Shale Microbial Ecology Affecting Reservoir Conditions

Djuna M. Gulliver

NETL – Research & Innovation Center

U.S. Department of Energy

National Energy Technology Laboratory

Oil & Natural Gas

2020 Integrated Review Webinar

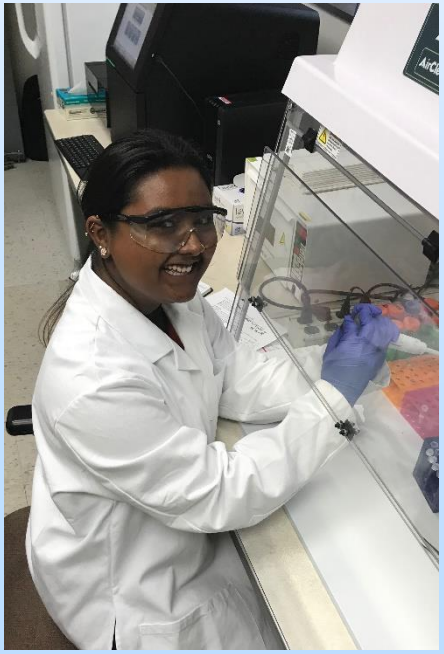
Program Overview:
Task 4 Funding and Project Participants

- Djuna Gulliver, NETL-RIC
- Kara Tinker, Leidos-NETL
- James Gardiner, Battelle-NETL
- Burt Thomas, Battelle-NETL
- Preom Sarkar, ORISE-RIC
- Joshua Miller, ORISE-RIC

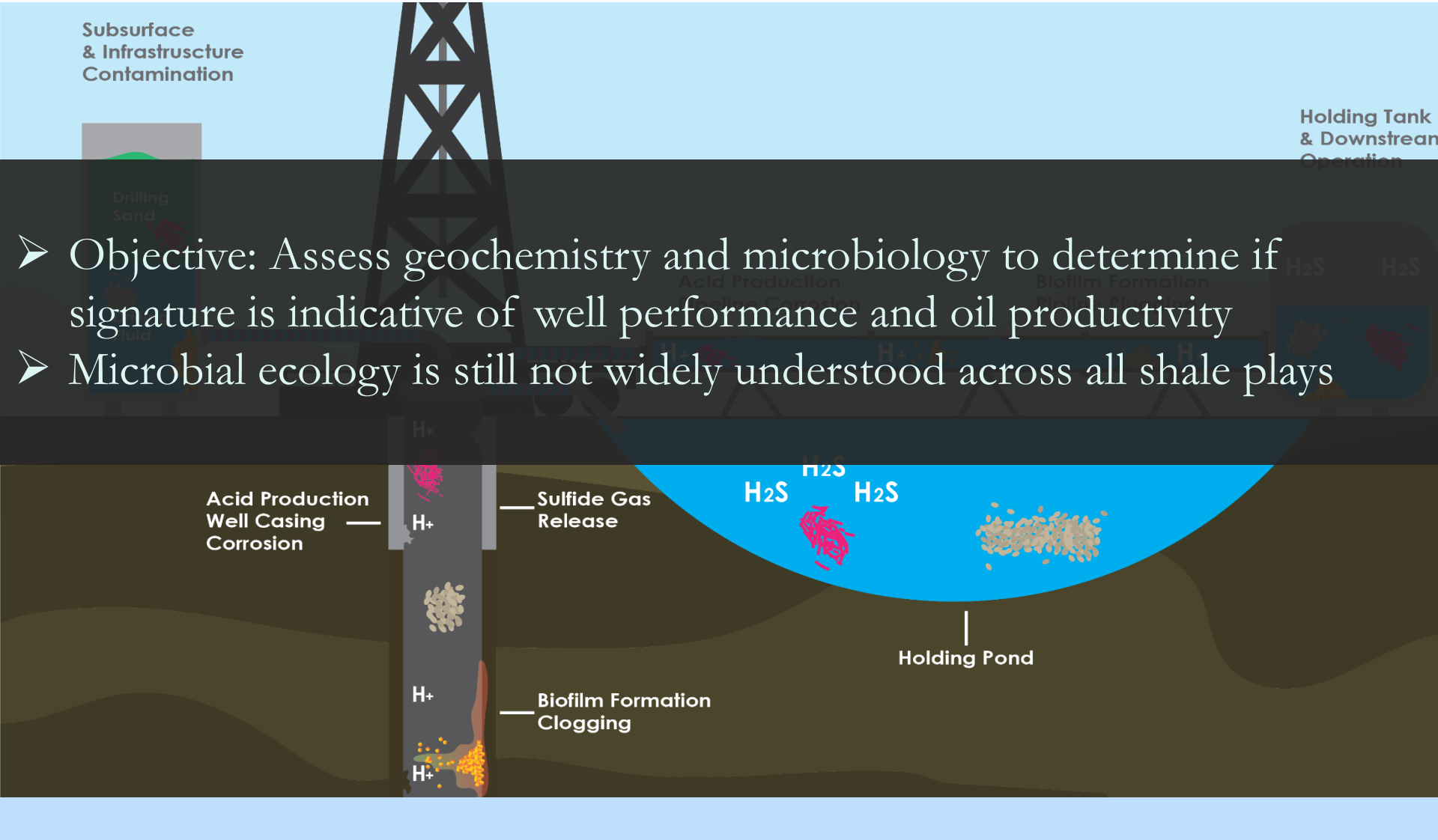
Funding ($k)

