

Survival Mode

Oceanic microbial communities are optimized for nutrient uptake

Proteomics resources at the Department of Energy's EMSL were critical to pioneering research in which scientists, for the first time, measured protein expression in microbial communities from the Sargasso Sea. The insight afforded by this research into oceanic microbial communities is important because such bacteria heavily influence biogeochemical cycles, affecting the concentrations of elements such as carbon – and therefore the greenhouse gas, carbon dioxide – in the Earth's air, water, and soil.

The team from Oregon State University, Pacific Northwest National Laboratory, and the University of California conducted their experiments using a new proteomics technique, *metaproteomics*, which allows identification of proteins in mixed cultures even without a complete genome to help. Metaproteomics analyses revealed that the lion's share of peptides detected in Sargasso Sea microbial communities were unique to *Prochlorococcus*, *Synechococcus*, or SAR 11 (*Pelagobacter ubique*), which is one of the most abundant organisms on earth. Further, these bacteria have adapted to their harsh environment, in which they are subjected to damage by light and oxidative stress, by expressing an abundance of transport proteins for nutrient uptake. This mechanism allows them to sequester the very limited essential nutrients needed for their survival from the waters that surround them.

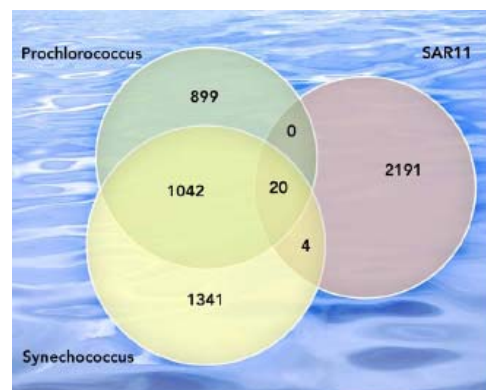
Scientific Impact: The team's work applies new proteomics methods to complex microbial community research and, furthermore, crosses the boundaries of many disciplines, connecting proteomics, microbiology, and climate research. In addition, these studies support EMSL's goal to predict biological functions from molecular and chemical data.

Societal Impact: Understanding how microbial communities use transport proteins to adapt to seasonal changes and fluctuations in the levels of atmospheric carbon yields insight into global carbon cycling and could help in the design of strategies to address global warming.

For more information, contact EMSL Communications Manager Mary Ann Showalter (509-371-6017).

Reference: Sowell SM, LF Wilhelm, AD Norbeck, MS Lipton, CD Nicora, DF Barofsky, CA Carlson, RD Smith, and SJ Giovanonni. 2009. "Transport Functions Dominate the SAR11 Metaproteome at Low Nutrient Extremes in the Sargasso Sea" *International Society for Microbial Ecology (ISME) Journal* 3:93-105. DOI:10.1038/ismej.2008.83

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A large proportion of the peptides detected in samples from the Sargasso Sea were unique to Prochlorococcus, Synechococcus, or SAR 11.