

LIDIANE COVELL

**METABOLIC RESPONSES TO NITROGEN DEFICIENCY AND RAPAMYCIN
TREATMENT IN FRESHWATER MICROALGAE STRAINS**

Thesis submitted to the Plant Physiology Graduate Program of the Universidade Federal de Viçosa in partial fulfillment of the requirements for the degree of *Doctor Scientiae*.

Adviser: Adriano Nunes Nesi

Co-adviser: Marcelo Gomes Marçal Vieira Vaz

**VIÇOSA - MINAS GERAIS
2022**

**Ficha catalográfica elaborada pela Biblioteca Central da Universidade
Federal de Viçosa - Campus Viçosa**

T

C873m
2022 Covell, Lidiane, 1978-
Metabolic responses to nitrogen deficiency and rapamycin
treatment in freshwater microalgae strains / Lidiane Covell. –
Viçosa, MG, 2022.
1 tese eletrônica (188 f.): il. (algumas color.).

Texto em inglês.

Inclui anexos.

Orientador: Adriano Nunes Nesi.

Tese (doutorado) - Universidade Federal de Viçosa,
Departamento de Biologia Vegetal, 2022.

Inclui bibliografia.

DOI: <https://doi.org/10.47328/ufvbbt.2022.337>

Modo de acesso: World Wide Web.

1. *Chlamydomonas reinhardtii*. 2. Microalga -
Metabolismo. 3. Microalga - Efeito do nitrogênio. 4. Microalga -
Efeito do stress. 5. Rapamicina. I. Nesi, Adriano Nunes, 1975-.
II. Universidade Federal de Viçosa. Departamento de Biologia
Vegetal. Programa de Pós-Graduação em Fisiologia Vegetal.
III. Título.

CDD 22. ed. 579.83

Bibliotecário(a) responsável: Bruna Silva CRB6/2552

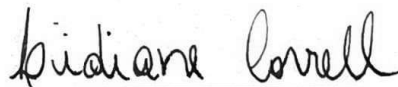
LIDIANE COVELL

**METABOLIC RESPONSES TO NITROGEN DEFICIENCY AND RAPAMYCIN
TREATMENT IN FRESHWATER MICROALGAE STRAINS**

Thesis submitted to the Plant Physiology Graduate Program of the Universidade Federal de Viçosa in partial fulfillment of the requirements for the degree of *Doctor Scientiae*.

APPROVED: February 18, 2022.

Assent:



Lidiane Covell
Author



Adriano Nunes Nesi
Adviser

ACKNOWLEDGMENT

To the Federal University of Viçosa for the opportunity for learning and academic improvement;

To the Department of Plant Biology, its faculty and staff for their academic contribution;

To the committee members, for their willingness to collaborate with the thesis;

Special thanks to my advisor, professor Adriano Nunes Nesi, for his attention, experience, patience, wisdom, confidence, guidance and support throughout my research;

To professor Marcio Arêdes for all his guidance, suggestions for improving my work and for the availability of using the Biofuels Laboratory;

To the Max Planck Institute of Molecular Plant Physiology in Potsdam-Germany for the support in the complementary analysis;

To Dr. Camila Caldana for advising me during my stay at Max Planck Institute of Molecular Plant Physiology;

To the Max Planck Institute of Molecular Plant Physiology staff, specially to Andrea Leiß and Anne Michaelis for their support and analytical procedures;

To the pos docs of Caldana's group for their help into data analysis and results discussion;

To the UCP members, for the assistance and good time, especially for the valuable advises from Marcelo Vaz, Mariana Machado and Dora Martins, who at different stages collaborated directly in my research;

To my friends and family, who deeply understand this harsh period of my life;

To my husband, Marcio, who accompanied me throughout the doctoral journey and was always present with care and encouragement for me to do my best;

To my mother and my brothers, Eduardo and Weliton, for all their patience and help in the most difficult times;

To my grandparents, Maria José and Silvio Lessa, for all the affection, support and cheering for me to reach my goal;

To Lucky, my lucky dog who always care about me.

To the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), to granting the scholarship.

BIOGRAPHY

Lidiane Covell, daughter of Adenir da Silva Lessa and Vanir Ribeiro Magalhães, was born on May 1, 1978, in the city of Viçosa, Minas Gerais. She concluded high school in her birth city in 1997.

She undergrad in Biological Sciences at the Federal University of Viçosa, on 2014.

In 2014 she started the Master's program in Plant Physiology at the Federal University of Viçosa, Minas Gerais, completing the requirements for obtaining the title of *Magister Scientiae* in October 2015.

In March 2017, she started her doctored in Plant Physiology at the Federal University of Viçosa, Minas Gerais, completing the requirements for obtaining the title of *Doctor Scientiae* on February 18, 2022.

“Es gibt einen Antrieb, der stärker ist als Dampf, als Elektrizität und als Atomenergie: Der Wille”
(“There is a driving force more powerful than steam, electricity and atomic energy: the will.”)

Albert Einstein

ABSTRACT

COVELL, Lidiane, D.Sc., Universidade Federal de Viçosa, February 2022. **Metabolic responses to nitrogen deficiency and rapamycin treatment in freshwater microalgae strains.** Adviser: Adriano Nunes Nesi. Co-adviser: Marcelo Gomes Marçal Vieira Vaz.

Nutrient deprivation causes significant stress to microalgae, which responds by altering their metabolic pathways. Following N deprivation, the accumulation of starch and triacylglycerols (TAGs) are significantly altered following reprogramming of cellular metabolism. In addition, the adaptation of cell growth and proliferation to environmental changes is essential for the surviving of biological systems. The evolutionary conserved Ser/Thr protein kinase (Target of Rapamycin - TOR) is crucial for the signaling pathway that integrates the sensing of growth signals to the regulation of metabolism and cellular growth. The TOR pathway controls cell growth by promoting anabolic processes, including protein synthesis and ribosome biogenesis, and inhibiting catabolic processes such as autophagy. Therefore, a greater understanding of the regulation of growth and metabolic pathways under N deprivation and TOR inhibition is necessary to understand the physiology and the mechanisms involved in the biosynthesis of storage compounds in Brazilian native microalgae. In this study, native microalgae, *Scenedesmus obliquus* BR003, *Chlorella vulgaris* BR017, *Chlamydomonas* sp. BR020 and *Monoraphidium* sp. BR023, and one consider model, *Chlamydomonas reinhardtii* CC503 were selected to evaluate the growth parameters, biochemical composition, and metabolite profile under different nitrogen concentrations and TOR pathway inhibition by rapamycin. Whereas N depletion leads to typical stress-related responses in all strains, including reduction of cell growth, chlorophyll and protein, differential accumulation of primary compounds, membrane lipid composition and fatty acid were also observed. The metabolic and physiological analysis showed not only differential sensitivity to the absence of N in relation to N-replete and N-saturated treatments but also differences between strains. The response of growth, dynamics, metabolism profile, and lipid profile to TOR-inhibition by rapamycin in the strains showed a decrease in both cell growth and strong changes in carbon and nitrogen partitioning in the direction of rapid conversion into carbon and nitrogen storage through an accumulation of starch, triacylglycerol and amino acids. Interestingly, the strains showed different metabolite levels, confirming the difference in reserve compound accumulation of each strain. Based on the results, this study indicates that, due to their metabolic profile, microalgae have different

responses in cell growth and metabolism, thus, a better understanding of the metabolic pathways in different strains is needed for biotechnological use.

Keywords: Chlorophytes. *Chlamydomonas reinhardtii*. Primary- and lipid- metabolism. Rapamycin. N-deprivation.

RESUMO

COVELL, Lidiane, D.Sc., Universidade Federal de Viçosa, fevereiro de 2022. **Respostas metabólicas à deficiência de nitrogênio e tratamento de rapamicina em linhagens de microalgas de água doce.** Orientador: Adriano Nunes Nesi. Coorientador: Marcelo Gomes Marçal Vieira Vaz.

A privação de nutrientes leva a diferentes estresses às microalgas, que respondem alterando as vias metabólicas. Após a privação de nitrogênio (N), os acúmulos de amido e triacilgliceróis (TAGs) são significativamente alterados pela reprogramação do metabolismo celular. Além disso, a adaptação do crescimento e proliferação celular às mudanças ambientais é essencial para a sobrevivência dos sistemas biológicos. A proteína quinase Ser/Thr evolutivamente conservada "Alvo da Rapamicina" (TOR) é crucial para a via de sinalização que integra a detecção de sinais de crescimento à regulação do metabolismo e crescimento celular. A via TOR controla o crescimento celular promovendo processos anabólicos, incluindo síntese de proteínas e biogênese de ribossomos, e inibindo processos catabólicos, como autofagia. Portanto, um maior entendimento da regulação do crescimento e das vias metabólicas sob privação de N e inibição de TOR é necessário para entender a fisiologia e os mecanismos envolvidos na biossíntese de compostos de armazenamento em microalgas nativas brasileiras. Neste estudo, microalgas nativas, *Scenedesmus obliquus* BR003, *Chlorella vulgaris* BR017, *Chlamydomonas* sp. BR020 e *Monoraphidium* sp. BR023, e a linhagem modelo, *Chlamydomonas reinhardtii* CC503 foram selecionados para avaliar os parâmetros de crescimento, composição bioquímica e perfil metabólico sob diferentes concentrações de N e inibição da via TOR pela rapamicina. Além de respostas típicas que a privação de N leva como redução do crescimento celular, níveis de clorofilas e proteínas, o acúmulo diferencial de compostos primários, composição lipídica da membrana e ácidos graxos também foram observados. A análise metabólica e fisiológica sugere que as linhagens não apresentam apenas sensibilidade diferencial à ausência de N em relação aos tratamentos repleto e saturado de N, mas também diferenças entre as linhagens observadas em condições ótimas de cultivo. A dinâmica de resposta de crescimento, perfil metabólico e lipídico à inibição de TOR pela rapamicina mostrou uma diminuição no crescimento celular e fortes mudanças na partição de carbono e N por meio de um acúmulo de amido, triacilglicerol e aminoácidos. As linhagens apresentaram diferentes níveis de metabólitos, confirmando a diferença no acúmulo de composto de reserva de cada linhagem. Com base nos resultados, este estudo indica que, devido ao seu perfil metabólico, as microalgas apresentam diferentes respostas no crescimento celular

e metabolismo sendo necessária uma melhor compreensão das vias metabólicas em diferentes linhagens para o uso biotecnológico.

Palavras-chave: Clorófitas. *Chlamydomonas reinhardtii*. Metabolismo primário e lipídico. Rapamicina. Privação de nitrogênio.

SUMMARY

GENERAL INTRODUCTION	13
REFERENCES	15
CHAPTER 1	19
TITLE: Metabolite reprogramming of freshwater microalgae strains during nitrogen depletion	19
1. INTRODUCTION.....	21
2. MATERIAL AND METHODS	22
2.1 Strains and culture media	22
2.2. Culture conditions and growth parameters.....	23
2.3. Extraction of chlorophyll, lipids and primary metabolites.....	24
2.4. Polar metabolite profiling.....	24
2.5. Determination of the chlorophyll and amino acids content.....	25
2.6. Extraction and determination of total water-soluble protein and starch content.....	25
2.7. Determination of neutral lipids.....	25
2.8. Determination of total lipids.....	26
2.9. Statistical analysis	26
3. RESULTS.....	26
3.1. Growth and biomass production.....	26
3.2. Metabolite levels	28
3.3 Metabolic profile	32
3.4 Lipid profile.....	34
3.5 Multivariate analysis	38
4. DISCUSSION.....	40
4.1. Biomass production and cellular components of the strains	40
4.2. Influence of N starvation on amino acid pools and TAG formation.....	41
5. CONCLUSION	43

6. REFERENCES	43
CHAPTER 2	51
TITLE: On the role of TOR signaling networks in freshwater microalgae strains	51
ABSTRACT	52
1. INTRODUCTION	53
2. MATERIAL AND METHODS.....	55
2.1 Strains and culture media	55
2.2 Culture conditions and growth parameters.....	55
2.2.1 Cultivation in microplate.....	55
2.2.2 Cultivation in Erlenmeyer flasks	56
2.2.3 Determination of growth parameters.....	56
2.3 Extraction of chlorophyll, lipids and primary metabolites	57
2.4 Polar metabolite profiling.....	57
2.5 Determination of the chlorophyll content.....	58
2.6 Extraction and determination of starch content.....	58
2.7 Determination of lipids.....	58
2.8 Statistical analysis	59
3. RESULTS.....	59
3.1 Growth curve and maximum growth rate (μ_{max}) of the selected strains with different rapamycin concentration.....	59
3.2 TOR inhibition results in reduced cell number	61
3.3 Rapamycin affects differently chlorophyll contents between strains.....	62
3.4 TOR inhibition alters primary metabolism differentially in three microalgae strains	63
3.5 Repression of the TOR kinase leads to higher levels of storage compounds per cell.....	65
3.6 Lipidomic analysis reveals changes between all strains in the composition of structural lipids	68
3.7 Multivariate analysis	70

4. DISCUSSION.....	71
4.1. TOR inhibition decreases differentialy the cell number in three strains of phylum Chlorophyta	71
4.2. Effect of TOR inhibition on primary metabolism of microalgae cells.....	72
4.3. TOR inhibition by rapamycin changes the carbon partitioning	73
4.4. TOR inhibition affects membrane lipid composition.....	74
5. CONCLUSION	75
6. REFERENCES:.....	76
CHAPTER 3	81
TITLE: The Target of Rapamycin (TOR) – a central growth regulator in microalgae.....	81
ABSTRACT	82
1 INTROCUCTION	83
2 TOR COMPLEXES	85
3 TOR COMPLEXES – CELULAR LOCALIZATION	87
4 EFFECTS OF RAPAMYCIN ON METABOLISM	88
5 TOR SIGNALING IN THE ACCUMULATION OF ENERGY STORAGE MOLECULES	89
6 CONTROL OF AUTOPHAGY BY TOR.....	91
7 ROLE OF TOR IN PROTEIN SYNTHESIS.....	92
8 PHOTOSYNTHETIC ORGANISMS – TOR SIGNALING IN CHLOROPLAST PROCESSES.....	94
9 PERSPECTIVES	95
10 REFERENCES	95
GENERAL CONSIDERATIONS.....	105
SUPPLEMENTARY DATA.....	107

GENERAL INTRODUCTION

During evolution microalgae species developed many protection mechanisms to survive under unfavorable conditions (e.g., variable salinity, temperature, nutrients, UV irradiation) that ultimately led them to produce a wide range of fascinating chemical compounds with novel structures and biological activities (Machado et al., 2016; Rocha et al., 2019). Microalgae are biological resources for a vast array of high-value compounds, are a rich source of protein, carbohydrates, lipids (especially essential fatty acids) and diversity of pigments (such as chlorophylls, carotenoids and phycobiliproteins) (Moreno-Garcia et al., 2017; Mobin and Chowdhury, 2019). The cultivation of these photosynthetic microorganisms represents an attractive process for obtaining biochemical components with high potential applications in the food, pharmaceutical, cosmetic, animal feed and biodiesel industries (Rizwan et al., 2018; Nagappan et al., 2020; Machado et al., 2021; Silva et al., 2021). Generally, the production of these bioproducts varies from species to species and even in the same species of algae (Mobin and Alam, 2017). Microalgae combine properties typical of plants (efficient oxygenic photosynthesis and simplicity of nutritional requirements) with biotechnological attributes properties of microbial cells (fast growth in liquid culture and ability to accumulate or secrete some metabolites) (Herrero et al., 2013; Rizwan et al., 2018; Kumar et al., 2020). This particular combination represents the basis of microalgal biotechnology for the use of these microorganisms on high-valued metabolites production (Rizwan et al., 2018; Kumar et al., 2020).

Microalgal metabolic pathways are heavily influenced by the environment (Gupta et al., 2019). Some stress strategies in culture have been studied for enhancing biomass and high-value compounds yields, like salinity, high temperature, nitrogen sources and other factors (Tan and Lee, 2016; Barsanti and Gualtieri, 2018; Choi et al., 2019). These conditions are defined as a significant deviation from the optimal conditions for the normal development and growth of microalgae and cause changes in all functional levels of the organism.

Limitation and starvation of nitrogen (N) are primary factors that influence cell growth and metabolism, and these conditions may be used to enhance lipids/starch biosynthesis with an optimal growth in microalgae (Machado et al., 2016; Soares et al., 2018; Batista et al., 2019). On the other hand, the regulation of metabolic homeostasis is critical to biosynthetic processes and cellular functions in microalgae (Ford et al., 2019). In this context, an emerging route is the TOR (Target of Rapamycin) kinase pathway (Wullschleger, 2006; Soulard et al., 2009). This

pathway is conserved in eukaryotes and acts as a center for the regulation of numerous cell cycle processes linking the perception of both nutrient availability and favorable external conditions to cell anabolic metabolism, growth, and division by recruiting and regulating the diverse TOR kinase substrates (Díaz-Troya et al., 2008b; Prioretti et al., 2017; Werth et al., 2019).

Nitrogen (N) is one of the most important nutrients for microalgae (Paskuliakova et al., 2018). Numerous studies have suggested that N limitation or starvation is one of the most effective approaches in inducing the accumulation of reserve compounds in microalgae (Arumugam et al., 2013; Singh et al., 2016). When N is insufficient to support protein synthesis, excess carbon (C) from photosynthesis is diverted into storage molecules such as triglycerides and starch (Zhu et al., 2014; Himanshu et al., 2016; Juergens et al., 2016; Zhu et al., 2019).

The TOR kinase plays an essential and conserved role in integrating nutritional and energy inputs for the proper regulation of cell growth in eukaryotes (Díaz-Troya et al., 2008b). TOR controls cell growth by promoting a number of anabolic processes, including translation, ribosome biogenesis, and transcription, and by antagonizing catabolic processes such as autophagy and mRNA degradation (Caldana et al., 2013; Shemi et al., 2015). The first experimental evidence of TOR conservation in these organisms was reported in the model green alga *Chlamydomonas reinhardtii* (Crespo et al., 2005). It has been reported that the growth of *Chlamydomonas* cells is inhibited by rapamycin and this sensitivity of *Chlamydomonas* cells, together with the easy manipulation of this organism, its simple life cycle, and a growing array of genetic and molecular tools (Menand et al., 2002), have positioned this green alga as a convenient model system to investigate the TOR network in photosynthetic eukaryotes. However, the changes in cell morphology, growth, biochemical composition, and photosynthetic performances of different microalgae during the process of N limitation or starvation and inhibition of the TOR signaling pathway still require more detailed studies. The optimization of biomass yield is an important parameter in cultivation of microalgae. Thus, it is essential to understand the behavior of selected microalgal species under different biotic and abiotic conditions.

The present study aimed at the cultivation of freshwater native Brazilian strains under various culture conditions to induce N-depletion and/or TOR pathway inhibition that are likely to influence algal growth and production of value-added products. The species were selected based on its growth rate and different accumulation of storage compounds ability (Rocha et al., 2017). The growth and biochemical and physiological parameters under different culture

conditions were evaluated. The thesis is organized into three independent chapters. The first chapter aimed to understand the adjustments in C/N metabolism in strains that accumulate in distinct amounts, the storage compounds starch/lipid under N depletion conditions. In the second chapter, the objective was to evaluate changes in metabolic compounds by the TOR signaling pathway inhibited by rapamycin in distinct strains. The last chapter presents a critical review of the current state of knowledge of TOR signaling pathway in microalgae.

REFERENCES

- Arumugam M, Agarwal A, Arya MC, Ahmed Z** (2013) Influence of nitrogen sources on biomass productivity of microalgae *Scenedesmus bijugatus*. *Bioresour Technol* **131**: 246–249
- Barsanti L, Gualtieri P** (2018) Is exploitation of microalgae economically and energetically sustainable? *Algal Res* **31**: 107–115
- Batista AD, Rosa RM, Machado M, Magalhães AS, Shalaguti BA, Gomes PF, Covell L, Vaz MGMV, Araújo WL, Nunes-Nesi A** (2019) Increased urea availability promotes adjustments in C/N metabolism and lipid content without impacting growth in *Chlamydomonas reinhardtii*. *Metabolomics*. doi: 10.1007/s11306-019-1496-3
- Caldana C, Li Y, Leisse A, Zhang Y, Bartholomaeus L, Fernie AR, Willmitzer L, Giavalisco P** (2013) Systemic analysis of inducible target of rapamycin mutants reveal a general metabolic switch controlling growth in *Arabidopsis thaliana*. *Plant J* **73**: 897–909
- Choi WJ, Chae AN, Song KG, Park J, Lee BC** (2019) Effect of trophic conditions on microalga growth, nutrient removal, algal organic matter, and energy storage products in *Scenedesmus* (*Acutodesmus*) *obliquus* KGE-17 cultivation. *Bioprocess Biosyst Eng* **42**: 1225–1234
- Crespo JL, Díaz-Troya S, Florencio FJ** (2005) Inhibition of target of rapamycin signaling by rapamycin in the unicellular green alga *Chlamydomonas reinhardtii*. *Plant Physiol* **139**: 1736–1749
- Díaz-Troya S, Pérez-Pérez ME, Florencio FJ, Crespo JL** (2008) The role of TOR in autophagy regulation from yeast to plants and mammals. *Autophagy* **4**: 851–865
- Ford MM, Smythers AL, McConnell EW, Lowery SC, Kolling DRJ, Hicks LM** (2019) Inhibition of TOR in *Chlamydomonas reinhardtii* Leads to Rapid Cysteine Oxidation Reflecting Sustained Physiological Changes. *Cells*. doi: 10.3390/cells8101171
- Gupta S, Pawar SB, Pandey RA, Kanade GS, Lokhande SK** (2019) Outdoor microalgae cultivation in airlift photobioreactor at high irradiance and temperature conditions: effect of

batch and fed-batch strategies, photoinhibition, and temperature stress. *Bioprocess Biosyst Eng* **42**: 331–344

Herrero M, Mendiola JA, Plaza M, Ibañez E (2013) Screening for Bioactive Compounds from Algae. *Screen Bioact Compd from Algae*. doi: 10.1007/978-1-4614-3348-4_35

Himanshu S, Manish RS, Basuthkar JR, Kandala VRC (2016) Regulation of starch, lipids and amino acids upon nitrogen sensing in *Chlamydomonas reinhardtii*. *Algal Res* **18**: 33–44

Juergens MT, Disbrow B, Shachar-Hill Y (2016) The relationship of triacylglycerol and starch accumulation to carbon and energy flows during nutrient deprivation in *Chlamydomonas reinhardtii*. *Plant Physiol* **171**: 2445–2457

Kumar G, Shekh A, Jakhu S, Sharma Y, Kapoor R, Sharma TR (2020) Bioengineering of Microalgae: Recent Advances, Perspectives, and Regulatory Challenges for Industrial Application. *Front Bioeng Biotechnol*. doi: 10.3389/fbioe.2020.00914

Machado M, Bromke M, Domingues Júnior AP, Marçal Vieira Vaz MG, Rosa RM, Vinson CC, Sabir JS, Rocha DI, Martins MA, Araújo WL, et al (2016) Comprehensive metabolic reprogramming in freshwater *Nitzschia palea* strains undergoing nitrogen starvation is likely associated with its ecological origin. *Algal Res*. doi: 10.1016/j.algal.2016.06.003

Machado M, Vaz MGMV, Bromke MA, Rosa RM, Covell L, Souza LP de, Rocha DI, Martins MA, Araújo WL, Szymański J, et al (2021) Metabolic stability of freshwater *Nitzschia palea* strains under silicon stress associated with triacylglycerol accumulation. *Algal Res* **60**: 102554

Menand B, Desnos T, Nussaume L, Bergert F, Bouchez D, Meyer C, Robaglia C (2002) Expression and disruption of the Arabidopsis TOR (target of rapamycin) gene. *Proc Natl Acad Sci U S A* **99**: 6422–6427

Mobin A, Chowdhury H (2019) Commercially important bioproducts from microalgae and their current applications – A review. *Energy Procedia* **160**: 752–760

Mobin S, Alam F (2017) Some Promising Microalgal Species for Commercial Applications: A review. *Energy Procedia* **110**: 510–517

Moreno-Garcia L, Adjallé K, Barnabé S, Raghavan GSV (2017) Microalgae biomass production for a biorefinery system: Recent advances and the way towards sustainability. *Renew Sustain Energy Rev* **76**: 493–506

Nagappan S, Devendran S, Tsai PC, Jayaraman H, Alagarsamy V, Pugazhendhi A, Ponnusamy VK (2020) Metabolomics integrated with transcriptomics and proteomics:

Evaluation of systems reaction to nitrogen deficiency stress in microalgae. *Process Biochem* **91**: 1–14

Paskuliakova A, McGowan T, Tonry S, Touzet N (2018) Microalgal bioremediation of nitrogenous compounds in landfill leachate – The importance of micronutrient balance in the treatment of leachates of variable composition. *Algal Res* **32**: 162–171

Prioretti L, Avilan L, Carrière F, Montané MH, Field B, Grégori G, Menand B, Gontero B (2017) The inhibition of TOR in the model diatom *Phaeodactylum tricornutum* promotes a get-fat growth regime. *Algal Res* **26**: 265–274

Rizwan M, Mujtaba G, Memon SA, Lee K, Rashid N (2018) Exploring the potential of microalgae for new biotechnology applications and beyond: A review. *Renew Sustain Energy Rev* **92**: 394–404

Rocha DN, Martins MA, Soares J, Vaz MGMV, de Oliveira Leite M, Covell L, Mendes LBB (2019) Combination of trace elements and salt stress in different cultivation modes improves the lipid productivity of *Scenedesmus* spp. *Bioresour Technol*. doi: 10.1016/j.biortech.2019.121644

Rocha RP, Machado M, Vaz MGMV, Vinson CC, Leite M, Richard R, Mendes LBB, Araujo WL, Caldana C, Martins MA, et al (2017) Exploring the metabolic and physiological diversity of native microalgal strains (Chlorophyta) isolated from tropical freshwater reservoirs. *Algal Res* **28**: 139–150

Shemi A, Ben-Dor S, Vardi A (2015) Elucidating the composition and conservation of the autophagy pathway in photosynthetic eukaryotes. *Autophagy* **11**: 701–715

Silva MET da, Leal MA, Resende M de O, Martins MA, Coimbra JS dos R (2021) *Scenedesmus obliquus* protein concentrate: A sustainable alternative emulsifier for the food industry. *Algal Res*. doi: 10.1016/j.algal.2021.102468

Singh P, Kumari S, Guldhe A, Misra R, Rawat I, Bux F (2016) Trends and novel strategies for enhancing lipid accumulation and quality in microalgae. *Renew Sustain Energy Rev* **55**: 1–16

Soares J, Kriiger Loterio R, Rosa RM, Santos MO, Nascimento AG, Santos NT, Williams TCR, Nunes-Nesi A, Arêdes Martins M (2018) *Scenedesmus* sp. cultivation using commercial-grade ammonium sources. *Ann Microbiol* **68**: 35–45

Soulard A, Cohen A, Hall MN (2009) TOR signaling in invertebrates. *Curr Opin Cell Biol* **21**: 825–836

- Tan KWM, Lee YK** (2016) The dilemma for lipid productivity in green microalgae: Importance of substrate provision in improving oil yield without sacrificing growth. *Biotechnol Biofuels* **9**: 1–14
- Werth EG, McConnell EW, Couso Lianez I, Perrine Z, Crespo JL, Umen JG, Hicks LM** (2019) Investigating the effect of target of rapamycin kinase inhibition on the *Chlamydomonas reinhardtii* phosphoproteome: from known homologs to new targets. *New Phytol* **221**: 247–260
- Wullschleger S** (2006) TOR signaling in growth and metabolism. *Cell*. doi: 10.1016/j.cell.2006.01.016
- Zhu L, Li S, Hu T, Nugroho YK, Yin Z, Hu D, Chu R, Mo F, Liu C, Hiltunen E** (2019) Effects of nitrogen source heterogeneity on nutrient removal and biodiesel production of mono- and mix-cultured microalgae. *Energy Convers Manag*. doi: 10.1016/j.enconman.2019.112144
- Zhu S, Huang W, Xu J, Wang Z, Xu J, Yuan Z** (2014) Metabolic changes of starch and lipid triggered by nitrogen starvation in the microalga *Chlorella zofingiensis*. *Bioresour Technol* **152**: 292–298

CHAPTER 1

TITLE: Metabolite reprogramming of freshwater microalgae strains during nitrogen depletion

Lidiane Covell¹, Marcelo Gomes Marçal Vieira Vaz¹, Mariana Machado¹, Auxiliadora Martins¹, Dilson Novais Rocha², Marcio Arêdes Martins², Camila Caldana³, Adriano Nunes-Nesi^{1*}

¹ Departamento de Biologia Vegetal, Universidade Federal de Viçosa, 36570-900, Brazil. lidianecovell@gmail.com, marcelogmvvaz@gmail.com, mmachado21@outlook.com, auxiliamartins82@gmail.com, nunesnesi@ufv.br

² Departamento de Engenharia Agrícola, Universidade Federal de Viçosa, 36570-900, Brazil. aredes@ufv.br, dilson.rocha@ufv.br

³ Max Planck Institute of Molecular Plant Physiology, Am Mühlenberg 1, 14476 Potsdam-Golm, Germany. caldana@mpimp-golm.mpg.de

*Corresponding author:

Adriano Nunes-Nesi

Departamento de Biologia Vegetal

Universidade Federal de Viçosa

36570-900 Viçosa, Minas Gerais, Brazil

Phone: +55-31-3612-5357

Email: nunesnesi@ufv.br

ABSTRACT

Nutrient deprivation causes significant stress to microalgae, which responds by altering their metabolic program. In nitrogen (N) deprivation, the accumulation of starch and triacylglycerols (TAGs) are significantly altered following massive reprogramming of cellular metabolism. Thus, a greater understanding of the regulation of metabolic pathways is necessary to understand the physiology and the mechanisms involved in the biosynthesis of storage compounds in microalgae strains. In this study, four uncharacterized microalgae strains, *Scenedesmus obliquus* BR003, *Chlorella vulgaris* BR017, *Chlamydomonas* sp. BR020 and *Monoraphidium* sp. BR023, and the model strain, *Chlamydomonas reinhardtii* CC503, were selected to evaluate the growth parameters, biochemical composition and metabolite profile under N depleted (0 mM), N replete (3.5 mM) and N saturated (7 mM) conditions. Whereas N depletion leads to typical stress-related responses in all strains, including reduction of cell growth, chlorophyll and protein, differential accumulation of primary compounds, membrane lipid composition and fatty acid were also observed. The metabolic and physiological analysis showed not only differential sensitivity to the absence of N in relation to N-replete and N-saturated treatments but also differences between strains. Many studies are driving to the hypothesis of a decrease in biomass accumulation and protein synthesis, with an increase on storage compounds. In this study, it was clearly demonstrated that the highest amount of storage compounds was obtained at the N starvation treatment, in which their growth and protein synthesis was the most affected. In addition, the strains showed different metabolic responses during cultivation. Biomass accumulation and protein content decreased in all strains in N depleted condition. Regarding amino acids, except for the *S. obliquus* BR003, all strains showed a decrease in amino acid content for N depleted treatment at the end of cultivation. It was also observed that only the *Monoraphidium* sp. BR023 did not change the chl *a* content between the treatments. For C contents, as expected, all strains showed an increase in starch and lipid contents for N depleted treatment. Taken together, this study describes an excellent cellular system for probing the N starvation and the consequent changes in carbon flow in relation to both starch/lipid accumulation and their re-mobilization and the changes in free amino acid pools in microalgae.

