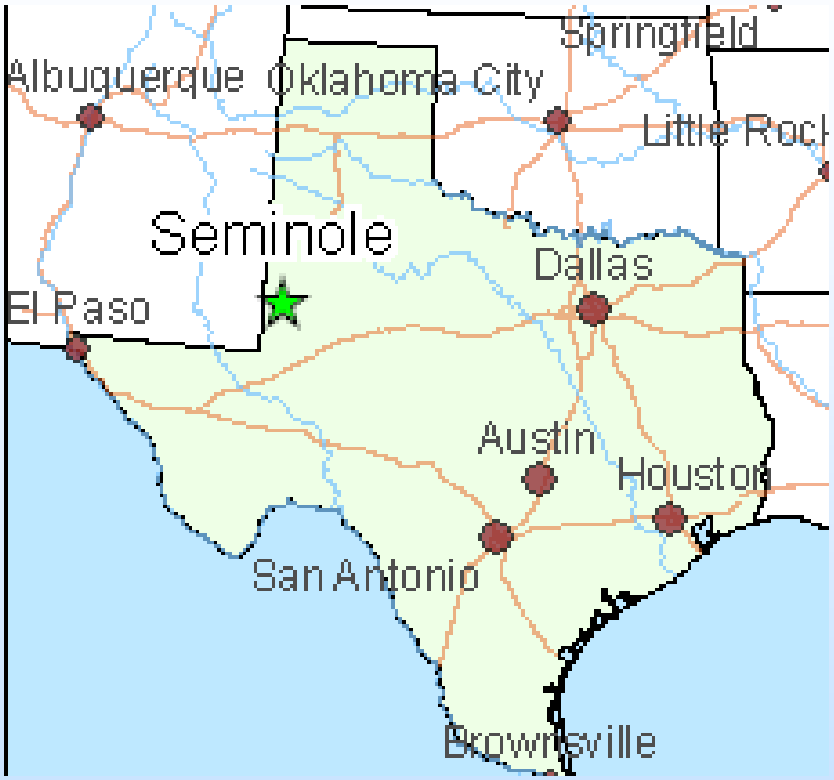


Figure by Jason Guinan at NETL MultiMedia

Technical Status



- April 2018 sampling
- 10 production wellheads, 6 groundwater wells

Technical Status: New Collaborations

- Take onsite measurements
  - pH, conductivity, temperature
  - O_2, CO_2, CO, H_2S
  - Alkalinity
- Prep samples onsite
  - IC
  - ICP-OES
  - Isotopes ($\delta^{18}O_{H2O}$, $\delta^{13}C$, $^{87}Sr/^{86}Sr$, $\delta^{7}Li$)
  - Metagenomics

Technical Status: New Collaborations

- Wellhead samples had oil and water
- Large variability in appearance

Lessons Learned

- Onsite sample prep challenges unique to oil and gas
- EOR reservoirs don't work on your schedule
- Onsite presence offers unique insights
  - Well behavior
  - Operator experience
  - Service industry/industry needs
- DNA extraction challenges unique to oil and gas

Project Summary

- Characterized microbial community from Plant Daniel freshwater aquifer
  - Identified high abundance microorganisms capable of CO_2 utilization
  - Demonstrated potential for sulfate precipitation and minor methane production
- Collected 10 new samples from existing collaboration in Seminole Texas

Synergy Opportunities

- Currently looking for new sample sites relevant to CO_2 storage, EOR, or CO_2 leakage aquifers
- Work with geochemists to correlate with microbiology for predicting subsurface reactions
  - Machine Learning modeling
- Demonstrate precipitation/dissolution reactions through simulation and imaging
- Communication with outside research groups characterizing other CO_2 exposed sites
- Comparison with other related subsurface reactions
  - Unconventional resource systems
  - Coal systems
- Comparison with CO_2 utilization technologies

FY18 Accomplishments to Date

- FY18 Milestone: Characterize Microbial Pore Plugging/Dissolution Processes from a CO_2 Storage Site of Existing Industrial Partnerships
  - Gulliver, D. M., Lipus, D., Ross, D. E., Bibby, K. 2018. "Metagenomic insights from a shallow CO2 leakage aquifer demonstrate microbial selection and adaption", *Environmental Microbiology Reports*.
  - Obtained Seminole samples for further investigation
- FY18 Milestone: Establish New Industrial Collaborations to Obtain a Sample from Uncharacterized CO_2 Storage Sites
  - Ongoing

Appendix

– These slides will not be discussed during the presentation, but are mandatory.

