Shale Microbiology Ecology Affecting Reservoir Performance

Djuna M. Gulliver

NETL – Research & Innovation Center

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

August 15, 2018

Presentation Outline

- Overview FY18
  - 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
- Eakalak Khan, University of Las Vegas
- Dhritikshama Roy, North Dakota State University
- Mengling Stuckman, AECOM-NETL
- Kyle Bibby, University of Notre Dame




Task 4 (FY18): Shale Microbiology Goals

Assess the geochemistry and microbiology of the reservoir for biogeochemical reactions that will indicate oil productivity and/or reservoir and infrastructure failure

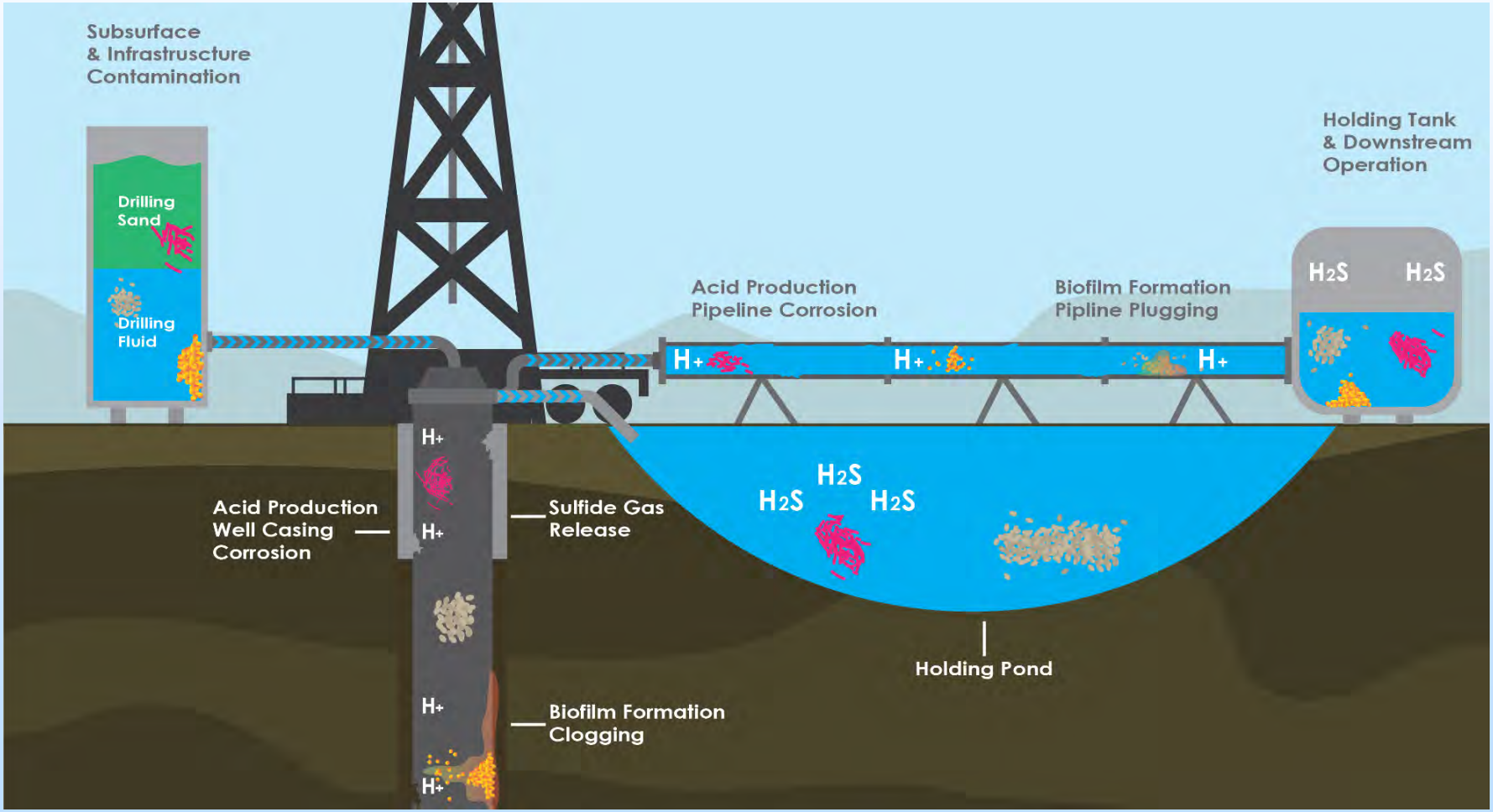


