

DNA analysis of microbes in a fracking site yields surprises

Pam Frost Gorder, Ohio State University

SAN FRANCISCO—Researchers have made a genetic analysis of the microbes living deep inside a deposit of Marcellus Shale at a hydraulic fracturing, or “fracking,” site, and uncovered some surprises.

They expected to find many tough microbes suited to extreme environments, such as those that derive from archaea, a domain of single-celled species sometimes found in high-salt environments, volcanoes, or hot springs. Instead, they found very few genetic biomarkers for archaea, and many more for species that derive from bacteria. They also found that the populations of microbes changed dramatically over a short period of time, as some species perished during the fracking operation and others became more abundant. One—an as-yet-unidentified bacterium—actually prospered, and eventually made up 90% of the microbial population in fluids taken from the fracked well.

Researchers may never know the exact species of bacteria in the fluids because of the difficulty in replicating the subsurface conditions in the laboratory, and the challenges associated with culturing unknown microbes from such environments, explained Paula Mouser, assistant professor of civil, environmental and geodetic engineering at Ohio State University and lead author of the study.

“There are millions of microbes that we can detect using biomarkers, but haven’t ever isolated or cultured from these environments before. Most are grouped into loose associations based on shared genetic characteristics—something akin to a human extended family,” Mouser said.

“Probably, the best we’ll be able to do is identify their microbial ‘cousins.’”

The study tracked the microbe species found in the water pumped out of a typical fracking site over a period of months during its normal operation. The rock at the site was a type of shale known as Marcellus, named for the city in New York where it was first identified.

To Mouser, the real value of the study is the new knowledge it offers on how microbes in fracking fluids compete and survive when the fluids are injected to the deep subsurface, as certain microbes could prove detrimental to oil and gas quality, or compromise well integrity.

She presented her team’s initial findings at the American Geophysical Union meeting this week.

“This kind of research is important, because everything we learn about subsurface

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microorganisms helps us understand ecology on Earth's surface," she said. "When water samples like this are shared, there is the potential for great discovery—this knowledge could open doors to new technology for improving gas extraction efficiency or for treating flowback fluids from these sites."

Because of the large cost for drilling and fracking one well—usually, millions of dollars—individual researchers must team together with industry for access to samples.

In fact, companies do not normally share the contents of their "flowback" fluids—the mix of water, oil, and gas that emerges from an active well—because they could reveal the proprietary mix of chemicals that the company is using to aid extraction.

The Ohio State study was able to take place only through a collaboration with the U.S. Department of Energy National Energy Technology Laboratory (NETL) in Pittsburgh. NETL is working with industry to study fracking technologies and provided Mouser's team with water samples donated by an unnamed shale gas operation.

When it comes to energy extraction, tiny microbes play a huge role, Mouser said.

As it happens, the chemicals that companies pump into the ground along with water to help fracture shale and release petroleum contain carbon, nitrogen, and phosphorous—in chemical formulations that microbes like to eat. So, left unchecked, the microbes in a fracking well can grow and reproduce out of control—so much so, that they may clog the fractures and block extraction, or foul the gas and oil with their waste, which contains sulfur.

This is no news to oil companies, Mouser added. They've long known about the microbes, and add biocides to the water to control the population. What isn't known: exactly what kinds of microbes live there, and what altering their populations does to the environment.

"Our goal is really to understand the physiology of the microbes and their biogeochemical role in the environment, to examine how industry practices influence subsurface microbial life and water quality," Mouser said.

Maryam Ansari, a master's student in environmental sciences at Ohio State, sequenced the microbes' DNA, and separated them into taxa, or taxonomic units—groups that could be thought of as microbial "cousins."

Of the 40 taxa the researchers identified from water samples taken at the start of the fracking operation, only six survived the first few weeks. Almost all of the bacteria at the site were classified as "halo-tolerant," similar to bacteria that live in deep saltwater environments.

The study is just beginning, and Mouser hopes that as they learn more, the researchers will be able to pin down how the microbes metabolize fracking fluids.

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Ultimately, they hope to meld those discoveries with a computer model that can predict fluid movement from shale formations to groundwater aquifers. The model would provide tools for commercial companies to assess the safety of possible fracking sites.

In the meantime, Mouser is very interested in teaming with other industry partners to also look at microbial dynamics in a different kind of rock: Ohio's Utica Shale.

Ohio State's Subsurface Energy Resource Center funded the genomic analyses, which were done at the university's Plant Microbe Genetics Facility. These early findings have earned Mouser a new grant from the National Science Foundation so that she can pursue the work further.

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