EY18	EY19	EY20	Total
$130	$143	$0	$273






Overall Project Objective



- Objective: Assess geochemistry and microbiology to determine if signature is indicative of well performance and oil productivity
- Microbial ecology is still not widely understood across all shale plays

Technology Background

Oct 2011 to Feb 2014	May 2014 to March 2018	April 2018 to March 2020
Project: Evaluation of the geochemical and biological composition of shale gas produced water	**Project: Evaluate relationship between fracturing fluids and microbial communities**	**Project: Geochemistry and Microbiology Explaining Reservoir and Wellbore Processes**
Focus on Marcellus Produced water impoundments and development of techniques to analyze microbiology in unconventional oil and gas produced water	Focus on Marcellus and Bakken wellhead/separator samples – collected for characterization of microbial community and related to published data on injected fluids	Focus on Bakken and Permian wellhead/separator samples – collected for characterization of both microbial community and chemistry to relate to actual processes within reservoir/well
PI: Rick Hammack	PI: Djuna Gulliver	PI: Djuna Gulliver

Technology: Prior Characterization

Previous Years: Characterize microbial community structure from Marcellus Shale and Bakken Shale

- Lipus, D., Vikram, A., **Gulliver, D. M.**, Bibby. K., 2019. Upregulation of peroxide scavenging enzymes and multidrug efflux proteins highlight an active sodium hypochlorite response in Pseudomonas fluorescens biofilms, *Biofouling*, 35(3), doi: 10.1080/08927014.2019.1605357.
- Lipus, D., Vikram, A., Hammack, R., Bibby. K, **Gulliver, D. M.**, 2018. The Effects of Sample Storage Conditions on the Microbial Community Composition in Hydraulic Fracturing Produced Water, *Geomicrobiology Journal*, 36(7), doi: 10.1080/01490451.2019.1599470.
- 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.

FY19: Characterize Permian Basin and incorporate geochemistry

- Tinker, Gardiner, J., K., Lipus, D., Sarkar, P., Stuckman, M., **Gulliver, D. M.**, 2020. Geochemistry and microbiology predict environmental niches with conditions favoring potential activity in the Bakken Shale, *Frontiers in Microbiology.*
- Tinker, K., Lipus, D., Sarkar, P., **Gulliver, D. M.**, 2020. The geochemistry and microbial ecology of produced waters from three different unconventional oil and gas regions, *Unconventional Resources Technology Conference*.