Figure by Jacob Howell at NETL MultiMedia

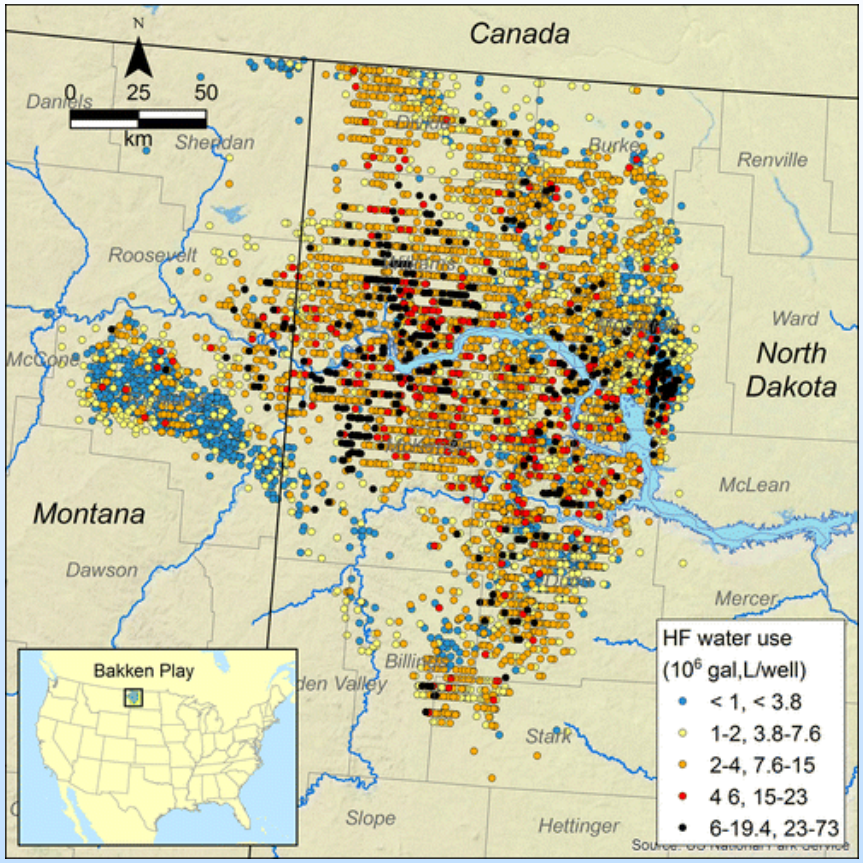
Task 4 (FY18): Shale Microbiology

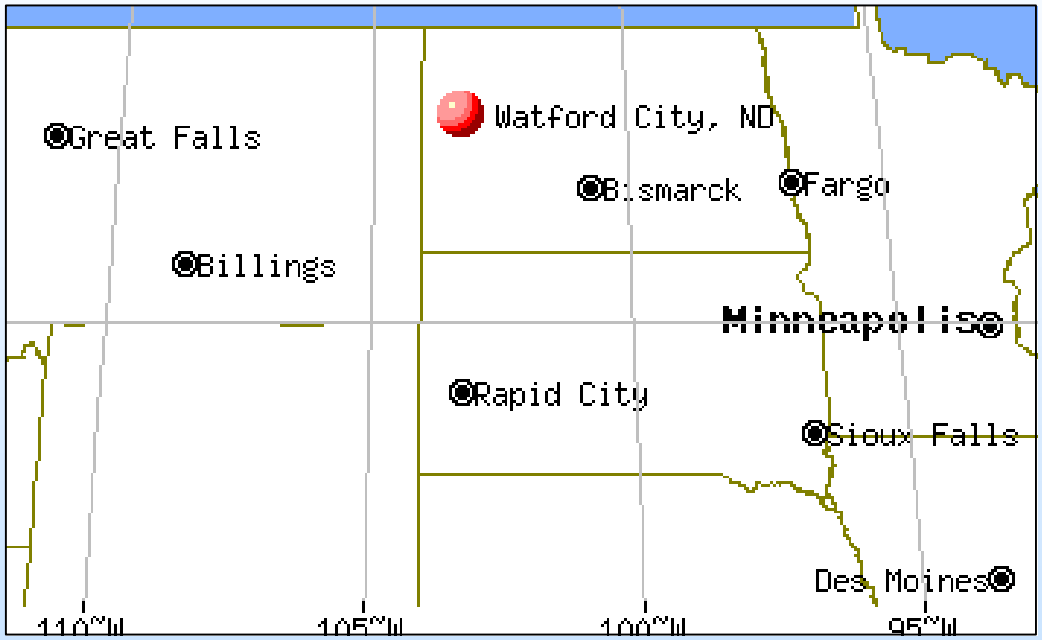
- **Subtask 4.1: Shale Microbial Ecology Affecting Reservoir Performance**
  - Characterize microbial communities from unconventional resource reservoirs of existing industrial partnerships
  - Establish new industrial collaborations to obtain sample from uncharacterized unconventional resource reservoirs
- **Use basin specific characterizations to develop guidance on the indicative ability of the microbial community to energy production and reservoir/infrastructure performance.**
  - Closely couple with geochemistry to predict reactions

Technical Status: Existing Partnerships

- **FY17: Characterized microbial ecology associated with Marcellus Shale**
  - 42 production wells
  - Lipus, D., Vikram, A., Ross, D., Bain, D., Gulliver, D. M., Hammack, R., Bibby. K., 2017. Predominance and metabolic potential of Halanaerobium in Marcellus Shale hydraulic fracturing produced water, *Applied Environmental Microbiology*
- **FY18: Characterized microbial ecology associated with Bakken Shale**
  - 118 Samples
    - 17 Separators
    - 17 Storage Tanks
  - Lipus, D., Roy, D., Khan, E., Vikram, A., Gulliver, D. M., Hammack, R., Bibby. K., 2018. Microbial communities in Bakken region produced water, *FEMS Microbiology Letters*

