

A promising genus for biofuel production with Chlorella microalgae genome

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A Chlorella algae "lawn" on a Petri dish, showing small circular "patches" (small lighter circles), revealing the presence of a virus. Credit: James L. Van Etten, University of Nebraska, Lincoln, Department of Plant Pathology

The analysis of the complete genome of Chlorella microalgae, a promising genus for biofuel production, has been completed by the Laboratoire Information Genomique et Structurale of CNRS, France, which is currently heading an international collaboration involving American and Japanese laboratories. The detailed elucidation of the Chlorella genome, also widely used as a food supplement, will make it possible to rationalize its industrial use. This analysis has also brought to



light unexpected findings at the fundamental level: it suggests that Chlorella could have a sexual cycle (which had gone unnoticed so far) and that a virus probably gave it the capacity to synthesize chitin-rich cell walls, a unique property in algae. This work is published online on *The Plant Cell* journal's website.

Microalgae are prime targets for research on biofuels. Leading candidates as alternative sources of biodiesel, their culture has the unquestionable advantage, compared to oleaginous land plants, of not competing with cultivated land necessary for human food. Producing fuel from water, sunlight and carbon dioxide from the atmosphere appears as a miracle solution that has fostered numerous research programs since the 1970s.

Chlorella is particularly interesting for the development of secondgeneration biodiesel thanks to its high lipid content (it only contains 30 % dry matter). Although several genomes of green algae (*Chlorophyta*) have already been sequenced (*Chlamydomonas, Micromonas and Ostreococcus*), *Chlorella* had not been analyzed until now, despite its economic role as long-established food supplement. The analysis of the Chlorella genome, coordinated by Guillaume Blanc, CNRS researcher, predicts 9,791 protein genes, a total comparable to that of its cousin *Micromonas*. This new genomic data will help to further rationalize the use of *Chlorella* in various industrial processes.

The comparative analysis of the different genomes of green algae has made it possible to paint a genetic portrait of their common ancestor, which seems to have already possessed most of the phytohormone biosynthesis pathways necessary to the development and growth of land plants.





Microphotograph of a Paramecium in symbiosis with hundreds of Chlorella cells (green circles). Credit: James L. Van Etten, University of Nebraska, Lincoln, Department of Plant Pathology

In an unexpected fashion, the analysis of the *Chlorella* genome has also revealed numerous genes governing the synthesis of flagellar proteins, which suggests that this species could have a sexual cycle that has gone unnoticed until now. Last but not least, the ability of *Chlorella* algae to synthesize chitin could have been inherited from a virus (itself endowed with chitinase activity) having secured exclusive use of its host against other viruses incapable of piercing through its protective shell. This "monopoly" scenario illustrates a new mode of co-evolution between viruses and their hosts.



Provided by CNRS

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