

# Differential expression of a model diatom in the early phases of lipid accumulation

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Diatoms are unicellular algae that contribute tremendously to the primary production of aquatic ecosystems. Their main primary storage products are lipids. We work with the main model species for pennate diatoms: *Phaeodactylum tricornutum*. The aim of our project is the creation of genetically modified *P. tricornutum* strains that have enhanced lipid productivity. Since the genetic basis of lipid accumulation during nutrient deprivation is still unknown we set out to catalog gene expression of diatoms during lipid accumulation. By using RNA-seq we profiled four conditions where lipid metabolism undergoes changes. Because the main interest of our research are the regulators of lipid metabolism we focussed on the first 24 hours, where, in our conditions, the cell shifts from growth to cell cycle arrest and increases lipid content. For these four conditions 10 timepoints were subjected to illumina 2X100bp sequencing and approximately 10% of the *P. tricornutum* transcriptome was differentially expressed. We linked the the RNA-seq to a metabolic analysis and flow cytometry to show that there are concurrent changes detectable in chrysolaminaran, lipid biosynthesis and the cell cycle. These changes are also detected on the transcriptome level. We are following up on this analysis by isolating and overexpressing candidate regulator genes. We have also shown that *P. tricornutum* lipid productivity can indeed be enhanced by overexpression of endogenous genes.

## References

Fabris M., M. Matthijs, S. Rombauts, W. Vyverman, A. Goossens and G.J. Baert. 2012. The metabolic blueprint of *Phaeodactylum tricornutum* reveals a eukaryotic Entner-Doudoroff glycolytic pathway. Plant J.70(6):1004-14. doi: 10.1111/j.1365-313X.2012.04941.x.