Technical Approach

Geospatially broad sampling

- **Heterogeneities in subsurface**
- **Differences during production lifetime**
- **72 Marcellus Samples, 67 Bakken Samples, 16 Permian Samples**
  - More samples to be processed

Onsite sampling

- **Observe systems**
- **Take onsite measurements**
- **Prep samples onsite**
  - Geochemistry
  - Taxonomy
  - Metagenomics

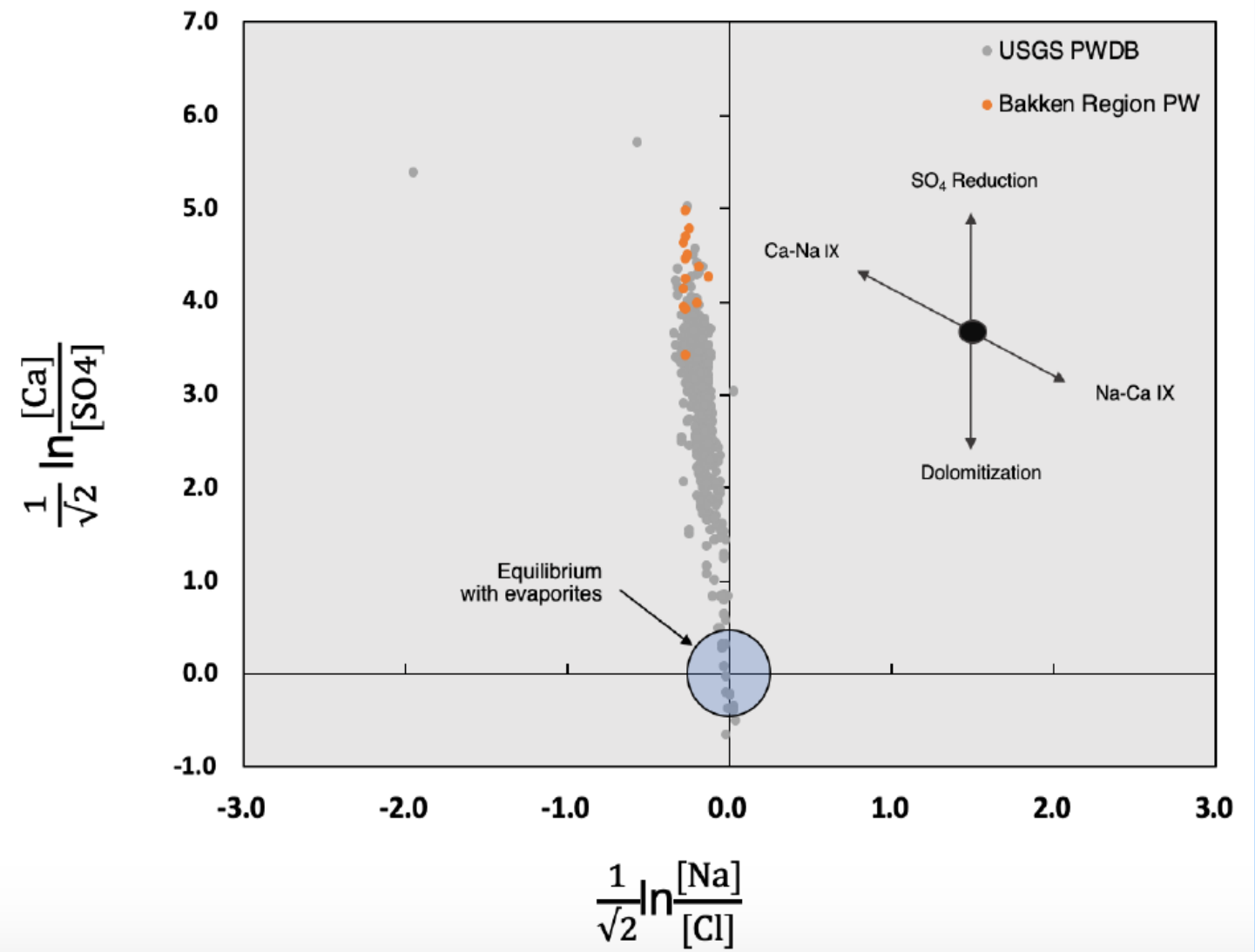
Project Scope

Number or Identifier	Type[1]	Regular or Stretch[2]	Expected Completion Date	Description
4.A	Progress	Regular	12/31/2019	**Completed.** Profile of relevant microbial pathways that may impact energy production in Bakken shale gas wells owned by the existing industrial partner.
4.B	Go/No Go	Regular	12/31/2019	**Completed**. Obtain access to a new field site in the Permian Basin in April 2018.
4.C	Progress	Regular	3/31/2020	**Completed**. Profile of relevant microbial pathways that may impact energy production in Permian Basin wells owned by new industrial collaborations.