Technical Status: Existing Partnerships



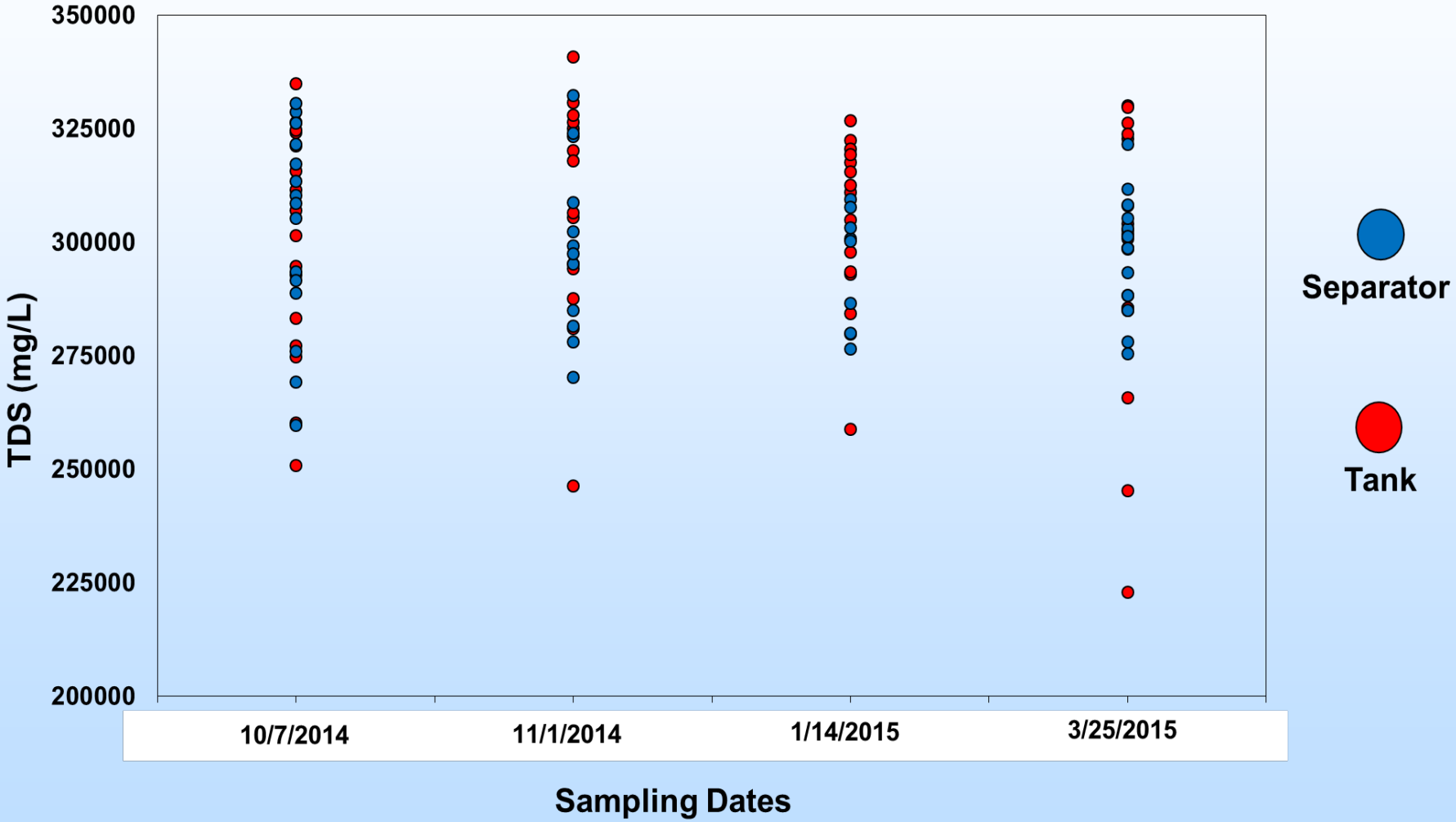


Technical Status: Existing Partnerships

Table 2. Physiochemical characteristics of analyzed produced water samples. Total dissolved solids (TDS), dissolved organic carbon (DOC), pH, alkalinity and turbidity were measured across all four sampling time points. Individual ions were measured for October 2014 samples. Ambient air temperatures were 8°C to 10°C on 10/7/2014 (October), 0°C to –2°C on 11/1/2014 (November), –3°C to –4°C on 1/14/2015 (January) and 15°C to 16°C on 3/25/2015 (March).

