

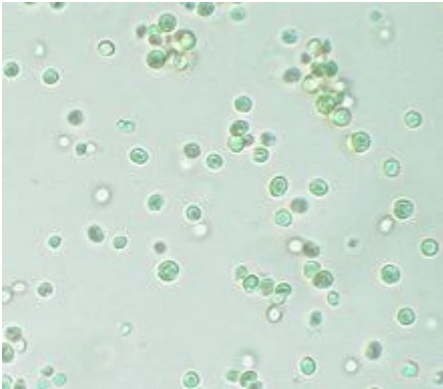
Nannochloropsis

Nannochloropsis is a genus of algae comprising six known species. The genus in the current taxonomic classification was first termed by Hibberd (1981).^[2] The species have mostly been known from the marine environment but also occur in fresh and brackish water.^[3] All of the species are small, nonmotile spheres which do not express any distinct morphological features that can be distinguished by either light or electron microscopy. The characterisation is mostly done by rbcL gene and 18S rRNA sequence analysis.^[4]

The algae of the genus *Nannochloropsis* differ from other related microalgae in that they have chlorophyll a and completely lack chlorophyll b and chlorophyll c. In addition they are able to build up a high concentrations of a range of pigments such as astaxanthin, zeaxanthin and canthaxanthin.^[5] They have a diameter of about 2 to 3 micrometers^[6] and a very simple ultrastructure with reduced structural elements compared to neighbouring taxa.

Nannochloropsis is considered a promising alga for industrial applications because of its ability to accumulate high levels of polyunsaturated fatty acids.^{[7][8]} Moreover, it shows promising features that can allow genetic manipulation aimed at the genetic improvement of the current oleaginous strains. Various species of *Nannochloropsis* indeed are transfectable and there has been evidence that some strains are able to perform homologous recombination.^[9] At the moment it is mainly used as an energy-rich food source for fish larvae and rotifers. Nevertheless, it has raised growing interest also for the investigation of biofuel production from photosynthetic organisms. (see Nannochloropsis and biofuels). *Nannochloropsis* is actually in use as food additive for human nutrition and it is also served at Restaurant "A Poniente" of El Puerto de Santa María (Cádiz, Spain) close to the natural environment where *Nannochloropsis gaditana* was first isolated and still grows.^[10] A 2020 study suggests it could be used for a highly performant, sustainable fish-free feed for farmed fish.^{[11][12]}

Nannochloropsis



Nannochloropsis viewed under a light microscope

Scientific classification

| | |
|---------|--|
| Clade: | <u>SAR</u> |
| Phylum: | <u>Ochrophyta</u> |
| Class: | <u>Eustigmatophyceae</u> |
| Order: | <u>Eustigmatales</u> |
| Family: | <u>Monodopsidaceae</u> |
| Genus: | <u><i>Nannochloropsis</i></u> <div>D.J.Hibberd, 1981^[1]</div> |

Type species

Nannochloropsis oculata
(Droop 1955) Hibberd 1981

Contents

- Species
- Sequenced genomes
- Accumulation of oil in nitrogen deprivation
- See also
- References

Species

The species currently recognised are:

- *Nannochloropsis australis* Fawley, Jameson & Fawley 2015
- *Nannochloropsis gaditana* Lubián 1982
- *Nannochloropsis granulata* Karlson & Potter 1996
- *Nannochloropsis limnetica* Krienitz et al. 2000
- *Nannochloropsis oceanica* Suda & Miyashita 2002
- *Nannochloropsis oculata* (Droop 1955) Hibberd 1981
- *Nannochloropsis salina* Hibberd 1981

Sequenced genomes

The scientific community has obtained the genomic sequence of different strains of *Nannochloropsis* belonging to two species: *N. gaditana*^{[13][14]} and *N. oceanica*.^{[15][16]} A genome portal (<https://web.archive.org/web/20131029184338/http://www.nannochloropsis.org/>) based on the *N. gaditana* B-31 (<https://web.archive.org/web/20131029184338/http://www.nannochloropsis.org/>) genome allows accessing much of the genomic information that concerns this micro-organism, moreover dedicated web pages are also available for the genomes of *N. gaditana* CCMP526 (<http://nannochloropsis.genomeprojectsolutions-databases.com/>) and *N. oceanica* CCMP1779 (<https://web.archive.org/web/20131030101356/http://www.bmb.msu.edu/nannochloropsis.html>).