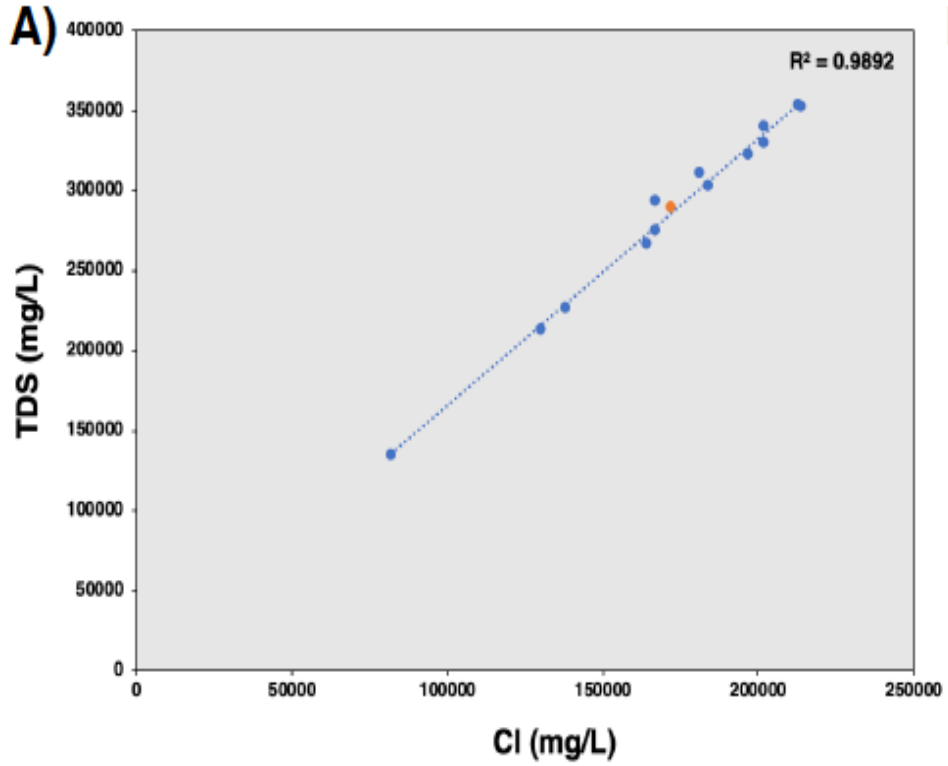
Current Status: Bakken

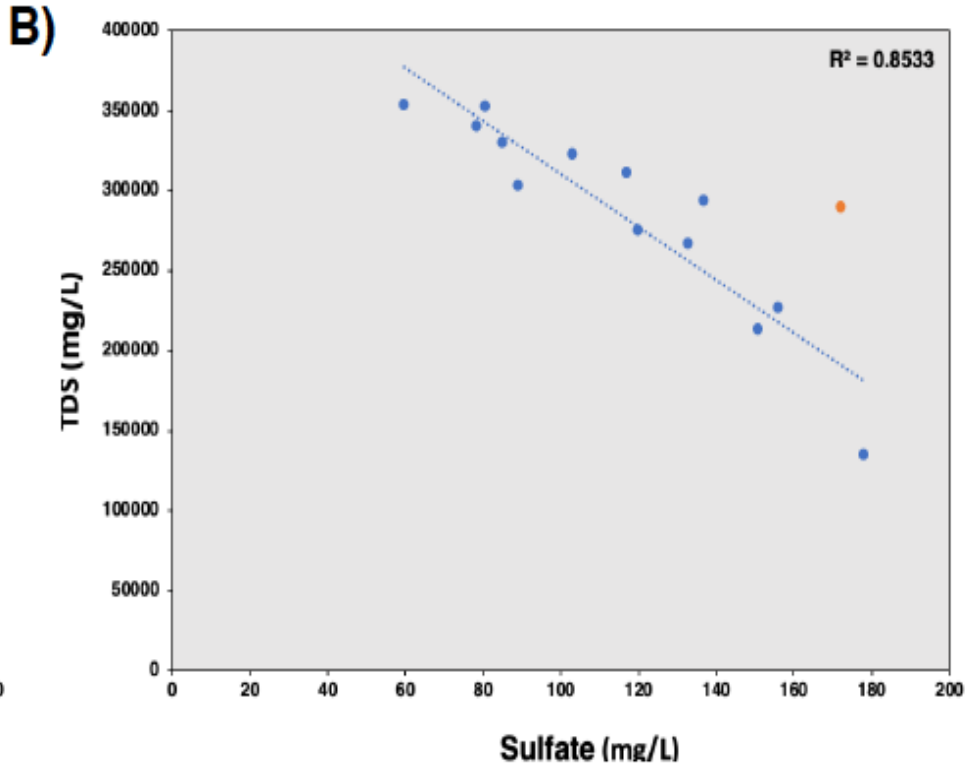
- Three Forks and Bakken Basin
- 14 Samples from 2018
- 53 Samples from 2015
- USGS Produced Water Database