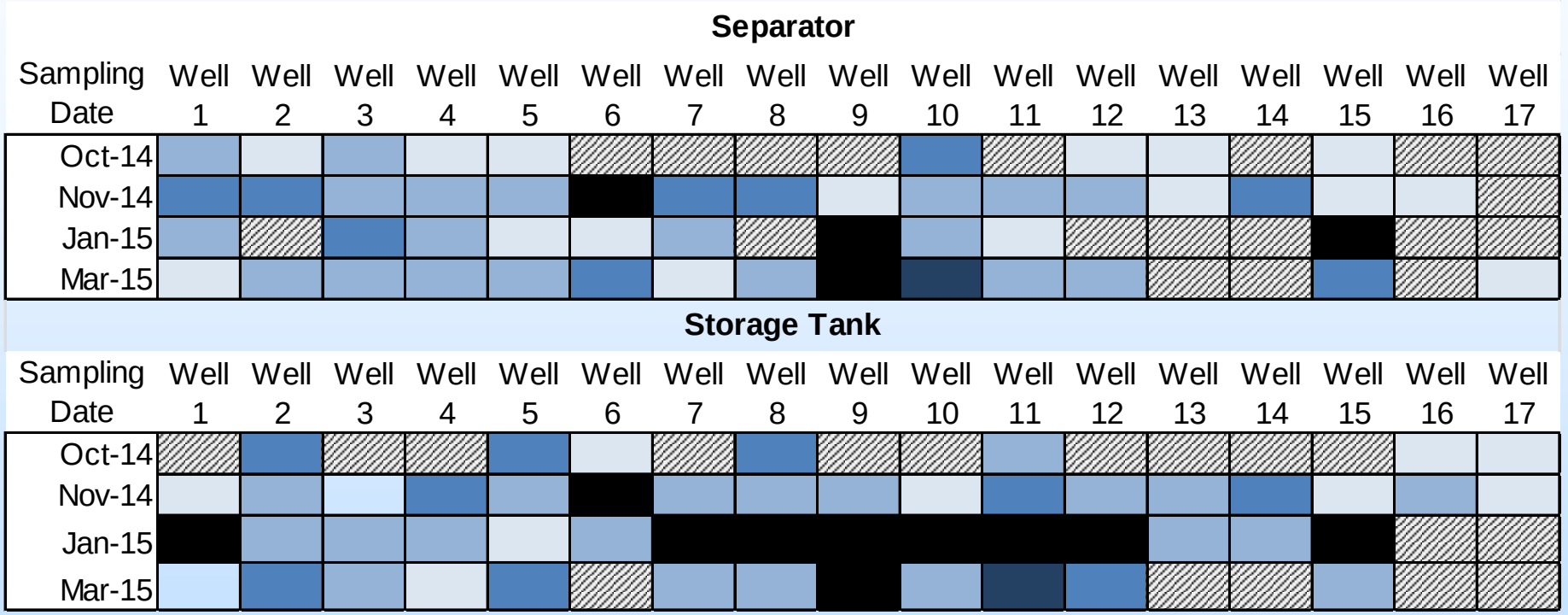
	Separator			Storage tank		
	Max	Min	Avg	Max	Min	Avg
TDS (mg/L)	340 750	223 000	301 507	332 250	196 000	296 803
DOC (mg/L)	225	19	70	132	14	65
pH	6.9	5.0	6.0	7.0	5.2	6.1
Alkalinity (mg/L)	900	300	550	900	250	525
Turbidity (NTU)	128.0	6.2	140.6	890.0	10.1	139.7
Ca (mg/L)	38 856	26 644	33 433	41 074	28 556	34 468
Na (mg/L)	135 847	99 027	119 339	108 179	132 899	121 777
Ba (mg/L)	55	35	47	36	36	50
Sr (mg/L)	3627	2451	3125	3988	2431	3201
Mg (mg/L)	2274	1760	1998	2310	1819	2051
Fe (mg/L)	365	55	195	249	50	529
K (mg/L)	15 665	9929	12 835	15 383	9973	13 567
B (mg/L)	861	638	738	881	662	783
S (mg/L)	425	306	366	441	346	389

Technical Status: Existing Partnerships



Technical Status: Existing Partnerships

Bakken Microbial Abundance



Concentration (gene copies/ml)				Other	
10^1		10^3		no data	
10^2		10^4		low biomass	

Technical Status: Existing Partnerships

A

Separator	October	November	January	March
Well 1				
Well 2				
Well 3				
Well 4				
Well 5				
Well 6				
Well 7				
Well 8				
Well 9				
Well 10				
Well 11				
Well 12				
Well 13				
Well 14				
Well 15				
Well 16				
Well 17				

