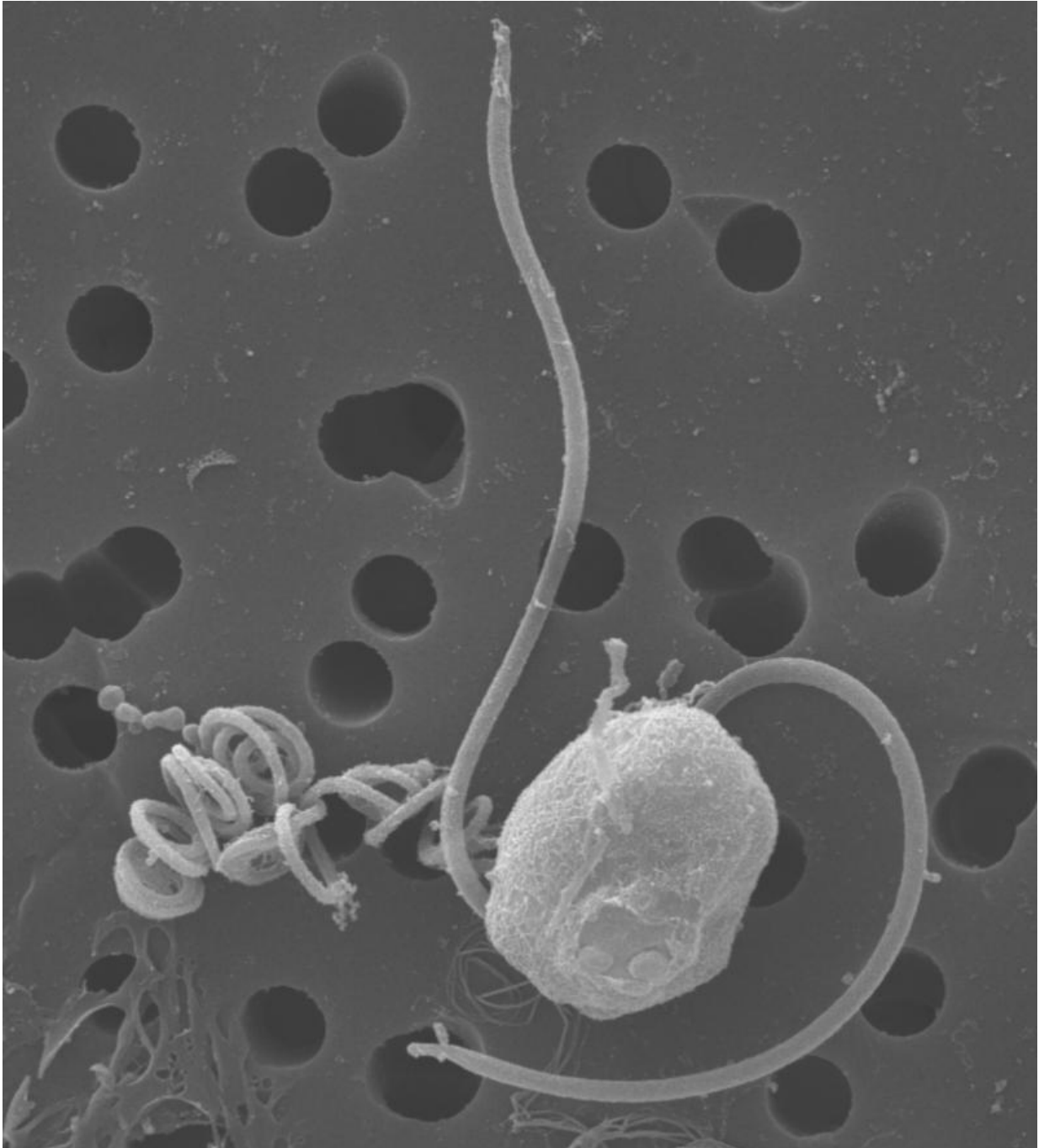


Sequencing algae's genome may aid biofuel production

November 19 2015, by James Urton



Close-up view of *Chrysochromulina tobin*. Credit: Rose Ann Cattolico

There's an ancient group of algae that evolved in the world's oceans

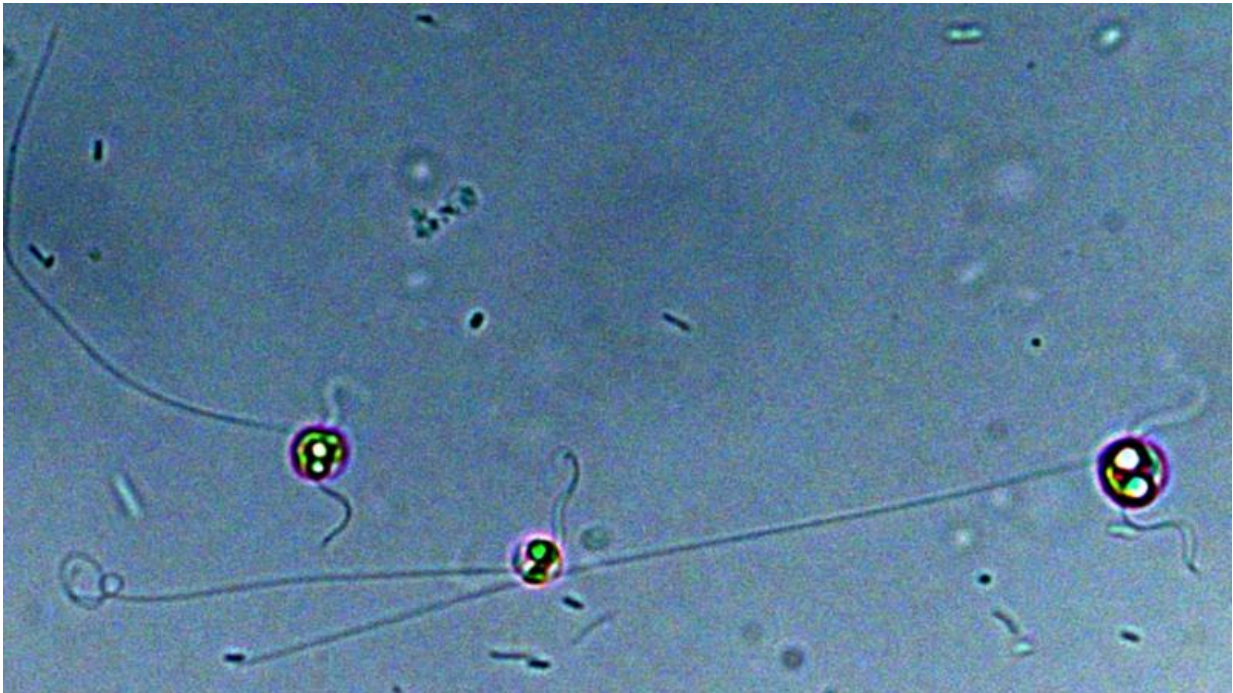
before our backboned ancestors crawled onto land. They are so numerous that their gigantic blooms can affect the weather, and they account for 30 to 40 percent of all photosynthesis in the world's oceans.

But until recently, scientists interested in these single-celled creatures knew next to nothing about their genes.

University of Washington scientists have sequenced the complete genetic makeup of one of these [algae](#). As they recently reported in the journal *PLOS Genetics*, it is only the second time that researchers have sequenced the genome of one of these ecologically important and plentiful algae, known as haptophytes. Researchers hope to better understand haptophytes and perhaps transform them into an important new tool for aquaculture, [biofuel production](#) and nutrition.

"Haptophytes are really important in carbon dioxide management and they form a critical link in the aquatic foodchain," said senior author and UW biology professor Rose Ann Cattolico. "This new genome shows us so much about this group."

The haptophyte Cattolico and her team studied is *Chrysochromulina tobin*, and it thrives in oceans across the globe. The researchers spent years on a series of experiments to sequence all of *Chrysochromulina*'s genes and understand how this creature turns different genes on and off throughout the day. In the process, they discovered that *Chrysochromulina* would make an ideal subject for investigating how algae make fat, a process important for nutrition, ecology and biofuel production.



Close-up view of *Chrysochromulina tobin*. Credit: Rose Ann Cattolico

"It turns out that their fat content gets high during the day and goes down during the night," said Cattolico. "A very simple pattern, and ideal for follow-up."

She believes that that these extreme changes in fat content—even within the span of a single day—may help ecologists understand when microscopic animals in the water column choose to feast upon these algae. But knowledge of how the algal species regulates its fat stores could also help humans.

