

New model reveals adaptations of world's most abundant ocean microbe

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Prochlorococcus, the most abundant photosynthetic microbe on the planet, is found in the Pacific Ocean (shown) and around the globe. Credit: Tara Clemente, University of Hawaii SOEST

Researchers from David Karl's laboratory at the University of Hawai'i at



Mānoa (UHM) and from Professor Jens Nielsen's laboratory at Chalmers University of Technology in Göteborg, Sweden, developed a computer model which takes into account hundreds of genes, chemical reactions, and compounds required for the survival of *Prochlorococcus*, the most abundant photosynthetic microbe on the planet. They found that *Prochlorococcus* has made extensive alterations to its metabolism as a way to reduce its dependence on phosphorus, an element that is essential and often growth-limiting in the ocean.

Revolutionary developments in <u>gene sequencing technology</u> have allowed scientists to catalog and investigate the genetic diversity and metabolic capability of life on Earth—from *E. coli* bacteria to humans, and much in between. Ocean monitoring and advances in oceanographic sensors have enabled a more detailed look than ever before at the environmental conditions that are both the consequence of microbial activity and act as stressors on the growth of microbes in the ocean.

This new metabolic model represents a window to the inner workings that enable microbes to dominate Earth's chemical and biological cycles, thrive in the harshest conditions, and make the planet habitable—a black box, in a sense.

Microbes are known to employ three basic strategies to compete for limiting elemental resources: cell quotas may be adjusted, stressed cells may synthesize molecules to make more efficient use of available resources, and cells may access alternatives or more costly sources of the nutrient.

In the case of phosphorus, a limiting resource in vast oceanic regions, the cosmopolitan *Prochlorococcus* thrives by adopting all three strategies and a fourth, previously unknown strategy.

"By generating the first detailed model of metabolism for an ecologically



important marine microbe, we found that *Prochlorococcus* has evolved a way to reduce its dependence on phosphate by minimizing the number of enzymes involved in phosphate transformations, thus relieving intracellular demands" said John Casey, an oceanography doctoral candidate in the UHM School of Ocean and Earth Science and Technology and lead author of the recently published study.

Prochlorococcus has an extremely minimal genome. If it were to lose the function of any one metabolic gene, its survival would be nearly a coin toss. To their surprise, Casey and co-authors discovered that the world's most abundant microbe has performed, through a process called "genome streamlining"—the concerted loss of frivolous genes over evolutionary time—a comprehensive re-design of the core metabolic pathways in response to the persistent limitation of phosphorus.

"The dramatic and widespread change in the metabolic network is really a shock," said Casey. "However, we're seeing that these changes provide a substantial growth advantage for this ubiquitous microbe in phosphoruslimited regions of the ocean, so it seems that where there's a will there's a way."

The computer model is built from an enormous library of genetic data compiled from researchers around the world, and the results are validated with data from numerous laboratory culture experiments and field studies.

"We're interested in the underlying principles guiding metabolism and physiology in marine microbes, and that is going to require a deep understanding of not only the 1-dimensional genetic code, but also the 4-dimensional product it codes for," said Casey. "So we're looking to a systems-level approach to incorporate a great variety of physiological and 'omics studies all in one computational structure, with the hope that we can start to learn from the design and interactions of these complex



systems."

In the future, the researchers plan to expand the model to include more representatives of the marine microbial community and to look deeper into micro-diversity within the *Prochloroccocus* genus.

"This will allow us to simulate marine microbial community metabolism at an unprecedented level of detail; embedding these fine-scale simulations within <u>global ocean circulation</u> models promises to deliver insights into how microbial assemblages interact with their environment and amongst each other," said Casey.

More information: *mSystems*, DOI: 10.1128/mSystems.00065-16

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