Genetic survey sheds light on Oceans' lean, mean microbial machines

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Water and microbial samples being collected by UBC researchers along Line P, a 1,425 kilometer (885 mile) survey line in the Northeast subarctic Pacific Ocean, originating in the coastal fjord Saanich Inlet, British Columbia and terminating at Ocean Station Papa on the southeast edge of the Alaskan Gyre. For over 50 years, hydrographic data have been collected along Line P, making it one of the longest running time-series in the global ocean. Credit: Jody Wright, Kendra Moss (Hallam Lab, University of British Columbia).

Planktonic bacteria inhabiting the world's oceans have streamlined their genetic makeup to become lean, mean survival machines, according to new research by an international team of researchers, including microbiologists at the University of British Columbia.

The findings, published this week in the *Proceedings of the National Academy of Sciences*, is the first direct evidence of widespread genome reduction—organisms evolving to cast off superfluous genes and traits in favor of simpler, specialized genetic make-ups optimized for rapid growth.

"Microbes are the dominant form of life on the planet and comprise a huge proportion of the oceans' biomass, but we know next to nothing about how populations exist, evolve and interact outside of the lab," says UBC microbiologist Steven Hallam, Canada Research Chair in Environmental Genomics and author on the paper.

"This widespread, signal cell genome sequencing of marine bacteria in the surface ocean has uncovered a surprising amount of metabolic specialization. This tendency toward genome reduction has profound implications for how microbial communities develop metabolic interactions that couple nutrient and energy flow patterns in the ocean. It could be a matter of survival of the most connected."

Says Ramunas Stepanauskas, director of the Bigelow Single Cell Genomics Centre and the paper's lead author: "We found that natural bacterioplankton are devoid of 'genomic pork' such as gene duplications and noncoding nucleotides, and utilize more diverse energy sources than previously thought."

Credits: Jody Wright, Kendra Moss (Hallam Lab, University of British Columbia).

Samples of planktonic bacteria were targeted from the Gulf of Maine, the Mediterranean, the South Atlantic and other sites. Data from northeast subarctic Pacific samples—taken over a six year period from the waters between Saanich Inlet and Ocean Station Papa along the Department of Fisheries and Oceans Line P transect was provided by Hallam's team.

More information: Prevalent genome streamlining and latitudinal divergence of planktonic bacteria in the surface ocean, www.pnas.org/cgi/doi/10.1073/pnas.1304246110

Provided by University of British Columbia