"Algae recently became more familiar to the general populace because of biofuel production," said Cattolico. "We needed a simple alga for looking at fat production and fat regulation."

This led Cattolico to team up with Blake Hovde, then a graduate student in the UW Department of Genome Sciences, to sequence the complete genome of this species. Hovde wanted to work on algae in biofuel production, and *Chrysochromulina* was ideally suited for the task because, unlike most other haptophytes, it has no protective cell wall.

Hovde and Cattolico uncovered other surprises in the *Chrysochromulina* genome. Like other algae and plants, *Chrysochromulina* uses light to make food, through the process of photosynthesis. But they also found another gene, called xanthorhodopsin, that may let the alga harvest light and do work outside of the traditional photosynthesis pathway. Cattolico does not know how the alga uses this gene, but would like to investigate this in the future.

In addition, they identified numerous genes that appear to harbor antibiotic activity, which may be useful as the need for new antibiotics continues to rise. But *Chrysochromulina* is not universally against bacteria. Through this project, Cattolico and her team discovered that there are at least 10 bacterial species that appear to enjoy living near *Chrysochromulina*.

"That leads to some interesting questions," said Cattolico. "Is *Chrysochromulina* selectively using its antimicrobials? Is it 'farming' beneficial bacteria in its neighborhood?"

Cattolico would like to understand how these bacteria affect which genes *Chrysochromulina* switches on and off. That information may pave the way for new studies of the ecology of haptophytes, which could be critical in the face of a changing global climate.

"Haptophytes are very important to our ocean health, especially with these massive —sometimes toxic—blooms they make," said Cattolico. "We need to understand this issue because ecosystems are only going to

get more compromised with climate change."

More information: Blake T. Hovde et al. Genome Sequence and Transcriptome Analyses of *Chrysochromulina tobin*: Metabolic Tools for Enhanced Algal Fitness in the Prominent Order Prymnesiales (Haptophyceae), *PLOS Genetics* (2015). [DOI: 10.1371/journal.pgen.1005469](https://doi.org/10.1371/journal.pgen.1005469)

Provided by University of Washington

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