

Natural algal population may explain how environmental changes affect global carbon cycles

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Transmission electron microscopy image of *Ostreococcus tauri* strain RCC4221.
Credit: Martin Hohmann-Marriott

Although they are invisible to the unaided eye, tiny green algae called *Ostreococcus* play a big role in how carbon, including carbon dioxide (CO₂), cycle through our world. Researchers have sequenced and analyzed the complete set of genes (the genome) of 13 members of a natural *Ostreococcus* population. The analysis revealed that the *O. tauri* population is larger than anticipated. It's also diverse in terms of its genetics and appearance. The algae's natural resistance to ocean viruses influenced the algae's diversity.

Ostreococcus is a model species to study [algae](#) in marine environments. Though microscopic, these picoplankton use sunlight together with CO₂ to create organic matter. The algae are significant primary producers (that is, they convert CO₂ into biomass). Thus, the algae contribute to the [global carbon cycle](#). This study offers insights into the genetic variability of various *Ostreococcus* strains. The results will help scientists see how environmental changes affect algae's ability to survive and thrive.

Picophytoplankton such as *Ostreococcus* are so small they are invisible to the naked eye. Despite their size, their global abundance means they are a widespread primary producer and form the bases of several [marine food webs](#). In coastal areas, they account for as much as 80 percent of the available biomass. A decade ago, the Joint Genome Institute (JGI), a U.S. Department of Energy (DOE) Office of Science user facility, sequenced one of the *Ostreococcus* strains. That genome, along with other genome sequences from three groups of the picophytoplankton

Ostreococcus, revealed the tiny algae's diversity and adaptation to different ecological niches around the world.

Now, a team led by researchers at the Oceanological Observatory of Banyuls, France, and including scientists at the DOE JGI, has resequenced and analyzed 13 members of a natural [population](#) of *Ostreococcus tauri* from the northwest Mediterranean Sea. The analysis offers a complete picture on the surprisingly large population and correspondingly high genetic and phenotypic diversity within *O. tauri* species. The team identified two large candidate mating type loci, consistent with the pervasive evidence of recombination and thus sexual reproduction within the population. The work reported in *Science Advances* was enabled in part by the DOE JGI's Community Science Program. A deeper understanding of algal genomic diversity and potential will help scientists track carbon (and nitrogen) traffic through marine ecosystems as well as provide insights into the structure and operation of algal plant communities.

More information: Romain Blanc-Mathieu et al. Population genomics of picophytoplankton unveils novel chromosome hypervariability, *Science Advances* (2017). [DOI: 10.1126/sciadv.1700239](https://doi.org/10.1126/sciadv.1700239)

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