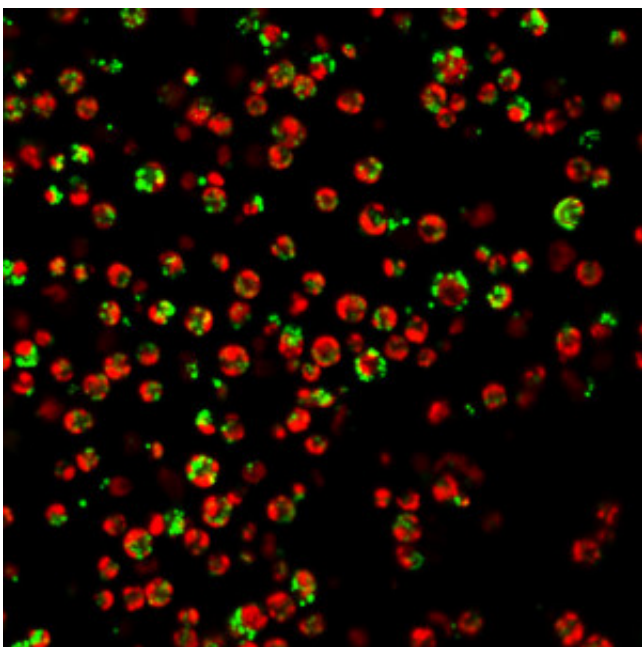


Identifying pathways in algae that produce oil without killing them

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Algal cells of *Chlamydomonas reinhardtii* grown under nitrogen starvation conditions to produce lipids. The red is the autofluorescence from the chlorophyll of the cells while the green indicates the lipid bodies following lipid staining with Lipidtox Green. Credit: Rita Kuo, DOE JGI.

While most people might know some algae as "pond scum," to the U.S. Department of Energy (DOE), they are tiny organisms that could provide a source of sustainable fuels. Like plants, they can convert light into energy-rich chemical compounds; unlike plants, they require less space and don't need arable soil to grow.

Some algae like *Chlamydomonas reinhardtii* (or "Chlamy," as it's known to its large research community) produce energy-dense oils or lipids when stressed, and these lipids can then be converted into fuels.

However, researchers walk a fine line in not killing the goose that lays the golden eggs, in this case, stressing the algae just enough to produce lipids, but not enough to kill them. Published ahead online July 27, 2015 in the journal *Nature Plants*, a team led by scientists from the U.S.

Department of Energy Joint Genome Institute (DOE JGI), a DOE Office of Science User Facility, analyzed the genes that are being activated during algal lipid production, and in particular the molecular machinery that orchestrates these gene activities inside the cell when it produces lipids.

"We know how to stress the algae," said the study's first author Chew Yee Ngan of the DOE JGI. "What we don't know is how to keep the algae alive at the same time, until now."

Stressful searches

As part of the DOE Office of Science's efforts to study [algae](#) for energy and environmental applications, the DOE JGI has published over 75 percent of all publicly available algal genomes. One of these is the Chlamy reference genome, which was released back in 2007. Until now, very little is known about the protein factor that can regulate lipid production. To find more of them, the team cultured Chlamy cells and starved them of nitrogen or sulfur, both of which are stress conditions to which Chlamy responds by producing lipids. They then analyzed the complex of DNA and proteins known as chromatin that define what genes are being activated, as well as the expression profiles or transcriptome, and compared these to non-stressed Chlamy cells.

"We're looking for changes in starved cells vs. cells that are happily growing," Ngan explained. Through careful analysis of genome-wide

data sets, they narrowed down their search to identify two transcription factors that appeared to play a pivotal role in lipid accumulation, and then studied one of them, PSR1, in detail. "In studying the chromatin modifications, we can read out changes in the proteins bound to DNA on a genome-wide scale and then specifically target those genes whose regulation profiles are changed under lipid-producing conditions."

"The study also demonstrated how cells can be tricked into producing lots of lipid without dying of starvation by overexpression of PSR1, which is a strategy that could potentially be applied in other industrial algal species better suited for large-scale biofuel production," said study co-author Axel Visel, DOE JGI Deputy for Science Programs.

Adding genomic technologies to the arsenal

While the work is expected to help algal bioenergy researchers develop more targeted approaches for producing lipids for fuels, corresponding author Chia-Lin Wei, head of DOE JGI's Sequencing Technologies Program, also pointed out that this study also successfully demonstrated an effective strategy for the integration of epigenomic and gene expression data, methods, i.e. the mapping of molecular tags that sit on top of the actual DNA sequence and affect its function, in an organism relevant to DOE missions in energy and environment.

"Such functional interrogation of the genomes, as part of the JGI's 10-Year Strategic Vision, is expected to be widely applicable to more plants and fungi whose gene regulatory pathways still prove elusive," Wei said, adding that Ngan and others at the DOE JGI are continuing this work in many other energy-related species.

More information: Lineage-specific chromatin signatures reveal a regulator of lipid metabolism in microalgae, *Nature Plants*, 2015. [DOI: 10.1038/nplants.2015.107](https://doi.org/10.1038/nplants.2015.107)

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