B

Tank	October	November	January	March
Well 1				
Well 2				
Well 3				
Well 4				
Well 5				
Well 6				
Well 7				
Well 8				
Well 9				
Well 10				
Well 11				
Well 12				
Well 13				
Well 14				
Well 15				
Well 16				
Well 17				

Bacillales

Relative abundance
<25%
25% - 50%
50% - 75%
75% - 100 %
low biomass
not sampled

C

Separator	October	November	January	March
Well 1				
Well 2				
Well 3				
Well 4				
Well 5				
Well 6				
Well 7				
Well 8				
Well 9				
Well 10				
Well 11				
Well 12				
Well 13				
Well 14				
Well 15				
Well 16				
Well 17				

D

Tank	October	November	January	March
Well 1				
Well 2				
Well 3				
Well 4				
Well 5				
Well 6				
Well 7				
Well 8				
Well 9				
Well 10				
Well 11				
Well 12				
Well 13				
Well 14				
Well 15				
Well 16				
Well 17				

Halanaerobiales

Relative abundance
not detected
<25%
25% - 50%
50% - 75%
75% - 100 %
low biomass
not sampled

E

Separator	October	November	January	March
Well 1				
Well 2				
Well 3				
Well 4				
Well 5				
Well 6				
Well 7				
Well 8				
Well 9				
Well 10				
Well 11				
Well 12				
Well 13				
Well 14				
Well 15				
Well 16				
Well 17				

F

Tank	October	November	January	March
Well 1				
Well 2				
Well 3				
Well 4				
Well 5				
Well 6				
Well 7				
Well 8				
Well 9				
Well 10				
Well 11				
Well 12				
Well 13				
Well 14				
Well 15				
Well 16				
Well 17				

Pseudomonadales

Relative abundance
<25%
25% - 50%
50% - 75%
75% - 100 %
low biomass
not sampled

Technical Status: Existing Partnerships

- Run a better characterization
  - Better chemical data
  - Metagenomic data
- Take onsite measurements
  - pH, conductivity, temperature,
  - Alkalinity
- Prep samples onsite
  - IC
  - ICP-OES
  - Ferric Iron
  - Metagenomics/metatranscriptomics

Technical Status: Existing Partnerships

- May 2018 sampling
- 17 Separators
  - 16 previously sampled, one newly online

Technical Status: New Collaborations

- April 2018 sampling
- 6 wellheads, 7 separators, injection fluid

Technical Status: New Collaborations

- Take onsite measurements
  - pH, conductivity, temperature,
  - O_2, CO_2, CO, H_2S, CH_4
  - Alkalinity
- Prep samples onsite
  - IC
  - ICP-OES
  - Isotopes ($^{87}Sr/^{86}Sr$, δ^7Li)
  - Metagenomics/Metatranscriptomics

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
- Oil 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 Bakken Shale samples
  - Identified high TDS, low biomass, and high diversity compared to Marcellus
  - Demonstrated potential for biocorrosion, biofouling, and H_2S production
- Collected 17 new samples from existing collaboration in Bakken Shale
- Collected 14 new samples from new collaboration in Permian Basin

Project Summary

Next Steps – Application of the datasets

- Correlation between geochemistry and microbiology for predicting subsurface reactions
- Investigating basin-specific trends between predicted subsurface reactions and oil/gas production and well performance
- Increase reliability of prediction with additional samples within and across different basins

Synergy Opportunities

- Machine Learning modeling
- Communication with outside research groups characterizing other basins
- Continued field-based collaboration to test new geochemical analyses
  - Organic chemistry
- Comparison with other related subsurface reactions
  - Carbon Storage reservoirs
  - EOR systems
  - Coal systems

FY18 Accomplishments to Date

- FY18 Milestone: Completed profile of relevant microbial pathways that may impact energy production in Bakken shale gas wells owned by the existing industrial partner.
  - Lipus, D., Roy, D., Khan, E., Vikram, A., Gulliver, D. M., Hammack, R., Bibby. K., 2018. Microbial communities in Bakken region produced water, *FEMS Microbiology Letters*
  - Obtained Bakken samples for further investigation
- FY18 Milestone: Obtained access to a new field site in the Permian Basin in April, 2018.