Keywords: Chlorophytes. *Chlamydomonas reinhardtii*. Metabolomics. Nitrogen nutrition. Biochemical composition. Lipids.

1. INTRODUCTION

Regardless of the intrinsic characteristics of each strain, the growth and metabolism of microalgae are affected by many environmental factors such as light, temperature and nutrient availability, which have a direct influence on the chemical cell composition, thus conditioning the biomass value as raw feedstock (Ikaran et al., 2015; Rocha et al., 2019). Nutrient availability is a vital factor that regulates the development of microalgal production system (Rai and Gupta, 2017). N is one of particularly essential elements for algal biomass production, playing a critical role in the regulation of biomass accumulation and composition (Park et al., 2015; Himanshu et al., 2016; Gargouri et al., 2017). N is an essential macronutrient that supports life in all living beings. This nutrient is an elemental constituent of biomolecules, such as nucleic acids, proteins, chlorophylls, cofactors, and signal molecules, among others (Zhu et al., 2018; Zhu et al., 2019).

N deprivation is a primary factor that influence cell growth and metabolism (Hu et al., 2008; Ikaran et al., 2015; Nagappan et al., 2020). When N is insufficient to support amino acids and protein synthesis, many microalgae are able to adapt their metabolic pathways and excess of carbon (C) from photosynthesis to storage molecules such as triacylglycerols (TAG) and starch (Sarat Chandra et al., 2016; Jagadevan et al., 2018; Mobin and Chowdhury, 2019). In several species, TAG constitute a greater fraction of cell weight, hence being considered the main C and energy storage form in such oleaginous strains (Ikaran et al., 2015; Mobin and Chowdhury, 2019). However, an enhanced TAG accumulation is not the unique metabolic response to N deprivation. Under such circumstances, it has been reported that carbohydrates (mainly starch) reached close to 50% of cell weigh in *Chlorella vulgaris* (Breuer et al., 2012; Chen et al., 2017). Simultaneous accumulation of both compounds has also been reported in some microalgae (Work et al., 2010; Cakmak et al., 2012; Zhu et al., 2014).

From a biological perspective, the accumulation of these C-rich compounds after N depletion occurs when the supply of C and energy through photosynthesis is higher than the metabolic C demand for growth (Hu et al., 2008; Ikaran et al., 2015). It has been also shown that the synthesis of these storage compounds would be mainly as a result of *de novo* C fixation by photosynthesis and its partition between glyoxylate pathways and gluconeogenesis (Work et al., 2010; Blaby et al., 2013). According to Fan et al. (2012), lipid and starch synthesis are competitive pathways in N starved cells of *C. reinhardtii* and C supply seems to be the major factor controlling C partitioning between starch and lipids accumulation in this species. On the other hand, the common physiological behavior associated with N deprivation is the reduction

in the level of nitrogenous compounds (Guerra et al., 2013; Sarat Chandra et al., 2016; Nagappan et al., 2020), mainly, chlorophyll and proteins. The chlorophyll degradation not only provides the cells with valuable N but also protects the cells from oxidative stress (Griffiths et al., 2011; Nama et al., 2015). Protein degradation generates N, which could be remobilized for the synthesis of new enzymes essential for cell viability under stress (López et al., 2010; Nama et al., 2015).

It is important to note that different metabolic responses have been reported in species belonging to the same genus, and that the degree of response can be different even among strains from the same species (Holbrook et al., 2014; Himanshu et al., 2016; Singh et al., 2016; El-Sheekh et al., 2018). Thus, it is essential to understand the behavior of selected microalgal species under stress conditions.

The selection and characterization of microalgal strains with high biomass production and reserve compounds are important to obtain appropriate strains for biotechnological applications and arrive at a better understanding of the relationship between microalgal metabolism and physiology. Therefore, the aim of this work is to evaluate the physiological and metabolic changes associated with different N supply in media containing different microalgae strains. It is known that different microalgae strains, under favorable growth conditions, have different behavior in relationship to biomass accumulation and the reserve compounds. According to Rocha et al., (2017), among the strains, *S. obliquus* BR003 was obtained the greatest biomass levels. However, *Chlamydomonas* sp. BR020 had the highest starch content. In contrast to its high starch content, *Chlamydomonas* sp. BR020 as well as *C. vulgaris* BR017 presented one of the lowest levels of lipids while the highest value was observed for *Monoraphidium* sp. BR023. Therefore, the hypothesis of this work is that the highest amount of reserve compounds will be more accumulated in the N starvation treatment, and of the other hand, growth and protein synthesis will be negatively affected, and that these responses are highly modulated by differential and species/strain-specific metabolic changes. The metabolite reprogramming observed for various pathways in relation to N starvation in microalgae, have been discussed.

2. MATERIAL AND METHODS

2.1 Strains and culture media

The four freshwater microalgae strains (Chlorophyta) used in this study are available at the Collection of Cyanobacteria and Microalgae at the Universidade Federal de Viçosa (CCM-UFV), available in the Laboratory of Phycology and Molecular Biology, Plant Biology

Department at the Universidade Federal de Viçosa, Viçosa, Minas Gerais State, Brazil (20°45'14"S, 42°52'54"W). *S. obliquus* BR003, *C. vulgaris* BR017, *Chlamydomonas* sp. BR020 and *Monoraphidium* sp. BR023 were isolated from water samples collected from freshwater reservoirs in the city of Viçosa/Brazil (Rocha et al., 2017). The model green microalga, *Chlamydomonas reinhardtii*, is widely selected for diverse experiments, because of its advantages, such as fast growth, short generation time, strong adaptability, easy cultivation and easy isolation of mutants (Harris, 2001).

The strains were cultivated in the mixotrophic Tris-Acetate-Phosphate (TAP) medium (Coleman, 1990). Before the addition of ammonium to the medium, the cultures were incubated for 12 h in TAP medium without N source to exhaust the original ammonium in the medium (Li et al., 2016). To investigate the effects of different N concentrations, we conducted three treatments with initial N-added concentrations of 0 mM (N-depleted), 3.5 mM (N-replete), and 7 mM (N-saturated) during 36 hours. Strains were cultivated under 24 ± 2 °C, with a 16 h/8 h (light/dark) photoperiod cycle, at a constant irradiance of $100 \mu\text{mol photons m}^{-2} \text{s}^{-1}$, under continuous shaking at 110 rpm. N-starved cells were then collected in stationary phase, washed twice in N-free media and used to inoculate a new culture at a starting density of around 0.2 $\text{OD}_{680\text{nm}}$, which corresponds to a cell dry weight of 100 mg L^{-1} .

2.2. Culture conditions and growth parameters

The experimental cultures were grown in 125 mL Erlenmeyer flasks, filled with 75 mL of culture medium and four repetitions per treatment. The experiments were carried out in a growth room, applying the same conditions described above. For the characterization of cell growth in different media and selection of sampling points we performed growth curves for each strain. The cellular growth was monitored hourly by absorbance on 680 nm and 750 nm in spectrophotometer (UVM 340, AsysHitech) for three days (Griffiths et al., 2011). Based on the obtained growth curves we selected four points to collect samples as indicated in the **Figure 1A**: at initial phase Lag 1 (0h), early logarithmic phase Log 1 (10h), late logarithmic phase Log 2 (18h); and stationary phase Sta 1 (36h).

The dry weight determination was performed by filtration of 10mL in nitrocellulose membranes $0,45 \mu\text{m}$ (Millipore®) (Griffiths et al., 2011). The ash-free dry weight was determined by subtraction of the dry weight by ash weight after calcination. The result was expressed in grams of ash-free weight per L of culture. These data were used to determine specific growth rate (μ) for all strains in exponential phase (Contois, 1959).

2.3. Extraction of chlorophyll, lipids and primary metabolites

Primary metabolites, chlorophyll and lipids were extracted as described elsewhere (Salem et al., 2016). About 5 mg of freeze-dried biomass cells were used for metabolite profiling. They were re-suspended in 1 mL of pre-cooled (-20°C) methyl tert-butyl ether (MTBE)-extraction buffer [methanol: methyl tert-butyl-ether (1 : 3; v/v) mixture; Biosolve, the Netherlands] (Salem et al., 2016). The resuspended cell pellets were immediately mixed before ultrasonification in an ice-cooled water bath for 10 min. Then the samples were incubated for 1h on an orbital shaker at 4°C. To induce the liquid: liquid-phase separation, 650 µL of UPLC-grade methanol : water (1 : 3; v/v; Biosolve, the Netherlands) was added to the homogenate and mixed, before centrifuging at 20 000 g for 5 min at 4°C in a table top centrifuge. The addition of the methanol: water mixture resulted in a separation of an upper MTBE-phase, containing lipids and chlorophyll, and a lower phase, containing the polar and semi-polar metabolites, next to a solid pellet in the bottom of the 1.5 mL plastic tube. The solid pellet contains the precipitated proteins next to starch and other insoluble polymers, such as cell wall fragments (Salem et al., 2016). For further analysis, 500 µL of the MTBE-phase and 650 µL of the lower, aqueous-phase were transferred to fresh 1.5 mL tubes. Samples of the lipid-phases (MTBE-phase) were dried in a vacuum concentrator and re-suspended in the proper resuspension buffer. The polar aliquots were also dried in a vacuum concentrator before storing the pellets at -80°C. The solid pellet was frozen in liquid N and stored at -80°C until further extraction. To measure the impact of contaminations from the extraction process, the whole extraction procedure was additionally performed with two–four empty, sample-free, 1.5 mL tubes (method blank).

2.4. Polar metabolite profiling

The derivatization of the polar-sample (primary metabolites) was performed on a gas chromatographer Agilent 6890 (Agilent) coupled to a Pegasus HT ToF mass spectrometer (LECO Instruments, St. Joseph, MI, USA) as outlined in a previous study (Lisec et al., 2006). Chromatograms were exported from ChromaToF v 3.25 (LECO Corp., St. Joseph, MI, USA) and processed using R. Peak detection, retention time alignment, and library matching were performed using the TargetSearch R package from Bioconductor, as performed by (Bromke et al., 2013). For data normalization, each analyte peak intensity was normalized by the median of all data and dry weight.

2.5. Determination of the chlorophyll and amino acids content

To determine the chlorophyll content, 100 μ L of the methyl tert-butyl ether (MTBE)-phase was mixed with 90% methanol and measured using an UV-VIS spectrometer at wavelengths of 665 nm and 652 nm to distinguish between chlorophyll *a* and chlorophyll *b*. The chlorophyll *a*, *b* and total content were determined using the equations described by Bar-Nun (Bar-nun and Ohad, 1980). Total amino acid contents were quantified as reported in Cross et al. (2006).

2.6. Extraction and determination of total water-soluble protein and starch content

Extraction of total protein water-soluble protein content was carried out according to Meijer and Wijffels (1998) and quantification was performed using the Bradford method (Bradford, 1976) at a wavelength of 595 nm in a microplate reader. As a standard, it was used as bovine serum albumin (BSA), and the results were expressed in mg / g of ash free dry mass.

In order to analyze the starch content, we optimized the standard protocol from Smith and Zeeman, 2006. The frozen cell pellet was first washed with 80% ethanol, incubated for 10 min at room temperature. Afterwards the pellet was dissolved in 250 μ l sterile water. Then 250 μ l 100 mM sodium acetate was added and starch was hydrolyzed by heating for 3h at 99 $^{\circ}$ C. The dissolved starch was digested into its glucose monomers over night with an enzyme mix of α -amylase (4.2 units per sample) and α -amylglucosidase (10 units per sample). The digested extract was centrifuged and the supernatant with the starch-derived glucose monomers was dissolved in 100 mM HEPES-buffer (pH 7) that contained 5 mM $MgCl_2$, 60 mg/ml ATP, 36 mg/ml NADP and glucose-6-phosphate-dehydrogenase (1 unit per sample). The baseline was measured at 340 nm and the subsequent addition of hexokinase started the reactions and the increase of $NADPH+H^+$ was measured at 340 nm with a plate reader in 96-well formats.

2.7. Determination of neutral lipids

Determination of total neutral lipids was performed according to (De la Hoz Siegler et al., 2012) with minor modifications using the lipophilic fluorescent dye Nile Red. Triolein was used to prepare the standard curve. 300 μ l of sample and 1 μ l of Nile Red dissolved in 1 mg/mL acetone were used. Nile Red fluorescence intensity was quantified in a microplate reader (Victor X5 – Perkin Elmer) using 485 nm filters for excitation and 595 nm for emission. A black 96-well plate was used to prevent fluorescence scattering. Fluorescence intensity data were normalized by cell density.

2.8. Determination of total lipids

Briefly, 650 μL of the lower aqueous phase of the MTBE extraction, described above, were transferred to fresh 1.5-ml Eppendorf tubes, dried in a SpeedVac and resuspended in a volume of 300 μL of a mixture of acetonitrile: isopropanol (7: 3; Biosolve, the Netherlands). Chromatograms were further processed using Excalibur software version 2.30 (Thermo-Fisher) and Progenesis CoMet software (Version 2.4; Nonlinear, Newcastle upon Tyne, UK). The UPLC/MS lipids data were processed using ToxID (Version 2.1.2; Thermo). To remove noise and contaminants, data for every lipid species with average peak height lower than the average peak height of the method blanks or with 50% of the values below 1,000 arbitrary counts were removed from the dataset. The remaining peaks were then assigned to annotated lipid species using an in-house-generated lipid database for *Arabidopsis* (Hummel et al., 2011). The data were normalized by the median of all data and dry weight. For some lipid species, more than one peak was detected having the same m/z and identical adducts but different retention times. In these cases, we added the letter A or B to the compound name, depending on their elution order.

2.9. Statistical analysis

The experiments were performed and analyzed following a completely randomized design with four replicates for each treatment. The values obtained for all variables were submitted to analysis of variance (ANOVA, $P < 0.05$) followed by Tukey's test ($P \leq 0.05$), and one analyses of the interaction effects, using the software R (Grace and Hudson, 2016). Primary metabolites and lipid profile data were log2 transformed. In addition , data were subjected to a principal component analysis (PCA) using the pcaMethods package in the software R (Stacklies et al., 2007).

3. RESULTS

3.1. Growth and biomass production

The analysis of growth parameters aimed to identify how cells produced biomass over time under different N concentrations. To determine the effect of N on the five strains grown under mixotrophic conditions, absorbance readings of OD_{680nm} were taken over a period of 36 hours (**Figure 1A-E**). The growth curve was noticeably affected by the differences in N availability. After 10 hours of cultivation, there was no or minor increase in cell growth during N-depleted condition. On the other hand, strains treated with N-saturated and N-replete showed a similar

growth pattern and displayed continuous growth throughout the culture time. Biomass measured as ash free dry weight (AFDW) is shown in four different point of cultivation, in which in the N group reached between 0.75 g.L^{-1} (*Monoraphidium* sp. BR023) and 0.983 g.L^{-1} (*C. reinhardtii* CC503) while the group without N were 0.335 g.L^{-1} (*Chlamydomonas* sp. BR020) and 0.502 g.L^{-1} (*C. reinhardtii* CC503) (**Figure 1F-J**). Additionally, the impacts of growth, in different culture media, were shown in maximum growth rate (μ_{max} , **Figure 1K**), and demonstrated that there is a difference for the 0 mM treatment when compared to the 7 mM and 3.5 mM treatments. All interactions between strain, time and concentration were statistically significant, even the triple interaction (Table S 1, supplementary material).

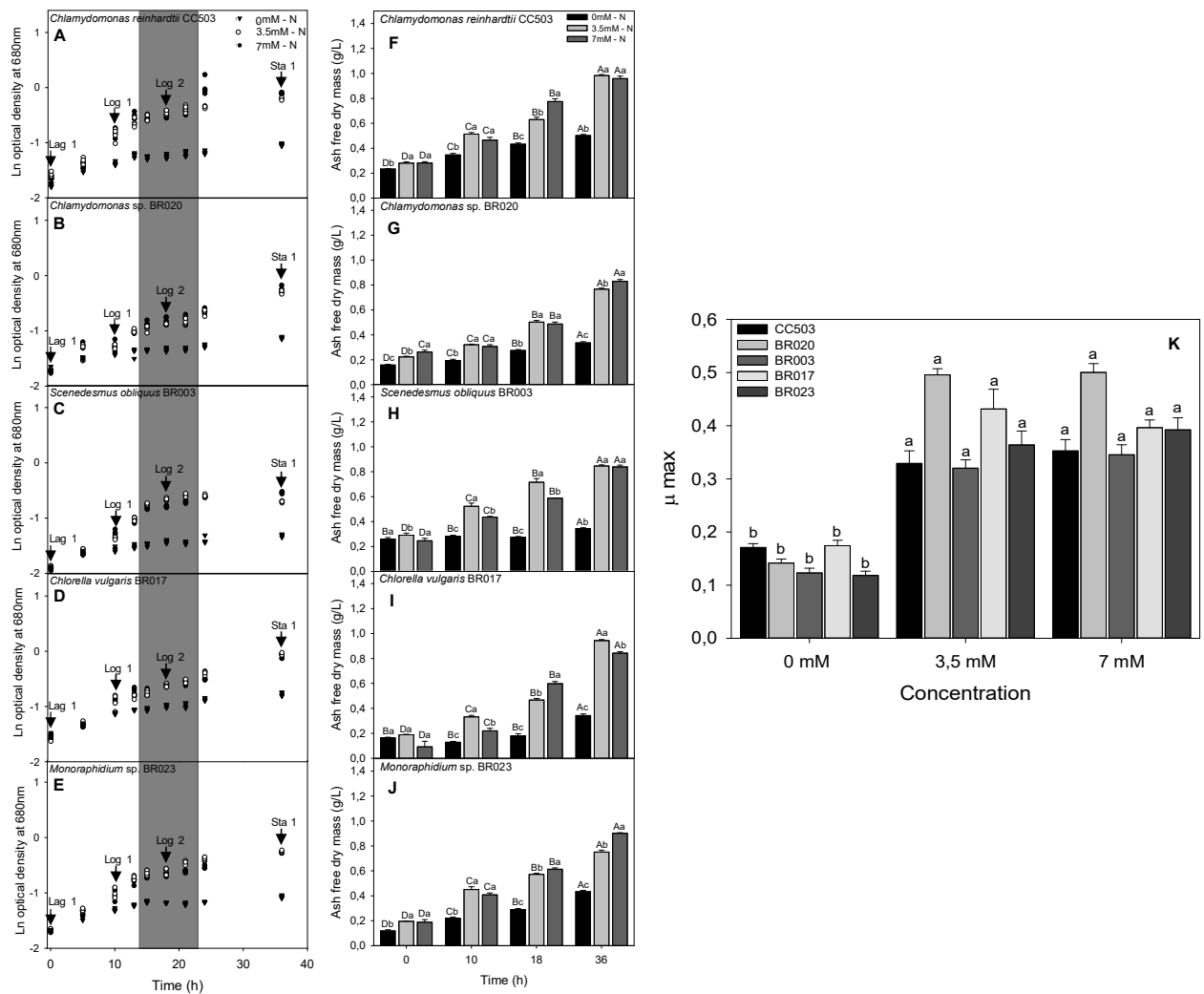


Figure 1. Growth parameters of five strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, *S. obliquus* BR003, *C. vulgaris* BR017 and *Monoraphidium* sp. BR023) cultivated under tree different nitrogen (N) concentration (0mM, 3.5mM and 7mM). Growth curves based on Optical Density (OD) at 680 nm (A-E), ash-free dry mass (F-J) and maximum growth rate (μ_{max}) (K). Period of dark highlighted in gray. Values represent the average error of four replications. Means followed by the same letters do not differ by the Tukey test ($P < 0.05$), lowercase letters compare different N concentration at the same growth phase and uppercase letters compare each treatment in different growth phases.

3.2. Metabolite levels

The analysis of variance for chlorophyll contents revealed that all interactions between strain, time of culture and N concentration were statistically significant, with the exception of interaction between strain and time for Chl *a/b* ratio (Table S 1). Chlorophyll levels, under N-replete and N-depleted both chlorophyll (Chl) *a* and *b* content were reduced in all strains throughout cultivation (Figure 2A-J). The Chl *a/b* ratio for these treatments decreased throughout cultivation in all strains, except for *S. obliquus* BR003 (Figure 2 K-O). For N-saturated, it was observed that at the end of the cultivation all strains had an increase in the chl *a* content, except for *Monoraphidium* sp. BR023 (Figure 2 A-E).

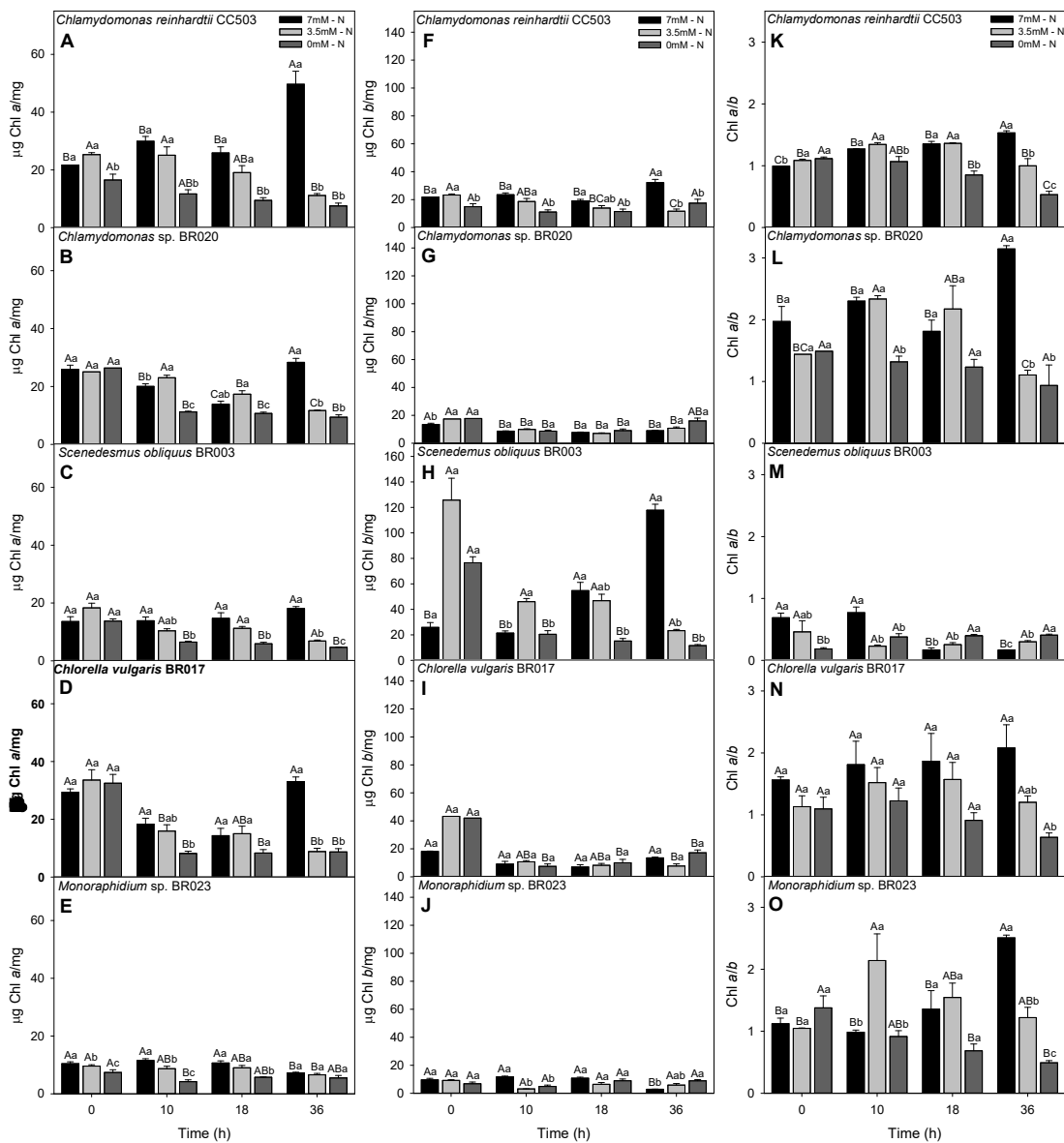


Figure 2. Chlorophyll *a* (A-E), *b* (F-J) content and Chlorophyll *a/b* ratio (K-O) of five strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, *S. obliquus* BR003, *C. vulgaris* BR017 and *Monoraphidium* sp. BR023) cultivated under three different nitrogen (N) concentration (0mM, 3.5mM and 7mM). Values represent the average error of four replications. Means followed by the same letters do not differ by the Tukey test ($P < 0.05$), lowercase letters compare different N concentration at the same growth phase and uppercase letters compare each treatment in different growth phases.

