

# **Team probes mysteries of oceanic bacteria: Wee creatures are key to Earth's environment**

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Microbes living in the oceans play a critical role in regulating Earth's environment, but very little is known about their activities and how they work together to help control natural cycles of water, carbon and energy.

A team of MIT researchers led by Professors Edward DeLong and Penny Chisholm is trying to change that.

Borrowing gene sequencing tools developed for sequencing the human genome, the researchers have devised a new method to analyze gene expression in complex microbial populations. The work could help scientists better understand how oceans respond to climate change.

"This project can help us get a better handle on the specific details of how microbes affect the flux of energy and matter on Earth, and how microbes respond to environmental change," said DeLong, a professor of biological engineering and civil and environmental engineering.

"The new approach also has other potential applications, for example, one can now realistically consider using indigenous microbes as in situ biosensors, as well as monitor the activities of human-associated microbial communities much more comprehensively," DeLong said.

Their technique, which has already yielded a few surprising discoveries, is reported in the March 3 issue of the *Proceedings of the National*

*Academy of Sciences.*

The work was facilitated by the Center for Microbial Oceanography: Research and Education (C-MORE), a National Science Foundation Science and Technology Center established in 2006 to explore microbial ocean life, most of which is not well understood.

The traditional way to study bacteria is to grow them in Petri dishes in a laboratory, but that yields limited information, and not all strains are suited to life in the lab. “The cast of characters we can grow in the lab is a really small percentage of what’s out there,” said DeLong, who is research coordinator for C-MORE.

The MIT team gathers microbe samples from the waters off Hawaii, in a part of the ocean known as the North Pacific Gyre.

Each liter of ocean water they collect contains up to a billion bacterial cells. For several years, researchers have been sequencing the DNA found in those bacteria, creating large databases of prevalent marine microbial genes found in the environment.

However, those DNA sequences alone cannot reveal which genes the bacteria are actually using in their day-to-day activities, or when they are expressing them.

“It’s a lot of information, and it’s hard to know where to start,” said DeLong. “How do you know which genes are actually important in any given environmental context?”

To figure out which genes are expressed, DeLong and colleagues sequenced the messenger RNA (mRNA) produced by the cells living in complex microbial communities. mRNA carries instructions to the protein-building machinery of the cell, so if there is a lot of mRNA

corresponding to a particular gene, it means that gene is highly expressed.

The new technique requires the researchers to convert bacterial mRNA to eukaryotic (non-bacterial) DNA, which can be more easily amplified and sequenced. They then use sequencing technology that is fast enough to analyze hundreds of millions of DNA base pairs in a day.

Once the sequences of highly expressed mRNA are known, the researchers can compare them with DNA sequences in the database of bacterial genes and try to figure out which genes are key players and what their functions are.

The team found some surprising patterns of gene expression, DeLong said. For example, about half of the mRNA sequences found are not similar to any previously known bacterial genes.

Source: Massachusetts Institute of Technology

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