Appendix

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

Benefit to the Program

Program Goals:

- Research and technology development that results in maximum ultimate recovery and operational efficiency basin by basin onshore.
- Under the Basin-Specific Strategy, fundamental shale research performed through the DOE National Laboratories is expected to assist in identifying key production factors across multiple scales.

Project benefits:

- There is a need to identify which microbial processes will occur during unconventional resource production, how much they impact energy production, 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 risks driven by microbial processes, potential mitigation strategies, and the potential for the microbiology to be indicative of energy production.

Project Overview:
Goals and Objectives

Subsurface microbial communities currently affect energy production, reservoir properties, and wellbore integrity which ultimately impacts recovery and operational efficiency. The goal of this task is to minimize these microbiology affects through the following phases:

- Characterize microbial communities from unconventional resource reservoirs of existing industrial partnerships
- Establish new industrial collaborations to obtain sample from uncharacterized unconventional resource reservoirs
- Characterize microbial communities unconventional resource reservoirs of new industrial partnerships
- Correlation between geochemistry and microbiology for predicting subsurface reactions
- Develop guidance on mitigation strategies for biological processes

Organization Chart

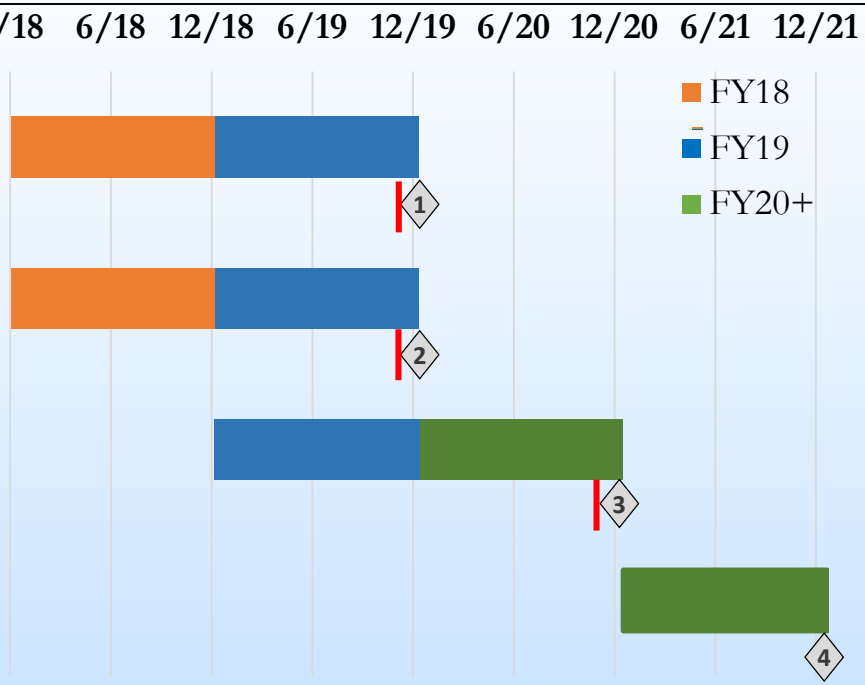
- Djuna Gulliver, NETL-RIC (PI - Task 4)
- Daniel Lipus, ORISE – NETL (Task 4)
- Kyle Bibby, Notre Dame University (Task 4)

