

# Macroalgae genetics study sheds light on how seaweed became multicellular

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A deep dive into macroalgae genetics has uncovered the genetic

underpinnings that enabled macroalgae, or "seaweed," to evolve multicellularity. Three lineages of macroalgae developed multicellularity independently and during very different time periods by acquiring genes that enable cell adhesion, extracellular matrix formation, and cell differentiation, researchers report in the journal *Molecular Plant*.

Surprisingly, many of these multicellular-enabling genes had viral origins. The study, which increased the total number of sequenced macroalgal genomes from 14 to 124, is the first to investigate macroalgal evolution through the lens of genomics.

"This is a big genomic resource that will open the door for many more studies," says co-first author and algal biologist Alexandra Mystikou of New York University Abu Dhabi and the Technology Innovation Institute, United Arab Emirates. "Macroalgae play an important role in global climate regulation and ecosystems, and they have numerous commercial and ecoengineering applications, but until now, there wasn't a lot of information about their genomes."

Macroalgae live in both fresh and seawater and are complex multicellular organisms with distinct organs and tissues, in contrast to microalgae, which are microscopic and unicellular. There are three main groups of macroalgae—red (Rhodophyta), green (Chlorophyta), and brown (Ochrophyta)—that independently evolved [multicellularity](#) at very different times and in very different environmental conditions. Rhodophytes and Chlorophytes both evolved multicellularity over a billion years ago, while Ochrophytes only became multicellular in the past 200,000 years.

To investigate the evolution of macroalgal multicellularity, the researchers sequenced 110 new macroalgal genomes from 105 different species originating from fresh and saltwater habitats in diverse geographies and climates.

The researchers identified several [metabolic pathways](#) that distinguish macroalgae from microalgae, some of which may be responsible for the success of invasive macroalgal species. Many of these metabolic genes appear to have been donated by algae-infecting viruses, and genes with a viral origin were especially prevalent in the more recently evolved brown algae.

They found that macroalgae acquired many new genes that are not present in microalgae on their road to multicellularity. For all three lineages, key acquisitions included genes involved in [cell adhesion](#) (which enables cells to stick together), [cell differentiation](#) (which allows different cells to develop specialized functions), cell communication, and inter-cellular transport.

"Many brown algal genes associated with multicellular functions had signature motifs that were only otherwise present in the viruses that infect them," says co-first author and bioinformatician David Nelson of New York University Abu Dhabi. "It's kind of a wild theory that's only been hinted at in the past, but from our data it looks like these horizontally transferred genes were critical factors for evolving multicellularity in the brown algae."

The team also identified other features that were distinct between the macroalgal lineages. They observed much more diversity between different species of Rhodophyte, which evolved multicellularity first and have thus had longer to diverge. They also found that Chlorophytes share many genomic features with [land plants](#), suggesting that these genes may have already been present in the last common ancestor of Chlorophytes and plants.

"By no means have we exhaustively explored all that there is in these genomes," says senior author and systems biologist Kourosh Salehi-Ashtiani of New York University Abu Dhabi. "There is a ton of

information that we have not touched in the present paper that can be mined by whoever who is interested."

The researchers are already digging into the dataset to investigate environmental and habitat adaptations among [macroalgae](#). In future, they hope to sequence and analyze even more macroalgal genomes.

"We want to explore some of these features in more detail, meaning more genomes if we can get our hands on them," says Salehi-Ashtiani.

**More information:** Macroalgal deep genomics illuminate multiple paths to aquatic, photosynthetic multicellularity, *Molecular Plant* (2024). DOI: [10.1016/j.molp.2024.03.011](https://doi.org/10.1016/j.molp.2024.03.011)

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