The genomes of the sequenced *Nannochloropsis* strains were between 28.5 and 29 Mega bases long, they had high density of genes, reduced intron content, short intergenic regions^[13] and very limited presence of repetitive sequences.^[15] The genes of the two species share extended similarity.

The analysis of the genomes revealed that these microalgae have set of genes for the synthesis and incorporation in the cell wall of cellulose and sulfated fucans and that they are able to store carbon in polymers of β -1,3- and β -1,6-linked glucose called chrysolaminarin.^[13] An NMR analysis of whole algal cells which were cultivated in autotrophic growth^[17] reports evidence of the presence of cellulose in the cell wall and of mobile chrysolaminarin, probably accumulated in solution in vacuoles inside the cell.

Comparison between the lipid metabolic genes of *N. gaditana* and of red/green/brown algae and diatoms provided some insights into the exemplary lipid production of *Nannochloropsis* cultures. The comparisons indeed highlighted the presence of an expanded repertoire of some of the genes involved in TAG assembly in *Nannochloropsis*.^[14] Numerous TAG lipases, which can affect TAG metabolism through either TAG degradation or lipid remodeling, were identified in *Nannochloropsis*,^[15] many of them belonging to a gene family which seems to be exclusive of *Nannochloropsis*.^[18]

Analysis of the genomic data suggested the presence in both the two species of *Nannochloropsis* of regulatory RNA and in particular miRNA.^{[13][15]}

Various orthologs of known blue light sensing proteins were found in the genomes of *Nannochloropsis* suggesting possible circadian regulation.^{[13][15]}

A research community from Qingdao Institute of Bioenergy and Bioprocess Technology (QIBEBT [1] (<http://www.singlecellcenter.org/en/index.aspx>)), Chinese Academy of Sciences, sequenced and compared six *Nannochloropsis* genomes that include two *N. oceanica* strains (IMET1 and CCMP531) and one strain from each of four other recognized species: *N. salina* (CCMP537), *N. gaditana* (CCMP526, which was previously reported^[14]), *N. oculata* (CCMP525) and *N. granulata* (CCMP529).^[19] They found that the six genomes share key oleaginous traits, such as the gene dose expansion of selected lipid biosynthesis genes compared to green algae *Chlamydomonas*. The most prominent example of gene dose expansion is Diacylglycerol acyltransferase (DGAT), which catalyzes the last step of triacylglycerol (TAG) synthesis. There are 13 DGAT genes in *Nannochloropsis*, representing the highest gene dose in known genomes.

Through a comprehensive phylogenetic analysis, researchers proposed that among the 11 DGAT-2s, one gene might originate from the red algae related secondary endosymbiont, four from green algae related endosymbiont, and the other six from the eukaryotic host genome. In addition, a large proportion (15.3%) of TAG biosynthesis related genes were acquired by *Nannochloropsis* via horizontal gene transfer (HGT) from bacteria. Therefore, multiple genome pooling and horizontal genetic exchange, together with selective inheritance of lipid synthesis genes and species-specific gene loss, have led to the enormous genetic apparatus for oleaginousness and the wide genomic divergence among present-day *Nannochloropsis* spp.

