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.
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

• **FY18: Characterized microbial ecology associated with Bakken Shale**

  – 118 Samples
    
    • 17 Separators
    • 17 Storage Tanks
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).

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

![Graph showing TDS (mg/L) over time with Sampling Dates: 10/7/2014, 11/1/2014, 1/14/2015, 3/25/2015. The graph includes data points for Separator and Tank.]
### Bakken Microbial Abundance

#### separator

<table>
<thead>
<tr>
<th>Sampling Date</th>
<th>Well 1</th>
<th>Well 2</th>
<th>Well 3</th>
<th>Well 4</th>
<th>Well 5</th>
<th>Well 6</th>
<th>Well 7</th>
<th>Well 8</th>
<th>Well 9</th>
<th>Well 10</th>
<th>Well 11</th>
<th>Well 12</th>
<th>Well 13</th>
<th>Well 14</th>
<th>Well 15</th>
<th>Well 16</th>
<th>Well 17</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oct-14</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nov-14</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Jan-15</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mar-15</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

#### Storage Tank

<table>
<thead>
<tr>
<th>Sampling Date</th>
<th>Well 1</th>
<th>Well 2</th>
<th>Well 3</th>
<th>Well 4</th>
<th>Well 5</th>
<th>Well 6</th>
<th>Well 7</th>
<th>Well 8</th>
<th>Well 9</th>
<th>Well 10</th>
<th>Well 11</th>
<th>Well 12</th>
<th>Well 13</th>
<th>Well 14</th>
<th>Well 15</th>
<th>Well 16</th>
<th>Well 17</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oct-14</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nov-14</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Jan-15</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mar-15</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

#### Concentration (gene copies/ml)

<table>
<thead>
<tr>
<th>Concentration</th>
<th>Other</th>
</tr>
</thead>
<tbody>
<tr>
<td>$10^1$</td>
<td>no data</td>
</tr>
<tr>
<td>$10^2$</td>
<td>low biomass</td>
</tr>
<tr>
<td>$10^3$</td>
<td></td>
</tr>
<tr>
<td>$10^4$</td>
<td></td>
</tr>
</tbody>
</table>
Technical Status: Existing Partnerships

Bacillales

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

Halanaerobiales

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

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,
  – O₂, CO₂, CO, H₂S, CH₄
  – Alkalinity

• Prep samples onsite
  – IC
  – ICP-OES
  – Isotopes (⁸⁷Sr/⁸⁶Sr, δ⁷Li)
  – 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
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.
  – 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.
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

<table>
<thead>
<tr>
<th>Section</th>
<th>Activity</th>
<th>Description</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>4.1.1</td>
<td><strong>Microbial communities from existing partnerships</strong></td>
<td>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.</td>
<td>Lipus, Gulliver, Bibby</td>
</tr>
<tr>
<td>4.1.2</td>
<td><strong>Establish new industrial collaborations</strong></td>
<td>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.</td>
<td>Lipus, Gulliver, Bibby</td>
</tr>
</tbody>
</table>
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:


Presentations:


