

## 'Coinage' of plankton -- viruses

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Sea experiments show there's a constant shuffling of genetic endowments among tiny plankton, say Massachusetts Institute of Technology researchers.

New evidence from open sea experiments shows there's a constant shuffling of genetic endowments going on among tiny plankton, and the "coinage" they use seems to be a flood of viruses, MIT scientists report.

The research, led by MIT Professor Sally W. Chisholm, is uncovering a challenging new facet of evolution, helping scientists see how photosynthesizing microbes manage to exploit changing conditions such as altered light, temperature and nutrients.

The work was reported in two articles in the March 24 issue of *Science*.

As a result of the new findings, "we are beginning to get a picture of gene diversity and gene flow in the most abundant photosynthetic cell on the planet, the Prochlorococcus group of planktonic microbes," said Chisholm, the Lee and Geraldine Martin Professor of Environmental Studies.

These photosynthesizing bacteria "form an important part of the food chain in the oceans, supply some of the oxygen we breathe, and even play a role in modulating climate. So it's very important that we understand what regulates their populations. And now genetic diversity seems to be an important factor," said Chisholm, who holds appointments in the Department of Civil and Environmental Engineering

(CEE) and in the Department of Biology.

In one of the journal reports, Chisholm and lead author Maureen I. Coleman, a CEE graduate student, suggest that gene-swapping in ocean microbes resembles the flow of genes already known to occur among disease-causing bacteria. In an ocean context, this exchange mechanism would offer marine microbes a diverse palette of potential gene combinations, each of which might be best suited for a particular environment. This should allow the overall population to persist despite complex and unpredictable environmental changes.

"We postulate that lateral gene transfer ... is an important mechanism for local specialization in the oceans," they wrote in *Science*. Eventually the scientists hope to provide a unified understanding of genomic evolutionary mechanisms and their impact on microbial ecology in the oceans.

The other paper from Chisholm's laboratory (lead authors are Zackary I. Johnson, now at the University of Hawaii, and Erik Zinser, now at the University of Tennessee), compares six known ecotypes, or subdivisions, of the *Prochlorococcus* microbes according to where they're found and under what conditions they thrive. Their geographic patterns suggest causal relations with environmental variables such as temperature, predators, light and nutrients.

Remarkably, despite centuries of oceanic research, tiny *Prochlorococcus* wasn't even known to exist two decades ago. It was discovered in 1985 during an open ocean research cruise by Rob Olson of the Woods Hole Oceanographic Institution and Chisholm.

Since then the science has progressed dramatically, and Chisholm can now describe *Prochlorococcus* in detail as "the smallest photosynthetic machine. It can convert the sun's energy into food through

photosynthesis using only 1,700 genes, something the human body cannot do with 30,000 genes. In fact, despite all of our technological ingenuity, we cannot even mimic this process."

Chisholm, who is co-director of MIT's Earth System Initiative, explained that as biological oceanographers she and her colleagues are trying to understand the bio-geo-chemistry of the oceans. That is, they're trying to learn "how these microbes function as a system in which they have not only co-evolved with each other, but also with the chemistry and physics of the oceans. These three - chemistry, physics and biology - are tightly linked as a system, meaning you can't change one without altering the other two."

Such work is based on the discovery that seawater is absolutely loaded with invisible microbes. In trying to understand how this microbial system works, the MIT team has focused on *Prochlorococcus* as a model.

The team's studies are showing that all *Prochlorococcus* strains "are very closely related, yet they display quite an array of physiologies, and astounding genetic diversity on top of that," Chisholm said. It's becoming clear, too, that "this genetic diversity is at the heart of the extraordinary stability of *Prochlorococcus* in the oceans, which maintains steady population sizes over vast regions" of the sea.

The collective *Prochlorococcus* community merely adjusts internally, with different groups (genome types) waxing and waning in relative abundance, depending on who is most fit under ever-changing circumstances.

But how do they do it?

"We decided to let the cells tell us what is most important to them" by

doing a systematic survey of relative abundances among six different types, or clades, of *Prochlorococcus* across vast environmental gradients in the oceans, Chisholm said. "We found first that two clades are orders of magnitude more abundant than all of the rest, and that temperature appeared to be very important in determining their distributions." Subsequent laboratory experiments with the cultured strains confirmed this idea.

Further analysis showed that most of the genetic differences between the two super-abundant strains are concentrated in a few "genomic islands," small zones where different kinds of genes get swapped in and swapped out, known among molecular geneticists as "hot spots" for gene exchange.

The distributors or carriers of new genes, they suspect, are the massive numbers of viruses also known to exist in seawater, some of which are adept at infecting ocean microbes such as *Prochlorococcus*. Such viruses, which carry genes of their own and sometimes transport odd genes picked up from an earlier host, are the most likely means of exchange - a natural way to get genes out of old cells and into new ones.

In essence, what all this means is that "our image of ocean microbes and their role in planetary maintenance is changing," Chisholm said. "We no longer think of the microbial community as being made up of species that have a fixed genetic makeup. Rather, it is a collection of genes, some of which are shared by all microbes and contain the information that drives their core metabolism, and others that are more mobile, which can be found in unique combinations in different microbes.

"So it is these unique combinations of genes that create the diversity we see, and which allow microbes to flourish in all environments on Earth," she added. "And if we can understand the details of this phenomenon in *Prochlorococcus*, the simplest free-living organism, it should be very

helpful toward understanding the diversity in all of life."

Additional MIT authors of the *Science* papers are Allison Coe, Nathan P. McNulty, Matthew S. Sullivan, Adam C. Martiny, Claudia Steglich (now at University Freiberg, Germany), and Professor Edward F. DeLong. Collaborators E. Malcolm S. Woodward and Kerrie Barry are from the Plymouth Marine Lab (U.K.) and the Department of Energy's Joint Genome Institute.

Source: MIT

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