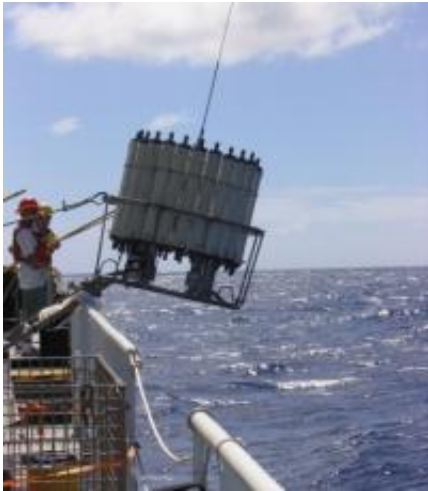


# Genomic comparison of ocean microbes reveals East-West divide in populations

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To obtain microbe samples, scientists on the R/V Kilo Moana oceanographic research ship lower a rosette holding 24 bottles that capture samples at different ocean depths in the Pacific Ocean. Photo: Maureen Coleman

Much as an anthropologist can study populations of people to learn about their physical attributes, their environs and social structures, some marine microbiologists read the genome of microbes to glean information about the microbes themselves, their environments and lifestyles.

Using a relatively new methodology called comparative population genomics, these scientists compare the entire genomes of different populations of the same microbe to see which genes are "housekeeping"

or core genes essential to all populations and which are population-specific. Scientists are able to read a genome and translate the genes into proteins that serve particular functions. Population-specific genes sometimes tell a very clear story about the environment, for instance temperature and the availability of light and particular elements, and over time, they can point to the microbes' [evolutionary adaptation](#) to changes in the ecosystem. Occasionally, as was the case with recent research at MIT, the population-specific genes reveal this information with crystal clarity, even providing unmistakable clues about lifestyle.

Professor Sallie (Penny) W. Chisholm of MIT's Department of Civil and Environmental Engineering (CEE) and former doctoral student Maureen Coleman compared the [genetic makeup](#) of two populations of the same oceanic photosynthetic [bacterium](#), Prochlorococcus, one living in the Atlantic Ocean and one in the Pacific.

They found that although a continent separates the populations, they differ significantly in only one respect: those in the Atlantic have many more genes specifically related to the scavenging of [phosphorus](#), an essential element for these microbes. And just as the variations in the beaks of Darwin's finches were evolutionary adaptations related to food availability, so too are the variations in the Prochlorococcus genes related to phosphorous gathering. Both are examples of a powerful evolutionary force at work.

"We expected to see some difference in the genes related to phosphorous, because the Atlantic Ocean has an order of magnitude lower concentration of phosphorus than the Pacific, so Atlantic populations of Prochlorococcus carry many more genes involved in extracting phosphorus from the seawater. They need more creative ways of gathering it. But we didn't expect it to be the only difference," said Chisholm. "This indicates that phosphorus availability is the dominant selective force in defining these populations."

The researchers also noted that the microbes in the Atlantic Ocean had increased numbers of phosphorous-related genes that helped them neutralize arsenic, an element they sometimes take up by mistake when they're scavenging for phosphorous. This finding "buttresses the assertion" that this is the result of a strong selective process, Chisholm said.

"We're really diagnosing the ecosystem using a specific species of microbe as a reporter," said Chisholm. "We're letting the cells tell us what they have to deal with in their environment."

She and Coleman also compared the genomes of two populations of a neighboring bacterium, *Pelagibacter*, and found that genes related to phosphorus gathering in that bacterium appear in far greater numbers in the Atlantic Ocean population, but with a twist. These microbes have a somewhat different repertoire of phosphorus-related genes, suggesting subtle differences between these two microbial groups with respect to how they scavenge phosphorus. This could reflect an adaptive behavior known as "niche partitioning," which allows cells sharing a microenvironment to apportion resources according to a cell's "lifestyle" rather than all competing for the same element or same form of that element.

To obtain these findings, which will appear in the online Early Edition of the *Proceedings of the National Academy of Sciences* the week of Oct. 11, the two scientists used the complete genomes of 13 strains of lab-cultured *Prochlorococcus* and *Pelagibacter* as reference genes, and compared these with the [genes](#) of well-documented wild microbe populations gathered at long-term oceanographic study stations near Bermuda (BATS) and Hawaii (HOTS). The work was funded by the Gordon and Betty Moore Foundation, the National Science Foundation and the U.S. Department of Energy.

The next step in this research is to make similar studies at different depths and locations to study the effects of temperature and chemical gradients on the genomes of microbial populations.

"How fast marine [microbes](#) adapt to environmental change is a big unknown," said Coleman, who is now a postdoctoral associate at Caltech. "One way to address this is to sample the population genomes over time, with parallel environmental monitoring. We might then be able to catch evolution in action. Long term study sites like HOT and BATS are crucial for this effort."

**More information:** "Ecosystem-specific selection pressures revealed through comparative population genomics," by Maureen L. Coleman and Sallie W. Chisholm, Proceedings of the National Academy of Sciences, 11 October, 2010. [www.pnas.org/content/early/2010/10/11/1009480107.abstract](http://www.pnas.org/content/early/2010/10/11/1009480107.abstract)

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