

EREF in the NEWS



Researchers ID microbe responsible for methane from landfills

Wednesday, April 6, 2011



Researchers have long known that landfills produce methane, but had a hard time figuring out why—since landfills do not start out as a friendly environment for the organisms that produce methane. New research from North Carolina State Univ. shows that one species of microbe is paving the way for other methane producers.

Researchers can use these findings to accelerate methane production for power generation. Credit: North Carolina State Univ.

Specifically, the researchers found that an anaerobic bacterium called *Methanosarcina barkeri* appears to be the key microbe.



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07 Apr 2011

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NEW ENERGY AND FUEL

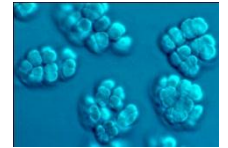
NEWS AND VIEWS FOR MAKING AND SAVING MONEY IN NEW ENERGY AND FUEL



FOUND! The Bug That Makes Methane In Garbage

"The starting bug has been found. That opens the door to engineering better landfills with better production management. Imagine a landfill with real economic prospects beyond getting the trash out of sight."

As an EREF scholar at North Carolina State University, current EREF President and CEO Bryan Staley's Ph.D. research identified a key microbe responsible for initiating methane from landfills under less than optimal conditions.



On April 6, 2011 North Carolina State University issued a press release with the results of this research project. The exciting findings were picked up by media outlets throughout the country.

APPLIED AND ENVIRONMENTAL MICROBIOLOGY, Apr. 2011, p. 2381-2391
0099-2240/11/\$12.00 doi:10.1128/AEM.02349-10
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Effect of Spatial Differences in Microbial Activity, pH, and Substrate Levels on Methanogenesis Initiation in Refuse¹

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Received 3 October 2010/Accepted 31 January 2011

The initiation of methanogenesis in refuse occurs under high volatile fatty acid (VFA) concentration and low pH (5.5 to 6.25), which generally are reported to inhibit methanogenic *Archaea*. One hypothesized mechanism for the initiation of methanogenesis in refuse decomposition is the presence of pH-neutral niches within the refuse that act as methanogenesis initiation centers. To provide experimental support for this mechanism, laboratory-scale landfill reactors were operated and destructively sampled when methanogenesis initiation was observed. The active bacterial and archaeal populations were evaluated using RNA clone libraries, RNA terminal restriction fragment length polymorphisms (TRFLP), and reverse transcription-quantitative PCR (RT-qPCR). Measurements from 81 core samples from vertical and horizontal sections of each reactor showed large spatial differences in refuse pH, moisture content, and VFA concentrations. No pH-neutral niches were observed prior to methanogenesis. RNA clone library results showed that active bacterial populations belonged mostly to *Chloroflexi*, and that methanogenic *Archaea* activity at low pH was attributable to *Methanosarcina barkeri*. After methanogenesis began, pH-neutral conditions developed in high-moisture-content areas containing substantial populations of *M. barkeri*. These areas expanded with increasing methane production, forming a reaction front that advanced to low-pH areas. Despite low-pH conditions in >50% of the samples within the reactors, the leachate pH was neutral, indicating that it is not an accurate indicator of landfill microbial conditions. In the absence of pH-neutral niches, this study suggests that methanogens tolerant to low pH, such as *M. barkeri*, are required to overcome the low-pH, high-VFA conditions present during the anaerobic acid phase of refuse decomposition.



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