Benefit to the Program

Program Goals:

- Validate/ensure 99% storage permanence.
- Develop best practice manuals for monitoring, verification, accounting, and assessment, site screening, selection and initial characterization

Project benefits:

- There is a need to identify which microbial processes will occur during carbon storage, how much they impact reservoir behavior, and how to properly utilize or mitigate these biopathways.
- This task is expected to provide insight into microbial processes that will occur in onshore unconventional resource reservoirs, giving guidance to the energy industry on potential microbially-driven barriers to the efficacy of current storage technology and infrastructure.

Project Overview:
Goals and Objectives

Subsurface microbial communities affect reservoir properties and wellbore integrity through plugging/dissolution processes such as biomineralization (scaling), acid formation (biocorrosion), and biofilm formation (biofouling). The goal of this task is to minimize these microbiology affects through the following phases:

- Characterize Microbial Pore Plugging/Dissolution Processes from a CO_2 Storage Site of Existing Industrial Partnerships
- Establish New Industrial Collaborations to Obtain a Sample from Uncharacterized CO_2 Storage Sites
- Characterize microbial communities from CO_2 storage site of new industrial partnerships
- Correlation between geochemistry and microbiology for predicting subsurface reactions
- Develop guidance on mitigation strategies for biological processes

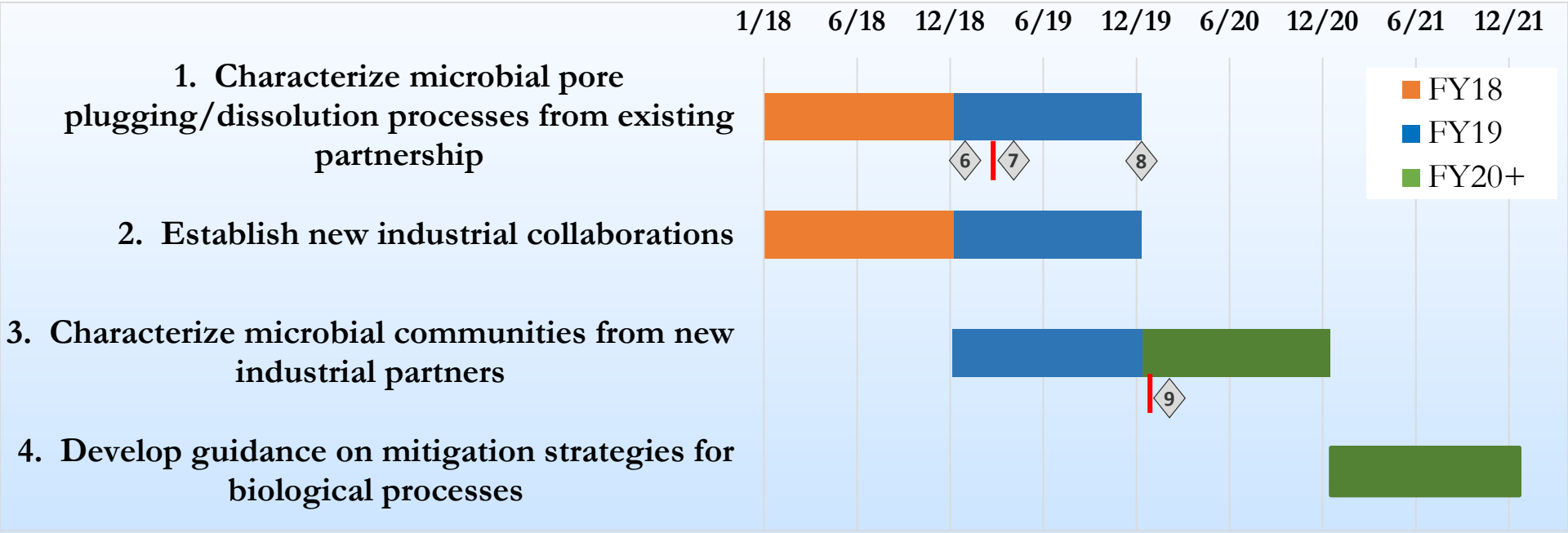
Organization Chart

- Djuna Gulliver, NETL-RIC (PI - Task 15)
- Daniel Lipus, ORISE – NETL (Task 15)
- Kyle Bibby, Notre Dame University (Task 15)
- Christina Lopano, NETL-RIC (Task 20, Task 21)
- James Gardiner, AECOM-NETL (Task 20, Task 21)
- R. Burt Thomas, AECOM – NETL (Task 20, Task 21)
- Mengling Stuckman, AECOM-NETL (Task 20)

Organization Chart

8.1.1	**Natural Geochemical Tracers in Groundwater (FY16)**	NETL currently has an existing industrial collaboration to characterize the geochemistry of carbon storage reservoirs. This existing industrial collaboration will be utilized to obtain fresh sample of microbial communities from CO2 storage sites for metagenomic/metatranscriptomic analysis	Gulliver, Lipus, Bibby
