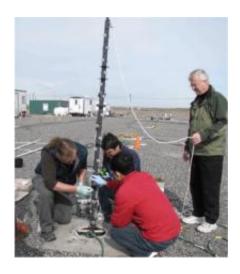


Same samples, different analytical strategies, complementary inferences

April 11 2012



Pacific Northwest National Laboratory scientists (from left) David Kennedy, Tom Resch, Xueju Lin, and Allan Konopka performing multi-level groundwater sampling at the Integrated Field Research Challenge Site, Hanford Site 300 Area.

(Phys.org) -- The results of two separate but complementary analyses on 400 samples of Hanford Site groundwater appeared together in the journal of the International Society for Microbial Ecology. The studies take different approaches, each providing unique insights that, when combined, result in a better understanding of what environmental forces affect the composition of microbial communities, and in turn, how those communities may influence the biogeochemistry of subsurface sediments.



In both studies, scientists at Pacific Northwest National Laboratory analyzed about 200,000 gene sequences from the groundwater's Bacteria and Archaea. Samples were taken from nine separate wells over a 10-month period. The first study analyzed the rate at which community composition changed over time and space. The results demonstrated that the intrusion of river water more than 200 meters (656 feet) inshore from the Columbia River impacted the composition of microbial assemblages. Consistent with the hydrodynamics of the aquifer, the effects were greatest near the top of the water table during the seasonal rise in the Columbia River.

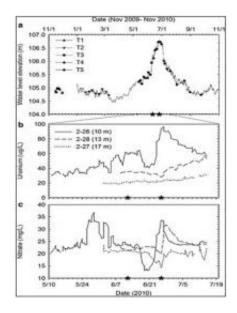
In the second study, scientists combined tools typically used in <u>plant</u> <u>ecology</u> with a randomization approach, called a null model, to predict what happens to a microbial community under stochastic conditions. Stochastic conditions arise when all organisms are ecologically similar, which results in the random assembly of ecological communities. Approaching the data with a different set of statistical tools paid off. The team discovered that river intrusion can indeed impact <u>microbial</u> <u>communities</u>, but only when river intrusion is combined with specific <u>geologic features</u>. When those conditions are not met, microbial community composition changed stochastically through time.

Microbial processes provide a wide variety of ecosystem services, including detoxification of contaminants, climate regulation, and bioprocessing to produce valuable products. Microorganisms in natural or engineered ecosystems rarely live alone, but instead function as integrated units—or communities—that process energy and materials and thereby affect their environment.

Despite their importance, scientists know little about microbial community function and behavior. By studying these communities, scientists can gain knowledge that will enable them to predict changes in microbial community dynamics during either natural cycles of change or



environmental perturbations—such as climate change or pollution.



Temporal variations in (a) water table elevation, estimated from river gauge data, (b) uranium, or (c) nitrate concentrations in groundwater at 10, 13, or 17 m. Sampling time points were grouped into five time clusters: T1-5. T3 and T4 represent samples taken before and after the Columbia River water intrusion, respectively. Stars on each x-axis indicate date of detectable river water intrusion (June 15) and peak of river water intrusion (June 26).

The samples used in both studies come from nine wells drilled into the unconfined subsurface aquifer at the U.S. Department of Energy's Hanford Site in south-central Washington state. The wells are located 250 meters from the Columbia River on the Hanford Site, WA. The wells were screened at depths ranging from 10 to 17 meters that differed in hydraulic conductivities.

Dr. James Stegen, a PNNL Linus Pauling Distinguished Postdoctoral Fellow who led the companion study, believes in starting at the top—the top of the microbial community system, that is. "I'm here to bring in a



different perspective on microbial communities. A lot of work takes a bottom-up or reductionist approach where the system is taken apart and then put back together. I'm at the other end," said Stegen.

He added, "I strive to provide a complementary approach by starting at the top, so we can understand the big picture and see broad patterns. By working towards each other, bottom-up and top-down approaches can together provide systems-level understanding that transcends spatial and temporal scales."

Stegen applied tools from phylogenetic, or evolutionary, community ecology combined with null modeling to mimic stochastic behavior. "In short, the model takes the names at the tips of the phylogenetic tree and shuffles them to different locations," he said. "We then recalculate the community-level metrics. This gives us an expectation of what each community should look like when the assembly is stochastic. This is useful, because when you see a big difference between what's observed and what's expected from the null model, you know there's something deterministic in the system. In our particular study, it showed that river intrusion deterministically caused a shift in community composition."

The goal is to link Stegen's top-down approach with bottom-up approaches to better understand subsurface systems. To that end, both studies took place in the context of two DOE subsurface programs at the Hanford Site: the Integrated Field Research Challenge, and the Subsurface Scientific Focus Area.

The other study, led by former PNNL postdoctoral researcher Dr. Xueju Lin, involved sequencing and analyzing genes in the samples' Bacteria and Archaea to document factors controlling microbial spatial and temporal dynamics. The approach was to measure changes in groundwater microbial abundances and community composition over time and in distinct subsurface strata.



The spatial and temporal patterns for several genes associated with particular functions, such as methane oxidizers and metal reducers, suggest dynamic changes in fluxes of electron donors and acceptors over an annual cycle. In addition, temporal dynamics in the abundance of eukaryotic microbes suggest that bacterial community dynamics could be affected not only by the physical and chemical environment, but also by top-down biological control.

Ecologists have recognized that the influx of groundwater into flowing surface waters, called the hyporheic zone, affects the ecology of streams. The results of these two studies are one of the first demonstrations that large river systems like the Columbia River may impact the biogeochemistry and microbial ecology of subsurface sediments. PNNL scientists will pursue a "whole systems" analysis of the hydrodynamics, geochemistry, and microbial functionality in the Columbia River's hyporheic zone to determine how these dynamics affect not just the composition of the microbial community but also its activity.

More information: Lin X, et al. 2012. "Spatial and temporal dynamics of the microbial community in the Hanford unconfined aquifer." *The ISME Journal* advance online publication, 29 March 2012; doi: 10.1038/ismej.2012.26

Stegen JC, et al. 2012. "Stochastic and Deterministic Assembly Processes in Subsurface Microbial Communities." *The ISME Journal* advance online publication, 29 March 2012; doi: 10.1038/ismej.2012.22.

Provided by Pacific Northwest National Laboratory

Citation: Same samples, different analytical strategies, complementary inferences (2012, April 11) retrieved 10 April 2024 from https://phys.org/news/2012-04-samples-analytical-strategies-



complementary-inferences.html

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.