Concerning the amount of other N-containing compounds, for all strains, except for *S. obliquus* BR003, the total free amino acids content decreased at the end of cultivation for N-depleted treatment, except *S. obliquus* BR003 that presented similar value during cultivation (Figure 3 A-E). The total protein content, for all strains showed a very similar behavior throughout the 36 hours of cultivation according to the analysis of variance (Table S1), and had a significant increase for N-saturated treatment and the lowest values for N-depleted (Figure 3 F-J).

The protein/amino acids ratio showed higher values for *C. reinhardtii* CC503 and *S. obliquus* BR003 during the cultivation when compared to the other strains (Figure 3 K-O).

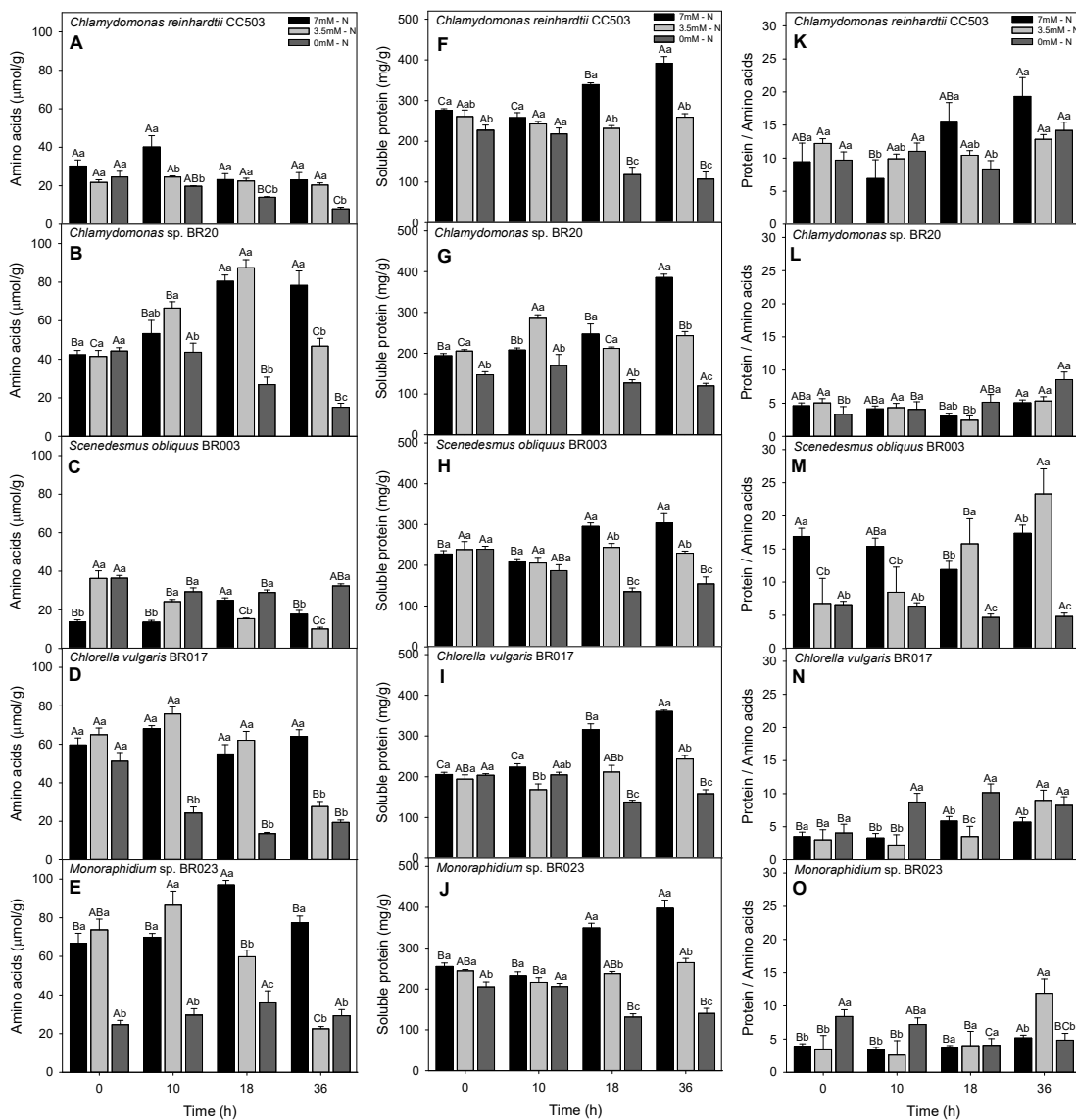


Figure 3: Nitrogen (N) containing metabolites of five strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, *S. obliquus* BR003, *C. vulgaris* BR017 and *Monoraphidium* sp. BR023) cultivated under three different nitrogen (N) concentration (0mM, 3.5mM and 7mM). (A-E) total free amino acids content, (F-J) total protein content and (K-O) protein / amino acids ratio. Values represent the average error of four replications. Means followed by the same letters do not differ by the Tukey test ($P < 0.05$), lowercase letters compare different N concentration at the same growth phase and uppercase letters compare each treatment in different growth phases.

Regarding the main C containing metabolites, the decrease in nitrogen concentration resulted in an increase in sucrose content for most strains, while for *S. obliquus* BR003 and *C. reinhardtii* CC503 the sucrose content was very low for all treatment (**Figure 4 A-E**). The increase in the concentration in the starch content is inversely proportional to the concentration of N. Increase in starch levels during different N concentration are shown in **Figure 4 F-J**. Starch levels increased after 10 hours of cultivation for N-depleted treatment for all strains. The highest starch content was for *C. reinhardtii* (944.80 mmol glucose equiv/md DW). Furthermore, N-replete treatment showed a greater increase in starch content at 36 hours when compared to the N- saturated treatment. N-depleted treatment promoted higher neutral lipids production in comparison with the other N concentrations (**Figure 4 K-O**). Interestingly that for *C. reinhardtii* CC503 the content of neutral lipids was higher during the 36 hours of cultivation for the N-depleted treatment when compared to the N-saturated and N-replete treatments (**Figure 4 K**). Although the highest value in the neutral lipids content was for *Monoraphidium* sp. BR023 (34.74 %) for N-depleted treatment, this strain also presented a high initial value in the neutral lipid levels (16.18 %) after 10 hours of cultivation (**Figure 4 O**).

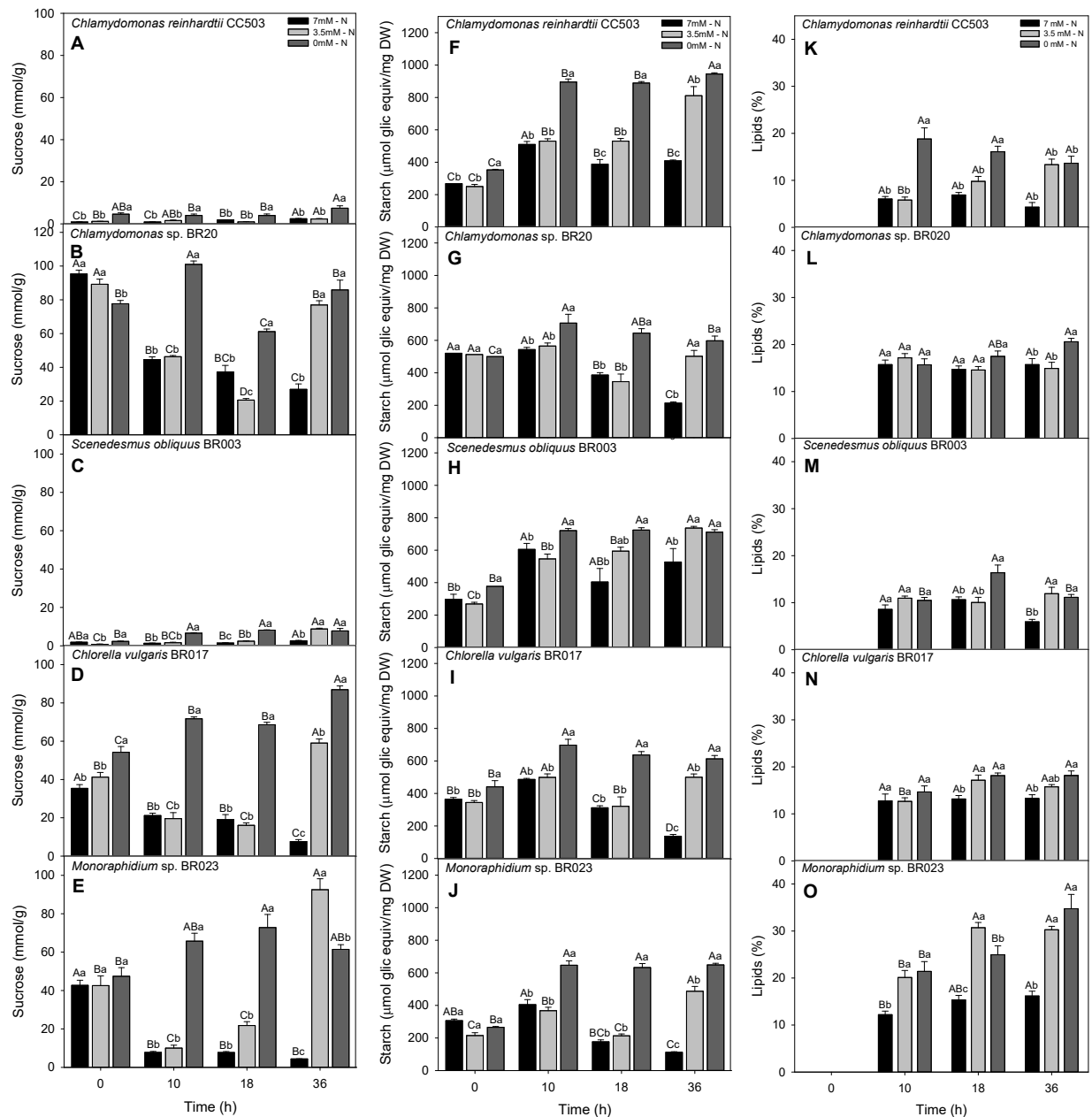


Figure 4: Carbon containing metabolites of five strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, *S. obliquus* BR003, *C. vulgaris* BR017 and *Monoraphidium* sp. BR023) cultivated under three different nitrogen (N) concentration (0mM, 3.5mM and 7mM). Sucrose content (A-E), starch content (F-J) and neutral lipids content (K-O). Values represent the average error of four replications. Means followed by the same letters do not differ by the Tukey test ($P < 0.05$), lowercase letters compare different N concentration at the same growth phase and uppercase letters compare each treatment in different growth phases.

3.3 Metabolic profile

In order to verify the metabolic alterations between different concentrations of N in the medium, we employed an established GC/TOF–MS based metabolite profiling platform. The metabolite profile is exhibited in a Heat map, wherein the colors red and blue mean increase and decrease, respectively, in relation to N-depleted in each growth phase (**Figure 5, Table S 2-6**). Heat map exhibited decrease in several amino acids during N-depleted in comparison with N-saturated and N-replete treatments in all strains during the 36 hours of cultivation. Still in relation to amino acid compounds, similar behavior was observed between *Chlamydomonas* sp. BR020 and *S. obliquus* BR003, and between *C. reinhardtii* CC503, *C. vulgaris* BR017 and *Monoraphidium* sp. BR023. Remarkably, the levels of alanine, arginine, and glutamine increased for *C. reinhardtii* CC503, *C. vulgaris* BR017 and *Monoraphidium* sp. BR023 strains in the N-saturated and N-replete treatments when compared to *Chlamydomonas* sp. BR020 and *S. obliquus* BR003 strains (**Table S 2-6**). For ornithine and tryptophan, there was a decrease and an increase, respectively, for *S. obliquus* BR003, different from the other strains. Regarding sugar content, it was possible to observe that *S. obliquus* BR003 strain presented higher values compared to the other strains.

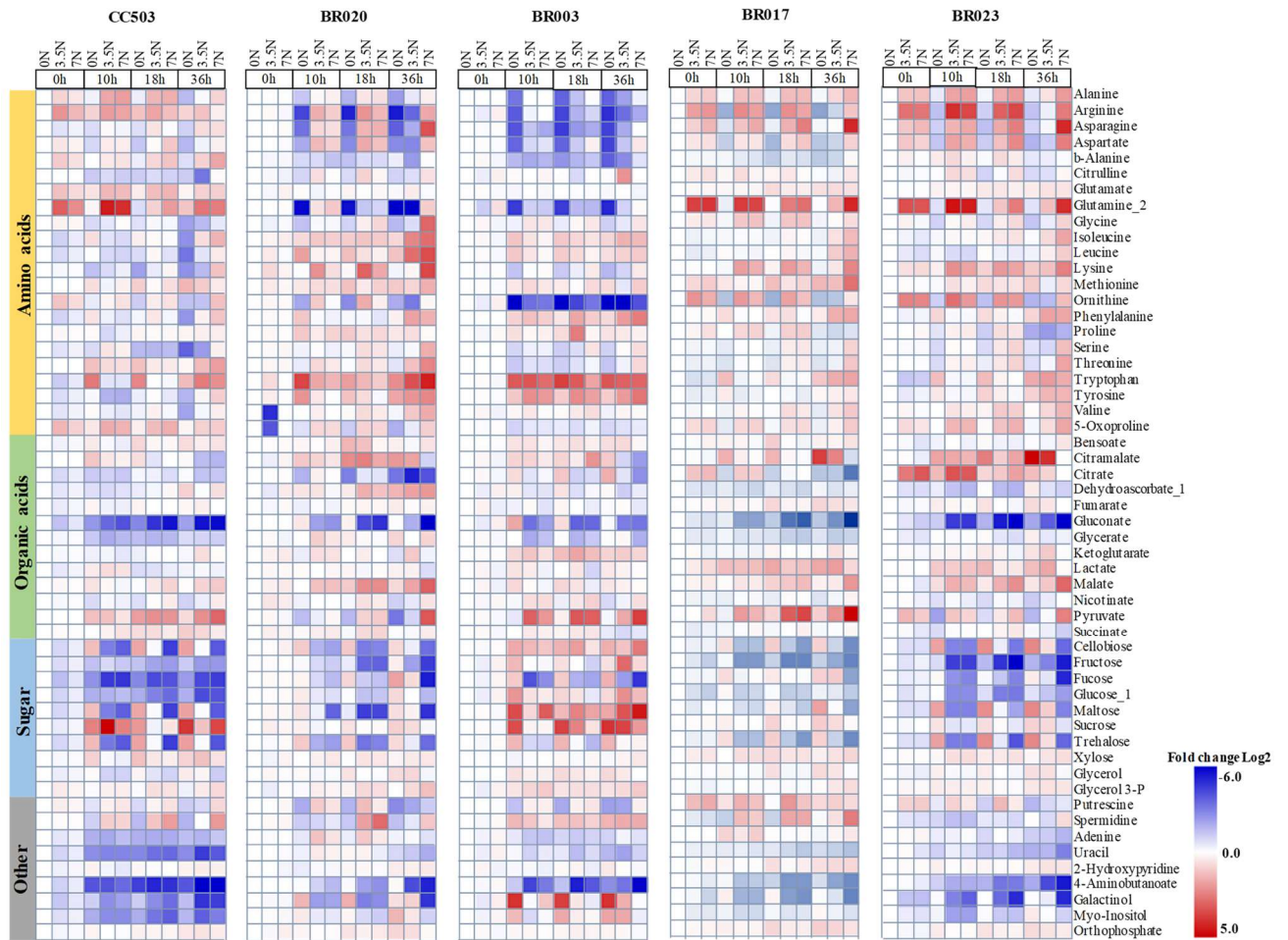


Figure 5. Heat map representing the changes in relative metabolite levels of five strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, *S. obliquus* BR003, *C. vulgaris* BR017 and *Monoraphidium* sp. BR023) cultivated under three different nitrogen (N) concentration (0mM, 3.5mM and 7mM). Data are scaled to the mean response measured for N-deplete 0h for each strain; values presented are means of four biological replicates. The average and statistical analysis are presented in supplementary table 2 - 6.

3.4 Lipid profile

It was detected 103 compounds from 8 different lipid classes among the identified metabolites 12 belongs to diacylglycerols (DAGs), 17 digalactosyldiacylglycerols (DGDGs), 6 Lysophosphatidylcholines (LysoPCs), 9 monogalactosyldiacylglycerols (MGDGs), 20 phosphatidylcholine (PCs), 21 phosphatidylethanolamines (PEs), 7 phosphatidylglycerol (PGs) and 11 sulfoquinovosyl diacylglycerol (SQDGs). The five strains showed different lipid profile (**Figure 6**). Accordingly, changes of lipid levels in BR020, BR017 and BR023 were more pronounced than in CC503 and BR003 during the cultivation (**Figure 6, Table S 7-11**). Intriguingly, during N-starvation there was a clear decrease in the levels of lipids from thylakoid membranes in BR020, BR017 and BR023 strains. Most of the chloroplast galactolipids (DAGs, MGDGs, DGDGs and SQDGs) increased in BR020, BR017 and BR023 cells under N-saturated conditions. Some phospholipids were not detected in CC503, namely PC 32:0, PC 32:1, PC 32:2, PC 32:3, PC 32:4, PC 34:2, PC 34:4, PC 34:5, PC 34:6, PC 36:3, PC 36:6, PC 38:3, PE 32:1, PE 32:2, PE 34:3, PE 34:4, PE 34:5, PE 36:3, PE 36:4, PE 36:5, PE 36:6, PE 40:1 and PG 32:1. Similarly, in BR017 PE 32:2, PE 34:4, PE 34:6, PE 36:3, PE 36:4, PE 38:3, PE 40:1, PE 40:3, PG 32:0, PG 32:1, PG 34:2, PG 34:3, PG 34:4, PG 36:1 and PG 36:2 were not detected. In the STA phase (36h) the remodeling of thylakoid membranes seems to be more severe in the BR020 strain, followed by CC503, as MGDGs decreased in N-replete and N-saturated treatments. Meanwhile under N-replete conditions these lipids are maintained at stable level in the other strains.

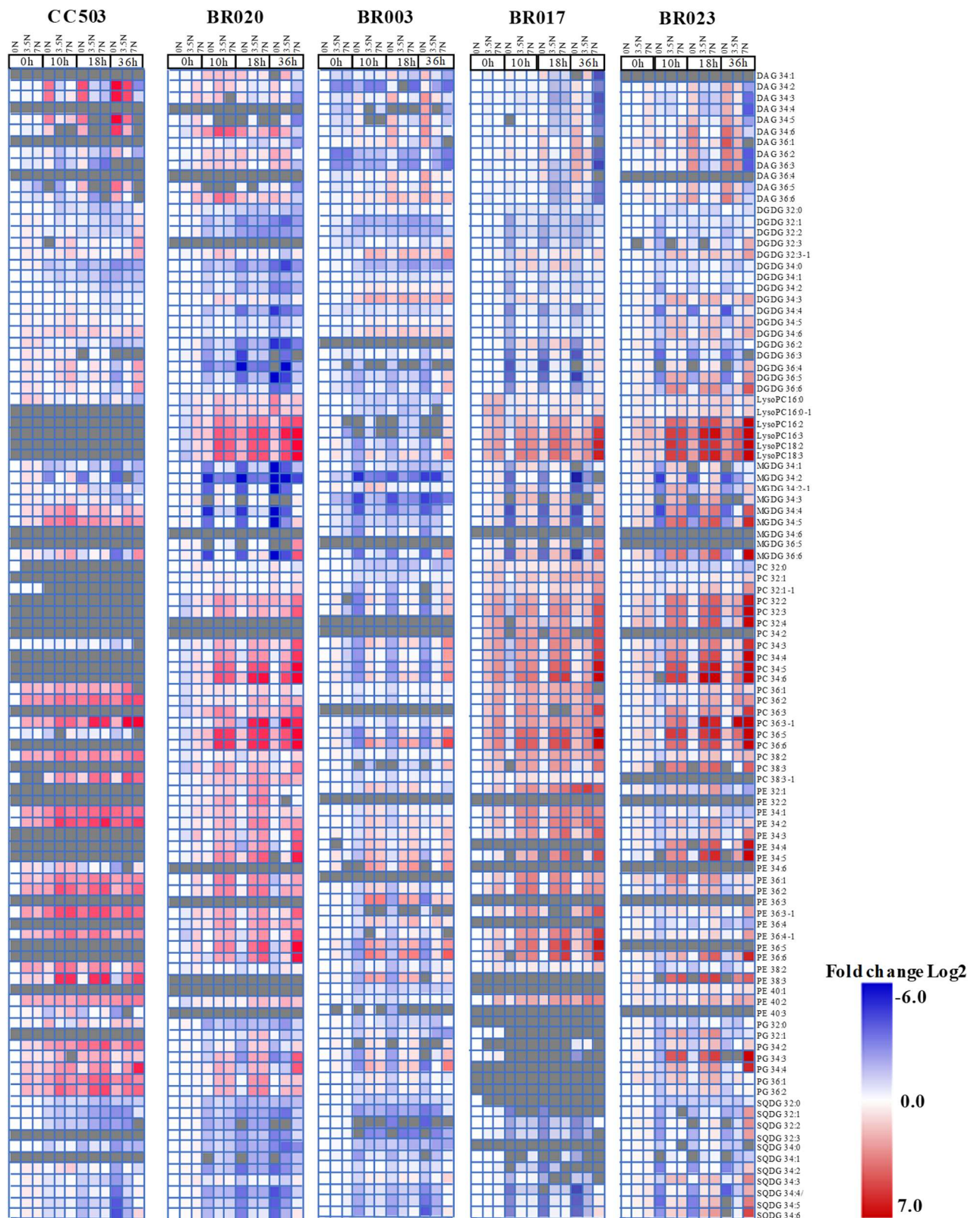


Figure 6. Heat map representing the changes in relative lipid contents of five strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, *S. obliquus* BR003, *C. vulgaris* BR017 and *Monoraphidium* sp. BR023) cultivated under tree different nitrogen (N) concentration (0mM, 3.5mM and 7mM). Data are scaled to the mean response measured for N-deplete 0h for each strain; values presented are means of four biological replicates. The average and statistical analysis are presented in supplementary table S 7 – 11.

The total fatty acids are presented in **Figure 7** and represent all fatty acids obtained from non-polar extracts. It was 20 fatty acids identified in the lipid samples harvested during LOG and STA phase. Saturated fatty acids (FA16:0, FA18:0, FA20:0 and FA26:0) and unsaturated fatty acid such as FA16:3, FA18:2, FA18:3, FA20:1 and FA22:1 showed higher abundance in BR003 and BR023 strains. While CC503, BR017 and BR020 strains were richer in saturated fatty acids like FA26:0, FA28:0 and FA30:0. Interestingly, BR003 showed a lower detection in the number of fatty acid. In addition, in all strains we observed a significant increase in C18:1 during N starvation.

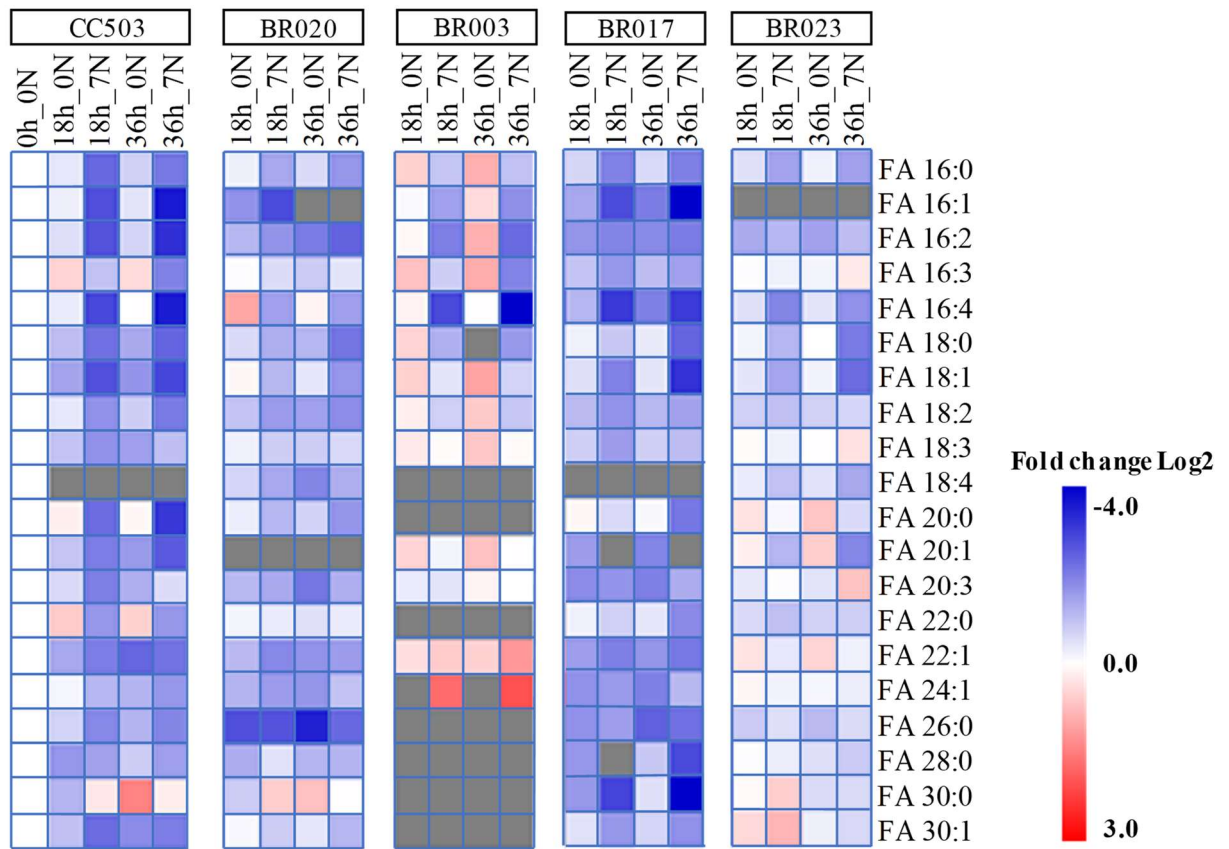


Figure 7. Heat map representing the changes in relative fatty acids contents (FA) of five strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, *S. obliquus* BR003, *C. vulgaris* BR017 and *Monoraphidium* sp. BR023) cultivated under two different N concentration (0mM and 7mM) in LOG (18h) and STA (36h) phase. Data are scaled to the mean response measured for N-deplete 0h for each strain; values presented are means of four biological replicates. The average and statistical analysis are presented in the supplementary table S 7 – 11.

In addition, all strains showed a marked accumulation of TAGs in N starvation in LOG and STA phase. Besides the chloroplast membrane lipids, a total of 79 TAGs were identified in the strains (**Figure 8**). Although all strains showed accumulation of lipid in the N-starvation treatment, BR003 and BR023 strains showed the greatest accumulation of lipid at 18h and 36h (LOG and STA phase), especially TAG 48, TAG 50 and TAG 52. On the other hand, regardless of the N concentration lowest lipid accumulation was observed in CC503 strain, which, in addition to having the lowest accumulation, also had the lowest number of identified TAGs, such as TAG 46:4, TAG 48:3, TAG 48:4, TAG 48:5, TAG 48:6, TAG 48:7, TAG 48:8, TAG 48:9, TAG 50:3, TAG 50:4, TAG 50:7, TAG 50:8, TAG 50:9, TAG 52:5, TAG 58:5 and TAG 58:6 were not detected in this strain.