Current Status: Bakken Geochemistry

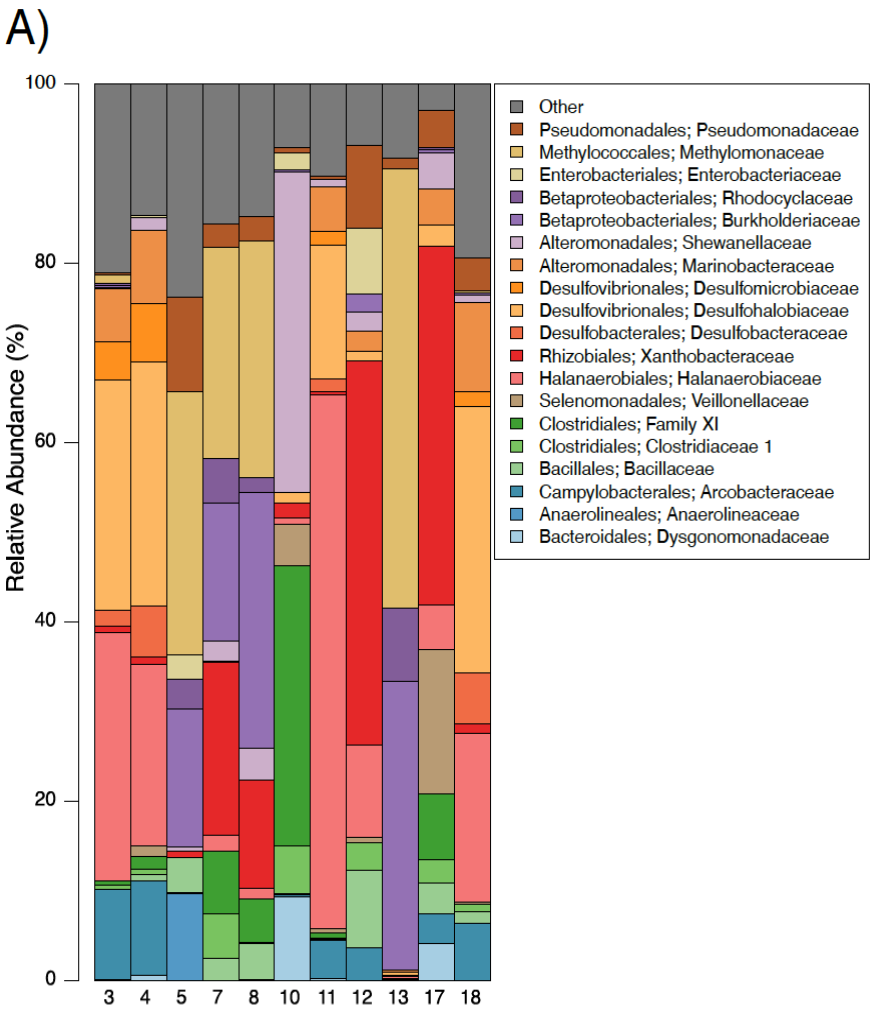


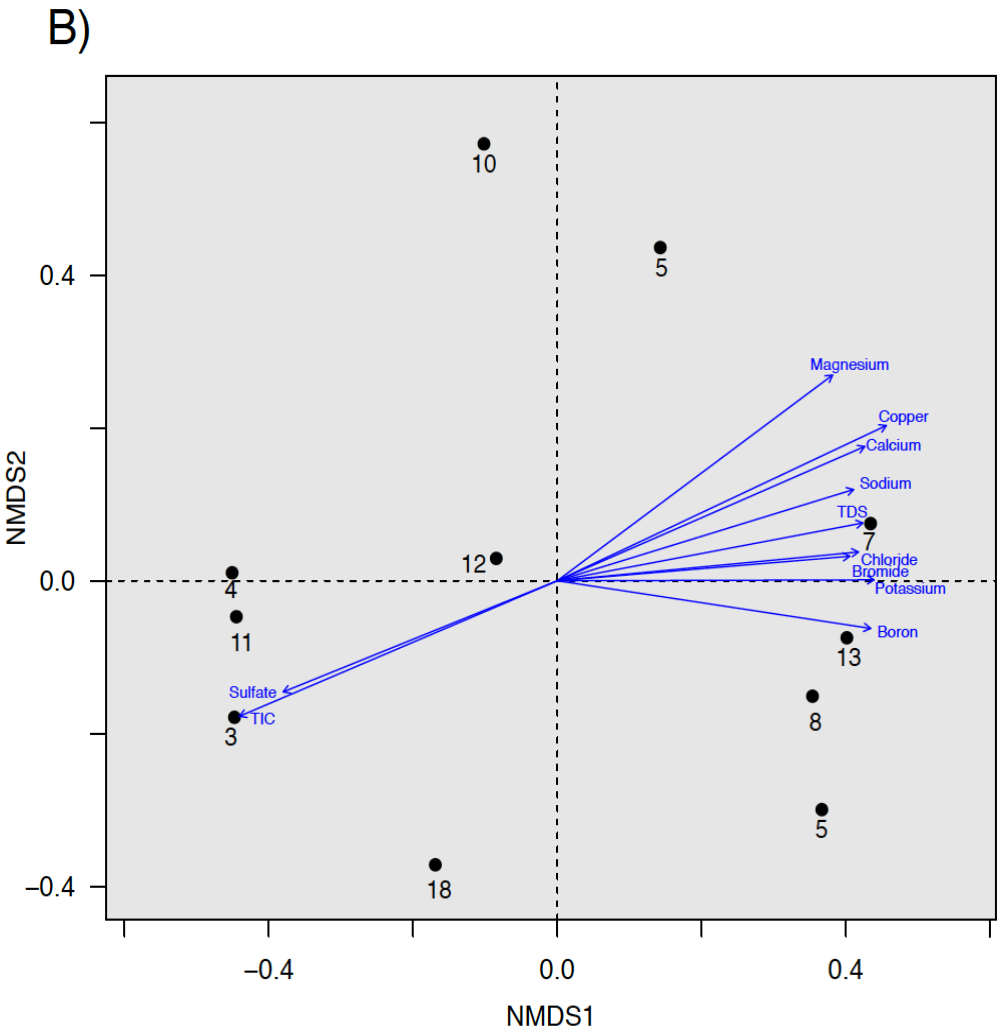
Current Status: Bakken Geochemistry





Current Status: Bakken Microbiology





Current Status: Bakken Conclusions

- Bakken Region demonstrates heterogeneities between wells
- Samples are a representative dataset for the Bakken Region, but with more indication of sulfate reduction
- Low TDS high sulfate areas provide "Hotspots" for microbial activity in a representative dataset
- To handle corrosion and scaling caused by microbiology, focus on low TDS wells for mitigation strategies

