

# Brown tide culprit sequenced: Genome of the first of algal bloom species

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This is an aerial view of Great South Bay, N.Y., during a brown tide bloom in June 2008. Billions of *A. anophagefferens* cells per liter crowded into the coastline and turned the water brown. Credit: Suffolk County Department of Health Services

Algae play key roles in the global carbon cycle, helping sequester significant amounts of carbon. Some algal species can bloom, or become so numerous, that they discolor coastal waters and reduce the amount of light and oxygen available in the ecosystem. Previously known as "red tide," the term "harmful algal blooms" (HABs) was introduced two decades ago to note accumulation of algal biomass can sometimes also turn the ocean waters brown or green and disrupt an ecosystem, or that red-colored waters can sometimes be harmless.

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[National Academy of Sciences](#), a team of researchers including U. S. Department of Energy (DOE) Joint Genome Institute (JGI) scientists led by Igor Grigoriev, reported the first complete and annotated genome sequence of a HAB species: *Aureococcus anophagefferens*.

At first glance the marine phytoplankton, so tiny that 50 of them side by side span the width of a single human hair, seems innocuous. "It's a photosynthetic organism that plays a big role in carbon cycling, particularly in coastal ecosystems, and can degrade organic carbon," noted first author Christopher Gobler of Stony Brook University. "When one of these blooms occurs and you get a billion cells per liter, it represents milligrams of carbon per liter, which is much higher than you typically see in coastal ecosystems." By sequencing its genome, or biological source code, scientists can examine its "parts list" for clues to *Aureococcus*' ability to capture CO<sub>2</sub>, survive in varying marine environments, exploit selenium in its proteins, and outgrow many of its competitors.

The 56-million base pair genome of *Aureococcus* was sequenced by the DOE JGI from a culture isolated sample collected from the shores of Long Island, NY, one of the areas most affected by the microalga when it first appeared 25 years ago on the east coast of the United States.

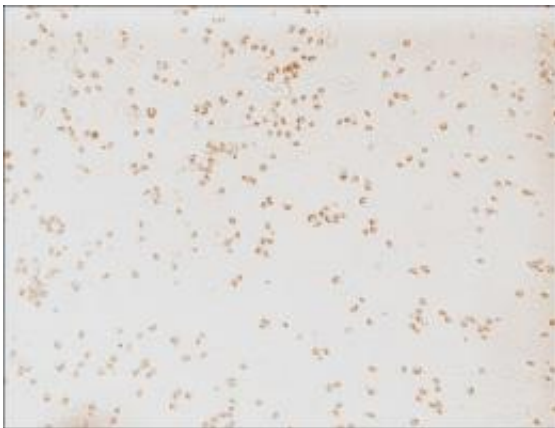
When billions of *Aureococcus* cells come together, however, they outcompete the other marine phytoplankton in the area, damaging the food chains in marine ecosystems as well as economically impacting the shellfish industry. Economic losses attributed to this and other HAB phenomena in the United States over the course of the last decade have been estimated at one billion dollars.

"In the decade since publishing the draft of the human genome, JGI has pioneered the exploration of marine algal genomics with sequences of the first diatoms, *Ostreococcus* and cyanobacteria," said Grigoriev.

"Compared to these phytoplankton inhabiting the same estuaries, *Aureococcus*, which outcompetes them, shows genome-encoded advantages to benefit from alternative nutrients, survive under variable light conditions, and encode the largest number of selenoproteins (which use the trace element selenium to perform essential cell functions) known to date."

Gobler elaborated on how *Aureococcus* can outcompete the other phytoplankton in a coastal estuary. "When we looked at the coastal ecosystems where we find *Aureococcus* blooms, we found they were enriched in organic matter, were very turbid and enriched in trace metals," he said. "And when we looked at the genome of *Aureococcus*, it ended up being enriched in genes to take advantage of these conditions. The surprise was the concordance between the genome and the ecosystem where it's blooming."

For example, this photosynthetic microalga is well-adapted to low light, and can survive for long periods in no-light conditions. The genomic study revealed that *Aureococcus* had 62 light-harvesting genes whereas its competitors had on average a couple of dozen of these genes.



These are the *Aureococcus anophagefferens* cells of a harmful algal bloom brown tide. Credit: Chris Gobler, Stony Brook University

"I think this paper says it all," said Don Anderson, a senior scientist at Woods Hole Oceanographic Institution who has studied harmful algal blooms for decades and is a tireless promoter of research efforts in this field. "For decades, scientists have been trying to understand why this species blooms, when it blooms, how it is able to dominate when there are so many other competing species in the water with it. With this new genomic data we have a new approach. We're getting answers based on the genes, though we still need other approaches that collect relevant oceanographic and chemical data to go along with the inferences drawn from the presence and absence of genes. It's a great advance - a great resource for our community. Even though there are major differences among HAB species, as we learn about *Aureococcus* with this approach, that knowledge will help us make similar advances with other HAB species."

Gobler said that one field of study that arose from the data involves these light-harvesting genes. "We know as a bloom occurs, the level of light in the estuary decreases gradually and becomes more turbid. Can we see the light-harvesting proteins expressed in *Aureococcus* turn on as a bloom occurs?" he asked. "Beyond gene expression, proteomics and looking at proteins synthesized during blooms are also other areas of future research to explore."

DOE JGI's Grigoriev also noted that the multidisciplinary approach of combining [genome](#) sequencing with other techniques allows researchers to explore a new area of ecogenomics, which is closely connected to the DOE mission in biogeochemistry. "Aligning the physico-chemical parameters of an ecosystem with the genomic potential of its inhabitants enables us to monitor changes in the environment. [Harmful algal blooms](#) are a recently reported phenomenon and could be connected to the growing human population along coastlines, which created conditions for

Aureococcus to thrive, in turn adversely affecting estuaries. On the other hand, massive algal blooms can reduce carbon dioxide in the atmosphere. So by employing the ecogenomics approach we can start building balanced models of targeted environments."

Gobler said that the work suggests a managerial next step. "We now know this organism is genetically predisposed to exploit certain characteristics of [coastal ecosystems](#). We also know the characteristics are there because of activities of man. If we continue to increase, for example, organic matter in coastal waters, then it's going to continue to favor brown tides since it's genetically predisposed to thrive in these conditions."

Provided by DOE/Joint Genome Institute

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