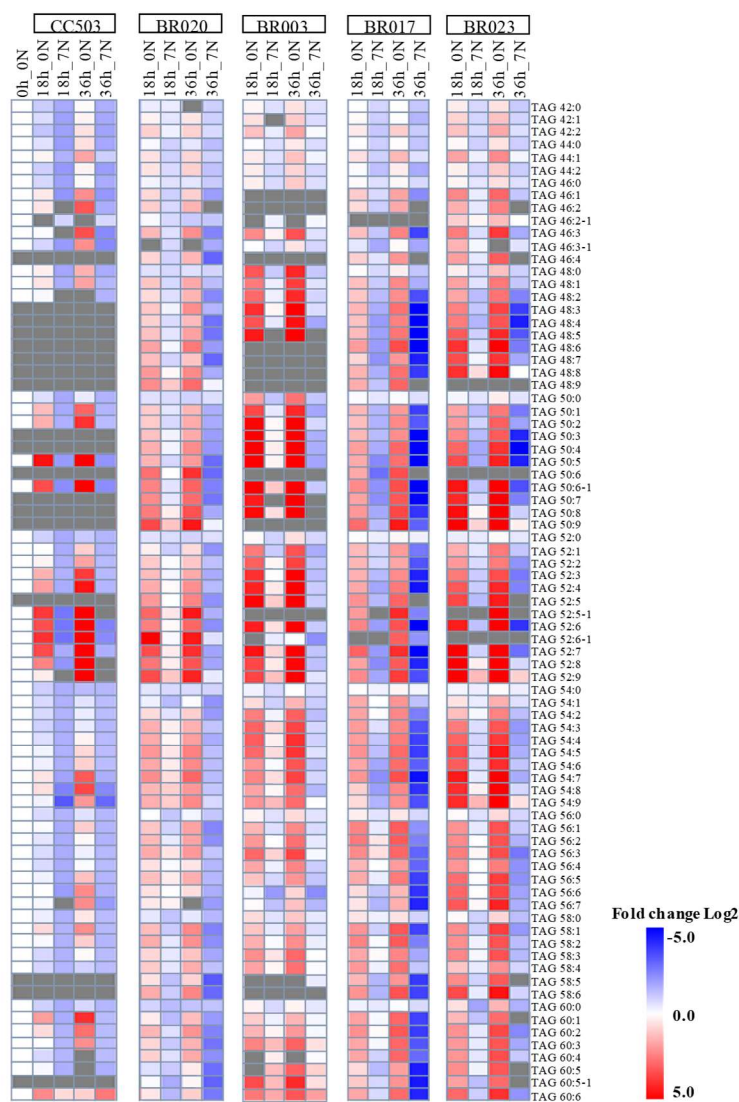
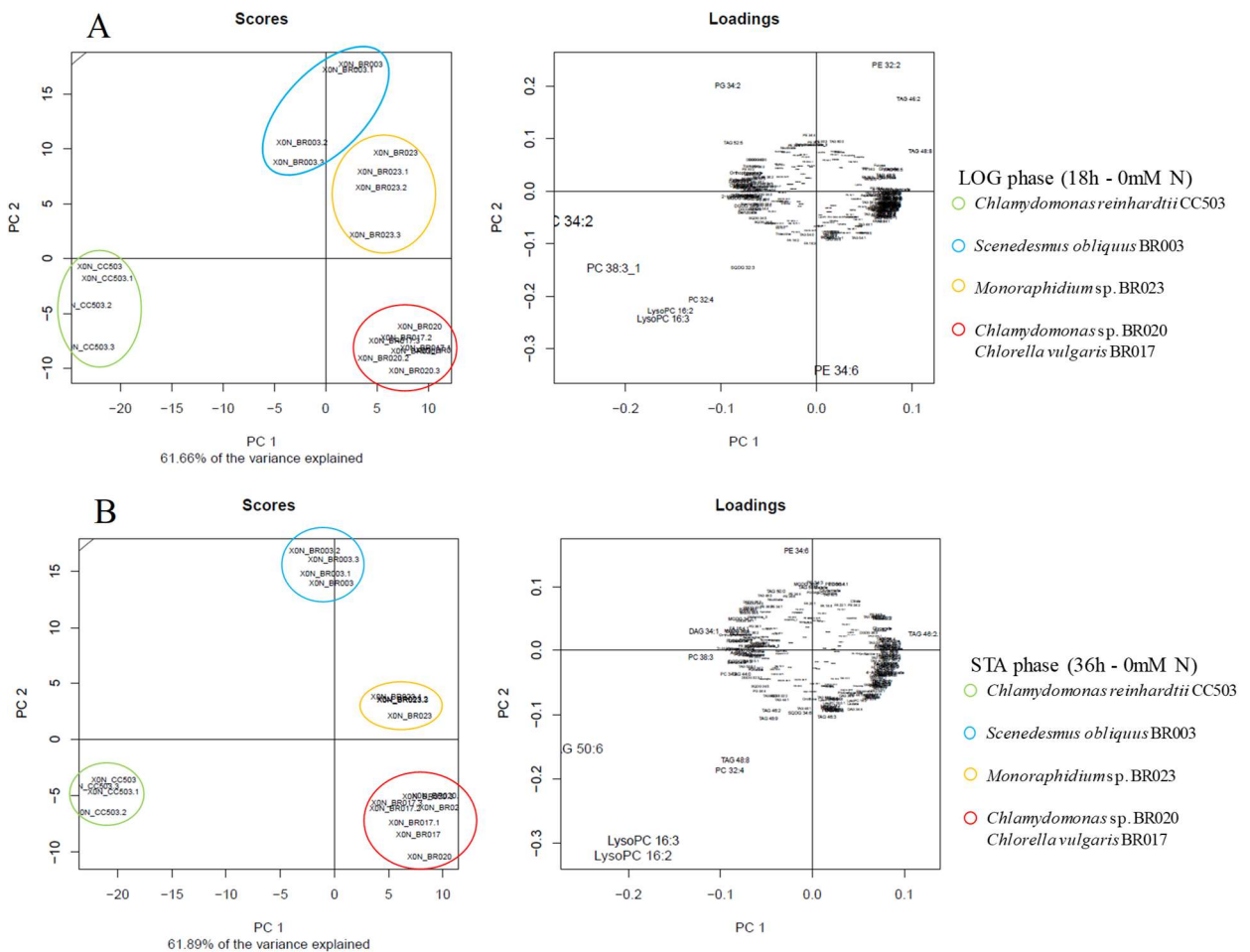


Figure 8. Heat map representing the changes in relative triacylglycerols (TAGs) contents of five strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, *S. obliquus* BR003, *C. vulgaris* BR017 and *Monoraphidium* sp. BR023) cultivated under two different nitrogen (N) concentrations (0mM and 7mM) in LOG (18h) and STA (36h) phase. Data are scaled to the mean response measured for N-deplete 0h for each strain; values presented are means of four biological replicates. The average and statistical analysis are presented in the supplementary table S 7 – 11.

3.5 Multivariate analysis

Principal component analysis (PCA) was performed to visualize the similarities between the treatments and thus explore in more detail the effect of the different N concentrations on growth and metabolic responses of the five strains. In the primary metabolite and lipids PCA (**Figure 9 Table S 2-11**) is evident the separation of the strains. N-depleted treatment, the principal components (PC1 and PC2) explained about 61% of the variance, and four groups were formed in the LOG and STA phase: (1) *C. reinhardtii* CC503; (2) *S. obliquus* BR003; (3) *Monoraphidium* sp. BR023 and (4) *Chlamydomonas* sp. BR020 and *C. vulgaris* BR017. Regarding N-saturated treatment, the principal components (PC1 and PC2) explained about 60% of the variance, and four groups were formed in the LOG phase, as in N-depleted treatment, however, in the STA phase five groups were formed: (1) *C. reinhardtii* CC503; (2) *S. obliquus* BR003; (3) *Monoraphidium* sp. BR023; (4) *Chlamydomonas* sp. BR020 and (5) *C. vulgaris* BR017. The analysis results indicated that the strains were clustered especially due to the high abundance of lipid compounds (**Figure 9A - D**).



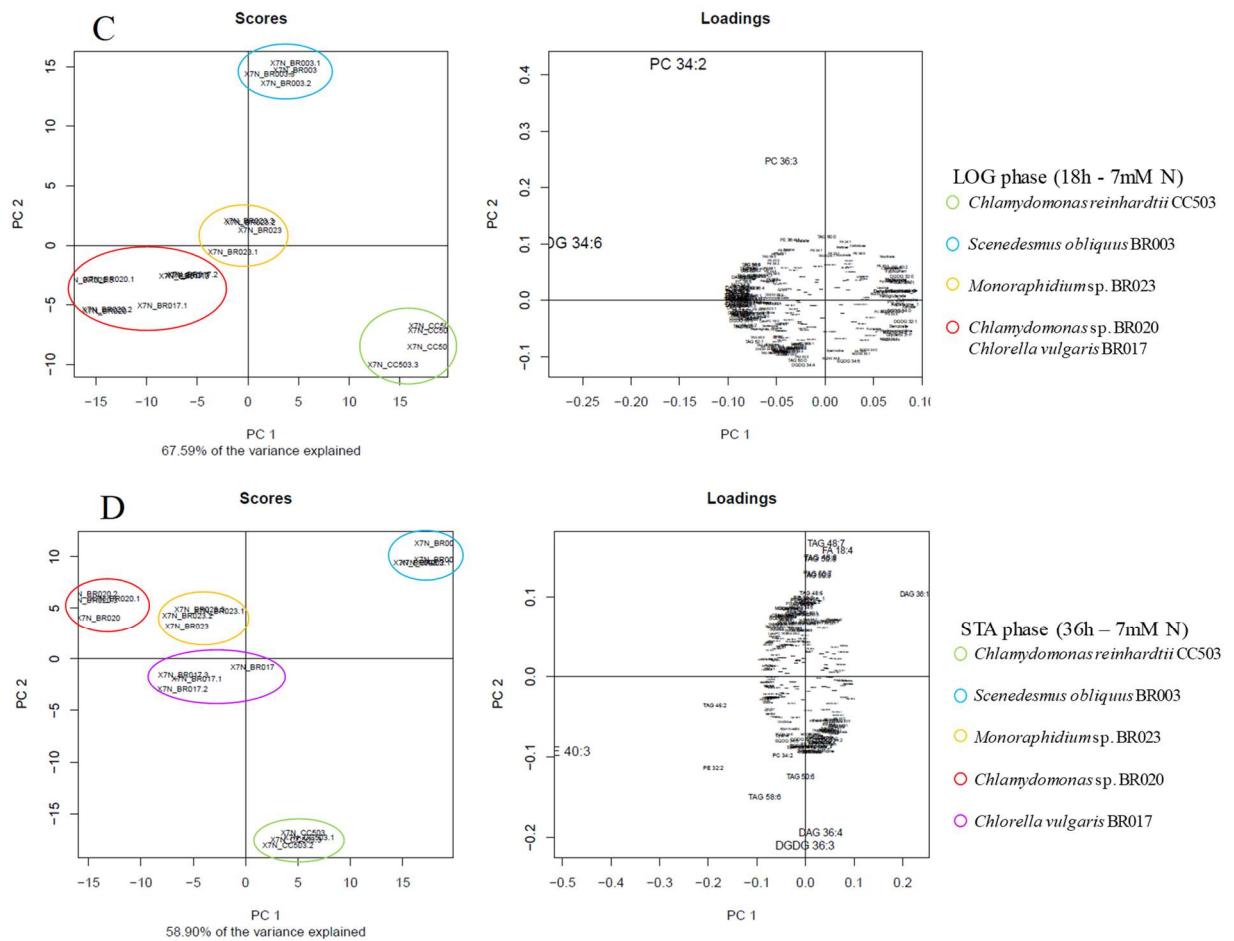


Figure 9. Principal component analysis (PCA) score plot derived data of five strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, *S. obliquus* BR003, *C. vulgaris* BR017 and *Monoraphidium* sp. BR023) cultivated under two different nitrogen (N) concentrations (0mM and 7mM) in LOG (18h) and STA (36h) phase. Primary metabolites and lipids profile displayed between 58.90% and 67.59% of the variance explained in the two principal components, PC1 and PC2. Values presented are means of four biological replicates. The average and statistical analysis are presented in the supplementary table S 2 – 11

4. DISCUSSION

Algal cell growth and metabolism can be manipulated by altering environmental conditions to optimize algal biomass production and composition through altering nutrient levels in the medium. Nitrogen limitation or starvation remarkably influences the growth and physiology of microalgae (Sanz-Luque et al., 2015; Dhup, 2016). Breuer et al. (2012) reported that the biomass of nine microalgae, significantly decreased during nitrogen starvation. It has been also demonstrated that nutrient limitation could enhance the accumulation of energy-rich compounds like starch and /or lipid in many microalgae (Zhu et al., 2014; Himanshu et al., 2016; Li-Beisson et al., 2019). Therefore, in this study, four microalgal strains isolated from freshwater reservoirs, and belonging to the phylum Chlorophyta and one model strain, *C. reinhardtii* CC503, were analyzed under different nitrogen concentration.

4.1. Biomass production and cellular components of the strains

As expected, N depletion caused relevant changes on the algal cell growth. Biomass concentration at the end of culture period (**Figure 1 F-J**) is an important factor, given that it indicates the productivity that can be achieved in culture systems (Nagappan and Kumar, 2021). The concentration obtained for the strains considered in this study for N-replete and N-saturated was about 0.8 ± 0.01 g/L while for N-depleted the highest value was 0.5 ± 0.009 g/L. Previous studies, using the same growth media and similar culture conditions (Park et al., 2015; Zhu et al., 2019), obtained similar results to those obtained here. The values obtained here are higher than those previously reported by Rocha et al., 2017, which varied between 0.134 and 0.054 mg mL⁻¹ day⁻¹ for these same freshwater algal strains. However, in the present study, a mixotrophic medium was used, which was reported to have greater growth potential for some species compared to autotrophic growth (Moon et al., 2013; Girard et al., 2014; Miao et al., 2016).

In this study, upon 10 hours of N starvation, chlorophyll *a* content had been significantly reduced. The degradation of chlorophyll not only provides the cells with valuable N but also protects the cells from oxidative stress (Breuer et al., 2012; Nagappan and Kumar, 2021). Like Yang et al., (2015). Here we demonstrated that the chl *a* content for *Monoraphidium* sp BR023 showed a small variation between treatments throughout the cultivation. Healey, (1978) reported that the ratios of chlorophyll *a* (the main pigment in most microalgal cells) to dry weight (DW) varied more than 30-fold with changes in species composition, temperature and nutrients, and light availability.

Cellular proteins perform the catalytic and structural roles in the form of enzymes, filaments, and tubules. As protein is majorly made up of N, the deprivation of the same has a profound impact on microalgae (Barsanti and Gualtieri, 2018; Nagappan et al., 2020). Five microalgal organisms have been exposed to different N concentration and protein changes have been observed. Protein decrease during N deprivation in all five species tested (**Figure 3 F-J**). A similar reduction in protein content was found for several microalgae during N deficiency (Li et al., 2016; Sarat Chandra et al., 2016; Kumar et al., 2020).

Starch and lipid are two major C and energy storage compounds of many plants and microalgal cells, particularly in response to stress conditions (Zhu et al., 2018; Batista et al., 2019; Covell et al., 2020). Upon depletion of the N in the growth medium, microalgae cease to synthesize N-rich molecules (e.g., proteins and nucleic acids) but continue to synthesize lipid and carbohydrates (Williams and Laurens, 2010). The first compound known to accumulate to high levels during N deprivation is starch (Klein, 1987) and the upregulation of starch synthesis gene expression has been reported during N deprivation (Ball et al., 1990; Miller et al., 2010; Juergens et al., 2015). Increases in starch levels during N deprivation are shown in Figure 4 F-J.

As mentioned earlier, prolonged N starvation of algae leads to multiple stresses associated with nutritional depletion, which in turn leads to major metabolic reorganization in the cell to form abundant amounts of starch and lipid. In this study, it was clear that the reserve compounds are strain-dependent. Here, *C. reinhardtii* CC503 under N-starvation showed increases in starch content throughout cultivation, which did not occur for lipid contents (**Figure 4F and 4K**). On the other hand, *Monoraphidium* sp. BR023 under the same conditions, showed an opposite behavior in relation to the accumulation of reserves (**Figure 4J and 4O**).

4.2. Influence of N starvation on amino acid pools and TAG formation

In recent years, there have been several attempts to study the metabolic, transcriptomic and proteome changes in various cellular systems in relation to their N starvation (Illman et al., 2000; Wu et al., 2013; Kiyota et al., 2014; Himanshu et al., 2016). A Heatmap was exhibited in order to assess whether the N starvation in the current study is accompanied by concomitant changes in cellular free amino acid pools while central C metabolism is readjusting. As expected, N starvation of cells led to overall drop in amino acid pool size (**Figure 5**). Remarkably, levels of glutamate decreased and methionine increased in the N-starvation treatment during the STA phase only for *C. reinhardtii* CC503. The pool levels of citrulline and

ornithine rise N-saturated treatment, as expected. These N-rich metabolites are not only N-rich but also critical regulatory metabolites that control a wide variety of biosynthetic reactions (Himanshu et al., 2016).

Lipid production in various algae is being explored as an alternate source of fuel and a major source of biofuel. Thus, the focus of the scientific community has been largely on understanding and maximizing the lipid production in *C. reinhardtii* and other algal strains (Huang et al., 2010; James et al., 2011; Li et al., 2015; Cheng et al., 2018). It is important to understand the important roles that fatty acids (FA) play in the interactions of microalgae cells with the environment. The biosynthesis of fatty acids and glycerolipids in plants and eukaryotic algae involves the cooperation of two subcellular organelles, plastids and the endoplasmic reticulum (ER) and for eukaryotic algae, this is also the case (Harwood, 2013). The fatty acids produced in plastids can be incorporated into the plastid pool of phosphatidate which can be subsequently converted into chloroplast membrane lipids, MGDG, DGDG, SQDG and PG (Harwood and Guschina, 2009; Harwood, 2013). Diacylglycerol (DAG) originating from a pool of endoplasmic reticulum PC, may be transferred from ER to plastids and be used there as a substrate for the synthesis of chloroplast lipids (Harwood, 2013; Liu and Benning, 2013). It has been suggested to be important, for normal photosynthetic function, the unique lipid composition in chloroplast membranes, (e.g. high level of fatty acid unsaturation) as well as the galactosylglycerides which are mainly located in these cell organelles (Siegenthaler and Murata, 2004). Investigation of various *Chlamydomonas* mutants with specific alterations in lipid composition showed to be a powerful tool to study structure-function relationships. Sato et al., (2003) compared the structural and functional properties of photosystem II (PSII) between a mutant of *C. reinhardtii* defective in SQDG (hf-2) and the wild type, to examine the role of SQDG in thylakoid membranes. It has been suggested that SQDG is involved in the maintenance of the normal properties of PSII (Sato et al., 2003).

Cells under N limitation display a rapid stress response, presumably related to the requirements for protein synthesis, whereas more sophisticated lipid-remodeling systems seem to be necessary during N limitation (Machado et al., 2016; Tan and Lee, 2016; Rocha et al., 2019). TAGs are accumulated in many algae species as storage products and the level of TAG accumulation is very variable (Thompson, 1996; John et al., 2002; Rocha et al., 2017; Li-Beisson et al., 2019) and may be stimulated by a number of environmental factors. When algal growth slows down and there is no requirement for the synthesis of new membrane compounds, the cells divert fatty acids into TAG synthesis before conditions improve and there is a need for

further growth (Harwood, 2013; Liu and Benning, 2013; Zienkiewicz et al., 2016). Nitrogen deprivation seems to be a major factor which is important for the stimulation of TAG synthesis (Goncalves et al., 2016; Li-Beisson et al., 2019). Many algae sustain a two- to three-fold increase in lipid content, predominantly TAG, under N limitation (Tan and Lee, 2016; Sivaramakrishnan and Incharoensakdi, 2017; Nagappan and Kumar, 2021).

5. CONCLUSION

In this study, the physiological analysis of the five strains grown in N depleted, N replete and N saturated regimes showed a decrease in biomass accumulation in N depleted conditions.

Regarding the metabolomic analysis, N starvation leads to typical stress-related responses such as reduction of chlorophyll and protein levels.

For C contents, as expected, all strains showed an increase in starch and lipid contents for N depleted treatment.

It seems reasonable to suggest that some microalgae are programmed to accumulate lipids, like *Monoraphidium* sp. BR023 while others, like *Chlamydomonas reinhardtii* CC503, accumulate starch during the stationary phase under nutritional stress as N deplete. All strains also markedly differ in membrane lipid composition, FA saturation and increase in TAGs.

Thus, reinforcing the importance of evolutionary and ecological constraints in the final phenotype of a strain.

6. REFERENCES

- Ball SG, Dirick L, Decq A, Martiat JC, Matagne RF** (1990) Physiology of starch storage in the monocellular alga *Chlamydomonas reinhardtii*. *Plant Sci* **66**: 1–9
- Bar-nun S, Ohad I** (1980) the accuracy of sometimes reported chloroplastic Mn abundance determinations based only on a presumed specific activity of Mn in the growth media. **69**: 363–374
- Barsanti L, Gualtieri P** (2018) Is exploitation of microalgae economically and energetically sustainable? *Algal Res* **31**: 107–115
- Batista AD, Rosa RM, Machado M, Magalhães AS, Shalaguti BA, Gomes PF, Covell L, Vaz MGMV, Araújo WL, Nunes-Nesi A** (2019) Increased urea availability promotes adjustments in C/N metabolism and lipid content without impacting growth in *Chlamydomonas reinhardtii*. *Metabolomics*. doi: 10.1007/s11306-019-1496-3

- Blaby IK, Glaesener AG, Mettler T, Fitz-Gibbon ST, Gallaher SD, Liu B, Boyle NR, Kropat J, Stitt M, Johnson S, et al** (2013) Systems-level analysis of nitrogen starvation-induced modifications of carbon metabolism in a *Chlamydomonas reinhardtii* starchless mutant. *Plant Cell* **25**: 4305–4323
- Bradford M** (1976) A Rapid and Sensitive Method for the Quantitation of Microgram Quantities of Protein Utilizing the Principle of Protein-Dye Binding. *Anal Biochem* **72**: 248–254
- Breuer G, Lamers PP, Martens DE, Draaisma RB, Wijffels RH** (2012) The impact of nitrogen starvation on the dynamics of triacylglycerol accumulation in nine microalgae strains. *Bioresour Technol* **124**: 217–226
- Bromke MA, Giavalisco P, Willmitzer L, Hesse H** (2013) Metabolic Analysis of Adaptation to Short-Term Changes in Culture Conditions of the Marine Diatom *Thalassiosira pseudonana*. *PLoS One* **8**: 1–11
- Cakmak T, Angun P, Demiray YE, Ozkan AD, Elibol Z, Tekinay T** (2012) Differential effects of nitrogen and sulfur deprivation on growth and biodiesel feedstock production of *Chlamydomonas reinhardtii*. *Biotechnol Bioeng* **109**: 1947–1957
- Chen H, Zheng Y, Zhan J, He C, Wang Q** (2017) Comparative metabolic profiling of the lipid-producing green microalga *Chlorella* reveals that nitrogen and carbon metabolic pathways contribute to lipid metabolism. *Biotechnol Biofuels*. doi: 10.1186/s13068-017-0839-4
- Cheng P, Wang Y, Osei-Wusu D, Wang Y, Liu T** (2018) Development of nitrogen supply strategy for *Scenedesmus rubescens* attached cultivation toward growth and lipid accumulation. *Bioprocess Biosyst Eng* **41**: 435–442
- Coleman AW** (1990) The *Chlamydomonas* sourcebook. A comprehensive guide to biology and laboratory use. *Trends Genet* **6**: 67
- Contois DE** (1959) Kinetics of Bacterial Growth: Relationship between Population Density and Specific Growth Rate of Continuous Cultures. *J Gen Microbiol* **21**: 40–50
- Covell L, Machado M, Vaz MGMV, Soares J, Batista AD, Araújo WL, Martins MA, Nunes-Nesi A** (2020) Alternative fertilizer-based growth media support high lipid contents without growth impairment in *Scenedesmus obliquus* BR003. *Bioprocess Biosyst Eng* **43**: 1123–1131
- Cross JM, Von Korff M, Altmann T, Bartzetko L, Sulpice R, Gibon Y, Palacios N, Stitt M** (2006) Variation of enzyme activities and metabolite levels in 24 arabidopsis accessions growing in carbon-limited conditions. *Plant Physiol* **142**: 1574–1588

- Dhup S** (2016) Understanding Urea Assimilation and its Effect on Lipid Production and Fatty Acid Composition of *Scenedesmus* Sp. *SOJ Biochem* **2**: 1–7
- El-Sheekh M, Abomohra AEF, Eladel H, Battah M, Mohammed S** (2018) Screening of different species of *Scenedesmus* isolated from Egyptian freshwater habitats for biodiesel production. *Renew Energy* **129**: 114–120
- Fan J, Yan C, Andre C, Shanklin J, Schwender J, Xu C** (2012) Oil accumulation is controlled by carbon precursor supply for fatty acid synthesis in *Chlamydomonas reinhardtii*. *Plant Cell Physiol* **53**: 1380–1390
- Gargouri M, Bates PD, Park JJ, Kirchhoff H, Gang DR** (2017) Functional photosystem i maintains proper energy balance during nitrogen depletion in *Chlamydomonas reinhardtii*, promoting triacylglycerol accumulation. *Biotechnol Biofuels* **10**: 1–21
- Girard JM, Roy ML, Hafsa M Ben, Gagnon J, Faucheux N, Heitz M, Tremblay R, Deschênes JS** (2014) Mixotrophic cultivation of green microalgae *Scenedesmus obliquus* on cheese whey permeate for biodiesel production. *Algal Res* **5**: 241–248
- Goncalves EC, Wilkie AC, Kirst M, Rathinasabapathi B** (2016) Metabolic regulation of triacylglycerol accumulation in the green algae: identification of potential targets for engineering to improve oil yield. *Plant Biotechnol J* **14**: 1649–1660
- Grace SC, Hudson DA** (2016) Processing and Visualization of Metabolomics Data Using R. *Metabolomics - Fundam Appl*. doi: 10.5772/65405
- Griffiths MJ, Garcin C, van Hille RP, Harrison STL** (2011) Interference by pigment in the estimation of microalgal biomass concentration by optical density. *J Microbiol Methods* **85**: 119–123
- Guerra LT, Levitan O, Frada MJ, Sun JS, Falkowski PG, Dismukes GC** (2013) Regulatory branch points affecting protein and lipid biosynthesis in the diatom *Phaeodactylum tricornutum*. *Biomass and Bioenergy* **59**: 306–315
- Harris EH** (2001) *Chlamydomonas* as a model organism. *Mol Biol* **52**: 363–406
- Harwood IAG ad JL** (2013) Algae for biofuels and energy. *Algae for Biofuels and Energy* 1–288
- Harwood JL, Guschina IA** (2009) The versatility of algae and their lipid metabolism. *Biochimie* **91**: 679–684
- Healey FP** (1978) Physiological indicators of nutrient deficiency in algae. *SIL Commun* 1953-1996 **21**: 34–41

