A Publication of the ENVIRONMENTAL RESEARCH AND EDUCATION FOUNDATION

RESEARCH BULLETIN

Environmental Research and Technologies for the Future *Issue 2, Volume 1 Winter 2004 www.erefdn.org*

Microbial Communities in Landfill Gas and Condensate

ABSTRACT: *Microbial Communities in Municipal Solid Waste Landfills Were Studied by an Examination of Landfill Gas and Gas Condensate.*

Landfills remain the most commonly used method for municipal solid waste disposal. However, soon after waste is buried, the organic portion begins to degrade because of microbial action. Although researchers have identified which microbes are responsible for waste degradation, limited studies have been performed on other landfill microbiology communities. For this study, landfill gas (LFG), landfill gas condensates (LFGC), and landfilled waste were used to study landfill microbial communities.

The study of microbial communities in the environment is difficult to understand with culture-based techniques alone. However, the recent developments of molecular techniques have overcome the limitations of culture dependent methods. In this study, landfill microbial communities were examined by using molecular techniques such as slot-blot hybridization with 16S rRNA and polymerase chain reaction (PCR) amplification. By using slot-blot hybridization, certain microorganism groups (e.g., *Bacteria*, *Archaea*, and *Eucarya*) can be quantified as to their relative abundances and PCR significantly increases the probability of detecting certain microorganisms in the samples.

A large number of LFG and LFGC samples were collected from the Burlington County Resource Recovery Complex in New Jersey. A gas sampling collection apparatus was attached to ports on the wellheads. Microbial cells were collected on membrane filters mounted in sterile holders. Filter holders were attached to wellheads through sterile tubing and syringe barrels.

Because the gas was saturated with water vapor, condensate formed when the gas cooled upon reaching the surface. In order to prevent formation of condensate on the membranes, the gas wells and filter holders were wrapped in heating tape and insulated with closed-cell foam pipe insulation. The temperature of the heating tape was set as close to the gas temperature as possible with temperature controllers. Landfill gas was withdrawn from the gas extraction wells by applying a vacuum to well heads.

Landfill gas condensate was collected from the landfill's condensate collection system at a point where the condensate drained into the sump. Gas condensate was collected in a clean bucket and transferred into polycarbonate bottles. Gas condensate was aseptically pumped through filter units to collect microbial biomass.

Landfilled waste was collected during the installation of gas extraction wells. Excavated wastes were collected every 20 feet and placed in airtight glass containers with metal lids. Nitrogen gas was purged into the containers before and after waste collection to maintain anaerobic conditions.

The results of PCR amplification were:

- Bacterial 16S rRNA was detected in all landfill samples (except in one gas sample);
- Archaeal 16S rRNA was detected in gas condensate and some raw wastes;
- A distinct pattern of *Archaea* present in the waste versus waste depth was not apparent, nor was *Archaea* detected in gas samples; and
- *Methanogens*, responsible for the terminal steps of anaerobic degradation of organic materials, were detected in gas condensate and in one waste sample.

