



A "brown tide" of harmful algae invades Moriches Bay, Long Island, in 2011.

Doug Kuntz

Harmful Algae Have the Right Genetic Stuff

Scientists from several institutions recently took a big step toward understanding the global rise in red and brown tides, the overwhelming blooms of harmful algae that cause environmental and economic damage in coastal waters. They analyzed the complete genome of the brown tide alga *Aureococcus anophagefferens*, the first harmful alga genome ever to be sequenced, and found that the alga has unique genes that may allow it to outcompete other marine phytoplankton in conditions that have been altered by human activities.

Specifically, *A. anophagefferens* has more genes than its competitors for metabolizing high levels of organic matter and toxic heavy metals from fertilizers and wastes found along heavily populated coastlines. It also has more genes to harvest light so it can survive for longer periods in murky estuaries clogged with organic matter.

"There are things it can do that the other algae can't, and those advantages are encoded at the genome level," said Sonya Dyrman, a biologist at Woods Hole Oceanographic Institution (WHOI). She and Louie Wurch, a graduate student in the MIT/WHOI Joint Program, were part of a multi-institution research group led by Chris Gobler of Stony Brook University that analyzed *A. anophagefferens* genes and compared them with other phytoplankton in the same estuaries.

A. anophagefferens produces opaque brown tides in U.S. East Coast estuaries and in South Africa. Unlike other harmful algae, they are not toxic to people, but they are environmentally devastating, blocking sunlight and killing sea-grass beds and commercial shellfish. No *A. anophagefferens* blooms were recorded

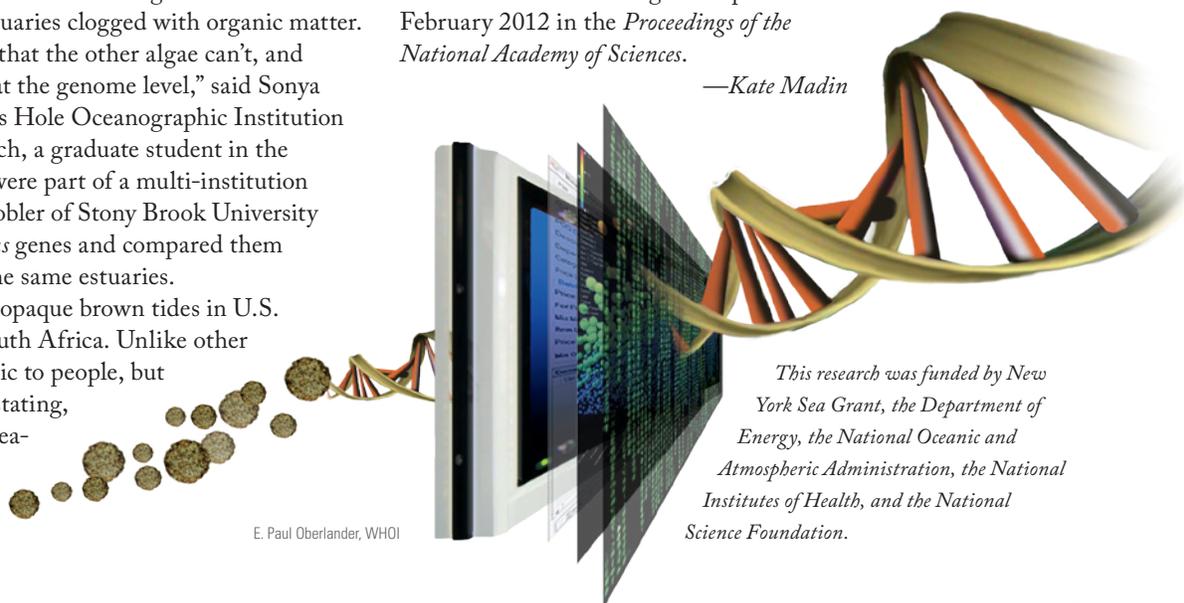
before 1985. Now they are annual summer events that cause severe losses to shellfisheries, especially in Long Island, N.Y. In 2007, the Department of Energy's Joint Genome Institute sequenced *A. anophagefferens*'s genome from cultured Long Island cells.

"It's really exciting to be able to apply these new tools and a molecular approach to old questions about how organisms are functioning and interacting with their environment," Dyrman said. "By looking at when the genes are transcribed through a bloom, we're hoping to provide the next piece in the puzzle—understanding what is fueling and causing the demise of blooms."

"It's incredible how much the technology has changed," Wurch said. "We couldn't do this when I first entered graduate school."

The scientists' findings were published in February 2012 in the *Proceedings of the National Academy of Sciences*.

—Kate Madin



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