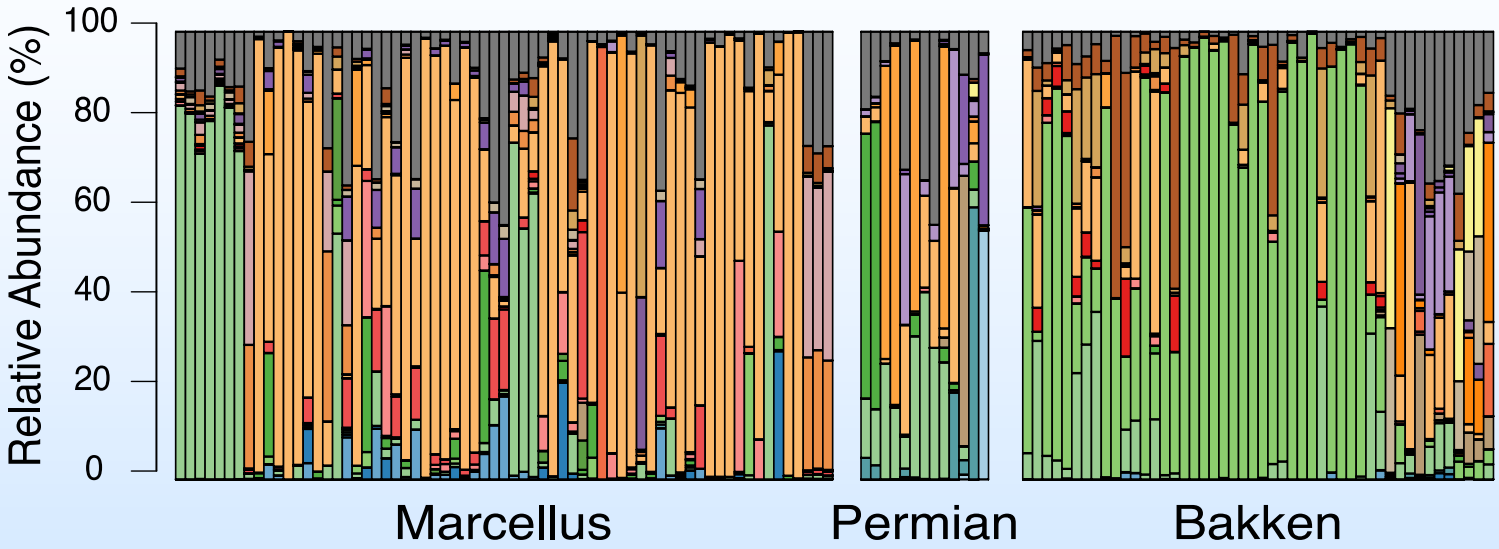
Current Status: Three-Basin Comparison

- **72 Marcellus Samples**
- **67 Bakken Samples**
- **16 Permian Samples**
  - 50 more samples yet to be processed

Current Status: Three-Basin Comparison

	Marcellus			Permian			Bakken		
	Avg	Min	Max	Avg	Min	Max	Avg	Min	Max
Barium (mg/L)	3425	65	7095	1	BDL	5	52	BDL	107
Bromide (mg/L)	N/A	N/A	N/A	447	229	614	921*	406*	1162*
Calcium (mg/L)	14014	764	31668	2868	1320	3830	27375	9080	27314
Chloride (mg/L)	71229	1745	147436	58480	29300	74500	174796*	81938*	214117*
Iron (mg/L)	N/A	N/A	N/A	52	14.7	86.8	193	63	275
Magnesium (mg/L)	N/A	N/A	N/A	575	504	623	1617	709	1643
Potassium (mg/L)	N/A	N/A	N/A	444	299	613	10322	3862	9662
Sodium (mg/L)	37364	1243	102716	33227	18000	42000	100114	37262	97276
Sulfate (mg/L)	9	BDL	29	2425	2070	2780	116*	60*	178*
TDS (mg/L)	132504	38749	223034	98113	53200	123000	299805	80034	348602
Alkalinity (mg/L $CaCO_3$)	N/A	N/A	N/A	412	95.2	737	558	241	1466
pH	N/A	N/A	N/A	6.78	6.42	7.27	6.05	4.58	6.94

Current Status: Three-Basin Comparison



- Selenomonadales; Veillonellaceae
- Clostridiales; Peptostreptococcaceae
- Clostridiales; Lachnospiraceae
- Clostridiales; Family XII
- Clostridiales; Family XI
- Clostridiales; Eubacteriaceae
- Clostridiales; Clostridiaceae 4
- Bacillales; Bacillaceae
- Campylobacterales; Arcobacteraceae
- Deferribacterales; Deferribacteraceae
- Bacteroidales; Prolixibacteraceae
- Bacteroidales; Muribaculaceae
- Methanobacteriales; Methanobacteriaceae
- Other
- Pseudomonadales; Pseudomonadaceae
- Pseudomonadales; Moraxellaceae
- Methylococcales; Methylomonaceae
- Betaproteobacteriales; Burkholderiaceae
- Alteromonadales; Shewanellaceae
- Desulfovibrionales; Desulfovibrionaceae
- Desulfovibrionales; Desulfohalobiaceae
- Sphingomonadales; Sphingomonadaceae
- Rhodobacterales; Rhodobacteraceae
- Rhizobiales; Xanthobacteraceae
- Halanaerobiales; Halobacteroidaceae
- Halanaerobiales; Halanaerobiaceae

