Shale Microbial Ecology Affecting Reservoir Conditions

Djuna M. Gulliver
NETL – Research & Innovation Center
# 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

<table>
<thead>
<tr>
<th>Funding ($k)</th>
<th>EY18</th>
<th>EY19</th>
<th>EY20</th>
<th>Total</th>
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<tr>
<td></td>
<td>$130</td>
<td>$143</td>
<td>$0</td>
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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

<table>
<thead>
<tr>
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<tr>
<td>Project: Evaluation of the geochemical and biological composition of shale gas produced water</td>
<td>Project: Evaluate relationship between fracturing fluids and microbial communities</td>
<td>Project: Geochemistry and Microbiology Explaining Reservoir and Wellbore Processes</td>
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<tr>
<td>Focus on Marcellus Produced water impoundments and development of techniques to analyze microbiology in unconventional oil and gas produced water</td>
<td>Focus on Marcellus and Bakken wellhead/separator samples – collected for characterization of microbial community and related to published data on injected fluids</td>
<td>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</td>
</tr>
<tr>
<td>PI: Rick Hammack</td>
<td>PI: Djuna Gulliver</td>
<td>PI: Djuna Gulliver</td>
</tr>
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</table>
Technology: Prior Characterization

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


FY19: Characterize Permian Basin and incorporate geochemistry

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
<table>
<thead>
<tr>
<th>Number or Identifier</th>
<th>Type¹</th>
<th>Regular or Stretch²</th>
<th>Expected Completion Date</th>
<th>Description</th>
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<tr>
<td>4.A</td>
<td>Progress</td>
<td>Regular</td>
<td>12/31/2019</td>
<td><strong>Completed.</strong> Profile of relevant microbial pathways that may impact energy production in Bakken shale gas wells owned by the existing industrial partner.</td>
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<td>4.B</td>
<td>Go/No Go</td>
<td>Regular</td>
<td>12/31/2019</td>
<td><strong>Completed.</strong> Obtain access to a new field site in the Permian Basin in April 2018.</td>
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<td>Progress</td>
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<td><strong>Completed.</strong> Profile of relevant microbial pathways that may impact energy production in Permian Basin wells owned by new industrial collaborations.</td>
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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

A) Relative Abundance (%)

B) NMDS analysis with correlation of variables
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

<table>
<thead>
<tr>
<th></th>
<th>Marcellus</th>
<th></th>
<th></th>
<th>Permian</th>
<th></th>
<th></th>
<th>Bakken</th>
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<tr>
<td></td>
<td>Avg</td>
<td>Min</td>
<td>Max</td>
<td>Avg</td>
<td>Min</td>
<td>Max</td>
<td>Avg</td>
<td>Min</td>
<td>Max</td>
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<td>7095</td>
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<td>229</td>
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<td>921*</td>
<td>406*</td>
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Current Status: Three-Basin Comparison

[Graph showing relative abundance of various bacterial groups across Marcellus, Permian, and Bakken basins.]

Legend:
- Selenomonadales; Veillonellaceae
- Clostridiales; Peptostreptococcaceae
- Clostridiales; Lachnospiraceae
- Clostridiales; Family XII
- Clostridiales; Family XI
- Clostridiales; Eubacteriaceae
- Clostridiales; Clostridiaceae 4
- Bacillales; Bacillaceae
- Campylobacterales; Arcobacteraceae
- Deferribacterales; Deferribacteraceae
- Bacteroidales; Prolibacteraceae
- Bacteroidales; Muribaculaceae
- Methanobacteriales; Methanobacteriaceae
- Other
- Pseudomonadales; Pseudomonadaceae
- Pseudomonadales; Moraxellaceae
- Methylcoccales; 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
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)
1. Characterize microbial communities from existing partnership
2. Establish new industrial collaborations
3. Characterize microbial communities from new industrial partners

**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.