- Himanshu S, Manish RS, Basuthkar JR, Kandala VRC** (2016) Regulation of starch, lipids and amino acids upon nitrogen sensing in *Chlamydomonas reinhardtii*. *Algal Res* **18**: 33–44
- Holbrook GP, Davidson Z, Tatara RA, Ziemer NL, Rosentrater KA, Scott Grayburn W** (2014) Use of the microalga *Monoraphidium* sp. grown in wastewater as a feedstock for biodiesel: Cultivation and fuel characteristics. *Appl Energy* **131**: 386–393
- Hu Q, Sommerfeld M, Jarvis E, Ghirardi M, Posewitz M, Seibert M, Darzins A** (2008) Microalgal triacylglycerols as feedstocks for biofuel production: Perspectives and advances. *Plant J* **54**: 621–639
- Huang GH, Chen F, Wei D, Zhang XW, Chen G** (2010) Biodiesel production by microalgal biotechnology. *Appl Energy* **87**: 38–46
- Hummel J, Segu S, Li Y, Irgang S, Jueppner J, Giavalisco P** (2011) Ultra performance liquid chromatography and high resolution mass spectrometry for the analysis of plant lipids. *Front Plant Sci* **2**: 1–17
- Ikaran Z, Suárez-Alvarez S, Urreta I, Castañón S** (2015) The effect of nitrogen limitation on the physiology and metabolism of *Chlorella vulgaris* var L3. *Algal Res* **10**: 134–144
- Illman AM, Scragg AH, Shales SW** (2000) Increase in *Chlorella* strains calorific values when grown in low nitrogen medium. *Enzyme Microb Technol* **27**: 631–635
- Jagadevan S, Banerjee A, Banerjee C, Guria C, Tiwari R, Baweja M, Shukla P** (2018) Recent developments in synthetic biology and metabolic engineering in microalgae towards biofuel production. *Biotechnol Biofuels* **11**: 1–21
- James GO, Hocart CH, Hillier W, Chen H, Kordbacheh F, Price GD, Djordjevic MA** (2011) Fatty acid profiling of *Chlamydomonas reinhardtii* under nitrogen deprivation. *Bioresour Technol* **102**: 3343–3351
- John U, Tillmann U, Medlin LK** (2002) A comparative approach to study inhibition of grazing and lipid composition of a toxic and non-toxic clone of *Chrysochromulina polylepis* (Prymnesiophyceae). *Harmful Algae* **1**: 45–57
- Juergens MT, Deshpande RR, Lucker BF, Park JJ, Wang H, Gargouri M, Omar Holguin F, Disbrow B, Schaub T, Skepper JN, et al** (2015) The regulation of photosynthetic structure and function during nitrogen deprivation in *Chlamydomonas reinhardtii*. *Plant Physiol* **167**: 558–573
- Kiyota H, Hirai M, Ikeuchi M** (2014) NblA1/A2-Dependent Homeostasis of Amino Acid Pools during Nitrogen Starvation in *Synechocystis* sp. PCC 6803. *Metabolites* **4**: 517–531

- Klein U** (1987) Intracellular Carbon Partitioning in *Chlamydomonas reinhardtii*. *Plant Physiol* **85**: 892–897
- Kumar G, Shekh A, Jakhu S, Sharma Y, Kapoor R, Sharma TR** (2020) Bioengineering of Microalgae: Recent Advances, Perspectives, and Regulatory Challenges for Industrial Application. *Front Bioeng Biotechnol*. doi: 10.3389/fbioe.2020.00914
- De la Hoz Siegler H, Ayidzoe W, Ben-Zvi A, Burrell RE, McCaffrey WC** (2012) Improving the reliability of fluorescence-based neutral lipid content measurements in microalgal cultures. *Algal Res* **1**: 176–184
- Li-Beisson Y, Thelen JJ, Fedosejevs E, Harwood JL** (2019) The lipid biochemistry of eukaryotic algae. *Prog Lipid Res* **74**: 31–68
- Li T, Gargouri M, Feng J, Park JJ, Gao D, Miao C, Dong T, Gang DR, Chen S** (2015) Regulation of starch and lipid accumulation in a microalga *Chlorella sorokiniana*. *Bioresour Technol* **180**: 250–257
- Li T, Xu J, Gao B, Xiang W, Li A, Zhang C** (2016) Morphology, growth, biochemical composition and photosynthetic performance of *Chlorella vulgaris* (Trebouxiophyceae) under low and high nitrogen supplies. *Algal Res* **16**: 481–491
- Lisec J, Schauer N, Kopka J, Willmitzer L, Fernie AR** (2006) Gas chromatography mass spectrometry–based metabolite profiling in plants. *Nat Protoc* **1**: 387–396
- Liu B, Benning C** (2013) Lipid metabolism in microalgae distinguishes itself. *Curr Opin Biotechnol* **24**: 300–309
- López CVG, del Carmen Cerón García M, Fernández FGA, Bustos CS, Chisti Y, Sevilla JMF** (2010) Protein measurements of microalgal and cyanobacterial biomass. *Bioresour Technol* **101**: 7587–7591
- Machado M, Bromke M, Domingues Júnior AP, Marçal Vieira Vaz MG, Rosa RM, Vinson CC, Sabir JS, Rocha DI, Martins MA, Araújo WL, et al** (2016) Comprehensive metabolic reprogramming in freshwater *Nitzschia palea* strains undergoing nitrogen starvation is likely associated with its ecological origin. *Algal Res*. doi: 10.1016/j.algal.2016.06.003
- Miao M sheng, Yao X dong, Shu L, Yan Y jie, Wang Z, Li N, Cui X tong, Lin Y min, Kong Q** (2016) Mixotrophic growth and biochemical analysis of *Chlorella vulgaris* cultivated with synthetic domestic wastewater. *Int Biodeterior Biodegrad* **113**: 120–125
- Miller R, Wu G, Deshpande RR, Vieler A, Gartner K, Li X, Moellering ER, Zauner S, Cornish AJ, Liu B, et al** (2010) Changes in transcript abundance in *Chlamydomonas*

reinhardtii following nitrogen deprivation predict diversion of metabolism. *Plant Physiol* **154**: 1737–1752

Mobin A, Chowdhury H (2019) Commercially important bioproducts from microalgae and their current applications – A review. *Energy Procedia* **160**: 752–760

Moon M, Kim CW, Park WK, Yoo G, Choi YE, Yang JW (2013) Mixotrophic growth with acetate or volatile fatty acids maximizes growth and lipid production in *Chlamydomonas reinhardtii*. *Algal Res* **2**: 352–357

Nagappan S, Devendran S, Tsai P, Jayaraman H, Alagarsamy V, Pugazhendhi A (2020) Metabolomics integrated with transcriptomics and proteomics: Evaluation of systems reaction to nitrogen deficiency stress in microalgae. *Process Biochem* 143393

Nagappan S, Kumar G (2021) Investigation of four microalgae in nitrogen deficient synthetic wastewater for biorefinery based biofuel production. *Environ Technol Innov* **23**: 101572

Nama S, Madireddi SK, Devadasu ER, Subramanyam R (2015) High light induced changes in organization, protein profile and function of photosynthetic machinery in *Chlamydomonas reinhardtii*. *J Photochem Photobiol B Biol* **152**: 367–376

Park JJ, Wang H, Gargouri M, Deshpande RR, Skepper JN, Holguin FO, Juergens MT, Shachar-Hill Y, Hicks LM, Gang DR (2015) The response of *Chlamydomonas reinhardtii* to nitrogen deprivation: A systems biology analysis. *Plant J* **81**: 611–624

Rai MP, Gupta S (2017) Effect of media composition and light supply on biomass, lipid content and FAME profile for quality biofuel production from *Scenedesmus abundans*. *Energy Convers Manag* **141**: 85–92

Rocha DN, Martins MA, Soares J, Vaz MGMV, de Oliveira Leite M, Covell L, Mendes LBB (2019) Combination of trace elements and salt stress in different cultivation modes improves the lipid productivity of *Scenedesmus* spp. *Bioresour Technol*. doi: 10.1016/j.biortech.2019.121644

Rocha RP, Machado M, Vaz MGMV, Vinson CC, Leite M, Richard R, Mendes LBB, Araujo WL, Caldana C, Martins MA, et al (2017) Exploring the metabolic and physiological diversity of native microalgal strains (Chlorophyta) isolated from tropical freshwater reservoirs. *Algal Res* **28**: 139–150

Salem MA, Jüppner J, Bajdzienko K, Giavalisco P (2016) Protocol: A fast, comprehensive and reproducible one-step extraction method for the rapid preparation of polar and semi-polar metabolites, lipids, proteins, starch and cell wall polymers from a single sample. *Plant Methods* **12**: 1–15

- Sanz-Luque E, Chamizo-Ampudia A, Llamas A, Galvan A, Fernandez E** (2015) Understanding nitrate assimilation and its regulation in microalgae. *Front Plant Sci.* doi: 10.3389/fpls.2015.00899
- Sarat Chandra T, Deepak RS, Maneesh Kumar M, Mukherji S, Chauhan VS, Sarada R, Mudliar SN** (2016) Evaluation of indigenous fresh water microalga *Scenedesmus obtusus* for feed and fuel applications: Effect of carbon dioxide, light and nutrient sources on growth and biochemical characteristics. *Bioresour Technol* **207**: 430–439
- Sato N, Aoki M, Maru Y, Sonoike K, Minoda A, Tsuzuki M** (2003) Involvement of sulfoquinovosyl diacylglycerol in the structural integrity and heat-tolerance of photosystem II. *Planta* **217**: 245–251
- Siegenthaler P-A, Murata N** (2004) Chapter 1: Lipids in photosynthesis - an overview. *Lipids Photosynth Struct Funct Genet* 1–20
- Singh P, Kumari S, Guldhe A, Misra R, Rawat I, Bux F** (2016) Trends and novel strategies for enhancing lipid accumulation and quality in microalgae. *Renew Sustain Energy Rev* **55**: 1–16
- Sivaramakrishnan R, Incharoensakdi A** (2017) Enhancement of total lipid yield by nitrogen, carbon, and iron supplementation in isolated microalgae. *J Phycol* **53**: 855–868
- Smith AM, Zeeman SC** (2006) Quantification of starch in plant tissues. *Nat Protoc* **1**: 1342–1345
- Stacklies W, Redestig H, Scholz M, Walther D, Selbig J** (2007) pcaMethods - A bioconductor package providing PCA methods for incomplete data. *Bioinformatics* **23**: 1164–1167
- Tan KWM, Lee YK** (2016) The dilemma for lipid productivity in green microalgae: Importance of substrate provision in improving oil yield without sacrificing growth. *Biotechnol Biofuels* **9**: 1–14
- Thompson GA** (1996) Lipids and membrane function in green algae. *Biochim Biophys Acta - Lipids Lipid Metab* **1302**: 17–45
- Williams PJLB, Laurens LML** (2010) Microalgae as biodiesel & biomass feedstocks: Review & analysis of the biochemistry, energetics & economics. *Energy Environ Sci* **3**: 554–590
- Work VH, Radakovits R, Jinkerson RE, Meuser JE, Elliott LG, Vinyard DJ, Laurens LML, Dismukes GC, Posewitz MC** (2010) Increased lipid accumulation in the *Chlamydomonas reinhardtii* sta7-10 starchless isoamylase mutant and increased carbohydrate synthesis in complemented strains. *Eukaryot Cell* **9**: 1251–1261

- Wu LF, Chen PC, Lee CM** (2013) The effects of nitrogen sources and temperature on cell growth and lipid accumulation of microalgae. *Int Biodeterior Biodegrad* **85**: 506–510
- Yang H, He Q, Hu C** (2015) Lipid accumulation by NaCl induction at different growth stages and concentrations in photoautotrophic two-step cultivation of *Monoraphidium dybowskii* LB50. *Bioresour Technol* **187**: 221–227
- Zhu FY, Chen MX, Chan WL, Yang F, Tian Y, Song T, Xie LJ, Zhou Y, Xiao S, Zhang J, et al** (2018) SWATH-MS quantitative proteomic investigation of nitrogen starvation in *Arabidopsis* reveals new aspects of plant nitrogen stress responses. *J Proteomics* **187**: 161–170
- Zhu L, Li S, Hu T, Nugroho YK, Yin Z, Hu D, Chu R, Mo F, Liu C, Hiltunen E** (2019) Effects of nitrogen source heterogeneity on nutrient removal and biodiesel production of mono- and mix-cultured microalgae. *Energy Convers Manag*. doi: 10.1016/j.enconman.2019.112144
- Zhu S, Huang W, Xu J, Wang Z, Xu J, Yuan Z** (2014) Metabolic changes of starch and lipid triggered by nitrogen starvation in the microalga *Chlorella zofingiensis*. *Bioresour Technol* **152**: 292–298
- Zienkiewicz K, Du ZY, Ma W, Vollheyde K, Benning C** (2016) Stress-induced neutral lipid biosynthesis in microalgae — Molecular, cellular and physiological insights. *Biochim Biophys Acta - Mol Cell Biol Lipids* **1861**: 1269–1281

CHAPTER 2

TITLE: On the role of TOR signaling networks in freshwater microalgae strains

Lidiane Covell¹, Marcelo Gomes Marçal Vieira Vaz¹, Mariana Machado¹, Auxiliadora Martins¹, Dilson Novais Rocha², Marcio Arêdes Martins², Wagner L. Araújo¹, Camila Caldana³, Adriano Nunes-Nesi^{1*}

¹ Departamento de Biologia Vegetal, Universidade Federal de Viçosa, 36570-900, Brazil. lidianecovell@gmail.com, marcelogmvvaz@gmail.com, mmachado21@outlook.com, auxiliamartins82@gmail.com, wlaraujo@ufv.br, nunesnesi@ufv.br

² Departamento de Engenharia Agrícola, Universidade Federal de Viçosa, 36570-900, Brazil. aredes@ufv.br, dilson.rocha@ufv.br

³ Max Planck Institute of Molecular Plant Physiology, Am Mühlenberg 1, 14476 Potsdam-Golm, Germany. caldana@mpimp-golm.mpg.de

*Corresponding author:

Adriano Nunes-Nesi

Departamento de Biologia Vegetal

Universidade Federal de Viçosa

36570-900 Viçosa, Minas Gerais, Brazil

Phone: +55-31-3612-5357

Email: nunesnesi@ufv.br

ABSTRACT

Responses of cell growth to environmental changes are essential for the survival of biological systems. The evolutionary conserved Ser/Thr protein kinase “Target of Rapamycin” (TOR) has emerged as a signaling node that integrates the sensing of numerous growth signals to the coordinated regulation of cellular metabolism and growth. The TOR pathway controls cell growth by promoting anabolic processes, such as protein synthesis and ribosome biogenesis, and inhibiting catabolic processes such as autophagy. The TOR kinase has been identified in plants and microalgae, indicating that this pathway is conserved in photosynthetic eukaryotes. A better understanding of the regulation of the metabolic pathways in freshwater microalgae with a different accumulation of reserve compounds is needed to understand the mechanisms involved in the regulation of biosynthesis and catabolism of storage compounds. In this study, two freshwater microalgae, *Chlamydomonas* sp. BR020 and *Chlorella vulgaris* BR017 and a model, *Chlamydomonas reinhardtii* CC503 were used to assess the effects of rapamycin-inhibited TOR signaling pathway on growth cell, biochemical composition and metabolic profile. We analyzed the dynamics responses of the strain metabolome and lipidome to TOR-inhibition by rapamycin. Consistent with the growth phenotype we observed strong changes in carbon (C) and nitrogen (N) partitioning in the direction of storage through an accumulation of starch, triacylglycerol and amino acids. Interestingly, the strains showed different metabolite levels, confirming the difference in reserve compound accumulation of each strain. This study clearly shows the complex picture of metabolic and lipidomic alterations in uncharacterized strains in TOR pathway affected by rapamycin. Furthermore, it reveals a complex regulation and adjustment of metabolite pools and lipid composition in response to TOR inhibition. This study show that TOR inhibition causes a severely reduced growth, leading to a reduction by 50% on the cell growth and TOR is involved in the regulation of cell growth in different strains. Next to the direct cell growth related results our data reveals that the obtained growth-phenotype was accompanied by strong accumulation of carbon (starch and TAGs) reserves. The amino acids profile exhibited a diverse pattern in relationship to the strains, which will aid in specifying the role and mechanism of individual compounds in the response to the rapamycin treatment. Taken together, the present data reveals a clear metabolite reprogramming in response to TOR inhibition in a strain specific mode.

Keywords: Chlorophytes. *Chlamydomonas reinhardtii*. Primary- and lipid- metabolism. Rapamycin.

1. INTRODUCTION

The modulation of growth and development is a central process in all organisms, and an intimate relationship exists between nutrient availability, energy status, and cell growth rate, which are influenced by dynamic and diverse environmental stresses (Pérez-Pérez et al., 2017; Pancha et al., 2020). Unicellular organisms, such as yeasts and algae, are in direct contact with environmental nutritional changes (Crespo and Hall, 2002). Multicellular organisms, such as plants and animals, must also sense and coordinate these cell-autonomous processes at the organism level via signals (Ren et al., 2013a). Those factors are reached over signaling networks that compose the sensing of local and systemic nutrient and energy sources and transmit this information to metabolic regulators and enzymes to control cellular anabolic and catabolic processes (Wullschleger, 2006; Dobrenel et al., 2016a).

One of the prominent and conserved nutrient sensing is performed by the Serine/Threonine protein kinase Target of Rapamycin (TOR) (Crespo and Hall, 2002; Soulard et al., 2009; Laplante and Sabatini, 2012). This protein kinase is a conserved and essential regulator of eukaryotic cell growth that is thought to integrate external and internal metabolic cues to balance cell growth with energy and nutrient supplies (Menand et al., 2002; Loewith and Hall, 2011; Xiong and Sheen, 2012; Rexin et al., 2015). As indicated by its name, TOR is the target of a molecule named rapamycin, which is a compound with antifungal and immunosuppressive properties that was first isolated in the 1970s from the soil bacterium *Streptomyces hygroscopicus* (Sehgal et al., 1975; Vézina and Kudelski, 1975). The elucidation of TOR as the target of rapamycin occurred in the budding yeast *Saccharomyces cerevisiae*, where two independent TOR genes were in the genome (Heitman et al., 1991). The presence of these two expressed genes opened the question of their functions and led to the discovery of two independent TOR complexes (TORC) in yeast (Loewith et al., 2002), but also in mammalian cell cultures (Hara et al., 2002; Kim et al., 2002). Both complexes, termed TOR complex 1 (TORC1) and Tor complex 2 (TORC2), were different in their composition, localization and functionality (Betz and Hall, 2013; Saxton and Sabatini, 2017). While TORC1 emerged as a highly conserved protein complex, composed of TOR, RAPTOR and LST8 whose homologs have been identified in all thus far studied eukaryotes, including fungi, mammals, worms, flies, plants and algae (Loewith et al., 2002; Wullschleger et al., 2005; Soulard et al., 2009; González and Hall, 2017), TORC2 seems to be less conserved. Studies performed in yeasts uncovered the unique mechanism of action of rapamycin. Rapamycin first binds the 12-kD FK506-binding protein

(FKBP12) and this complex inhibits the TOR Ser/Thr kinase. FKBP12 is a member of the FK506- and rapamycin-binding protein (FKBP) family.

The TOR kinase has been described in plants and algae, indicating that this signaling pathway is also conserved in photosynthetic organisms (Loewith et al., 2002; Menand et al., 2002; Wullschleger, 2006). However, in contrast to yeasts, mammals, or flies, the vegetative growth of *Arabidopsis* and other plants such as *Oryza sativa*, *Nicotiana tabacum*, or *Brassica napus*, is not sensitive to rapamycin (Menand et al., 2002). A feasible explanation to rapamycin resistance of land plants might be the inability of plant FKBP12 to bind this drug. Indeed, studies previously reported that plant FKBP12 has evolved structural changes that hamper this protein to mediate the action of its drug ligands against the functional targets (Xu et al., 1998).

Several photosynthetic red and green algae, including the green model alga species *Chlamydomonas reinhardtii* have been proven to be sensitive to the TOR inhibiting drug rapamycin (Pérez-Pérez et al., 2017). TOR inhibition in *Chlamydomonas* was not only globally affecting growth and development (Crespo et al., 2005; Jüppner et al., 2018), but its function was also shown to negatively control catabolic process like autophagy (Pérez-Pérez and Crespo, 2010a; Couso et al., 2018), while anabolic process like protein translation were positively controlled by active TORC1 (Díaz-Troya et al., 2011). Still, even though evidence was accumulating that TOR is regulating several metabolic pathways on species like yeast and mammals (Jewell and Guan, 2013; Ben-Sahra and Manning, 2017; González and Hall, 2017), only few studies have been analyzing the impact of TOR inhibition on primary (Lee and Fiehn, 2013; Kleessen et al., 2015) or lipid metabolism (Imamura et al., 2015; Couso et al., 2016; Werth et al., 2019) in *Chlamydomonas* or other green alga.

Since most studies involving inhibition of the TOR signaling pathway by rapamycin are conducted with the model strain *C. reinhardtii*, the hypothesis of this study is that other strains with different growth rates, accumulation of different storage compounds following N starvation have distinct metabolic responses and signaling pathway mechanisms. Therefore, we decided to conduct an experiment to better understand the function and response of the model alga *C. reinhardtii* CC503 and two Brazilian freshwater strains, *Chlamydomonas* sp. BR020 and *Chlorella vulgaris* BR017 induced by rapamycin to TOR inhibition. According to Rocha et al., 2017, under favorable growth conditions, BR020 and BR017 are characterized by different behavior in relationship to biomass accumulation and the reserve compounds. While the BR020 strain had the highest starch content, BR017 showed high levels of amino acids, protein and sucrose. Although all strains in this study showed a decrease in cell growth, when submitted to

rapamycin treatment, *C. reinhardtii* CC503 and *C. vulgaris* BR017 had the highest starch content when compared to *Chlamydomonas* sp. BR020. However, *C. reinhardtii* CC503 and *Chlamydomonas* sp. BR020 presented higher TAG contents compared to *C. vulgaris* BR017.

2. MATERIAL AND METHODS

2.1 Strains and culture media

Two freshwater microalgae strains used in this study Chlorophyceae are available at the Collection of Cyanobacteria and Microalgae (CCM-UFV), available in the Laboratory of Phycology and Molecular Biology, Plant Biology Department at the Universidade Federal de Viçosa, Viçosa, Minas Gerais State, Brazil (20°45'14"S, 42°52'54"W). Both strains, *Chlamydomonas* sp. BR020 and *C. vulgaris* BR017 were isolated from water samples collected from freshwater reservoirs on the university campus. The model green microalga, *C. reinhardtii*, is widely selected for diverse experiments, because of its advantages, such as fast growth, short generation time, strong adaptability, easy cultivation and easy isolation of mutants (Harris, 2001a).

The strains were cultivated in the mixotrophic medium Tris-Acetate-Phosphate (TAP) (Coleman, 1990). Strains were cultivated under 24±2 °C, with a 16 h/8 h (light/dark) photoperiod cycle, at a constant irradiance of 100 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$, under continuous shaking at 110 rpm.

2.2 Culture conditions and growth parameters

2.2.1 Cultivation in microplate

For the determination of a suitable growth inhibitory concentration, various dilutions of rapamycin, re-suspended in dimethyl sulfoxide (DMSO), were applied to liquid cultures. A first set of growth curves in three different concentrations (2.5, 5.0, and 10.0 μM) of rapamycin were carried out aiming to evaluate the maximum growth rate at logarithmic phase (μ_{max}), a selection of sampling points as well as the cell concentration after 70 hours of cultivation, which was obtained by means of absorbance at 680nm (Optic density – OD680nm) (Griffiths et al., 2011).

The rapamycin screening assays were conducted in two steps. Firstly, growth curves were carried out in microplate (96 wells) in order to access the effect of the rapamycin concentration on the growth of the strains. For that, the experiment was carried out in a growth room, applying the same conditions described above (item 2.1). Each microplate well was filled with 280 μL

of TAP medium, 10 μL of strain inoculum (initial cell density of 1.5×10^6 cells mL^{-1}) and a final concentration of 2.5, 5.0 and 10.0 μM rapamycin was applied to each of the treatments, while the same concentrations of drug vehicle (DMSO) were added to the control cultures for the comparison. The treatments were applied at the beginning of experiment and cellular growth was monitored hourly by absorbance measurements at 680 nm (OD_{680nm}) in spectrophotometer (UVM 340, AsysHitech) (Griffiths et al., 2011). The experiment was performed with eight repetitions during 71 hours of growth cultivation.

2.2.2 Cultivation in Erlenmeyer flasks

Subsequently, the concentration of 5 μM of rapamycin was chosen for experiments carried out in Erlenmeyer flasks (Jüppner et al., 2018; Mubeen et al., 2018). Accordingly, in this second round of experiments, besides the cell growth, physiological and biochemical parameters were also evaluated. This experiment was carried out in a growth room, applying the same conditions described in item 2.1. Cultivations were carried out in 125 mL Erlenmeyer flasks filled with 75 mL useful volume. The flasks were filled with 60 mL of TAP medium, 15 mL of strain inoculum (initial cell density of 1.5×10^6 cells mL^{-1}) and a final concentration of 5 μM rapamycin was applied to each of the treatments, while similar concentrations of drug vehicle were added to the control cultures for the comparison. The treatments were applied at the beginning of cultivation and it was performed in quadruplicates. Based on the obtained growth curves we selected three points to collect samples, 0h, 24h and 48h.

2.2.3 Determination of growth parameters

A total of 2 mL homogenous cell suspension was removed from each culture at the 0h, 24h and 48h and fixed with Transeau solution (1:1 sample: fixator) for use in the determination of cell density. Cell counts were carried out using a light microscope with a bright-line hemocytometer (Neubauer's chamber hemocytometer). These data were used to determine specific growth rate (μ), generation time (G_2), mass per cell and specific growth rate at each growth phase as previously described (Contois, 1959). And at the same time cellular growth was monitored by absorbance measurements at 680 nm in spectrophotometer (UVM 340, AsysHitech) (Griffiths et al., 2011).

2.3 Extraction of chlorophyll, lipids and primary metabolites

Primary metabolites, chlorophyll and lipids were extracted with minor changes as described elsewhere (Salem et al., 2016). Snap-frozen cell pellets, harvested by centrifugation were re-suspended in 1 mL of pre-cooled (-20°C) methyl tert-butyl ether (MTBE)-extraction buffer [methanol: methyl tert-butyl-ether (1 : 3; v/v) mixture; Biosolve, the Netherlands] as mentioned previously (Salem et al., 2016). The resuspended cell pellets were immediately mixed before ultrasonification in an ice-cooled water bath for 10 min. Then the samples were incubated for 1 h on an orbital shaker at 4°C. To induce the liquid: liquid-phase separation, 650 µL of UPLC-grade methanol : water (1 : 3; v : v; Biosolve, the Netherlands) was added to the homogenate and mixed, before centrifuging at 20 000 g for 5 min at 4°C in a table top centrifuge. The addition of the methanol: water mixture resulted in a separation of an upper MTBE-phase, containing lipids and chlorophyll, and a lower phase, containing the polar and semi-polar metabolites, next to a solid pellet in the bottom of the 1.5 mL plastic tube. The solid pellet contains the precipitated proteins next to starch and other insoluble polymers, such as cell wall fragments (Salem et al., 2016). For further analysis, 500 µL of the MTBE-phase and 650 µL of the lower, aqueous-phase were transferred to fresh 1.5 mL tubes. Samples of the lipid-phases were dried in a vacuum concentrator and re-suspended in the proper resuspension buffer. The polar aliquots were also dried in a vacuum concentrator before storing the pellets at -80°C. The solid pellet was frozen in liquid N and stored at -80°C until further extraction. To measure the impact of contaminations from the extraction process, the whole extraction procedure was additionally performed with two–four empty, sample-free, 1.5 mL tubes (method blank).

