

# Bacteria involved in sewer pipe corrosion identified

October 23 2012

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Microbes corrode sewer pipes from the inside, a process that can lead to spills, bad odors, disease outbreaks, and the need for costly repairs. In a first step towards reducing the corrosion, researchers have identified the culprit microbes. The research is published in the October *Applied and Environmental Microbiology*.

Surprisingly, they found two different communities, on the wall and the ceiling of the pipes, respectively, says first author Barry Cayford of the University of Queensland. "This separation into two different communities suggests that different types of corrosion may be taking place, and this needs to be considered in the management of the problem," says Cayford.

Earlier work had suggested that *Acidithiobacillus thiooxidans*, [microbes](#) that oxidize [hydrogen sulfide](#) to sulfuric acid, were key constituents of the sewer pipe corrosion community. Cayford and his colleagues found that the ceiling species were instead dominated by bacteria from the genera *Acidiphilium* and *Mycobacterium*. The former species are known to grow in high acidity, where they oxidize [sulfur compounds](#) to sulfuric acid. The wall-associated genera included Xanthomonadales, Burkholderiales, Sphingobacteriales, and others.

Besides bacteria, a range of eukaryotic sequences were detected, but at low abundance, and mostly in wall-associated samples.

"The research resulted from complaints about the smell of sewer systems

from people living near large sewer pipes," says Cayford. The complaints forced a major reduction in sewer pipe ventilation, which had been a method for controlling corrosion, he explains. That was the germ of the research. Cayford and his collaborators decided to study the microbiology of the corrosion, in an effort to find other ways to mitigate the problem.

"We hypothesized that we could improve on the limited knowledge of this environment through the use of state-of-the-art microbial ecology tools," says Cayford. His team sequenced the 16S ribosomal RNA genes of the microbes using high-throughput molecular ecology analysis. "The approach provides a much more detailed account of the microbes present than had been possible before." But the current research is only the first step, he says. "We aim to build on this work to deliver a much improved model of sewer corrosion."

**More information:** B.I. Cayford, P.G. Dennis, J. Keller, G.W. Tyson, and P.L. Bond, 2012. High-throughput amplicon sequencing reveals distinct communities within a corroding concrete sewer system. *Appl. Environ. Microbiol.* 78:7160-7162. [bit.ly/asmtip1012b](http://bit.ly/asmtip1012b)

Provided by American Society for Microbiology

Citation: Bacteria involved in sewer pipe corrosion identified (2012, October 23) retrieved 23 April 2024 from <https://phys.org/news/2012-10-bacteria-involved-sewer-pipe-corrosion.html>

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