

Hydrothermal vents: Hot spots of microbial diversity

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Thousands of new kinds of marine microbes have been discovered at two deep-sea hydrothermal vents off the Oregon coast by scientists at the MBL (Marine Biological Laboratory) and University of Washington's Joint Institute for the Study of Atmosphere and Ocean.

Their findings, published in the October 5 issue of the journal *Science*, are the result of the most comprehensive, comparative study to date of deep-sea microbial communities that are responsible for cycling carbon, nitrogen, and sulfur to help keep Earth habitable.

Using a new analytical technique called "454 tag sequencing," the scientists surveyed one million DNA sequences of bacteria and archaea, two of the three major domains of life. The DNA was taken from samples collected from two hydrothermal vents on the Pacific deep-sea volcano, Axial Seamount.

The researchers discovered that while there may be as few as 3,000 different kinds of archaea at these sites, the bacteria exceed 37,000 different kinds.

"Most of these bacteria had never been reported before, and hundreds were so different from known microbes that we could only identify them to the level of phylum," says lead author, Julie Huber of the MBL.

"Clearly, additional sampling of these communities will be necessary to determine the true diversity."

The research also revealed that the microbial population structures differed between vent sites due to their different geochemical environments. The ability to link environmental characteristics with microbial population structures using 454 tag sequencing allows scientists to assess how natural and manmade environmental changes are affecting diverse habitats on Earth.

Until now, microbiologists have had limited tools for assessing microbial populations and diversity. The MBL's 454 tag sequencing strategy is an important contribution to the young science of metagenomics, which seeks to characterize communities of organisms through genomic analysis. While other metagenomic studies look at all the genes in an environmental sample, such as a bucket of seawater or scoop of sediment, 454 tag sequencing examines one tiny, highly variable region of one gene that all microbes have (the 16s rRNA gene). It is much more efficient and cost effective than other environmental microbial survey tools.

“The tremendous diversity we found using 454 tag sequencing suggests that even the largest metagenomic surveys--which capture only the most highly abundant taxa-- inadequately represent the full extent of microbial diversity,” says MBL scientist David Mark Welch, one of Huber's co-authors. “Even with tag sequencing, statistical tests of our data suggest we still only sampled about half of the total number of species that were actually present.”

The new findings also underscore just how daunting understanding marine microbial diversity is. “This research demonstrates that surveys of hundreds of thousands of sequences will be necessary to capture the vast diversity of microbial communities, and that different patterns in evenness for both high and low-abundance taxa may be important in defining microbial ecosystem dynamics,” says Mitchell Sogin, director of the MBL's Josephine Bay Paul Center for Comparative Molecular

Biology and Evolution.

This research is part of the ongoing International Census of Marine Microbes, a massive effort to inventory the world's marine microbial diversity. It is also part of a major MBL initiative to study microbial ecology and evolution to understand how microbial communities are evolving in response to natural and human-induced environmental changes.

Source: Marine Biological Laboratory

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