Accumulation of oil in nitrogen deprivation

When cultured in normal growth conditions in standard f/2 medium (<http://www.ccap.ac.uk/media/documents/f2.pdf>) supplemented with nitrogen, *Nannochloropsis* cells have an oil content of about 30% of their dry weight. This oil can be used to produce biodiesel. In order to produce biodiesel, the oil content of *Nannochloropsis* cultures must be increased. Fatty acid biosynthesis in *N. oceanica* was shown to be integrated with the regulation of the cholesterol biosynthetic pathway, suggesting new genetic engineering or chemical biology approaches for enhanced oil production in microalgae.^[20] On the other hand, various culturing conditions were observed to increase the average oil content per cell, supporting however only slow growth rates of the cultures (see the related section *Nannochloropsis* and biofuels), and decreasing the overall productivity. Among these conditions, nitrogen deprivation has been one of the most vastly studied. Studies have examined the behaviour of the cultures in nitrogen stress in various culturing set-ups, as well as the physiological and molecular response of the cells to nitrogen deprivation.

Various strains of *Nannochloropsis* were shown to accumulate up to 60–70% of their overall biomass as lipids in nitrogen limitation.^{[8][21]} In this condition not only the amount of lipids changes, but also the composition. It was observed that triacylglycerols largely increase in nitrogen depletion while other lipids, mainly polar glycerolipids, free fatty acids and diacylglycerols, slightly decrease. The increase in triacylglycerols in nitrogen depletion is much larger than the decrease in the other glycerolipids, supporting the hypothesis that the cells actively synthesise new triacylglycerols rather than just transforming the existing lipids into triacylglycerols.^[22]

While triacylglycerols accumulate and lipid droplets enlarge, other important morphological changes take place. The chloroplasts became smaller and the amount of lipids that are characteristic of the photosynthetic membranes decrease significantly. Photosynthetic yield decreases in the nitrogen depleted cells, but it is still sufficient to drive cell survival and growth. If photosynthesis is inhibited indeed, *Nannochloropsis* cells stop growing, indicating that they rely on photosynthetic solar energy conversion and not on stored carbohydrates or lipids as energy source.^[22]

Nannochloropsis cultivated in normal growth condition and deprived of a nitrogen source continues growing for 4–5 days. The analysis of gene expression reveals that mechanisms for nitrogen assimilation and redistribution are activated in the cells in nitrogen scarcity and allow survival through a partial reorganisation of the cellular metabolism. The genes responsible for the incorporation of free ammonium into glutamate ($\text{L-glutamine} + 2\text{-oxoglutarate} + \text{NADPH} + \text{H}^+ \leftarrow \rightarrow 2 \text{ L-glutamate} + \text{NADP}^+$) are up-

regulated . Their up-regulation increases the capability of the cells to assimilate minimal amount of ammonium eventually present in the medium and, more importantly, allows them to assimilate the intracellular ammonium that can be released by degradative processes. Transcriptomic data of nitrogen-deprived *Nannochloropsis* cultures show that various enzymes responsible for degradative processes that release ammonium are indeed up regulated. Moreover, the expression of genes coding for proteins involved in controlled degradation of proteins increase, together with others involved in the formation of cytosolic sequestering vesicles used for degradation and recycling of cellular components.^[13]

The machinery of gene expression of chloroplast and mitochondrion is down regulated in *Nannochloropsis* in response to nitrogen depletion.^{[13][14]}

Corteggiani Carpinelli and coworkers (2013)^[13] report a complete analysis of the gene expression of *Nannochloropsis* cultures grown in normal conditions and nitrogen deprivation for 3 days and 6 days. Data on similar conditions were also collected by Radakovits et al. (2012)^[14] and Vieler et al. (2012).^[15] The all of this data show that genes involved in fatty acid and triacylglycerol biosynthesis are always abundant in the cells and their expression is not correlated with the amount of oil accumulated. Also the expression of the genes involved in triacylglycerols degradation is not significantly down-regulated as triacylglycerols accumulate. The general conclusion suggested by the experimental data is that *Nannochloropsis* constitutively produces triacylglycerols and that the metabolic reorganisation that follows nitrogen deprivation increases the flux of substrates through this pathway, which is in turn capable to sustain the increased metabolic flux. Corteggiani Carpinelli and coworkers (2013)^[13] advance the hypothesis that, in their experimental conditions, photosynthesis is the main energy source and the down-regulation of the metabolic activity of the mitochondrion is determinant in increasing the amount of substrates that enter the fatty acid biosynthetic pathway. If more precursors are available, more fatty acids are synthesised and as a consequence more triacylglycerols are produced and accumulated into the cells as oil droplets.