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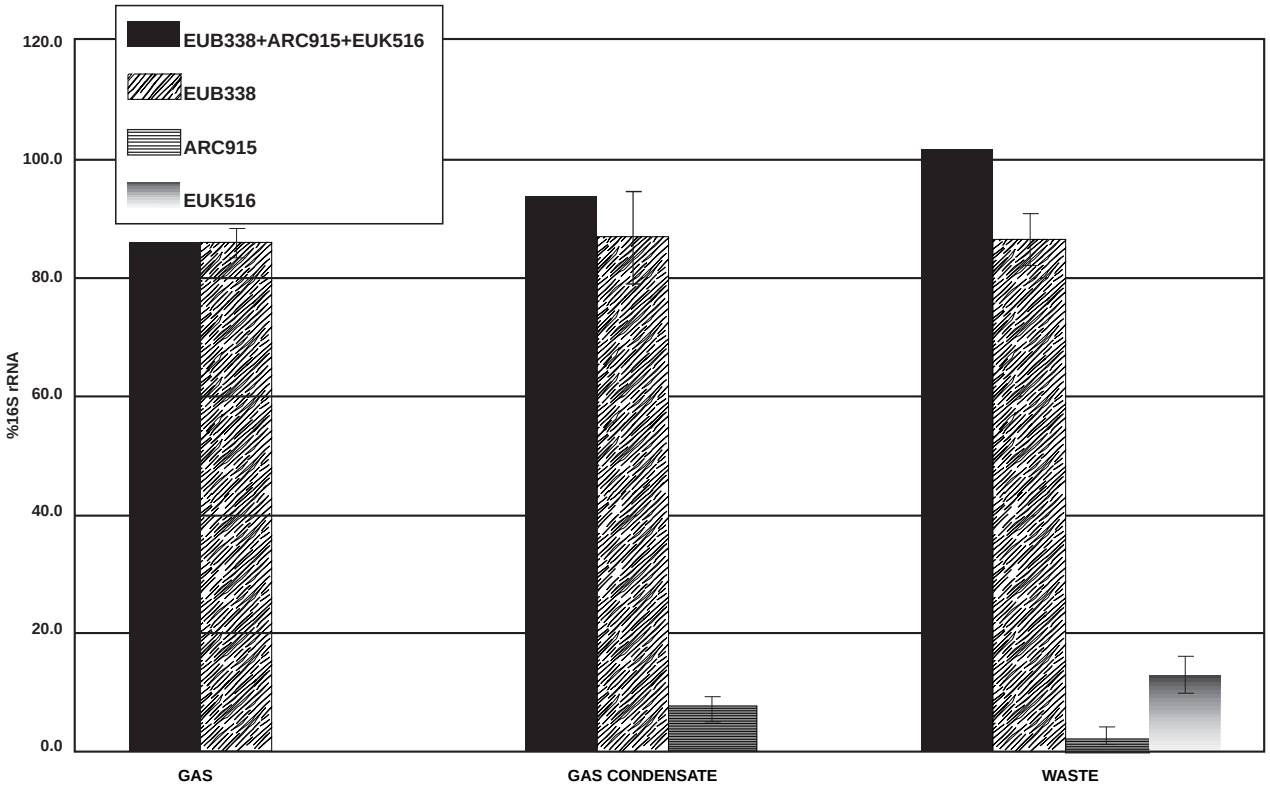

Figure 1. Hybridization Results (Bacteria: EUB338; Archaea: ARC915; Eucarya: EUK516)

The results of hybridization were (Figure 1):

- Bacterial 16S rRNA was dominant in all the landfill samples (86-87%);
- The relative abundance of *Archaea* was 7.2 percent in gas condensate and 2.1 percent in wastes, while not detected in the gas; and
- *Eucarya* was only detected in waste samples (13.1%).

The study found that *Bacteria* dominated and *Archaea* seemed to be a minor component in the landfill microbial communities. This result was similar to observations made in natural anaerobic systems and in anaerobic digesters.

The lack of *Archaea* (including *Methanogens*) in the gas streams was probably caused by low cell numbers in the gas rather than complete absence. Landfills are often compared with anaerobic digesters. However, unlike an engineered anaerobic digester, which often operates under optimum conditions, the study found that *Methanogens* were not the major member of the *Archaea* in the landfill environments.

The results of the study showed that gas and gas condensates provided representative samples from the landfill environments and provide the basis for a comprehensive investigation of the microbial processes involved in landfill waste degradation.

Therefore, information from slot-blot hybridization and PCR amplification can be used as references for future studies of the landfill environment. Also, this is the first report to investigate the landfill microbial community using gas or gas condensate coupled with molecular techniques. The protocols developed in the study could be used to monitor in-situ microbial activity using landfill gas and gas condensate in order to provide information for site management.

This study on the microbiological communities in landfill gas has the potential to allow landfill owners and operators an alternate method to determine the rate of waste degradation in a landfill without obtaining waste samples. The study also provides owners and operators with information necessary for optimal site management especially if bioreactor operations are undertaken.

Ms. Mijin Kim conducted this study for the Foundation in partial fulfillment of the requirements for the degree of Doctor of Philosophy from Drexel University, Philadelphia, Pennsylvania.