

Archaea and Bacteria Community Dynamics During Thermophilic Composting of Cattle Manure Revealed 100 ENERGY using 16S rRNA PhyloChip Microarray Technology

Jennifer Anders^{1,2}, Eric Dubinsky², Yvette Piceno², Francine Reid², Todd deSantis^{2,3}, Garv Andersen² ¹College of Marin, ²Lawrence Berkeley National Laboratory, ³Second Genome

Abstract

Proper management of agricultural manure (solid biowaste) is important to protect water supplies, and mitigate green house gas emissions. Thermophilic composting of solid biowaste is a proposed alternative to current management practices. Compost and raw manure samples were collected from a field scale operation. To prepare these samples for PhyloChip microarray analysis, total DNA extractions were performed. The 16S rBNA gene was amplified by polymerase chain reaction (PCR) from the extracted genomic DNA and quantified using gel electrophoresis. The PCR product was hybridized to the G3 PhyloChip microarray. The hybridization intensities were used to determine the taxa of archaea and bacteria present in each sample as well as compare corresponding relative population abundances. Archaea phyla Thaumarchaeota and Thermoprotei phyla Actinobacteria and Firmicutes dramatically increased the number of different detected subfamilies. Hybridization intensity values for ammonia oxidizing prokaryotes increased under thermophilic conditions and remained high in the endpoint, mesophilic compost samples suggesting potentially high levels of nitrification. Increased intensity values for methanogens in thermophilic conditions suggest a potential increase in methane production during composting. Conversely, the vast majority of detected methanotrophs had higher intensities in old mesophilic compost and sharply decreased with increasing temperature. More study is needed to definitively determine what taxa are dominant and which metabolic pathways are active relative to green house gas emissions

Introduction

California dairies produce 70 billion pounds of solid waster per year, 80% more solid waste than states' residents. This study characterizes microbial community dynamics of archaea and bacteria, and community dynamics of functional groups involved in GHG emissions during thermophilic composting.

> Land Application of Manure - Current waste management practice -

Benefits Supply nutrients to crops Increase overall soil quality

Leaching of nutrients Public health safety Green House Gas emissions

Areas of Concern

Thermophilic Composting of Solid Waste - Proposed alternative

The biological process by which microbial activity decomposes raw organic material.

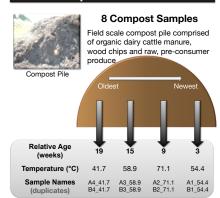


PhyloChip Technology

PhyloChip, a high-density microarray, utilizes conserved regions of the 16s rRNA gene possessed by all bacteria and archaea.

Can detect relative abundance values on level below subfamily called Operational Taxonomic Unit (OTU).

Sample Collection



3 Manure Samples Organic dairy cow manure used for compost piles. Served as "time-zero". No manure temperatures recorded.

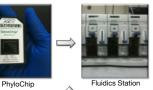
Sample Processing

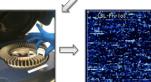
Manure Pile

Mortar and pestle used to homogenize samples.

- ODNA extractions performed using Zymo-ZR Fecal DNA MiniPrep according to manufacturers protocol.
- 9 16S rRNA PCR amplification and guantification using universal primers.

PhyloChip Processing:

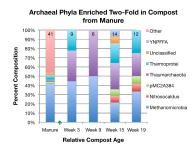




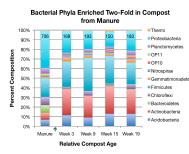
PhyloChip Scanner PhyloChip Array Image

Results

Richness of Archaea and Bacteria Phyla



Archaeal Phyla Enriched Two-Fold in Composit from Manure: Composition reflects those subfamilies, which had any OTU whose average relative abundance increase two-fold to that of the manure samples, and were detected in at least one of the sample replicates, based on subfamily binary present/absent calls. The Manure samples served as baseline samples, and are representative of all the subfamilie within each phylum originally detected prior to compost treatment. Graph is scaled to 100%. The numbers at the top of each bar represent the total number of different subfamilies within that age group. The green arrow between Manure and Week 3 indicates the addition of food waste and wood chips.



Bacterial Phyla Enriched Two-Fold in Compost from Manure: Composition reflects those subfamilies, which had any OTU whose average relative abundance increased two-fold to that of the manure samples, and were detected in at least one of the sample replicates. based on subfamily binary present/absent calls. The Manure samples served as base samples, and are representative of all the subfamilies within each phylum originally detected samples, and are representative or an me subnammes within each physicin organized prior to composite treatment. Graph is scaled to 100%. Number at the top of each bar represents the total amount of subfamilies in the age group. The green arrow betwee Manure and Week 3 indicates the addition of food waste and woodchips.

Green House Gas (GHG) Implications

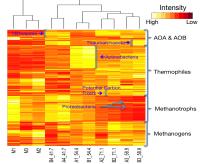
Based on community dynamics of functional groups

Methanogens Organic Compounds \rightarrow CH ₄		$\begin{array}{c} \text{Methanotrophs} \\ \text{CH}_4 \twoheadrightarrow \text{CO}_2 \end{array}$	
Ammonia Oxidizers $NH_3 \rightarrow NO_3, NO_2$		Photosynthetic Carbon Fixers $CO_2 \rightarrow Organic Compounds$	

Results

U.S. DEPARTMENT OF

Heatmap of Functional Groups



Heatmap of Functional Groups: Displays shifts in relative abundance values for those OTU involved in ammonia axidation (AOA & AOB), methane formation (methanogens), methane consumption (methanotrophis) as well as thermophilic organisms including those which and clustered similarly. All compost samples clustered separately from narrues samples. Ad: 17. and B. 4.17. and B. mesophilic samples from week 18th of clustered sparately final hermophilic, which all 5.4.4 and B. 15.4.4 are pro-pased than hermophilic, which all 5.4.4 and B. 15.4.4 are pro-pased thermophilic and A3_5.8.9 and B3_5.8.9 are post peak thermophilic.

Conclusions

- Phyla Actinobacteria, Firmicutes, Thaumarchaeota and Thermoprotei dramatically increase in richness with composting.
- Q Nitroscaldus subfamilies were only detected in 15 and 19 week old samples.
- O Bacteriodetes and Proteobacteria decrease in richness with composting.
- Ammonia oxidizing organisms increased in hybridization intensities under thermophilic conditions, suggesting high levels of nitrification.
- O Thermophilic organisms increased in intensity values with increased temperatures, including organisms with phototrophic carbon fixation pathways. 0
- Methanogen and methanotroph intensities were inversely related, suggesting increased methane emissions during the thermophilic phase.

Acknowledgements

This work was supported by the Center for Science and Engineering Education at the Lawrence Berkeley National Laboratory, the U.S. Department of Energy in partnership with the College of Marin and the Marin Carbon Project. I would like to personally thank Gary Andersen, Fernando Agudelo-Silva, Jeff Creque, Andrew Cullen, Eric Dubinsky, John Hulls, Yvette Piceno, Francine Reid, and John Wick for their unwavering support and guidance.