Dong et al. (2013)^[23] report a quantification of the abundance of various proteins in cultures of *Nannochloropsis* grown with a supplement of CO₂ and deprived of nitrogen. Despite the different experimental conditions, also the proteomic study seems to support the hypothesis that the accumulation of triacylglycerols is due to an increase of the metabolic flux through the fatty acid biosynthetic pathway. The authors advance the hypothesis that, in their experimental conditions, the degradation of storage sugars and the up-regulation of glycolysis are responsible for the increase of substrates through the pathway.

More recently Li and coworkers (2014)^[24] collected extensive experimental data from cultures of *Nannochloropsis oculata* IMET1 grown in nitrogen sufficient and nitrogen depleted media. According to their analysis it is the catabolism of carbohydrates and proteins together with the up-regulation of genes assigned to various pathways (the cytosolic glycolysis pathway, which produces pyruvate; the PDHC bypass, which yields additional acetyl-CoA; and the coupling of TCA reactions with mitochondrial β-oxidation) that have to be claimed for increasing the supply of carbon precursors to the fatty acid biosynthetic pathway. Nevertheless, the authors suggest that it isn't the increased synthesis of fatty acids that leads to accumulation of oil inside the cells, but it is rather the up-regulation of genes involved in the assembly of triacylglycerols that determines the final oil concentration. In other words, under nitrogen depletion, it is the up-regulation of the transcript level of the key genes in triacylglycerol assembly, rather than those in fatty acids biosynthesis, that leads to accelerated triacylglycerol production.

In 2017, a study jointly funded by ExxonMobil and Synthetic Genomics achieved a breakthrough in lipid percentages in *Nannochloropsis gaditana* through applications of the CRISPR-Cas9 reverse-genetics pipeline and nitrogen starving—improving partitioning of total carbon to lipids from 20% (wild type) to 40-45% (mutant type).^[25]


See also

- Microalgae
- Planktonic algae
- Nannochloropsis and biofuels
- Biofuel
- Sustainable aviation fuel
- Energy content of biofuel

