

Genome of marine organism reveals hidden secrets

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William Gerwick seeks marine organisms with biomedical potential in Papua New Guinea in 2006. Credit: Scripps Institution of Oceanography, UC San Diego

An international team of researchers led by scientists at Scripps Institution of Oceanography at UC San Diego has deciphered the genome of a tropical marine organism known to produce substances potentially useful against human diseases.

Tiny photosynthetic microorganisms called cyanobacteria are some of the oldest forms of life on the planet. At times their emergence as toxic blooms causes a threat to humans and animals. But despite the recognized capability of marine strains of the cyanobacterial genus *Lyngbya*, and specifically the species *L. majuscula*, to create hundreds of natural products with biomedical promise, surprisingly little is known about the genetics underlying their production.

In this week's online early edition of the [Proceedings of the National Academy of Sciences](#), a research team led by Scripps graduate student Adam Jones and postdoctoral fellow Emily Monroe, both in the Gerwick laboratory at Scripps Institution of Oceanography's Center for Marine Biotechnology and Biomedicine (CMBB), provide the first insights of the [genome](#) of *Lyngbya majuscula* 3L, a Caribbean organism that generates compounds that are being developed for potential treatment against cancer and [neurodegenerative diseases](#).

"These compounds have gained considerable attention due to their pharmaceutical and biotechnology potential, but they are also notorious for their environmental toxicity and threats to humans, wildlife and livestock," the authors note in their paper.

In the marine environment the wiry, or "filamentous," cyanobacteria play a vital role in the [global carbon cycle](#). *Lyngbya* strains are known to disrupt the healthy growth of [coral reefs](#) and are behind the agents responsible for a skin rash known as "swimmer's itch."

Achieving the first genomic sequencing of its kind for the filamentous *Lyngbya majuscula* 3L, the research team overcame several obstacles due to the organism's complex, intermeshed growth in the wild with a range of other bacteria, muddying a clear picture of the genome. The team undertook several different research tactics and experiments, including single cell genome amplification, protein and metabolite profiling.

The results revealed a complex gene network suggesting an enhanced ability of the organism to adapt to shifting conditions in the marine environment.

Sequencing was done at the Max Planck Institute in Berlin, Germany and at the J.Craig Venter Institute in Rockville, Maryland. Much of the

assembly was conducted by Sheila Podell, a project scientist in the Eric Allen laboratory at Scripps. Jones and Monroe traced the genomic pathways and performed tests to understand which genes encoded the production of different natural products.

Yet as much as the genome revealed about *Lyngbya majuscula* 3L, the researchers also uncovered key information about its limitations and shortcomings. For example, it's been assumed that *Lyngbya majuscula* 3L and its cousins in the *Lyngbya* genus convert, or "fix," nitrogen from the atmosphere into organic molecules, a fundamental natural process in the global environment. To their surprise, *Lyngbya majuscula* 3L lacks the genes necessary for nitrogen fixation, even though reports exist that this species fixes nitrogen.

"It's possible that strains of *L. majuscula* reported to fix nitrogen may have been misidentified because it is visually very similar to other filamentous cyanobacteria species and we found that this marine strain doesn't seem capable of fixing nitrogen on its own," said Monroe. "This feature could be a distinction between the freshwater and the marine strains of what is currently characterized as *Lyngbya*."



Adam Jones collects samples in Papua New Guinea. Credit: Scripps Institution of Oceanography, UC San Diego

And while marine *Lyngbya* strains are proven prolific generators of natural products with biomedical and pharmaceutical potential, the new study shows that more work is needed to pinpoint which species generates which natural products. Jones says that more than 250 compounds are attributed to marine *Lyngbya* strains. Of those, nearly three-quarters are linked to *Lyngbya majuscula*. However, the *Lyngbya majuscula* 3L strain was found to only produce a small number of natural products.

"This particular strain doesn't produce nearly as many (natural products) as we thought it might, which shows that many of the interesting molecules discovered to date are probably scattered among multiple organisms," said Jones. "The lesson learned is that not all marine

Lyngbya strains are created equal."

"This may change the way we start looking at things in the field and give us new ways to identify organisms," said Lena Gerwick, the faculty member who organized this genomic project from the beginning. "We might be able to turn things around and use the compounds they make as a new way of determining what kinds of species they are."

Provided by University of California - San Diego

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