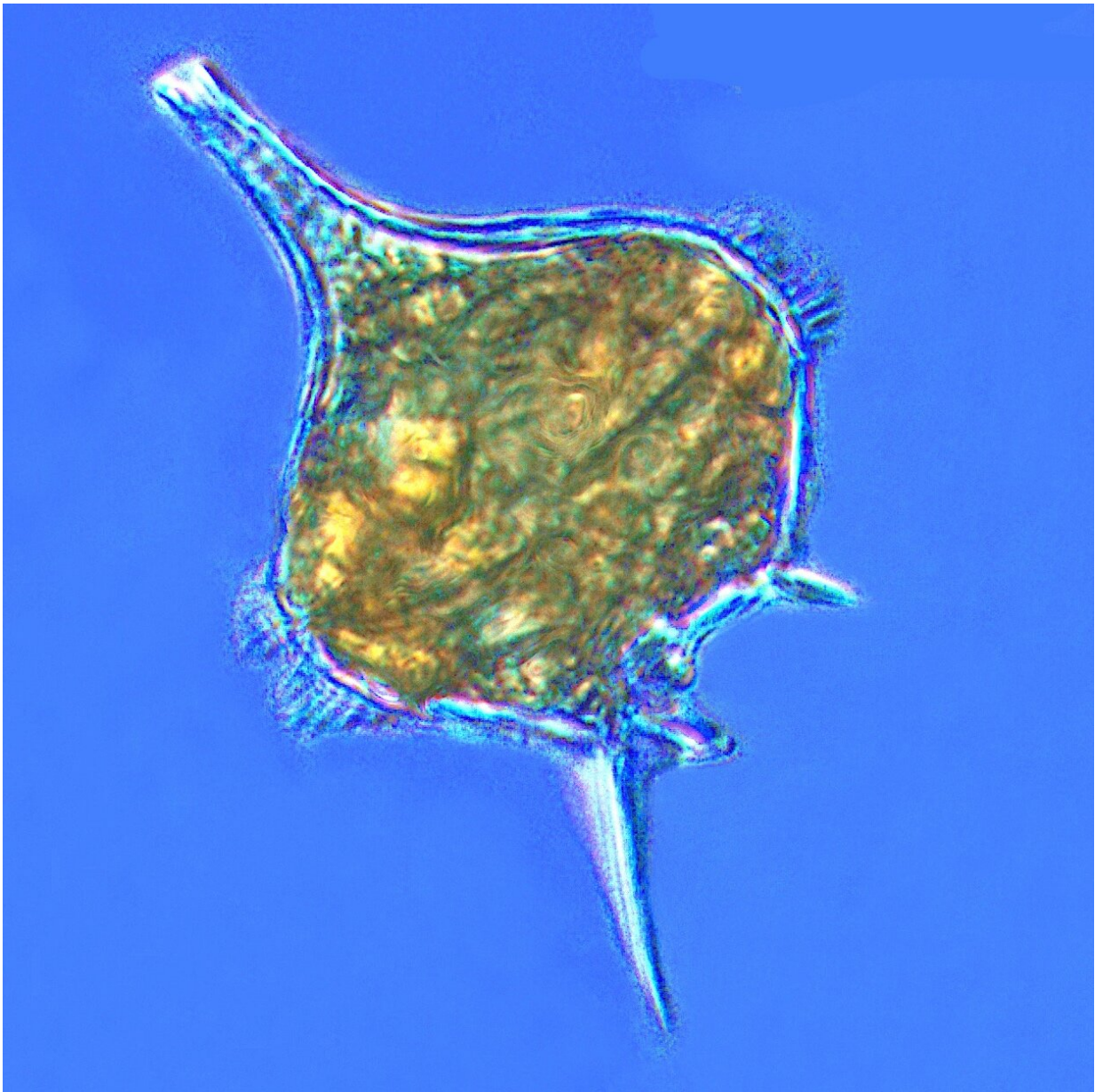


# Unraveling a mystery of dinoflagellate genomic architecture

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Microzooplankton, the major grazers of the plankton: spiny-globe  
Protozooidinium dinoflagellate. Credit: Wikimedia / Creative Commons  
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New work from a Stanford University-led team of researchers including Carnegie's Arthur Grossman and Tingting Xiang unravels a longstanding mystery about the relationship between form and function in the genetic material of a diverse group of algae called dinoflagellates.

Their findings, published in *Nature Genetics*, have implications for understanding genomic organizational principles of all organisms.

Dinoflagellates include more than 2,000 species of marine and freshwater plankton, many of which are photosynthetic, and some of which also ingest other organisms for food. They play a wide variety of roles in various ecosystems, including [extreme environments](#), and are predominantly known to humans as the cause of toxic "red tides" and as the source of most ocean bioluminescence.

Some photosynthetic dinoflagellates are also crucial to the health of coral reefs. These algae are taken up by individual coral cells and form mutually beneficial relationships through which nutrients are exchanged. Ocean warming and pollution can cause this relationship between the alga and animal to break down, resulting in ghostly white "bleached" corals that are at risk of starvation, which could lead to the death of reef ecosystems.

"Like animals and plants, dinoflagellates are complex eukaryotic organisms and are evolutionarily interesting because their [genetic material](#) is packaged in a way that is unique among organisms with complex [cellular architecture](#)," said lead author Georgi Marinov of

Stanford University.

One defining characteristic of eukaryotes is that their DNA is housed inside a nucleus within each cell and is organized as separate units called chromosomes. Furthermore, in most eukaryotes, segments of DNA are wound around a spool-like complex of proteins called a nucleosome. This organization is thought to predate the common ancestor of all eukaryotes. It helps to condense the genetic material into a small space and control access to the DNA and how the genes encoded in it are activated to direct the cell's physiological functions.

"By contrast, even though dinoflagellates are eukaryotes, their [genome](#) is not packaged as nucleosomes, but rather appears to be permanently condensed and exist in a liquid crystal state," Grossman explained. "We still have so much to learn about how genome architecture influences genome function in all eukaryotes; so, [dinoflagellate](#)'s exceptional 'tight' packaging of DNA may help us understand the similarities and differences in organizational principles among [eukaryote](#) genomes."

To delve into this question, the research team—which also included Stanford's Alexandro E. Trevino, Anshul Kundaje, and William J. Greenleaf—used sophisticated technology to map the 3D spatial relationships of the genetic material of the dinoflagellate *Breviolum minutum*.

"Our work revealed topological features in the *Breviolum* genome that differ from the various models of dinoflagellate genome organization that have been predicted since the 1960s," said Xiang.

They found evidence of large self-interacting regions of DNA in the dinoflagellate genome called "topologically associating domains." The work suggests that this genomic architecture is induced by the process by which genes are transcribed into RNA; this RNA is subsequently

translated into proteins that perform the cell's various activities.

In fact, when transcription was inhibited, the architecture 'loosened up,' indicating that the rigidly preserved topographical features are, indeed, a function of gene activity.

"There are many more questions raised by these results, which represent a big step forward in unraveling the mysteries of the dinoflagellate genome. They are also providing a new perspective on structure-function relationships inherent to chromosomes," Grossman concluded.

**More information:** Georgi K. Marinov et al, Transcription-dependent domain-scale three-dimensional genome organization in the dinoflagellate *Breviolum minutum*, *Nature Genetics* (2021). [DOI: 10.1038/s41588-021-00848-5](https://doi.org/10.1038/s41588-021-00848-5)

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