References

1. Hibberd, D. J. (1981). "Notes on the taxonomy and nomenclature of the algal classes Eustigmatophyceae and Tribophyceae (synonym Xanthophyceae)". *Botanical Journal of the Linnean Society*. **82** (2): 93–119. doi:10.1111/j.1095-8339.1981.tb00954.x (<https://doi.org/10.1111%2Fj.1095-8339.1981.tb00954.x>).
2. Hibberd (1981). "Notes on the taxonomy and nomenclature of the algal classes Eustigmatophyceae and Tribophyceae (Synonym Xanthophyceae)". *Botanical Journal of the Linnean Society*. **82** (2): 93–119. doi:10.1111/j.1095-8339.1981.tb00954.x (<https://doi.org/10.1111%2Fj.1095-8339.1981.tb00954.x>).
3. Fawley (2007). "Observations on the Diversity and Ecology of Freshwater Nannochloropsis (Eustigmatophyceae), with Descriptions of New Taxa". *Protist*. **158** (3): 325–336. doi:10.1016/j.protis.2007.03.003 (<https://doi.org/10.1016%2Fj.protis.2007.03.003>). PMID 17576099 (<https://pubmed.ncbi.nlm.nih.gov/17576099>).
4. Andersen, R. A.; Brett, R. W.; et al. (1998). "Phylogeny of the Eustigmatophyceae based upon 18s rDNA, with emphasis on Nannochloropsis". *Protist*. **149** (1): 61–74. doi:10.1016/S1434-4610(98)70010-0 (<https://doi.org/10.1016%2FS1434-4610%2898%2970010-0>). PMID 23196114 (<https://pubmed.ncbi.nlm.nih.gov/23196114>).
5. Lubian, L. M.; et al. (2000). "Nannochloropsis (Eustigmatophyceae) as source of commercially valuable pigments". *Journal of Applied Phycology*. **12** (3/5): 249–255. doi:10.1023/A:1008170915932 (<https://doi.org/10.1023%2FA%3A1008170915932>). S2CID 620002 (<https://api.semanticscholar.org/CorpusID:620002>).
6. Kandilian, R.; Lee, E.; Pilon, L. (2013). "Radiation and optical properties of Nannochloropsis oculata grown under different irradiances and spectra". *Bioresource Technology*. **137**: 63–73. doi:10.1016/j.biortech.2013.03.058 (<https://doi.org/10.1016%2Fj.biortech.2013.03.058>). PMID 23587810 (<https://pubmed.ncbi.nlm.nih.gov/23587810>).
7. Assaf Sukenik, Y. C. T. B. (1989). "Regulation of fatty acid composition by irradiance level in the Eustigmatophyte Nannochloropsis sp". *Journal of Phycology*. **25** (4): 686–692. doi:10.1111/j.0022-3646.1989.00686.x (<https://doi.org/10.1111%2Fj.0022-3646.1989.00686.x>). S2CID 84590502 (<https://api.semanticscholar.org/CorpusID:84590502>).
8. Boussiba, S.; Vonshak, A.; Cohen, Z.; Avissar, Y.; Richmond, A. (1987). "Lipid and biomass production by the halotolerant microalga Nannochloropsis salina". *Biomass*. **12**: 37–47. doi:10.1016/0144-4565(87)90006-0 (<https://doi.org/10.1016%2F0144-4565%2887%2990006-0>).
9. Kilian, O.; Benemann, C. S. E.; Niyogi, K. K.; Vick, B. (2011). "High-efficiency homologous recombination in the oil-producing alga Nannochloropsis sp" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3248512>). *Proc. Natl. Acad. Sci. U.S.A.* **108** (52): 21265–21269. doi:10.1073/pnas.1105861108 (<https://doi.org/10.1073%2Fpnas.1105861108>). PMC 3248512 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3248512>). PMID 22123974 (<https://pubmed.ncbi.nlm.nih.gov/22123974>).
10. Lubian, L. M. (1982). "Nannochloropsis gaditana sp. nov., a new Eustigmatophyceae marina strain". *Lazaroa*. **4**: 287–293.
11. "Research breakthrough achieves fish-free aquaculture feed that raises key standards" (<http://phys.org/news/2020-11-breakthrough-fish-free-aquaculture-key-standards.html>).

phys.org. Retrieved 9 December 2020.

