

Driving evolution: Sequencing of ocean microbiome shows nutrient limitation plays key role

Microbes dominate the planet, especially the ocean, and help support the entire marine food web. In a recent report published in *Nature Microbiology*, University of Hawai'i at Mānoa (UHM) oceanography professor Ed DeLong and his team report the largest single-site microbiome gene catalog constructed to date. With this new information, the team discovered nutrient limitation is a central driver in the evolution of ocean microbe genomes.

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Water samples were collected over two years, and modern [genome](#) sequencing technologies were used to decode the genes and genome...

"In surface waters, [microbial genomes](#) are much smaller, and their proteins contain less nitrogen—a logical adaptation in this nitrogen-starved environment," said Daniel Mende, post-doctoral researcher at the UHM School of Ocean and Earth Science and Technology (SOEST) and lead author on the paper...

"These results suggest that the availability of nutrients in the environment may actually shape how microbial genomes and proteins evolve in the wild," said DeLong.

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"These new data will provide an important tool for understanding the nature and function of the [ocean's](#) microbiome today, as well as help predict its trajectory into the future," said DeLong.

The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion, and analysis. Read full, original post: [New gene catalog of ocean microbiome reveals surprises](#)