Bacterial Bio-indicators of Marcellus Shale Activities in Pennsylvania: A Molecular Ecology Survey

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Introduction

- Hydraulic fracturing has become more prevalent over the years in Pennsylvania, which contains gas-rich Marcellus Shale formations.
- This process has been found to reduce species richness and evenness in streams near wells pads.
- Bacterial communities readily respond to perturbations in the environment.
- Knowledge of the biodegradative capabilities of the microorganisms associated with hydrofracking operations and potential recipients (e.g., aquifers, surface waters, and streambed sediments) enables predictions about the longevity of compounds of environmental concern and the likelihood they will be biologically degraded.

Objectives

- To identify additional microbial taxa in Northeast and Southwest PA that are heavily impacted by fracking.
- Investigate the presence of microbial biomarkers related to biodegradation and bicarbonate resistance.
- Compare impacted sites with unimpacted sites as baseline samples.

Methods

- Microbial Sample Collection
  - Impacted and unimpacted water and sediment samples (Northeastern PA n=45 and Southwestern PA n = 12).
  - UOG+ (n=22), UOG− (n=22), UOG abandoned (n=1), HF+ (n=6), and Control (n=6).
- Genomic DNA and RNA extraction
  - Illumina-tag 16S rRNA library prep and sequencing (MiSeq)
- DNA Amplification
  - A Polymerase Chain Reaction of the 16S rRNA gene, which is a good thumbprint for this research.
  - PCR products are approximately 390 bp
- Analysis of 2,977,011 million 16S sequences from the Northeast region and 593,700 sequences from the Southwest region with Qime and R
  - Greengenes 97% similarity
  - Computation of Beta Diversity and LEfSe plots

Results

Figure 1: LEfSe plot of biomarkers between UOG+ and UOG− sites in Northeastern PA. Samples are plotted by relative abundances including sample identities.

Figure 2: LEfSe plot of biomarkers between HF+ and Control samples in Southwestern PA. Biomarkers such as Blautia and GN07 are abundant in the HF+ sites.

Figure 3: A bar plot showing the enriched taxa for the UOG+ and UOG− sites. The OTUs are classified to the family level.

Figure 4: A bar plot showing the enriched taxa for the HF+ and control sites. They are classified to the genus level.

Figure 5: An overview of the phyla in the Northeastern project sample sites. The bars do not show a clear difference. Proteobacteria appears to be the most abundant phylum for almost all of the samples.

Figure 6: An overview of the phyla in Southwestern PA.
- Acidobacteria seem to be more common in sediment samples than in water samples.

Discussion & Future Directions

- This study shows that there may be some new biomarkers for fracking activity in addition to other biomarkers that were identified in our previous study.
- Several biomarkers identified are known to survive saline conditions and bicarbonate.
- The phylum bar plots provide an overview of the microbial communities in the different samples (Figures 3&4).
- Acidobacteria appear to be more common in samples with fracking activity.
- However, LEfSe analysis showed several taxa in that phylum, such as CCU21, were significantly enriched in UOG+ sites.
- We will continue our studies by sequencing more DNA samples for the Southwestern project and analyzing the functional profile of several of the Northeastern project samples.
- We will also continue researching information to explain why certain taxa are enriched based on the presence or absence of fracking activity.

References


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