

## The early nitrogen starvation response of the diatom *Phaeodactylum tricornutum*

Matthijs Michiel<sup>1,2,3</sup>, Michele Fabris<sup>1,2,3</sup>, T. Obata<sup>4</sup>, Stefaan Broos<sup>5,6</sup>, Gino Baart<sup>1,2,3</sup>, A.R. Fernie<sup>4</sup>, Wim Vyverman<sup>3</sup> and Alain Goossens<sup>1,2</sup>

<sup>1</sup> Department of Plant Systems Biology, VIB, Technologiepark 927, B-9052 Ghent, Belgium  
E-mail: [mimat@psb.vib-ugent.be](mailto:mimat@psb.vib-ugent.be)

<sup>2</sup> Department of Plant Biotechnology and Genetics, Ghent University, Technologiepark 927, B-9052 Ghent, Belgium

<sup>3</sup> Department of Biology, Ghent University, Krijgslaan 281, B-9000 Ghent, Belgium

<sup>4</sup> Max Planck Institute of Molecular Plant Physiology, Wissenschaftspark Golm, Am Mühlenberg 1, D-14476 Potsdam-Golm, Germany

<sup>5</sup> Department for Molecular Biomedical Research, VIB, Technologiepark 927, B-9052 Ghent, Belgium

<sup>6</sup> Department of Biomedical Molecular Biology, Ghent University, B-9052 Ghent, Belgium

In this study we investigated the transcriptomic and metabolic response of *Phaeodactylum tricornutum* to nitrogen starvation and other stresses during the first 24 hours. *P. tricornutum* is a unicellular marine alga of the coastal zone. These algae live in a varied environment where nutrient and light availability can fluctuate substantially. Nitrogen starvation induces the accumulation of lipids in algae which has potential biotechnological purposes. The aim of the study was to find transcriptional regulators that coordinate this process.

Using RNA-seq, we sequenced a total of ten points across the different timepoints and conditions. The response in the primary metabolism was found to be dramatically different when compared to nitrogen starvation in green algae. The citric acid cycle especially was under tight transcriptional control and likely plays a central role in the repurposing of carbon and nitrogen in the cell. To investigate this further metabolic labeling experiments are being performed.

Additionally, in the promoters of genes upregulated during nitrogen starvation several overrepresented motifs were found. By employing a Yeast One Hybrid screen, a potentially novel transcription factor termed NMB1 was found. NMB1 was previously unannotated but appears evolutionary conserved in the heterokontae. *P. tricornutum* contains two other members of this gene family. The expression profiles of two out of three putative transcription factors cluster together with a substantial part of the nitrogen salvaging and amino acid breakdown genes, implying a functional link with the target process. NMB1 would be the first transcription factor known to be involved in nutrient responses in diatoms.