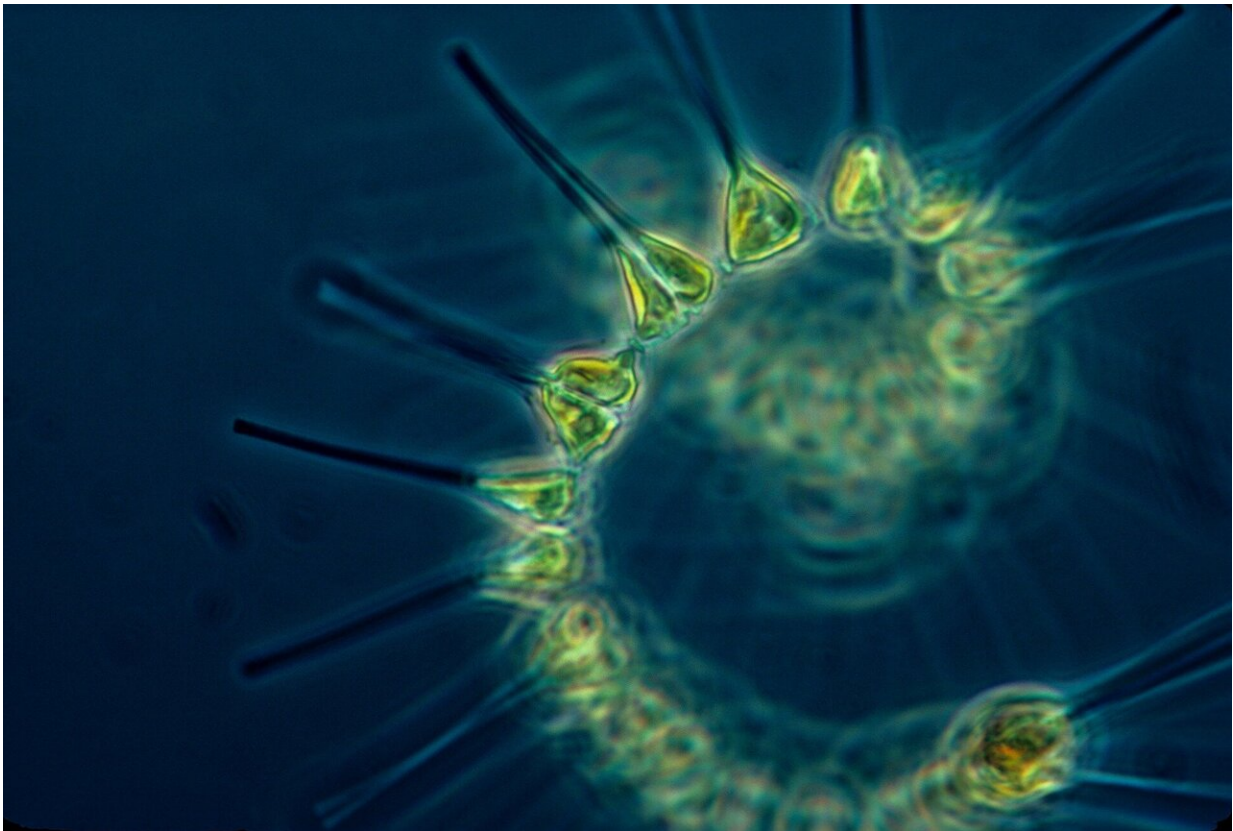


The new gene technology makes it easier to characterize phytoplankton assemblages

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Credit: CC0 Public Domain

Unicellular microorganisms are the most abundant form of life on Earth in terms of quantity and variety. In the doctoral dissertation under review at the University of Jyväskylä, a new gene technology was developed to

replace the laborious microscopic identification of small phytoplankton species. The method can be useful, for example, in detecting phenomena caused by climate change. The new method can be used to monitor blooms of harmful cyanobacterial.

Microbes play an important role in the Earth's ecosystem. They are virtually everywhere, although hidden from the human eye. Exploring the [microbial world](#) is a challenge, and new, more accurate methods are constantly being developed.

"Although invisible, microbes inhabit our bodies, our food, our habitat, the air and almost every corner of our environment. New methods are needed to better understand the role of microbes in the changing world," says Anita Mäki, Ph.D. student at the University of Jyväskylä.

In her [doctoral dissertation](#), Mäki focused especially on [phytoplankton](#). These microbes are the primary producers of oceans, lakes and rivers, and they are largely responsible for producing essential oxygen while consuming carbon dioxide. Both laboratory-grown phytoplankton species and samples collected from 83 Finnish lakes were used in the study.

"Blooms of harmful cyanobacteria, due to increased nutrient input and climate change, is an example why it is important to monitor phytoplankton samples. The new genetic method offers more efficient ways to do this," says Mäki.

The new method allows more comprehensive analysis of different organisms

Anita Mäki developed a new high-throughput sequencing method based on expressed RNA. The method allows more comprehensive analysis of different organisms, both nucleated and non-nucleated microbes simultaneously.

"It is estimated that we share the earth with about 10^{11} - 10^{12} microbial species and about 99.999 percent of these species are not yet identified. The human gut is estimated to contain about 10^{14} [bacterial cells](#), and the [total number](#) of bacterial and archaeal cells in the entire globe is estimated to be 10^{30} . Characterizing microbial communities, at both organismal and global levels is therefore challenging. Our knowledge of the ecological significance of [microbes](#) has increased, and new, sufficiently practical and effective research methods are increasingly needed," says Mäki.

More information: Development of Genetic Phytoplankton Monitoring, JYU Dissertations, Jyväskylä 2019, urn.fi/URN:ISBN:978-951-39-7822-8

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