2.4 Polar metabolite profiling

The derivatization of the polar-sample (primary metabolites) was performed on a gas chromatographer Agilent 6890 (Agilent) coupled to a Pegasus HT ToF mass spectrometer (LECO Instruments, St. Joseph, MI, USA) as outlined in a previous study (Lisec et al., 2006). Chromatograms were exported from ChromaToF v 3.25 (LECO Corp., St. Joseph, MI, USA) and processed using R. Peak detection, retention time alignment, and library matching were performed using the TargetSearch R package from Bioconductor, as performed by (Bromke et al., 2013). For data normalization, each analyte peak intensity was normalized by the median of all data and dry weight.

2.5 Determination of the chlorophyll content

To determine the chlorophyll content, 100 μL of the MTBE-phase was mixed 1 : 10 (v : v) with 90% methanol and measured using an UV-VIS spectrometer at wavelengths of 665 nm and 652 nm to distinguish between chlorophyll *a* and chlorophyll *b*. The chlorophyll *a*, *b* and total content were determined using the equations described by Bar-Nun (Bar-nun and Ohad, 1980).

2.6 Extraction and determination of starch content

In order to analyze the starch content, we used the standard protocol from Smith and Zeeman, 2006. The frozen cell pellet was first washed with 80% ethanol, incubated for 10 min at room temperature. Afterwards the pellet was dissolved in 250 μl sterile water. Then 250 μl 100 mM sodium acetate was added and starch was hydrolyzed by heating for 3h at 99 °C. The dissolved starch was digested into its glucose monomers over night with an enzyme mix of α -amylase (4.2 units per sample) and α -amylglucosidase (10 units per sample). The digested extract was centrifuged and the supernatant with the starch-derived glucose monomers was dissolved in 100 mM HEPES-buffer (pH 7) that contained 5 mM MgCl_2 , 60 mg/ml ATP, 36 mg/ml NADP and glucose-6-phosphate-dehydrogenase (1 unit per sample). The baseline was measured at 340 nm and the subsequent addition of hexokinase started the reactions and the increase of $\text{NADPH}+\text{H}^+$ was measured at 340 nm with a plate reader in 96-well formats.

2.7 Determination of lipids

Briefly, 650 μL of the lower aqueous phase of the MTBE extraction, described above, were transferred to fresh 1.5-ml Eppendorf tubes, dried in a SpeedVac and resuspended in a volume of 300 μL of a mixture of acetonitrile: isopropanol (7: 3; Biosolve, the Netherlands). Chromatograms were further processed using Excalibur software version 2.30 (Thermo-Fisher) and Progenesis CoMet software (Version 2.4; Nonlinear, Newcastle upon Tyne, UK). The UPLC/MS lipids data were processed using ToxID (Version 2.1.2; Thermo). To remove noise and contaminants, data for every lipid species with average peak height lower than the average peak height of the method blanks or with 50% of the values below 1,000 arbitrary counts were removed from the dataset. The remaining peaks were then assigned to annotated lipid species using an in-house-generated lipid database for *Arabidopsis* (Hummel et al., 2011). The data were normalized to sample dry weight. For some lipid species, more than one peak was detected

having the same m/z and identical adducts but different retention times. In these cases, we added the letter A or B to the compound name, depending on their elution order.

2.8 Statistical analysis

The experiments were performed and analyzed following a completely randomized design with four replicates for each treatment. The values obtained for all variables were submitted to analysis of variance (ANOVA, $P < 0.05$) followed by Tukey's test ($P \leq 0.05$), and one analyses of the interaction effects, using the software R (Grace and Hudson, 2016). In addition, data were subjected to a principal component analysis (PCA) performed using the `pcaMethods` package in the software R (Stacklies et al., 2007), therefore primary metabolites and lipid profile data were \log_2 transformed.

3. RESULTS

3.1 Growth curve and maximum growth rate (μ_{max}) of the selected strains with different rapamycin concentration

The analysis of growth parameters aimed to identify how cells grew and accumulated biomass over time. From these data, the growth parameters were calculated allowing other inferences about the behavior of the culture over time. Growth curves based on optical density (OD) at 680nm indicated a similar pattern for *Chlamydomonas* sp. BR020 and *C. vulgaris* BR017 which a decreased in growth of rapamycin treatments compared to the control between 10 and 50 hours (**Figure 1 B and C**). In *C. reinhardtii* CC503 rapamycin treatments seem to have a more evident effect during all the cultivation (**Figure 1 A**). Regarding the specific growth rate (μ), only for *Chlamydomonas* sp. BR 020 there was no statistical difference between control and treatments, however for *C. reinhardtii* CC503 and *C. vulgaris* BR017 showed lowest growth rate for the treatments with rapamycin, thus differing statistically from the control (**Figure 1 D**). The value for control was 0.38 d^{-1} , 0.20 d^{-1} and 0.23 d^{-1} for CC503, BR020 and BR017, respectively. While for $5\mu\text{M}$ rapamycin these values were 0.31 d^{-1} , 0.18 d^{-1} and 0.20 d^{-1} . According to these results and current literature (Jüppner et al., 2017; Jüppner et al., 2018), we chose $5\mu\text{M}$ rapamycin and 0h, 24h and 48 h to perform the experiment in Erlenmeyer's and the biochemical analyses.

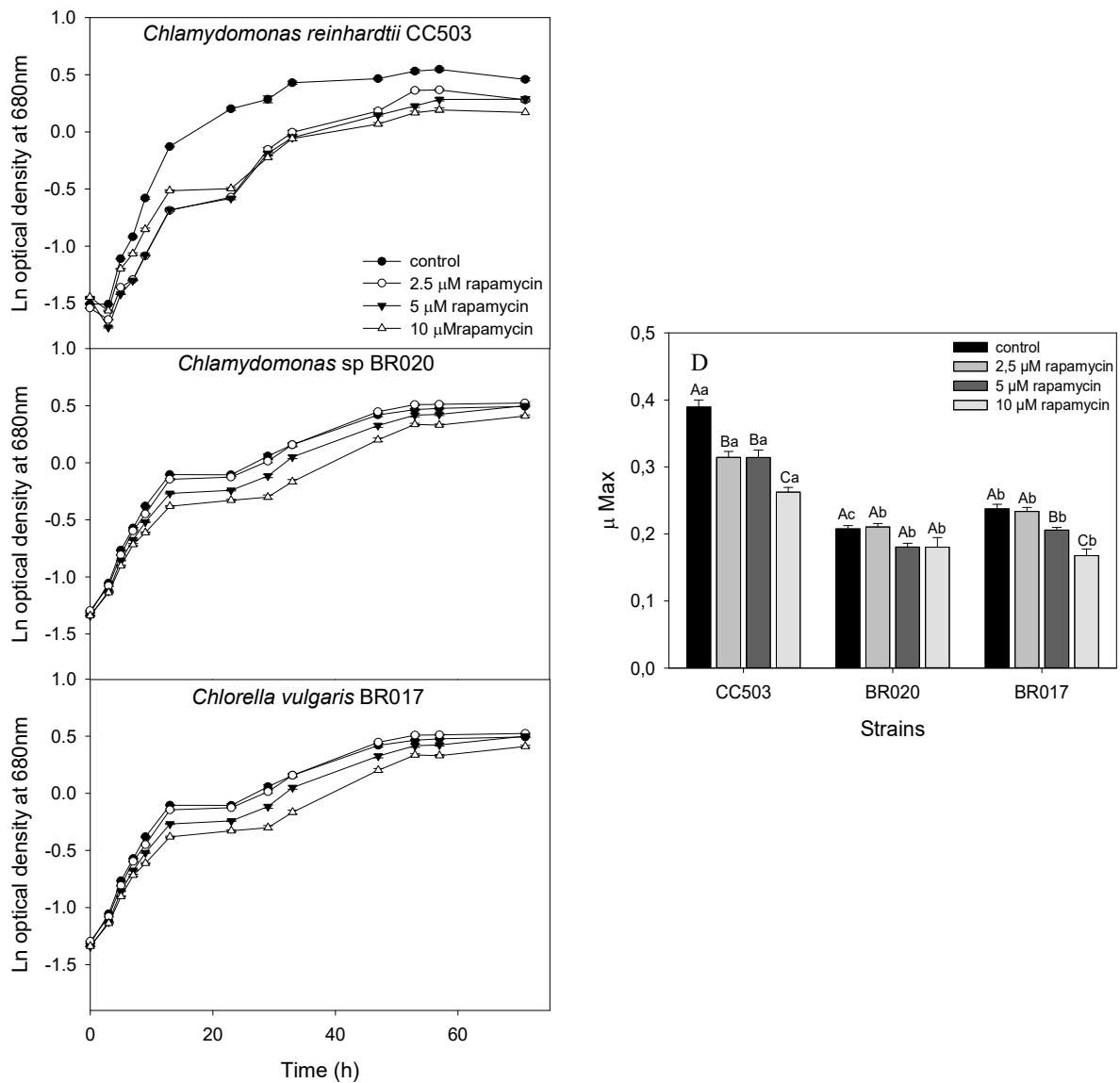


Figure 1. Growth parameters of three freshwater strains (*Chlamydomonas reinhardtii* CC503, *Chlamydomonas* sp. BR020 and *Chlorella vulgaris* BR017) cultured in TAP medium under three different rapamycin concentrations (2.5; 5 and 10 μ M) and control; Growth curves based on Ln Optical Density (OD) at 680 nm (A-C) and maximum growth rate (μ_{max}) (D). Values represent the average error of eight replications. Means followed by the same letters do not differ by the Tukey test ($P < 0.05$), uppercase letters compare the rapamycin concentration in each strain and lowercase letters compare each treatment in all strains.

3.2 TOR inhibition results in reduced cell number

The cell number was monitored at three different times of strains growth (**Figure 1**). The treatment of 5 μM rapamycin reduced the cell number at 48h growth period by approximately 50% compared with control conditions (**Figure 2 A - C**). Also, the three strains exhibited a reduced number of cells in the first hours of culture when cultivated with 5 μM of rapamycin. Regarding the specific growth rate (μ), all strains showed a statistical difference between control and 5 μM rapamycin treatment, which it is possible to observe a slowdown growth in rapamycin treatment (**Figure 2 D**). All interactions between strain, time and concentration were statistically significant, even the triple interaction (Table S 12, supplementary material).

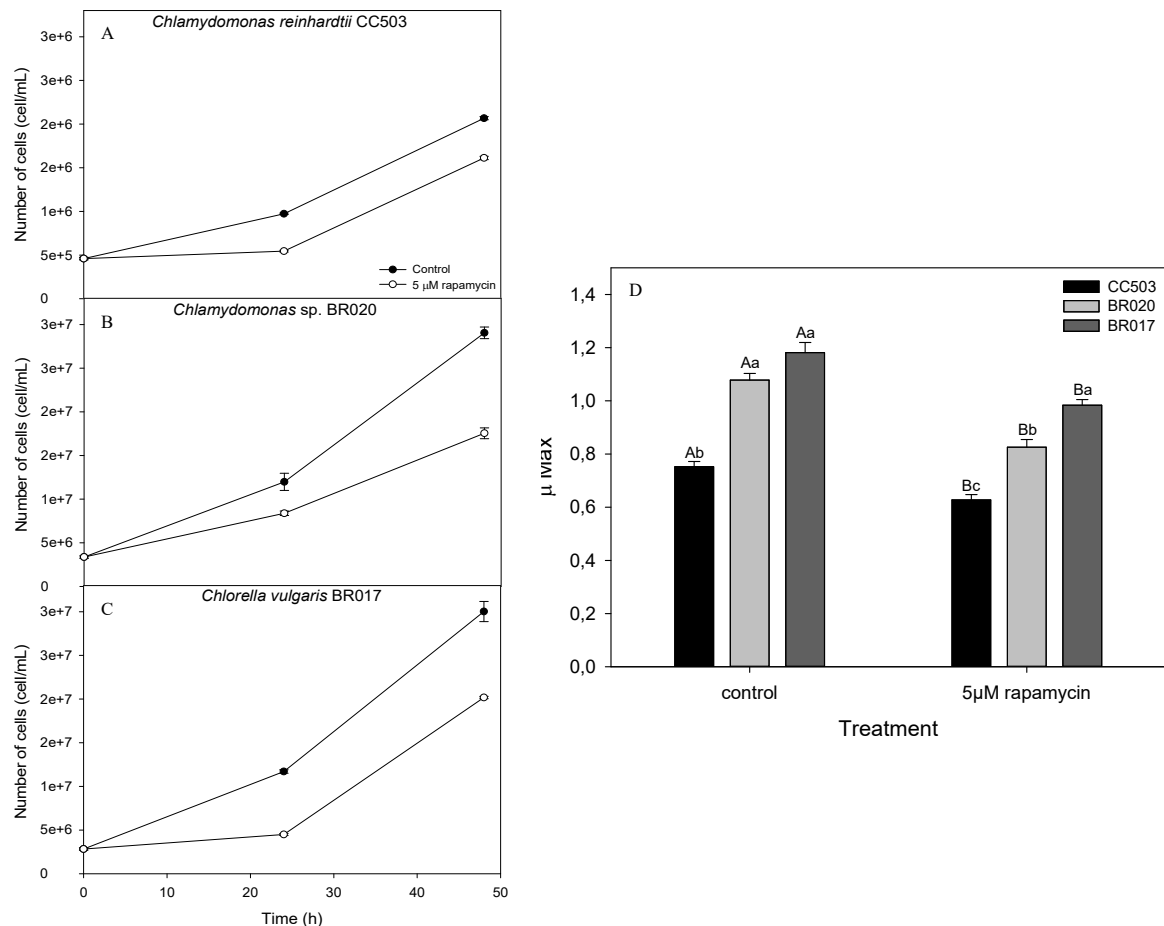


Figure 2. Growth parameters of three freshwater strains (*Chlamydomonas reinhardtii* CC503, *Chlamydomonas* sp. BR020 and *Chlorella vulgaris* BR017) cultured in TAP medium with 5 μM rapamycin and control. Growth curves based on cell number (**A – C**) and maximum growth rate (μ_{max}) (**D**). Values represent the average error of eight replications. Means followed by the same letters do not differ by the Tukey test ($P < 0.05$), uppercase letters compare the rapamycin concentration in each strain and lowercase letters compare each treatment in all strains.

3.3 Rapamycin affects differently chlorophyll contents between strains.

Regarding pigments content, all strains exhibited very similar behavior (**Figure 3**). The analysis of variance for chlorophyll contents revealed that all interaction between strain, time and concentration were statistically significant for Chl *b*. However, for Chl *a* the interaction between strain and concentration, as well as the triple interaction were not significant (**Table S 12**). The levels of chlorophyll *a* and *b* decreased in rapamycin treatment at the end of cultivation for all strains (**Figure 3 A-B, D-E and G-H**). The levels of chlorophyll *a/b* ratio were also affected by rapamycin treatment (**Figure 3 C, F and I**), suggesting that the applied treatment was stressful to the microalgae cells.

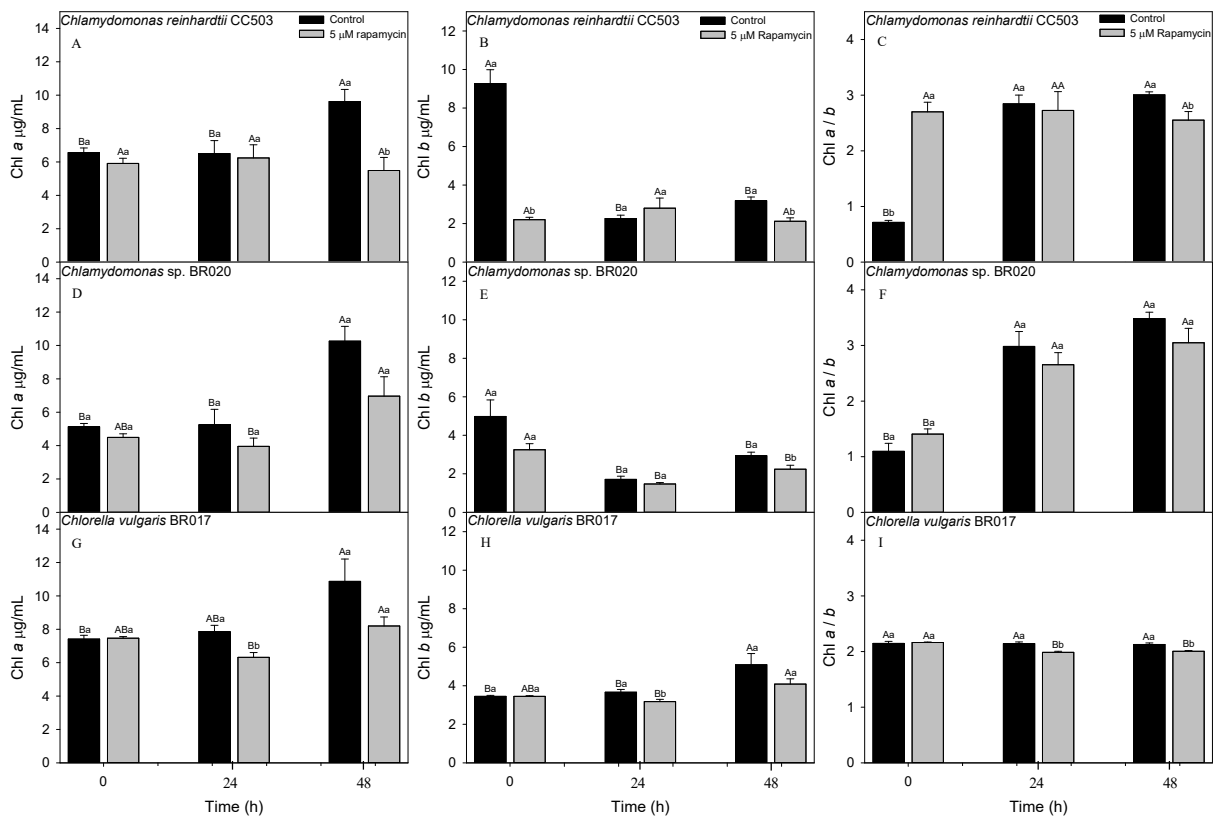


Figure 3. Chlorophyll content of of three freshwater strains (*Chlamydomonas reinhardtii* CC503 (**A – C**); *Chlamydomonas sp.* BR020 (**D – F**) and *Chlorella vulgaris* BR017 (**G – I**)) cultured in TAP medium with 5µM rapamycin and control. Values represent the average error of eight replications. Means followed by the same letters do not differ by the Tukey test ($P < 0.05$), uppercase letters compare the rapamycin concentration in each strain and lowercase letters compare each treatment in all strains.

3.4 TOR inhibition alters primary metabolism differentially in three microalgae strains

A possible mechanism contributing to increased amino acid accumulation after TOR inhibition might be the immediate induction of amino acid synthesis. The metabolic analysis in *C. reinhardtii* CC503 revealed that all measured amino acids at 24 h exhibited an increase after rapamycin application. Most of these initially elevated amino acids did not maintain the increased concentrations, compared with the control samples (**Figure 4, Table S 13 - 15**). Similar behavior was also observed in *Chlamydomonas* sp. BR 020 and *C. vulgaris* BR 017 but only for metabolites aspartate, citrulline, glutamate, glutamine, histidine, ornithine, proline, serine, threonine and valine (**Figure 4**).

The pool sizes of intermediates from glycolysis and tricarboxylic acid (TCA) cycle showed a more variable pattern between control and the rapamycin treated cells for the three strains. The three TCA cycle intermediates citrate, succinate and malate did show consistent differences between the strains. While *C. reinhardtii* CC503 and *C. vulgaris* BR017 showed a citrate and succinate increase at 24h in rapamycin treatments, malate did not differ between control and rapamycin treatments for any of the strains (**Figure 4**). Surprisingly, these data also show that fructose-6-phosphate and glucose-6-phosphate, which are products of glycolysis, were differentially regulated after TOR inhibition only for *C. vulgaris* BR017, which increased in the TOR-inhibited cultures at 24 h, while *C. reinhardtii* CC503 and *Chlamydomonas* sp. BR020 did not show consistent differences between the control and rapamycin treatments (**Figure 4**).

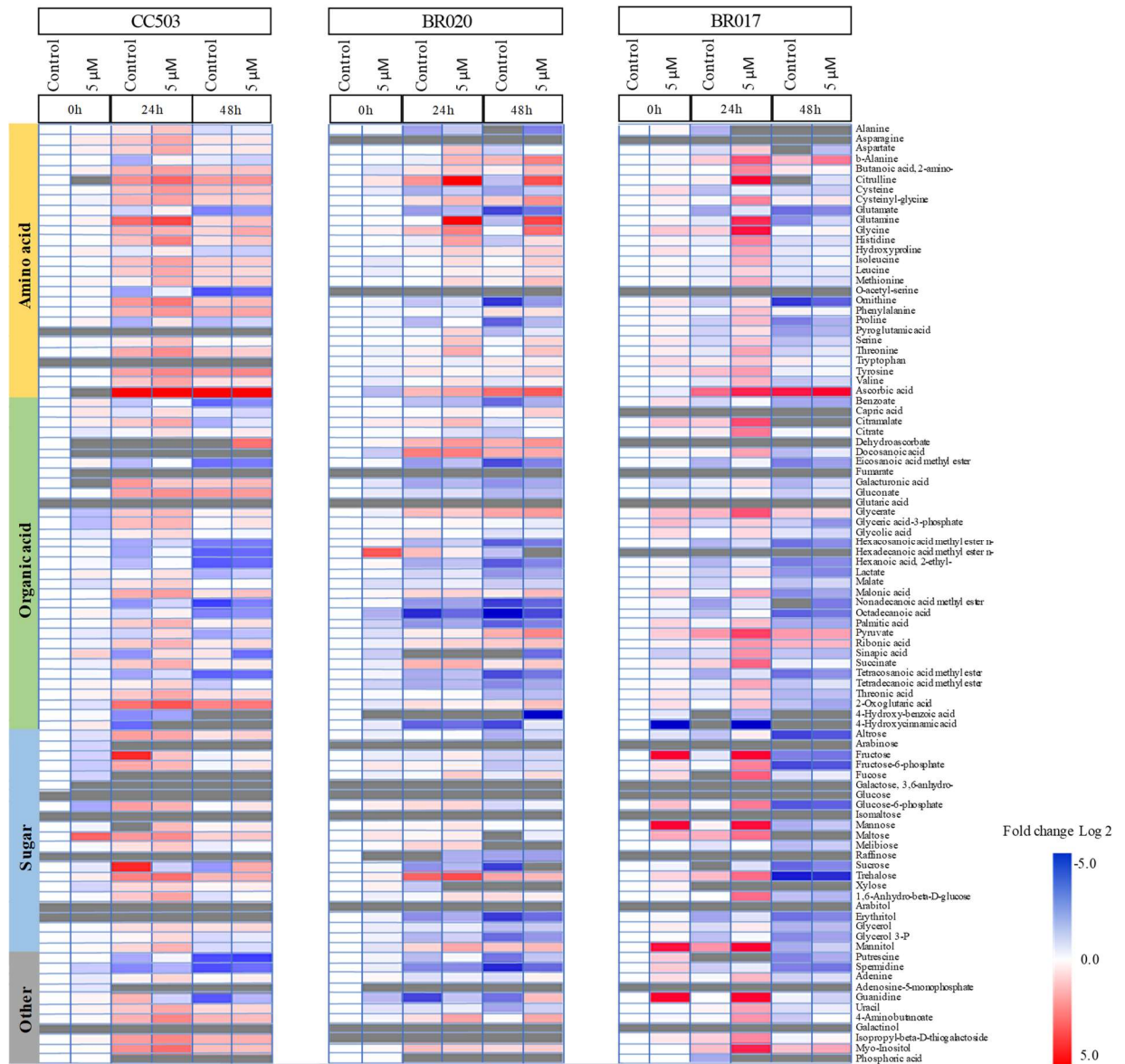


Figure 4. Heat map representing the changes in relative levels of primary metabolites of three freshwater strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, and *C. vulgaris* BR017) cultured in TAP medium with 5 μM rapamycin and control. Data are scaled to the mean response measured for control 0h for each strain, values presented are means of four biological replicates. The complete dataset and statistics are presented in the supplementary table S13 – 15.

3.5 Repression of the TOR kinase leads to higher levels of storage compounds per cell

To determine if increased levels of stored carbon occur after inhibition of TOR, we extracted starch and lipids from the cultures and analyzed these compounds during three cultivation time. The two main storage carbon pools, TAGs and starch, clearly follow the expectation that growth and carbon storage are inversely proportional in *C. reinhardtii* CC503 and *C. vulgaris* BR017. While we detected a twofold decrease in the cell number of the rapamycin-treated cultures (**Figure 2 A – C**), there was an increase in starch content at the end of 24 h in the rapamycin-treated cultures for *C. reinhardtii* CC503 and *C. vulgaris* BR017 (**Figure 5 A and C**), followed by a decrease at 48 h. Surprisingly, *Chlamydomonas* sp. BR020 strain had the lowest starch content when treated with rapamycin, both in 24 h and 48 h of cultivation (**Figure 5 B**).

The relationship between growth and accumulation of TAGs was different of starch, all three strains showed an increase in TAG levels, especially at 24 h of treatment. The highest levels of TAG were in 24 h of cultivation, however, BR020 strain was the one that showed the greatest increase when compared to the control, followed by BR017 and CC503 strains, respectively (**Figure 6**). Although strain CC503 had the lowest composition of TAGs when compared to the other two strains analyzed, it was possible to observe an increase in DAGs at the end of cultivation, which leads to an increase in the content of TAGs (**Figure 6**). It has been demonstrated that *C. reinhardtii* may employ a distinct pathway that uses DAG derived almost exclusively from the chloroplast to produce TAG (J. Fan, 2011).

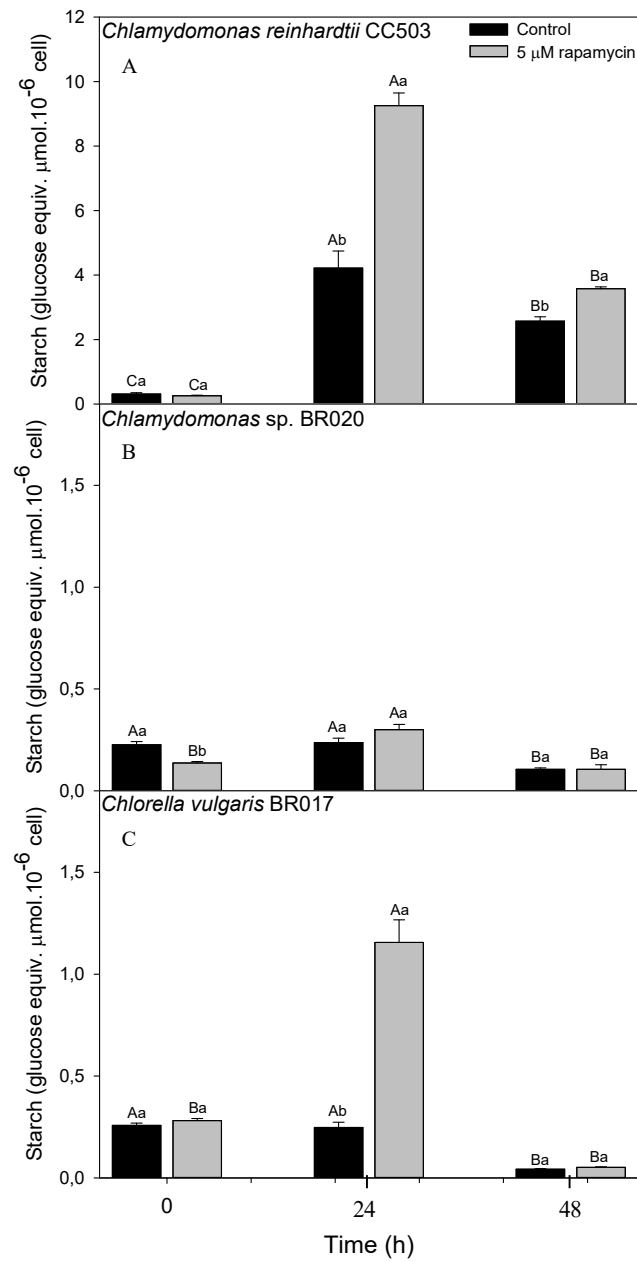


Figure 5. Starch content of three freshwater strains cultured in TAP medium with 5 μM rapamycin and control. *Chlamydomonas reinhardtii* CC503 (A); *Chlamydomonas* sp. BR020 (B) and *Chlorella vulgaris* BR017 (C). Values represent the average error of eight replications. Means followed by the same letters do not differ by the Tukey test ($P < 0.05$), uppercase letters compare the rapamycin concentration in each strain and lowercase letters compare each treatment in all strains.