12. Sarker, Pallab K.; Kapuscinski, Anne R.; McKuin, Brandi; Fitzgerald, Devin S.; Nash, Hannah M.; Greenwood, Connor (12 November 2020). "Microalgae-blend tilapia feed eliminates fishmeal and fish oil, improves growth, and is cost viable" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7665073>). *Scientific Reports*. **10** (1): 19328. Bibcode:2020NatSR..1019328S (<https://ui.adsabs.harvard.edu/abs/2020NatSR..1019328S>). doi:10.1038/s41598-020-75289-x (<https://doi.org/10.1038/s41598-020-75289-x>). ISSN 2045-2322 (<https://www.worldcat.org/issn/2045-2322>). PMC 7665073 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7665073>). PMID 33184333 (<https://pubmed.ncbi.nlm.nih.gov/33184333>).  Available under CC BY 4.0 (<https://creativecommons.org/licenses/by/4.0/>).
13. Corteggiani Carpinelli, E.; et al. (2013). "Chromosome scale genome assembly and transcriptome profiling of *Nannochloropsis gaditana* in nitrogen depletion" (<https://doi.org/10.1093/mp/sst120>). *Molecular Plant*. **7** (2): 323–335. doi:10.1093/mp/sst120 (<https://doi.org/10.1093/mp/sst120>). PMID 23966634 (<https://pubmed.ncbi.nlm.nih.gov/23966634>).
14. Radakovits, R.; et al. (2012). "Draft genome sequence and genetic transformation of the oleaginous alga *Nannochloropsis gaditana*" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3293424>). *Nat Commun*. **3** (2): 686. Bibcode:2012NatCo...3..686R (<https://ui.adsabs.harvard.edu/abs/2012NatCo...3..686R>). doi:10.1038/ncomms1688 (<https://doi.org/10.1038/ncomms1688>). PMC 3293424 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3293424>). PMID 22353717 (<https://pubmed.ncbi.nlm.nih.gov/22353717>).
15. Vieler, A.; et al. (2012). "Genome, Functional Gene Annotation, and Nuclear Transformation of the Heterokont Oleaginous Alga *Nannochloropsis oceanica* CCMP1779" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3499364>). *PLOS Genet*. **8** (11): e1003064. doi:10.1371/journal.pgen.1003064 (<https://doi.org/10.1371/journal.pgen.1003064>). PMC 3499364 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3499364>). PMID 23166516 (<https://pubmed.ncbi.nlm.nih.gov/23166516>).
16. Liang, C.; et al. (2012). "De Novo Sequencing and Global Transcriptome Analysis of *Nannochloropsis* sp. (Eustigmatophyceae) Following Nitrogen Starvation". *Bioenerg. Res*. **6** (2): 494–505. doi:10.1007/s12155-012-9269-0 (<https://doi.org/10.1007/s12155-012-9269-0>). S2CID 207395605 (<https://api.semanticscholar.org/CorpusID:207395605>).
17. Arnold, A. A.; et al. (2014). "Identification of lipid and saccharide constituents of whole microalgal cells by ¹³C solid-state NMR" (<https://doi.org/10.1016/j.bbamem.2014.07.017>). *Biochimica et Biophysica Acta (BBA) - Biomembranes*. **1848** (1 Pt B): 369–377. doi:10.1016/j.bbamem.2014.07.017 (<https://doi.org/10.1016/j.bbamem.2014.07.017>). PMID 25065670 (<https://pubmed.ncbi.nlm.nih.gov/25065670>).
18. Elisa Corteggiani Carpinelli e Nicola Vitulo Unpublished data available through the *Nannochloropsis gaditana* genome portal (<http://www.nannochloropsis.org>) Archived (<https://web.archive.org/web/20131029184338/http://www.nannochloropsis.org/>) 2013-10-29 at the Wayback Machine
19. Wang, Dongmei; Ning, Kang; Li, Jing; et, al.; Xu, Jian (January 2014). "Nannochloropsis Genomes Reveal Evolution of Microalgal Oleaginous Traits" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3886936>). *PLOS Genetics*. **10** (1): e1004094. doi:10.1371/journal.pgen.1004094 (<https://doi.org/10.1371/journal.pgen.1004094>). PMC 3886936 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3886936>). PMID 24415958 (<https://pubmed.ncbi.nlm.nih.gov/24415958>).
20. Lu; et al. (2014). "Regulation of the cholesterol biosynthetic pathway and its integration with fatty acid biosynthesis in the oleaginous microalga *Nannochloropsis oceanica*" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4052811>). *Biotechnology for Biofuels*. **7**: 81. doi:10.1186/1754-6834-7-81 (<https://doi.org/10.1186/1754-6834-7-81>). PMC 4052811 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4052811>). PMID 24920959 (<https://pubmed.ncbi.nlm.nih.gov/24920959>).

