



www.cnrs.fr



NATIONAL PRESS RELEASE | PARIS | 12 JUNE 2013

NB : Embargoed until 19:00 pm, 12 June 2013

Emiliana genome sequenced

The genome of *Emiliana huxleyi*, an emblematic species of marine phytoplankton, has been sequenced for the first time by an international consortium including French teams from CNRS, UPMC, INRA, Aix-Marseille Université and ENS¹. The scientists found that the genome of this extremely abundant single-celled microorganism contains one third more genes than the human genome, but is twenty times smaller. Another surprising finding is the complexity of this genome, which gives *Emiliana* a high adaptation capacity. Sequencing was performed at the Department of Energy (DOE) Joint Genome Institute in the US and results were published in *Nature* on 13 June 2013.

The oceans produce more than half of the planet's oxygen through the photosynthesis of marine phytoplankton. Most of this photosynthesis is performed by protists: a little known group of unicellular, eukaryotic (having a nucleus) marine microorganisms, which are sometimes photosynthetic. Protists cannot be classified as bacteria, viruses, plants or animals. They display both anatomical and physiological plasticity, and have a complex metabolism. The protist *Emiliana huxleyi* is a haptophyte². Because of its abundance, this tiny planktonic cell is an emblematic species of marine phytoplankton. With its varied fundamental metabolism (photosynthesis, calcification, etc.), it is known for its calcareous micro-skeleton, which turns the ocean a milky-white color that is visible from space when cells of the species multiply in giant blooms.

To decipher the genome of *Emiliana*, which is the first haptophyte genome to be sequenced, the scientists examined thirteen strains of this species from all of the world's oceans (some came from the large collection at *Station Biologique de Roscoff*, which contains more than 500 *Emiliana* accessions). The researchers then isolated these strains in different laboratories. With 141 million base pairs (compared with about 24 million for the diatom and around 3,200 million for the human genome), the team found that the genome of *Emiliana huxleyi* is twenty times smaller than the human genome — but surprisingly contains one third more genes. The consortium highlighted more than 30,000 genes coding for all kinds of proteins and functions, more than half of which were totally unknown to existing genetic databases.

Furthermore, the thirteen strains sequenced were thought to be closely related but turned out to share only three-quarters of their genes: the 'core' of the *Emiliana* genome. This means that 25% of genes are only present in certain strains and that this 'dispensable' part of the genome is composed of genes specific to certain strains. This 'pan-genome' structure (with a core surrounded by variably distributed genes) is typical of bacteria and archaea. How it arose in *Emiliana* remains to be determined. The presence of such

¹ The laboratory 'Adaptation et diversité en milieu marin' (CNRS/UPMC) and the Laboratory 'Végétaux marins et biomolécules' (CNRS/UPMC), both at the *Station Biologique de Roscoff* (CNRS/UPMC), laboratory 'Information génomique et structurale' (CNRS/AMU), *Institut de biologie de l'Ecole normale supérieure* (CNRS/ENS/Inserm) and *Unité de recherches en Génomique-Info* (INRA)

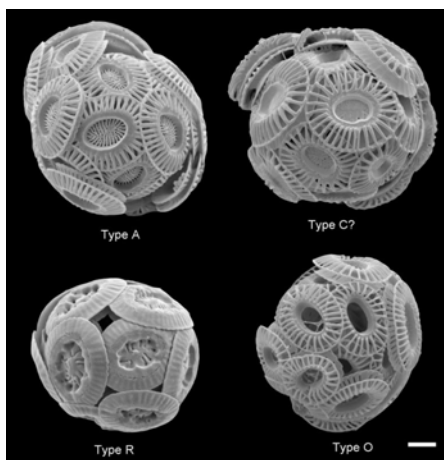
² Haptophyte protists have a filiform appendage known as a haptoneme



www.cnrs.fr



a high proportion of genes specific to certain strains is remarkable for a sexually reproducing eukaryotic organism. It certainly gives *Emiliana* both genome flexibility and a high adaptation capacity.



Different strains of *Emiliana huxleyi*

© Kyoko Hagino-Tomioka

Bibliography

Pan genome of the phytoplankton *Emiliana* underpins its global distribution, Betsy A. Read, Jessica Kegel, Mary J. Klute, Alan Kuo, Stephane C. Lefebvre, Florian Maumus, Christoph Mayer, John Miller, Adam Monier, Asaf Salamov, Jeremy Young, Maria Aguilar, Jean-Michel Claverie, Stephan Frickenhaus, Karina Gonzalez, Emily K. Herman, Yao-Cheng Lin, Jonathan Napier, Hiroyuki Ogata, Analissa F. Sarno, Jeremy Shmutz, Declan Schroeder, Colomban de Vargas, Frederic Verret, Peter von Dassow, Klaus Valentin, Yves Van de Peer, Glen Wheeler, *Emiliana huxleyi* Annotation Consortium, Joel B. Dacks, Charles F. Delwiche, Sonya T. Dyrman, Gernot Glöckner, Uwe John, Thomas Richards, Alexandra Z. Worden, Xiaoyu Zhang & Igor V. Grigoriev, *Nature*, 13 June 2013

Contacts information

Researcher | Colomban de Vargas | T +33 (0)2 98 29 25 28 | vargas@sb-roscoff.fr

Jean-Michel Claverie | T +33 (0)4 91 82 54 20 | claverie@igs.cnrs-mrs.fr

Florian Maumus | T +33 (0)1 30 83 31 74 | florian.maumus@versailles.inra.fr

CNRS Press Officer | Priscilla Dacher | T +33 (0)1 44 96 46 06 | priscilla.dacher@cnrs-dir.fr