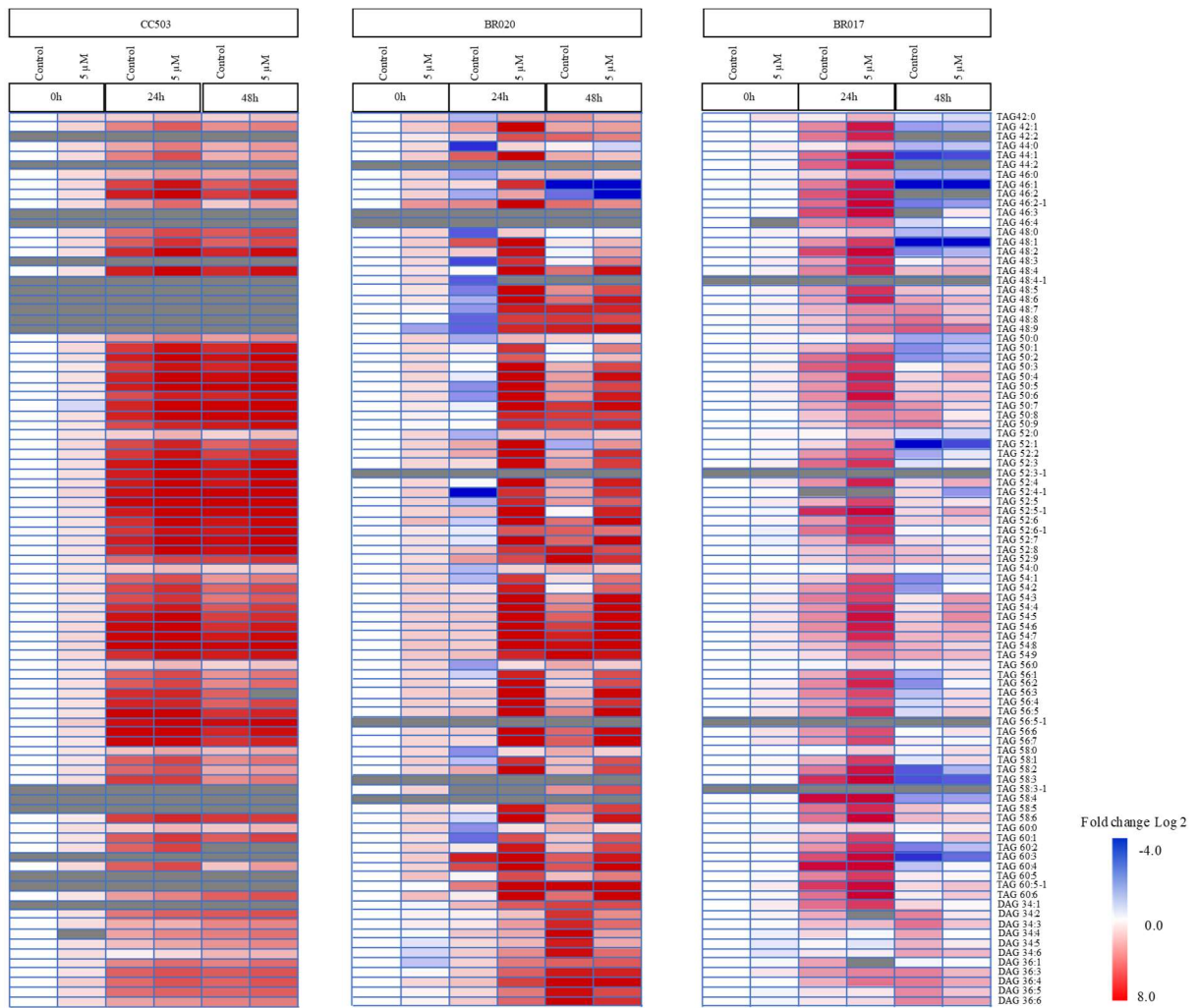


Figure 6. Heat map representing the changes in relative triacylglycerols (TAGs) of three freshwater strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, and *C. vulgaris* BR017) cultured in TAP medium with 5 μM rapamycin and control. Data are scaled to the mean response measured for control 0h for each strain, values presented are means of four biological replicates. The complete dataset and statistics are presented in the supplementary table S 16 – 18).

3.6 Lipidomic analysis reveals changes between all strains in the composition of structural lipids

As there were severe changes in the composition of the storage compounds, especially the storage lipids, we hypothesized if the other lipid classes were also affected after rapamycin treatment. To obtain an overview of the data we prepared a heat map, where the colors blue and red mean decrease and increase in relation to control in each growth phase (**Figure 7**). In total 106 compounds from 8 different lipid classes were determined. Of the identified metabolites 16 belongs to digalactosyldiacylglycerols (DGDGs), 12 monogalactosyldiacylglycerols (MGDGs), 10 sulfoquinovosyl diacylglycerol (SQDGs), 10 Lysophosphatidylcholines (LysoPCs), 20 phosphatidylcholine (PCs), 16 phosphatidylethanolamines (PEs), 5 phosphatidylglycerol (PGs) and 17 Fatty acids (FAs) and lipid profile for the three strains were different (**Figure 7, Table S 16 - 18**). In keeping with the diverse structure of different algae, the quantitative and qualitative compositions of lipids vary considerably (Harwood and Guschina, 2009; Li-Beisson et al., 2019). In the present study, CC503 strain showed a lower number of lipids compositions (173) in relationship to BR020 (194) and BR017 (195) strains (**Figure 7**). For CC503 strain, the lipid compositions TAG (10), PC (6), LysoPC (2) and DGDG, MGDG and DAG (1) were not found.

Most of the chloroplast galactolipids (MGDG, DGDG and SQDG) increased in BR017 and BR020 cells under control conditions at the end of cultivation. Under rapamycin-treatment, only CC503 cells increased at 48 h of cultivation. Three phospholipids, phosphatidylcholine (PC), phosphatidylethanolamine (PE) and phosphatidylglycerol (PG), are the major phosphoglycerides identified in most algae species (Borowitzka and Moheimani, 2013). In the present study, we observed that rapamycin treatment did not alter the levels of PC, PE, and PG in CC503 and BR020, but reduced levels of PE were present in BR017 cells.

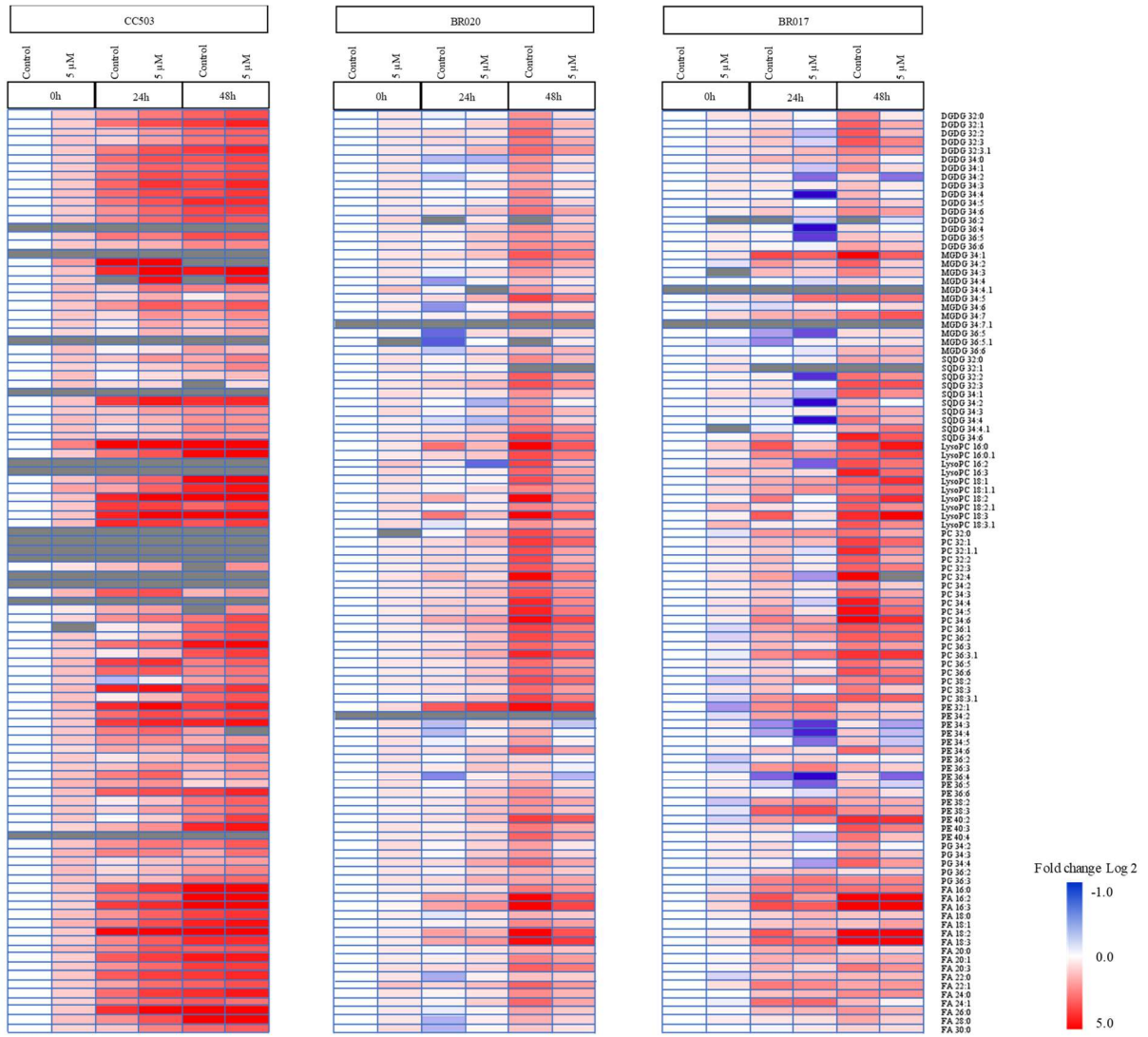
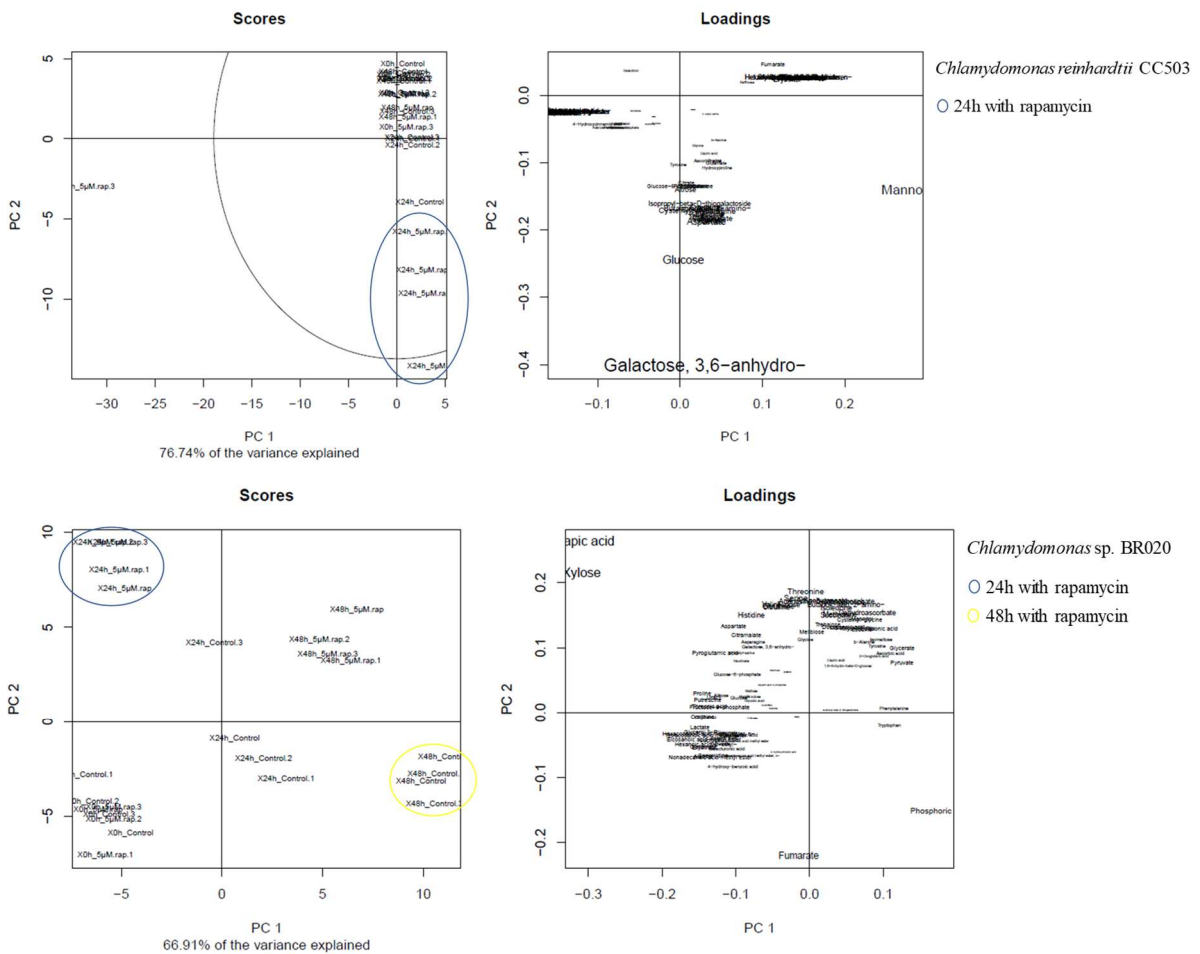


Figure 7. Heat map representing the changes in relative lipid levels contents of three freshwater strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, and *C. vulgaris* BR017) cultured in TAP medium with 5 μM rapamycin and control. Data are scaled to the mean response measured for control 0h for each strain, values presented are means of four biological replicates. The complete dataset and statistics are presented in the supplementary table S 16 – 18).

3.7 Multivariate analysis

Principal component analysis (PCA) was performed to visualize the results between control and rapamycin treatment and thus explore the effect of rapamycin inhibition of the TOR pathway on growth and metabolism of three strains. The primary metabolite PCA (**Figure 8**) shows the difference between the strains. For *C. reinhardtii* CC503 and *C. vulgaris* BR017, the principal components (PC1 and PC2) explained 76.74% and 71.82% of the variance, respectively. The analysis results indicated that the 5 μ M rapamycin treatment at 24h was clustered because of glucose and galactose, 3, 6-anhydro for *C. reinhardtii* CC503 (**Figure 8A**) while for *C. vulgaris* BR017 was clustered by glutaric acid (**Figure 8C**). Regarding *Chlamydomonas* sp. BR020, the principal components (PC1 and PC2) explained 66.91% of the variance and two groups were formed. The 5 μ M rapamycin treatment at 24h was clustered because of sinapic acid and Xylose, while 5 μ M rapamycin treatment at 48h was clustered by phosphoric acid (**Figure 8B**).



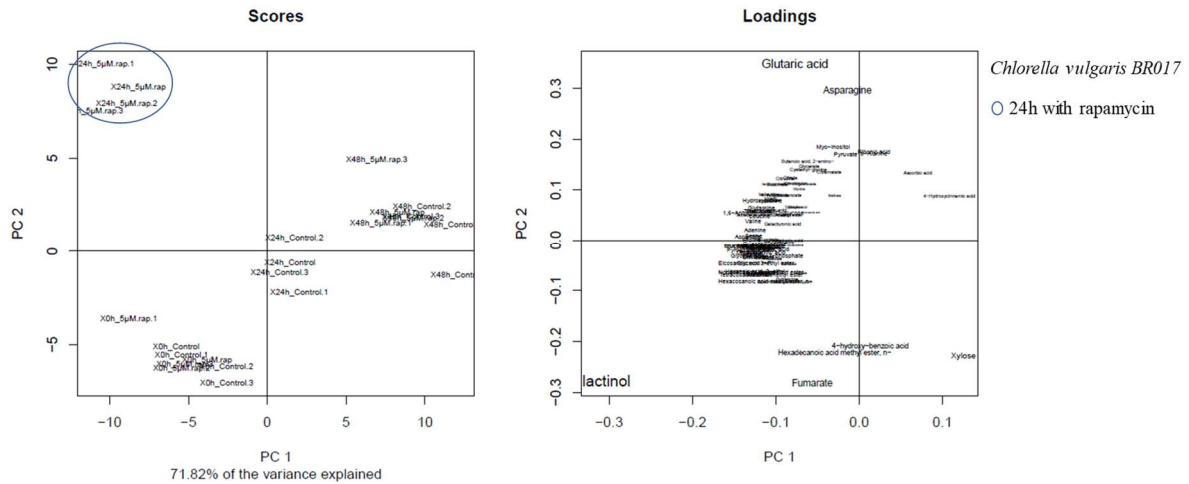


Figure 8. Principal component analysis (PCA) score plot derived data of three freshwater strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, and *C. vulgaris* BR017) cultured in TAP medium with 5 μ M rapamycin and control in three collect points (0h, 24h and 48h). Primary metabolites profile displayed between 66.91% and 76.74% of the variance explained in the two principal components, PC1 and PC2.

4. DISCUSSION

4.1. TOR inhibition decreases differentially the cell number in three strains of phylum Chlorophyta

The phenotype of the rapamycin treatment was characterized by a 50% reduction in the total cell number when compared to control (**Figure 2 A - C**). This partial repression of the cell number is in full agreement with previous studies elucidating the function of TOR in *Chlamydomonas* (Crespo et al., 2005; Lee and Fiehn, 2013; Kleessen et al., 2015; Couso et al., 2016; Jüppner et al., 2018). Part of the explanation for the partial growth repression was traced back to the fact that the native FKBP12 (FK506 binding protein 12 kDa) protein in *Chlamydomonas* does not effectively bind rapamycin (Crespo et al., 2005; Pérez-Pérez et al., 2017). The sensitivity of the *Chlamydomonas* FKBP12 protein to the drug could be increased by two point mutations but, still, contrary to the yeast system, where rapamycin treatment leads to a full growth arrest in G1 cell cycle (Barbet et al., 1996; Oldenhof et al., 2007; Jüppner et al., 2018), *Chlamydomonas* cells were not fully inhibited in growth (Pancha et al., 2020). To overcome, at least in part, this problem, we used the rapamycin concentration by 10-fold to 5 μ M, to make sure that we obtained maximal inhibition of the TOR complex (**Figure 2 A - C**). Our results show that rapamycin inhibits the growth of a photosynthetic organism and strongly suggests the presence of a TOR signaling cascade, not only in the model strain, *C. reinhardtii*, but also in other strains belonging to the same phylum. According to the strain, concentration and time interaction results, *C. reinhardtii* CC503, *Chlamydomonas* sp BR020 and *C. vulgaris* BR017 showed a reduced number of cells between the control and the treatment with rapamycin

(Table S 12). All strains exhibited reduced growth at the end of 48 hours of cultivation with the use of rapamycin (Figure 2 A - C).

4.2. Effect of TOR inhibition on primary metabolism of microalgae cells

Transition from a growing state to a stationary state or vice versa profoundly changes the metabolism of cells. Broadly speaking, there is a metabolic shift from anabolic processes for the *de novo* synthesis of macromolecules (growing or proliferating cells) towards catabolic processes for breakdown of macromolecules to release energy (stationary phase cells) (Mubeen et al., 2018). The TOR kinase has emerged as a signaling node that promotes cell growth and proliferation by the activation of key anabolic processes (Howell et al., 2013). The aim of this study was to describe the metabolic changes within the cell growth of three strains and compare these results to cells where the TOR signaling pathway was inhibited by rapamycin.

The sensitivity of *Chlamydomonas* to rapamycin has been considered an experimental advantage to explore the function of TOR in a photosynthetic organism. Transcriptomic and metabolomic analyses of *Chlamydomonas* cells treated with this drug have been recently reported (Lee and Fiehn, 2013; Li et al., 2014; Mubeen et al., 2018). Metabolomic studies revealed that the TCA cycle is largely affected by the inhibition of TOR, and some TCA cycle intermediates including malate, succinate, and citrate accumulated in rapamycin-treated cells (Lee and Fiehn, 2013; Kleessen et al., 2015; Pérez-Pérez et al., 2017). As in the present study (Figure 4), these metabolites had similar behavior and increased in rapamycin treatment. The negative effect on the TCA cycle intermediates is accompanied by the simultaneous down-regulation of some amino acids such as glutamic acid, asparagine, or glutamine in *C. reinhardtii* (Lee and Fiehn, 2013; Pérez-Pérez et al., 2017), which can be observed for the results in figure 4. It has been proposed that the decrease of these amino acids in rapamycin-treated cells can be associated with the activation of nutrient recycling processes such as senescence or autophagy (Lee and Fiehn, 2013; Pérez-Pérez and Crespo, 2017), which are activated by rapamycin. Thus, TOR seems to play a prominent role in the control of primary metabolism in *Chlamydomonas*, as previously reported in *Arabidopsis* mutant plants with decreased TOR expression (Xiong and Sheen, 2015; Dobrenel et al., 2016). Metabolomics data also indicated that cysteine pool was strongly affected in CC503, BR020 and BR017 strains cells treated with rapamycin (Figure 4). A cysteine and methionine metabolism is needed for the assimilation of sulfur and the synthesis of glutathione, a highly abundant free soluble thiol that maintains the intracellular redox balance in the cell (Foyer and Noctor, 2011). The altered metabolism of cysteine and

methionine in rapamycin-treated cells suggests that proper TOR function might be required to maintain redox homeostasis. In close agreement with this hypothesis, it has been shown that the down-regulation of TOR in *Arabidopsis* results in the enhanced synthesis of glutathione (Caldana et al., 2013; Ren et al., 2013). Furthermore, pyruvate can be produced by the degradation of the amino acids glycine, alanine, tryptophan, threonine, serine and cysteine (Bhatnagar et al., 2011). As the amino acids are strongly accumulated after rapamycin treatment, they might support the accumulation of pyruvate (**Figure 4**). Ketogenic amino acids, as leucine, lysine, isoleucine, phenylalanine, tryptophan, tyrosine and threonine can be converted to acetyl-CoA (Johnson and Alric, 2013; Mubeen et al., 2018). Among these, leucine, lysine and the aromatic amino acids (phenylalanine, tryptophan, tyrosine) show a weaker accumulation after rapamycin treatment compared to other amino acids (**Figure 4**). This might indicate that breakdown of ketogenic amino acids contributes to pools for fatty acid synthesis.

4.3. TOR inhibition by rapamycin changes the carbon partitioning

Starch is one of the main products of photosynthetic carbon fixation and serves as a transient carbon reserve for the night. It has already been shown that *Chlamydomonas* cells, grown under a light-dark regime, accumulate starch within the chloroplast during the light and degrade it in the dark (Klein, 1987; Batista et al., 2019; Covell et al., 2020). The accumulation of starch was accompanied by a decrease of hexoses phosphate, as glucose-6-phosphate (G6P), fructose-6-phosphate (F6P), during the cultivation (**Figure 4**). This is in agreement with observation made by Lee and Fiehn in *Chlamydomonas* after TOR inhibition (Lee and Fiehn, 2013) and was also reported for artificial micro RNA lines of TOR (amiR-tor) in *Arabidopsis* (Caldana et al., 2013). After starch, non-membrane forming neutral lipids as the TAGs represent a major storage for highly reduced carbon and energy (Johnson and Alric, 2013). It has been shown that plant leaves typically do not accumulate high amounts of storage lipids, but they do in fact synthesize significant amounts of TAGs during the day and degrade them during the night (Lin and Oliver, 2008; Caldana et al., 2013). The results show that similar to starch TAGs can increase during the light phase (**Figure 6**).

In agreement with results from yeast (Barbet et al., 1996; Schmelzle et al., 2004), fruit fly (Teleman et al., 2005; Bjedov et al., 2010) and *Arabidopsis* (Caldana et al., 2013; Mubeen et al., 2019), we found that the inhibition of TOR in the all strains leads to an increased accumulation of starch (**Figure 5**) and TAGs (**Figure 6**). It has been already shown in *Chlamydomonas* cells subjected to N starvation that the TAG accumulation lags behind that of

starch (Fan et al., 2012; Himanshu et al., 2016). Interestingly, it was also reported that rapid TAG synthesis occurs only when carbon supply exceeds the capacity of starch synthesis (Smith and Gilmour, 2018). Therefore, our results might imply that TOR has a dominant role in the regulation of TAG biosynthesis and in the regulation of starch.

4.4. TOR inhibition affects membrane lipid composition

Studies published over the last few years have shown that TOR controls lipogenesis through the regulation of the transcription factor sterol regulatory element-binding protein1 (SREBP1) and the phosphatidic acid phosphatase LIPIN1 (Porstmann et al., 2008; Peterson et al., 2011; Lamming and Sabatini, 2013). Beside the strong accumulation of TAG, the analysis of lipids revealed that TOR inhibition in *Chlamydomonas* strongly affects the composition of membrane lipids on the level of saturation and fatty acid chain length (Jüppner et al., 2017; Pancha et al., 2020). Several studies mainly focused on lipid content as a way to evaluate the nutritional value of different microalgal species (Phong et al., 2018; Silva et al., 2019; Kumar et al., 2020; Amorim et al., 2021; Silva et al., 2021).

The major plastid lipids, galactosylglycerides, are polar lipids. In plants, MGDG and DGDG account for 40–55% and 15–35% of the total lipids in thylakoid membranes, respectively (Harwood, 2006; Borowitzka and Moheimani, 2013). The identified lipid classes in this study are presented in a heat map (**Figure 6 and 7**), and the largest number of annotated lipid species belong to the class of structural polar glycosylglycerides MGDGs, DGDGs and SQDGs and the neutral storage, glycerolipids of the TAG class. Furthermore, we found that with minor exceptions the most abundant lipid species within the membrane lipids consists of 34 carbons in their two fatty acids, most of which are polyunsaturated. This was not surprising as it has already been shown that the dominant chain lengths of the total fatty acid composition in *Chlamydomonas* were C16 and C18 (Giroud et al., 1988; Harwood, 2006; Huerlimann et al., 2010; Li-Beisson et al., 2019). Plastid galactolipids are characterized by a very high content of polyunsaturated fatty acids (Giroud et al., 1988; Harwood, 2006). The glycolipids from some algal species, e.g. green algae *Trebouxia* spp., *Coccomyxa* spp., *Chlamydomonas* spp., *Scenedesmus* spp., may also be esterified with unsaturated C16 acids, such as hexadecatrienoic (C16:3n-3/C16:3n-2) and hexadecatetraenoic (C16:4) (Harwood and Guschina, 2009; Huerlimann et al., 2010; Li-Beisson et al., 2019). Three phospholipids, phosphatidylcholine (PC), phosphatidylethanolamine (PE) and phosphatidylglycerol (PG), are the major phosphoglycerides identified in most algae species (Borowitzka and Moheimani, 2013). In the

present work, it was possible to find 41 of those phospholipids (**Figure 7**), practically half of the total lipids. The phospholipids are located in the extrachloroplast membranes with the exception of PG. This phospholipid is present in substantial quantities in thylakoid membranes. PG accounts for around 10 and 20% of the total polar glycerolipids in eukaryotic green algae (Harwood and Guschina, 2009; Borowitzka and Moheimani, 2013).

