

New Carbon-Fixation Pathway Unveiled in Ocean Depths



Understanding the flow and processing of carbon in the world's oceans, which cover 70 percent of Earth's surface, is central to understanding global climate cycles, with many questions remaining unanswered. Between 200 and 1,000 meters below the ocean surface exists a "twilight zone" where insufficient sunlight penetrates for microorganisms to perform photosynthesis. Despite this, it is known that microbes resident at these depths capture carbon dioxide that they then use to form cellular structures and carry out necessary metabolic reactions so that they can survive and reproduce.

Details are now emerging about a microbial metabolic pathway that helps solve the mystery of how certain bacteria do this in the dark ocean. These research results, which are enabling a better understanding of what happens to the carbon that is fixed in the oceans every year, were published by a team of researchers, including those from the U.S. Department of Energy (DOE) Joint Genome Institute (JGI), in the Sept. 2, 2011 edition of *Science*.

Carbon fixation in the dark ocean has so far been attributed primarily to the Archaea, single-celled organisms that often live in extreme environmental conditions. In this region of the ocean, the bacteria living there were thought to rely on organic compounds for both energy and carbon. According to DOE JGI collaborator Ramunas Stepanauskas, Director of the Bigelow Laboratory Single Cell Genomics Center and senior author of the *Science* paper, "Previous oceanographic models suggested that Archaea do not adequately account for the amount of carbon that is being fixed in the dark ocean. Our study discovered specific types of Bacteria rather than Archaea, and their likely energy sources that may be responsible for this major, unaccounted component of the dark ocean carbon cycle."

To overcome the challenge that had hindered studies of deep ocean microbes, which have not yet been cultivated in the laboratory, researchers employed innovative single-cell genomics techniques, where DOE JGI's Tanja Woyke and Alexander Sczyrba, Bigelow Laboratory's Ramunas Stepanauskas

and their teams are among the pioneers. Study co-author Woyke explained, "After we sequenced the genomes of single cells that were isolated by our colleagues at Bigelow, it was possible to verify the predominant bacterial lineages capable of trapping carbon in this deep underwater region. "This study represents a pristine example for the use of single cell genome sequencing to decipher the metabolic capabilities of uncultured natural microbial consortia, providing a powerful complement to metagenomics."

Stepanauskas attributed the success of the project to the combined efforts of the DOE JGI, the Bigelow Laboratory, the Monterey Bay Aquarium Research Institute, the University of Vienna, and MIT. "This is the first application of a single-cell genomic approach to the deep ocean, one of the largest and least known biomes on the planet," emphasized David Kirchman, Harrington Professor of Marine Biosciences at the University of Delaware. "The paper radically changes our view about how microbes gain energy and flourish in the oceans."