20.1.1	**New Geochemical Signal Methodologies**	This activity will develop isotopic methods for purposes of tracking CO2 impacts.	Lopano, Thomas, Gardiner, Stuckman
21.1.1	**Geochemical Signal Processing for Leakage Assessment**	Provide a matrix of aqueous geochemical signals that can be used for assessing leakage under a range of geologically relevant systems.	Lopano, Thomas, Gardiner

Gantt Chart



Upcoming Milestones

6. M.15.6 – Complete white paper summarizing previous years results, implications, and path forward (Q4, January 2019)
7. Complete metagenomic sequencing of samples from sites owned by Tabula Rasa (Q4, March 2019)
8. Complete profile of relevant microbial processes that may impact pore plugging/dissolution of the carbon storage sites owned by Tabula Rasa (Q3, December 2019)
9. Obtain access to a new samples relevant to carbon storage (Q4, January 2020)

Go / No-Go

1. To move to this milestone enough DNA must be isolated from samples provided by Tabula Rasa to complete metagenomic sequencing.
2. To move to upcoming milestones, a new industrial collaboration must be made.
3. To move to this milestone enough DNA must be isolated from samples provided by new industrial collaborator to complete metagenomic sequencing

Bibliography

Publications

- Gulliver, D. M., Lipus, D., Ross, D. E., Bibby, K. 2018. "Metagenomic insights from a shallow CO2 leakage aquifer demonstrate microbial selection and adaption", *Environmental Microbiology Reports*, in review.
- Gulliver, D. M., Lowry, G. V., Gregory, K. B., 2016. "Comparative study of effects of CO2 concentration and pH on microbial communities from a saline aquifer, a depleted oil reservoir, and a freshwater aquifer", *Environmental Engineering Science*, 33(10) 806.
- Gulliver, D. M., Lowry, G. V., Gregory, K. B., 2016. "Effects of CO_2 concentration on shallow freshwater microbial communities under simulating a CO2 leakage scenarios", *Environmental Science and Technology Letters*, 1(12) 479

Presentations

- Gulliver, D. M., Lipus, D., Bibby, K., CO2 exposure on a freshwater microbial community from simulated carbon storage leakage, Gordon Research Seminar, Applied and Environmental Microbiology, Spring 2017, South Hadley, MA.
- Gulliver, D. M., Lipus, D., Bibby, K., Characterization of Curvibacter from a simulated geologic carbon storage leakage. American Society of Microbiology, Spring 2017, New Orleans, LA.