Organization Chart

4.1.1	**Microbial communities from existing partnerships**	This activity will characterize microbial communities from unconventional reservoirs of existing industrial partnerships. NETL currently has an existing industrial collaboration to characterize the geomicrobiology of the Bakken Shale. This existing industrial collaboration will be utilized to obtain fresh sample of microbial from the Bakken Shale for immediate metagenomic/metatranscriptomic analysis	Lipus, Gulliver, Bibby
4.1.2	**Establish new industrial collaborations**	This activity will establish new industrial collaborations to obtain sample from uncharacterized unconventional resource reservoirs. NETL has begun discussion with future industrial collaborators to characterize the geochemistry and geomicrobiology of the Permian Basin. Communication will continue to ensure several sampling events to characterize the temporal variation of the microbial community and reservoir conditions.	Lipus, Gulliver, Bibby

Gantt Chart

1. **Characterize microbial communities from existing partnership**
2. **Establish new industrial collaborations**
3. **Characterize microbial communities from new industrial partners**
4. **Develop guidance on mitigation strategies for biological processes**



Milestones

1. Complete profile of relevant microbial pathways that may impact energy production in Bakken shale gas wells owned by the existing industrial partner. (Q3, December 2019)
2. Obtain access to a new field site in the Permian Basin. (Q3, December 2019)
3. Complete profile of relevant microbial pathways that may impact energy production in Permian Basin wells owned by new industrial collaborations. (Q3, December 2020)
4. Complete guidance outlining the expected microbial processes in unconventional resource reservoirs and infrastructure. (Q3, December 2022)

Go / No-Go

1. To move to this milestone enough DNA must be isolated from Bakken shale samples to complete metagenomic sequencing.
2. To move to this milestone, a formal agreement with a new industrial collaborator in the Permian Basin must be completed.
3. To move to this milestone enough DNA must be isolated from Permian Basin samples to complete metagenomic sequencing.

Bibliography

Publications:

- Lipus, D., Roy, D., Khan, E., Vikram, A., Gulliver, D. M., Hammack, R., Bibby. K., 2018. Microbial communities in Bakken region produced water, *FEMS Microbiology Letters*, doi: 10.1093/femsle/fny107.
- Lipus, D., Vikram, A., Ross, D., Bain, D., Gulliver, D. M., Hammack, R., Bibby. K., 2017. Predominance and metabolic potential of Halanaerobium in Marcellus Shale hydraulic fracturing produced water, *Applied Environmental Microbiology*, doi: 10.1128/AEM.02659-16.
- Lipus, D., Ross, D., Bibby. K., Gulliver, D. M., 2017. Draft genome sequence of *Pseudomonas* sp. BDAL1 reconstructed from a Bakken Shale hydraulic fracturing produced storage tank metagenome, *Genome Announcements*, 5(11): e00033-17.

Presentations:

- Lipus, D., Vikram, A., Bain, D., Gulliver, D., Hammack, R., and Bibby, K., Produced Water Microbial Community Analysis from 42 Marcellus Shale Wells, Gordon Research Conference – Applied and Environmental Microbiology, 16-21 July, 2017, South Hadley, MA.
- Lipus, D., Vikram, A., Ross, D., Bain, D., Gulliver, D., Hammack, R., and Bibby, K., Predominance and Metabolic Potential of Halanaerobium in Marcellus Shale Hydraulic Fracturing Produced Water, American Society of Microbiology, 1-5 June, 2017, New Orleans, LA.
- Lipus, D. Roy, D., Khan, E., Ross, D., Vikram, A., Gulliver, D., Hammack, R., and Bibby, K., Microbial Activity in Hydraulic Fracturing Produced Water from Two Shale Gas Reservoirs, National Groundwater Association, 25-26 April, 2017, Columbus, OH.
- Lipus, D. Roy, D., Khan, E., Ross, D., Vikram, A., Gulliver, D., Hammack, R., and Bibby, K., Microbial Communities in Bakken Region Hydraulic Fracturing Produced Water, American Chemical Society, 1-6 April, 2017, San Francisco, CA.