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Microbe's Genome Reveals Insights Into Ocean Ecology Local Baltimore Scientist's work highlighted in Nature Magazine

A new study uncovers unexpected findings about the genetic makeup of a marine microbe, and has given scientists a new perspective on how bacteria make a living in the ocean – a view that may prove useful in wider studies of marine ecology. By deciphering and analyzing the DNA sequence of *Silicibacter pomeroyi*, a member of an important group of marine bacteria, scientists have found that the metabolic workings of marine bacteria are more diverse and less conventional than previously thought.

The study, which appears in the December 16 issue of *Nature*, was a collaborative effort among scientists from the University of Maryland Biotechnology Institute's Center of Marine Biotechnology together with lead researchers at the University of Georgia's (UGA) Department of Marine Sciences and The Institute for Genomic Research (TIGR) in Rockville, MD. The project was sponsored by the National Science Foundation, and led by UGA's Dr. Mary Ann Moran and by TIGR's Assistant Investigator Dr. Naomi Ward, along with collaborators that included: Dr. Ron Kiene of the University of South Alabama; Dr. Gary King of the University of Maine; Dr. Clay Fuqua of Indiana University; Dr. Robert Belas of the University of Maryland Biotechnology Institute's Center of Marine Biotechnology, and Dr. José González of the University of La Laguna, Spain.

In one surprise, the study found that *S. pomeroyi* has the genetic tools to enable it to use inorganic compounds (such as inorganic sulfur and carbon monoxide) for energy, which allows the microbes to use scarce resources more efficiently in low-nutrient ocean environments. *S. pomeroyi*, is a member of an important group of marine microbes, the Roseobacter clade, found in both coastal and open oceans. Those bacteria account for an estimated 15 percent of the production of new microbial cells in the ocean.

"This is a prime example of how using tools of genomics enables us to understand how abundant marine microbes contribute to nutrient and energy cycles in the open ocean," said Dr. Yonathan Zohar, Director of UMBI's Center of Marine Biotechnology. "These microbial processes contribute not only to marine life, but also to our atmosphere, the global climate, and life on earth."

Further analysis of the genome sequence also showed that the microbe has adapted in ways that allow it to take advantage of so-called ocean "hot spots" – microscopic areas of the ocean that are rich in organic matter, typically associated with living and dead cells, of other microbes, such as phytoplankton and dinoflagellates. "The interaction of Roseobacter clade bacteria with dinoflagellates, some of which are the causative agents of "red tides", also known as harmful algal blooms, is important because an analysis of the *S. pomeroyi* genome has revealed genes that may be important for the interaction between *S. pomeroyi* and the dinoflagellate cells," said Dr. Belas. Research into the nature of *S. pomeroyi* genes "could

ultimately lead to more effective means to control harmful algal blooms in the ocean and in the Chesapeake Bay.”

The *Nature* paper’s first author, Mary Ann Moran, says the DNA sequence sheds new light on ecological strategies that sustain microbial life in the world’s oceans. “This genome is especially significant for the new theories it will generate about the workings of the ocean,” Moran said. “It provides ideas and tools for investigating how microbes control carbon, sulfur, and nitrogen cycling on a global scale.”

The *S. pomeroyi* genome offers the first real glimpse at the genetic material harbored by the Roseobacter group of bacteria, which have evolved metabolic strategies that allow them to flourish in marine environments. While scientists knew from laboratory studies that the microbe could metabolize sulfur, the genome sequence offered several surprises about how bacteria make a living in the ocean.

The genomic analysis showed evidence of “lithoheterotrophy,” the ability of marine bacteria that typically rely on organic carbon fixed by primary producers as their source of cell material to also use inorganic compounds (carbon monoxide and sulfur, in this case) for energy. In that way, the microbes can save more of the organic compounds for biosynthetic processes – allowing more efficient use of organic carbon in an environment that has relatively little to go around.

“The microbe’s predicted ability to use such inorganic compounds was surprising,” said Dr. Ward of TIGR. “This study demonstrates how genome analysis allows us to propose new hypotheses of biological activity for a well-studied organism. We were able to test and confirm some of those hypotheses in the lab, providing more evidence for this lithohetrotropic strategy.”

The genomic analysis also confirms experimental evidence that *S. pomeroyi* swims through the oceans aided by flagella, which act like propellers. “In most motile bacteria, a set of evolutionarily conserved proteins is used to control the rotation of flagella in a behavior known as chemotaxis”, said Dr. Belas. “However, the genome of *S. pomeroyi* lacks the genes to make these conserved proteins, suggesting that chemotaxis of *S. pomeroyi* is controlled by an unknown mechanism. This is both unusual and potentially important to understanding how these bacteria interact with dinoflagellates. In other words, this microbial organism is able to sense and smell its food and move towards it without having the typical proteins needed by other microbes to perform the same task. Suggesting, that this microbe has a brand new way of sensing food and moving towards it. It is likely this is an adaptation, through evolution, that has allowed this microbe to live in a nutrient-limited environment. Better understanding this microbe and how it functions, may lead to interesting new discoveries as to how nutrient poor waterways continue to support life. And, these applications, could actually help us better understand the life of the Chesapeake Bay as well as the open ocean.”

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Dr. Robert Belas, a native of Plantsville, Connecticut, currently resides in Catonsville, Maryland. He received his Ph.D. in Microbiology from the University of Maryland College Park in 1981 and is an Associated Professor at UMBI’s Center of Marine Biotechnology since 1989. His area of expertise is in microbial genetics, cell to cell communication, and sensory transduction with emphasis on how regulation of gene

expression helps microorganisms adapt to a changeable environment. To learn more about UMBI and its Center of Marine Biotechnology, visit www.umbi.umd.edu