Plans for future development: Network Analysis

- Desulfohalobium – sulfate reducer, hub score of 1
- Marinobacter – hydrocarbon reducer, hub score of 0.98
- Desulfovermiculus – sulfate reducer, hub score of 0.85

Take-aways

- These may be targeted for as an indicator of well performance and oil productivity
- When these microorganisms are removed, the entire microbial community is broken down – target for biocide mitigation if necessary
- Sulfur cycling is an important pathway in the reservoir ecosystem across all three basins

Summary Slide

- Heterogeneities in unconventional reservoirs lead to “hotspots” for microbial activity
- Common microorganisms amongst differing basins, but also basin specificity
- Keystone species can be indicators or target for mitigation strategy
- Sulfur cycling is important across basins

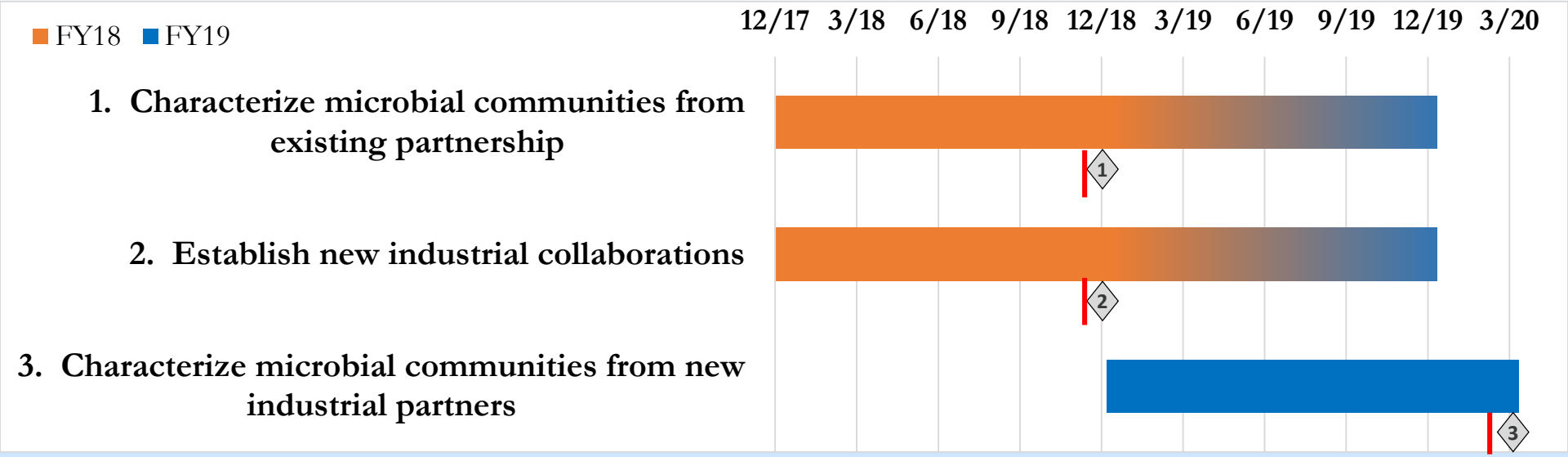
Appendix

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

Organization Chart

- Djuna Gulliver, NETL-RIC (PI – Task 4)
- Kara Tinker, Leidos-NETL (Task 4)
- James Gardiner, Battelle-NETL (Task 4)
- Burt Thomas, Battelle-NETL (Task 4)
- Preom Sarkar, ORISE-RIC (Task 4)
- Joshua Miller, ORISE-RIC (Task 4)

Gantt Chart



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. (Q4, March 2020)

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.