21. Rodolfi, L; Zittelli, Chini; et al. (2008). "Microalgae for oil: strain selection, induction of lipid synthesis and outdoor mass cultivation in a low-cost photobioreactor". *Biotechnology and Bioengineering*. **102** (1): 100–12. doi:10.1002/bit.22033 (<https://doi.org/10.1002%2Fbit.22033>). PMID 18683258 (<https://pubmed.ncbi.nlm.nih.gov/18683258>). S2CID 28285869 (<https://api.semanticscholar.org/CorpusID:28285869>).
22. Simionato, Diana; Block, Maryse A.; Rocca, Nicoletta La; Jouhet, Juliette; Maréchal, Eric; Finazzi, Giovanni; Morosinotto, Tomas (2013). "The response of *Nannochloropsis gaditana* to nitrogen starvation includes de novo biosynthesis of triacylglycerols, a decrease of chloroplast galactolipids, and reorganisation of the photosynthetic apparatus" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3647774>). *Eukaryotic Cell*. **12** (5): 665–676. doi:10.1128/EC.00363-12 (<https://doi.org/10.1128%2FEC.00363-12>). PMC 3647774 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3647774>). PMID 23457191 (<https://pubmed.ncbi.nlm.nih.gov/23457191>).
23. Dong, HP; Williams, E; Wang, DZ; Xie, ZX; Hsia, RC; Jenck, A; Halden, R; Li, J; Chen, F; Place, AR (2013). "Responses of *Nannochloropsis oceanica* IMET1 to long-term nitrogen starvation and recovery" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3668043>). *Plant Physiology*. **162** (2): 1110–1126. doi:10.1104/pp.113.214320 (<https://doi.org/10.1104%2Fpp.113.214320>). PMC 3668043 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3668043>). PMID 23637339 (<https://pubmed.ncbi.nlm.nih.gov/23637339>).
24. Li, Jing; Han, Danxiang; Wang, Dongmei; Ning, Kang; Jia, Jing; Wei, Li; Jing, Xiaoyan; Huang, Shi; Chen, Jie (2014). "Choreography of transcriptomes and lipidomes of *Nannochloropsis* reveals the mechanisms of oil synthesis in microalgae" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4036577>). *Plant Cell*. **26** (4): 1645–1665. doi:10.1105/tpc.113.121418 (<https://doi.org/10.1105%2Ftpc.113.121418>). PMC 4036577 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4036577>). PMID 24692423 (<https://pubmed.ncbi.nlm.nih.gov/24692423>).
25. Ajjawi, Imad; Verruto, John; Aqui, Moena; Soriaga, Leah B; Coppersmith, Jennifer; Kwok, Kathleen; Peach, Luke; Orchard, Elizabeth; Kalb, Ryan (2017). "Lipid production in *Nannochloropsis gaditana* is doubled by decreasing expression of a single transcriptional regulator". *Nature Biotechnology*. **35** (7): 647–652. doi:10.1038/nbt.3865 (<https://doi.org/10.1038%2Fnbt.3865>). PMID 28628130 (<https://pubmed.ncbi.nlm.nih.gov/28628130>). S2CID 8175045 (<https://api.semanticscholar.org/CorpusID:8175045>).

External links

- Guiry, M.D.; Guiry, G.M. (2008). "Nannochloropsis" (http://www.algaebase.org/search/genus/detail/?genus_id=44568). *AlgaeBase*. World-wide electronic publication, National University of Ireland, Galway. Retrieved 2009-02-21.
 - *Nannochloropsis gaditana* genome portal (<https://web.archive.org/web/20131029184338/http://www.nannochloropsis.org/>)
 - *Nannochloropsis* latest news and scientific reports (<https://web.archive.org/web/20131029193230/http://www.nannochloropsis.org/blog/>)
 - *Nannochloropsis gaditana* CCMP526 web page (<http://nannochloropsis.genomeprojectsolutions-databases.com/>)
 - *Nannochloropsis oceanica* CCMP1779 web page (<https://web.archive.org/web/20131030101356/http://www.bmb.msu.edu/nannochloropsis.html>)
-

Retrieved from "<https://en.wikipedia.org/w/index.php?title=Nannochloropsis&oldid=1043650254>"

Text is available under the Creative Commons Attribution-ShareAlike License; additional terms may apply. By using this site, you agree to the Terms of Use and Privacy Policy. Wikipedia® is a registered trademark of the Wikimedia Foundation, Inc., a non-profit organization.