5. CONCLUSION

Cells of *C. reinhardtii* CC503 and native Brazilian strains, *Chlamydomonas* sp. BR020 and *C. vulgaris* BR017, were used to analyze the impact of TOR inhibition on cell growth. The results from this study clearly show that TOR inhibition causes a severely reduced growth, leading to a reduction by 50% on the cell growth. The present data therefore reveals that TOR is involved in the regulation of cell growth in different strains.

Next to the direct cell growth related results our data reveals that the obtained growth-phenotype was accompanied by strong accumulation of carbon (starch and TAGs) reserves. The amino acids profile exhibited a diverse pattern in relationship to the strains, which will aid in specifying the role and mechanism of individual compounds in the response to the rapamycin treatment. Taken together, the present data reveals a clear metabolite reprogramming in response to TOR inhibition in a strain specific mode (**Figure 9**).

Therefore, further analyses using *C. reinhardtii*, together with other algae, will provide important information on the regulatory mechanism of reserve compounds accumulation and TOR signaling pathway. Furthermore, such data will be useful for the construction of algae being targeted to specific goals.

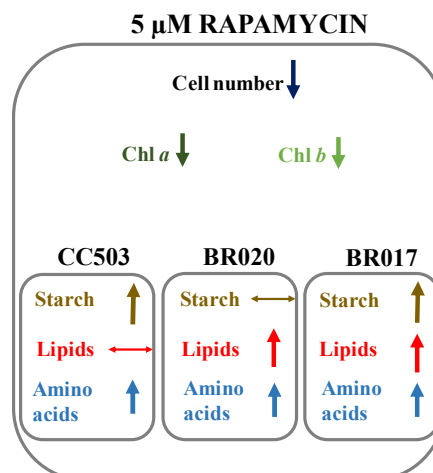


Figure 9. Summary representation of principal responses in *Chlamydomonas reinhardtii* CC503, *Chlamydomonas* sp. BR020 and *Chlorella vulgaris* BR017 according to the rapamycin treatment compared to control. Up arrows indicate increase, down arrows indicate decrease and vertical double arrows indicate there were no difference. The thickness of the arrows was related to the values of compounds or parameters evaluated.

6. REFERENCES:

- Amorim ML, Soares J, Coimbra JS dos R, Leite M de O, Albino LFT, Martins MA** (2021) Microalgae proteins: production, separation, isolation, quantification, and application in food and feed. *Crit Rev Food Sci Nutr* **61**: 1976–2002
- Bar-nun S, Ohad I** (1980) the accuracy of sometimes reported chloroplastic Mn abundance determinations based only on a presumed specific activity of Mn in the growth media. **69**: 363–374
- Barbet NC, Schneider U, Helliwell SB, Stansfield I, Tuite MF, Hall MN** (1996) TOR controls translation initiation and early G1 progression in yeast. *Mol Biol Cell* **7**: 25–42
- Batista AD, Rosa RM, Machado M, Magalhães AS, Shalaguti BA, Gomes PF, Covell L, Vaz MGMV, Araújo WL, Nunes-Nesi A** (2019) Increased urea availability promotes adjustments in C/N metabolism and lipid content without impacting growth in *Chlamydomonas reinhardtii*. *Metabolomics*. doi: 10.1007/s11306-019-1496-3
- Bhatnagar A, Chinnasamy S, Singh M, Das KC** (2011) Renewable biomass production by mixotrophic algae in the presence of various carbon sources and wastewaters. *Appl Energy* **88**: 3425–3431
- Bjedov I, Toivonen JM, Kerr F, Slack C, Jacobson J, Foley A, Partridge L** (2010) Mechanisms of Life Span Extension by Rapamycin in the Fruit Fly *Drosophila melanogaster*. *Cell Metab* **11**: 35–46
- Borowitzka MA, Moheimani NR** (2013) Algae for biofuels and energy. *Algae for Biofuels and Energy* 1–288
- Bromke MA, Giavalisco P, Willmitzer L, Hesse H** (2013) Metabolic Analysis of Adaptation to Short-Term Changes in Culture Conditions of the Marine Diatom *Thalassiosira pseudonana*. *PLoS One* **8**: 1–11
- Caldana C, Li Y, Leisse A, Zhang Y, Bartholomaeus L, Fernie AR, Willmitzer L, Giavalisco P** (2013) Systemic analysis of inducible target of rapamycin mutants reveal a general metabolic switch controlling growth in *Arabidopsis thaliana*. *Plant J* **73**: 897–909
- Contois DE** (1959) Kinetics of Bacterial Growth: Relationship between Population Density and Specific Growth Rate of Continuous Cultures. *J Gen Microbiol* **21**: 40–50
- Couso I, Evans BS, Li J, Liu Y, Ma F, Diamond S, Allen DK, Umen JG** (2016) Synergism between inositol polyphosphates and TOR kinase signaling in nutrient sensing, growth control, and lipid metabolism in *Chlamydomonas*. *Plant Cell* **28**: 2026–2042

- Covell L, Machado M, Vaz MGMV, Soares J, Batista AD, Araújo WL, Martins MA, Nunes-Nesi A** (2020) Alternative fertilizer-based growth media support high lipid contents without growth impairment in *Scenedesmus obliquus* BR003. *Bioprocess Biosyst Eng* **43**: 1123–1131
- Crespo JL, Díaz-Troya S, Florencio FJ** (2005) Inhibition of target of rapamycin signaling by rapamycin in the unicellular green alga *Chlamydomonas reinhardtii*. *Plant Physiol* **139**: 1736–1749
- Dobrenel T, Caldana C, Hanson J, Robaglia C, Vincentz M, Veit B, Meyer C** (2016) TOR Signaling and Nutrient Sensing. *Annu Rev Plant Biol* **67**: 261–285
- Fan J, Yan C, Andre C, Shanklin J, Schwender J, Xu C** (2012) Oil accumulation is controlled by carbon precursor supply for fatty acid synthesis in *Chlamydomonas reinhardtii*. *Plant Cell Physiol* **53**: 1380–1390
- Foyer CH, Noctor G** (2011) Ascorbate and glutathione: The heart of the redox hub. *Plant Physiol* **155**: 2–18
- Giroud C, Gerber A, Eichenberger W** (1988) Lipids of *Chlamydomonas reinhardtii*. Analysis of molecular species and intracellular site(s) of biosynthesis. *Plant Cell Physiol* **29**: 587–595
- Grace SC, Hudson DA** (2016) Processing and Visualization of Metabolomics Data Using R. *Metabolomics - Fundam Appl*. doi: 10.5772/65405
- Griffiths MJ, Garcin C, van Hille RP, Harrison STL** (2011) Interference by pigment in the estimation of microalgal biomass concentration by optical density. *J Microbiol Methods* **85**: 119–123
- Harwood JL** (2006) Membrane Lipids in Algae. *Lipids Photosynth Struct Funct Genet* 53–64
- Harwood JL, Guschina IA** (2009) The versatility of algae and their lipid metabolism. *Biochimie* **91**: 679–684
- Himanshu S, Manish RS, Basuthkar JR, Kandala VRC** (2016) Regulation of starch, lipids and amino acids upon nitrogen sensing in *Chlamydomonas reinhardtii*. *Algal Res* **18**: 33–44
- Howell JJ, Ricoult SJH, Ben-Sahra I, Manning BD** (2013) A growing role for mTOR in promoting anabolic metabolism. *Biochem Soc Trans* **41**: 906–912
- Huerlimann R, de Nys R, Heimann K** (2010) Growth, lipid content, productivity, and fatty acid composition of tropical microalgae for scale-up production. *Biotechnol Bioeng* **107**: 245–257

- Hummel J, Segu S, Li Y, Irgang S, Jueppner J, Giavalisco P** (2011) Ultra performance liquid chromatography and high resolution mass spectrometry for the analysis of plant lipids. *Front Plant Sci* **2**: 1–17
- J. Fan CA** (2011) A Chloroplast pathway for the de novo biosynthesis of triacylglycerol in *Chlamydomonas reinhardtii*. 1985–1991
- Johnson X, Alric J** (2013) Central carbon metabolism and electron transport in *Chlamydomonas reinhardtii*: Metabolic constraints for carbon partitioning between oil and starch. *Eukaryot Cell* **12**: 776–793
- Jüppner J, Mubeen U, Leisse A, Caldana C, Brust H, Steup M, Herrmann M, Steinhauser D, Giavalisco P** (2017) Dynamics of lipids and metabolites during the cell cycle of *Chlamydomonas reinhardtii*. *Plant J* **92**: 331–343
- Jüppner J, Mubeen U, Leisse A, Caldana C, Wiszniewski A, Steinhauser D, Giavalisco P** (2018) The target of rapamycin kinase affects biomass accumulation and cell cycle progression by altering carbon/nitrogen balance in synchronized *Chlamydomonas reinhardtii* cells. *Plant J* **93**: 355–376
- Kleessen S, Irgang S, Klie S, Giavalisco P, Nikoloski Z** (2015) Integration of transcriptomics and metabolomics data specifies the metabolic response of *Chlamydomonas* to rapamycin treatment. *Plant J* **81**: 822–835
- Klein U** (1987) Intracellular Carbon Partitioning in *Chlamydomonas reinhardtii* . *Plant Physiol* **85**: 892–897
- Kumar G, Shekh A, Jakhu S, Sharma Y, Kapoor R, Sharma TR** (2020) Bioengineering of Microalgae: Recent Advances, Perspectives, and Regulatory Challenges for Industrial Application. *Front Bioeng Biotechnol*. doi: 10.3389/fbioe.2020.00914
- Lamming DW, Sabatini DM** (2013) A central role for mTOR in lipid homeostasis. *Cell Metab* **18**: 465–469
- Lee DY, Fiehn O** (2013) Metabolomic response of *Chlamydomonas reinhardtii* to the inhibition of target of rapamycin (tor) by rapamycin. *J Microbiol Biotechnol* **23**: 923–931
- Li-Beisson Y, Thelen JJ, Fedosejevs E, Harwood JL** (2019) The lipid biochemistry of eukaryotic algae. *Prog Lipid Res* **74**: 31–68
- Li J, Kim SG, Blenis J** (2014) Rapamycin: One drug, many effects. *Cell Metab* **19**: 373–379
- Lin W, Oliver DJ** (2008) Role of triacylglycerols in leaves. *Plant Sci* **175**: 233–237
- Lisec J, Schauer N, Kopka J, Willmitzer L, Fernie AR** (2006) Gas chromatography mass spectrometry–based metabolite profiling in plants. *Nat Protoc* **1**: 387–396

- Mubeen U, Giavalisco P, Caldana C** (2019) TOR inhibition interrupts the metabolic homeostasis by shifting the carbon-nitrogen balance in *Chlamydomonas reinhardtii*. *Plant Signal Behav* **14**: 1670595
- Mubeen U, Jüppner J, Alpers J, Hinch DK, Giavalisco P** (2018) Target of rapamycin inhibition in *Chlamydomonas reinhardtii* triggers de novo amino acid synthesis by enhancing nitrogen assimilation[open]. *Plant Cell* **30**: 2240–2254
- Oldenhof H, Zachleder V, Van Den Ende H** (2007) The cell cycle of *Chlamydomonas reinhardtii*: The role of the commitment point. *Folia Microbiol (Praha)* **52**: 53–60
- Pancha I, Chokshi K, Tanaka K, Imamura S** (2020) Microalgal Target of Rapamycin (TOR): A Central Regulatory Hub for Growth, Stress Response and Biomass Production. *Plant Cell Physiol* **61**: 675–684
- Pérez-Pérez ME, Couso I, Crespo JL** (2017) The TOR signaling network in the model unicellular green alga *Chlamydomonas reinhardtii*. *Biomolecules* **7**: 1–13
- Pérez-Pérez ME, Crespo JL** (2017) Monitoring Autophagy in the Model Green Microalga *Chlamydomonas reinhardtii*. *Cells* **6**: 36
- Peterson TR, Sengupta SS, Harris TE, Carmack AE, Kang SA, Balderas E, Guertin DA, Madden KL, Carpenter AE, Finck BN, et al** (2011) MTOR complex 1 regulates lipin 1 localization to control the srebp pathway. *Cell* **146**: 408–420
- Phong WN, Show PL, Ling TC, Juan JC, Ng EP, Chang JS** (2018) Mild cell disruption methods for bio-functional proteins recovery from microalgae—Recent developments and future perspectives. *Algal Res* **31**: 506–516
- Porstmann T, Santos CR, Griffiths B, Cully M, Wu M, Leever S, Griffiths JR, Chung YL, Schulze A** (2008) SREBP Activity Is Regulated by mTORC1 and Contributes to Akt-Dependent Cell Growth. *Cell Metab* **8**: 224–236
- Ren M, Venglat P, Qiu S, Feng L, Cao Y, Wang E, Xiang D, Wang J, Alexander D, Chalivendra S, et al** (2013) Target of rapamycin signaling regulates metabolism, growth, and life span in arabidopsis. *Plant Cell* **24**: 4850–4874
- Salem MA, Jüppner J, Bajdzienko K, Giavalisco P** (2016) Protocol: A fast, comprehensive and reproducible one-step extraction method for the rapid preparation of polar and semi-polar metabolites, lipids, proteins, starch and cell wall polymers from a single sample. *Plant Methods* **12**: 1–15
- Schmelzle T, Beck T, Martin DE, Hall MN** (2004) Activation of the RAS/Cyclic AMP Pathway Suppresses a TOR Deficiency in Yeast. *Mol Cell Biol* **24**: 338–351

- Silva MET da, Correa K de P, Martins MA, da Matta SLP, Martino HSD, Coimbra JS dos R** (2019) Food safety, hypolipidemic and hypoglycemic activities, and in vivo protein quality of microalga *Scenedesmus obliquus* in Wistar rats. *J Funct Foods* 103711
- Silva MET da, Leal MA, Resende M de O, Martins MA, Coimbra JS dos R** (2021) *Scenedesmus obliquus* protein concentrate: A sustainable alternative emulsifier for the food industry. *Algal Res.* doi: 10.1016/j.algal.2021.102468
- Smith AM, Zeeman SC** (2006) Quantification of starch in plant tissues. *Nat Protoc* **1**: 1342–1345
- Smith RT, Gilmour DJ** (2018) The influence of exogenous organic carbon assimilation and photoperiod on the carbon and lipid metabolism of *Chlamydomonas reinhardtii*. *Algal Res* **31**: 122–137
- Stacklies W, Redestig H, Scholz M, Walther D, Selbig J** (2007) pcaMethods - A bioconductor package providing PCA methods for incomplete data. *Bioinformatics* **23**: 1164–1167
- Teleman AA, Chen YW, Cohen SM** (2005) Drosophila melted modulates FOXO and TOR activity. *Dev Cell* **9**: 271–281
- Xiong Y, Sheen J** (2015) Novel links in the plant TOR kinase signaling network. *Curr Opin Plant Biol* **28**: 83–91

CHAPTER 3

TITLE: The Target of Rapamycin (TOR) – a central growth regulator in microalgae

Lidiane Covell¹, Marcelo Gomes Marçal Vieira Vaz¹, Mariana Machado¹, Camila Caldana², Adriano Nunes-Nesi^{1*}

¹ Departamento de Biologia Vegetal, Universidade Federal de Viçosa, 36570-900, Brazil. lidianecovell@gmail.com, marcelogmvvaz@gmail.com, mmachado21@outlook.com, nunesnesi@ufv.br

² Max Planck Institute of Molecular Plant Physiology, Am Mühlenberg 1, 14476 Potsdam-Golm, Germany. caldana@mpimp-golm.mpg.de

*Corresponding author:

Adriano Nunes-Nesi

Departamento de Biologia Vegetal

Universidade Federal de Viçosa

36570-900 Viçosa, Minas Gerais, Brazil

Phone: +55-31-3612-5357

Email: nunesnesi@ufv.br

ABSTRACT

The central role that microalgae play in global biomass production, together with the high biotechnological potential of these organisms in industrial sectors like agriculture or biofuel production has drawn attention to the study of proteins that regulate its cell growth including the Target of rapamycin (TOR) kinase. This protein is an evolutionarily conserved protein kinase which plays an important role in the regulation of cell growth and the sensing of nutrient and energy status in eukaryotes. TOR functions in two distinct multiprotein complexes termed TOR complex 1 (TORC1) and TOR complex 2 (TORC2). While the structure and functions of TORC1 are highly conserved in all eukaryotes, including algae and plants, TORC2 core proteins seems to be missing in photosynthetic organisms. In yeasts and mammals, the roles of TOR have been already well described. Several functions of TOR signaling in plant lineages have also been revealed during the last years. In microalgae, most of functions of TOR have been primarily studied in the model green alga *Chlamydomonas reinhardtii*. Indeed, the development of tools for the functional analysis of TOR have helped to reveal the involvement of TOR in microalgae in many functions, including transcription, translation, accumulation of energy storage molecules, autophagy, etc. In this review, we discuss recent findings relating to TOR signaling and its roles in microalgae.

Keywords: Microalgae. Cell growth. Metabolism. Signaling pathway.

1 INTROCUCTION

The amount and quality of nutrients regulate cell growth and development in all living organisms (Dobrenel et al., 2016a; Pérez-Pérez et al., 2017). This modulation is a central process in organisms and there is a specific relationship between nutrient availability, energy state and cell growth rate, influenced by stresses and various environmental challenges (Wullschleger, 2006; Dobrenel et al., 2013; Xiong and Sheen, 2014). Availability of nutrients, energy, oxygen and stress signals determine the transition and balance between anabolic and catabolic processes (Dibble and Manning, 2013; Howell et al., 2013; Shimobayashi and Hall, 2014). In eukaryotes, nutrient availability and growth output have evolved different signaling pathways (Chantranupong et al., 2015; Efeyan et al., 2015). One of such highly conserved signaling cascades is Target of Rapamycin (TOR) kinase (Crespo and Hall, 2002; Jewell and Guan, 2013; Yuan et al., 2013).

The TOR kinase related pathway controls cell growth by promoting anabolic processes, including protein synthesis, transcription and ribosome biogenesis, and inhibiting catabolic processes such as autophagy and mRNA degradation (Díaz-Troya et al., 2011; Loewith and Hall, 2011; Ingargiola et al., 2020). In yeasts and mammals, TOR is composed of two structurally and functionally different protein complexes: TOR complex 1 (TORC1) and TOR complex 2 (TORC2), and core components of these complexes are, like TOR, evolutionarily conserved. TORC1 mainly responds to the nutrient and energy status of cells and accordingly alters their growth and metabolism (Wullschleger, 2006; Hall, 2016), while TORC2 is mainly responsible for the regulation of the cytoskeleton and other cellular processes through phosphorylation of several targets (Maegawa et al., 2015; Gaubitz et al., 2016; Saxton and Sabatini, 2017). TORC1 is sensitive to the drug rapamycin, while TORC2 is not (Loewith et al., 2002; Pérez-Pérez and Crespo, 2017). The macrolide antibiotic rapamycin is produced by the bacterium *Streptomyces hygroscopicus* and was originally identified as a potent antifungal agent with immunosuppressive activity and anticancer properties (Vézina and Kudelski, 1975; Pérez-Pérez and Crespo, 2010b).

Target of Rapamycin (TOR) is a conserved serine/threonine-protein kinase, member of the phosphatidylinositol 3-kinase-related kinase family (Heitman et al., 1991) and was originally identified by mutations, TOR1-1 and TOR2-1, that confer resistance to the growth inhibitory properties of rapamycin, in the budding yeast *Saccharomyces cerevisiae* (Heitman et al., 1991).

Rapamycin first binds the FKBP12 (FK506-binding protein of 12 kDa) immunophilin, and this complex specifically inhibits TOR function by restricting the access of substrates to the (FRB) domain in TOR, adjacent to the catalytic kinase domain (Wullschleger, 2006; Ren et al., 2013b).

Every eukaryote genome examined (including yeasts, algae, slime mold, plants, worms, flies, and mammals) contains a TOR gene. Unlike yeast, which in some cases possess two TOR genes, eukaryotes possess only a single TOR gene (Loewith et al., 2002; Laplante and Sabatini, 2012; Gaubitz et al., 2015). Heitman et al. (1991) succeeded to identify two target genes, namely TOR1 and TOR2 by employing a genetic mutant screening in the budding yeast *S. cerevisiae*. Whereas rapamycin treatment leads to a growth arrest at G1 state in growing yeast, the two mutants affected in either TOR1 or TOR2 did not show any growth phenotype. This result provided the starting point for the investigation and elucidation of the function and regulation of TOR and leads to the identification of TOR homologues in all eukaryotic organisms, including fungi, mammals, worms, flies, plants, and algae (Crespo and Hall, 2002; Menand et al., 2002; Porstmann et al., 2008; Shimobayashi and Hall, 2014).

Although rapamycin potently inhibits cell growth in most eukaryotes, the vegetative growth of *Arabidopsis* and other plants such as *Oryza sativa*, *Nicotiana tabacum*, or *Brassica napus* is not sensitive to rapamycin (Menand et al., 2002) due to the inability of plant FKBP12 to form a stable complex with this drug (Xu et al., 1998; Sormani et al., 2007; Xiong and Sheen, 2012). Unlike plants, the growth of the unicellular green alga *Chlamydomonas reinhardtii* is sensitive to rapamycin, indicating the presence of a rapamycin-sensitive TOR signaling cascade in this photosynthetic organism (Crespo et al., 2005; Prioretti et al., 2019). The sensitivity of *Chlamydomonas* cells to rapamycin, together with the easy manipulation of this organism, its simple life cycle, and a growing array of genetic and molecular tools (Harris, 2001b; Cross and Umen, 2015; Imamura et al., 2016), have positioned this green alga as a convenient model system to investigate the TOR network in photosynthetic eukaryotes.

Several new TOR functions and signaling pathways have since been revealed in various microalgae by a few research groups using different comprehensive omics tools and other analyses (Mukaida et al., 2016; Imamura et al., 2018; Pancha et al., 2020; Prioretti et al., 2020). The central role that this microalga and native Brazilian strains, play in global biomass production, together with their high biotechnological potential in biofuel generation, animal food, and pharmacology, has boosted our research focused on improving cell growth and better understanding of metabolic pathways.

2 TOR COMPLEXES

Unlike most eukaryotes, *S. cerevisiae* has two TOR genes named TOR1 and TOR2. The TOR kinase resides in two distinct multiprotein complexes, termed TORC1 and TORC2 (Loewith et al., 2002). TORC1 and TORC2 differ in protein composition, although some proteins are common in both complexes (Helliwell et al., 1994; Pérez-Pérez and Crespo, 2010b). In addition to TOR kinase, a TOR-interacting protein, LST8 protein, is present in all TORC1 and TORC2 complexes described (Loewith et al., 2002; Kim et al., 2003; Wedaman et al., 2003; Hayashi et al., 2007; Matsuo et al., 2007). Together with TOR kinase and LST8 is composed of regulatory-associated protein of TOR (RAPTOR) or also known as Kontroller of Growth 1 (KOG1) (Moreau et al., 2012; Saxton and Sabatini, 2017), whereas the core of TORC2 contains AVO1/hSIN1 and AVO3/RICTOR, the rapamycin-insensitive companion of TOR complex (Gaubitz et al., 2016; Burkart and Brandizzi, 2021).

Mammals also have two TOR-containing complexes but only one gene encoding mTOR. mTOR complex 1 (mTORC1) consists of raptor, mLST8, PRAS40, and Deptor (Laplante and Sabatini, 2012; Tulin et al., 2021). mTOR is a serine/threonine protein kinase that responds to a variety of environmental cues, including nutrient, energy, and growth factor levels, as well as diverse forms of stress, to regulate many anabolic and catabolic processes (Howell et al., 2013; Kim et al., 2013; Prioretti et al., 2019).

In both yeasts and mammals, the FKBP12-rapamycin complex targets and inhibits TORC1 but curiously not TORC2 (Hara et al., 2002; Kim et al., 2002; Schmelzle et al., 2004). A thorough analysis of the molecular architecture of TORC2 revealed that AVO3, a subunit unique of this complex, could mask the FKBP12-rapamycin-binding (FRB) domain of TOR2, thereby conferring insensitivity to inhibition by FKBP12-rapamycin (Figure 1A and B) (Gaubitz et al., 2015; Gaubitz et al., 2016; McCready et al., 2020).

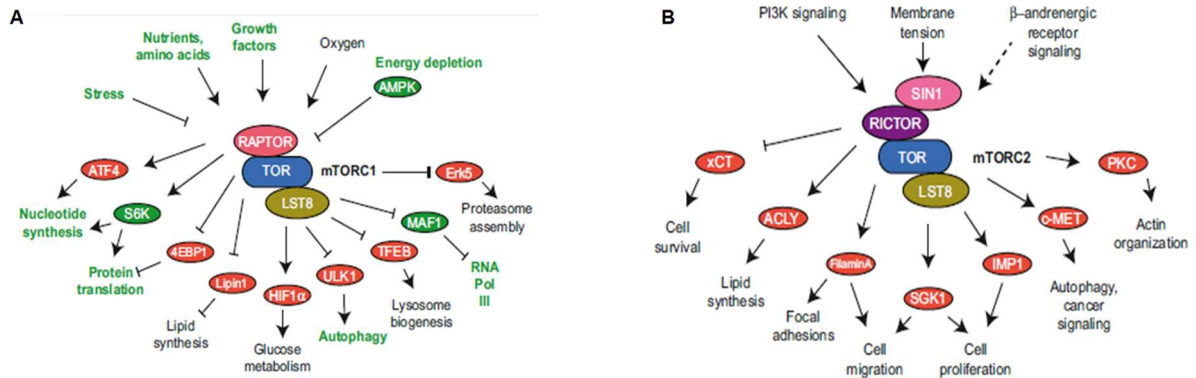


Figure 1. Overview of Mammalian Target of Rapamycin Complex (mTORC) Signaling. **(A)** Upstream activators/repressors and downstream effectors of mTORC1 regulate numerous metabolic and catabolic processes. Activators, effectors, and processes in green are conserved TOR-regulated processes in plants. **(B)** Signaling through mTORC2 modulates diverse cellular functions. Abbreviations: LST8, lethal with SEC13 protein 8; PI3K, phosphoinositide 3-kinase; PKC, protein kinase C; RAPTOR, regulatory-associated protein of mTOR; S6K1, S6 KINASE β -1; RICTOR, rapamycin-insensitive companion of mTOR; SIN1, SAPK-interacting protein 1 (Burkart and Brandizzi, 2021).

The current knowledge about control of cell growth by TOR in photosynthetic organisms is limited compared to other eukaryotes. The TOR kinase has been identified in the model photosynthetic systems *Arabidopsis thaliana* and *Chlamydomonas reinhardtii* (Pérez-Pérez and Crespo, 2010a). The high degree of conservation of TOR proteins throughout the eukaryotic kingdom was leading to the identification of a TOR homolog in plants (Menand et al., 2002; Dobrenel et al., 2011) and a subsequent identification of TOR in *C. reinhardtii* (Crespo et al., 2005; Pérez-Pérez and Crespo, 2010b), including freshwater and marine species from the Chlorophyta, Rhodophyta and Chromalveolata clades (Shemi et al., 2015).

The presence of a single RAPTOR gene and a functional LST8 gene also seems to be conserved in algae, LST8 was copurified with TOR and FKBP12 in the presence of rapamycin, suggesting its involvement in the formation of rapamycin-sensitive TORC1 (Díaz-Troya et al., 2008a). In addition, CrTOR and CrLST8 exist in high-molecular-mass complexes that associate with microsomal membranes in high abundance in the peri-basal body region (Loewith et al., 2002; Li et al., 2014). Unlike TORC1 components, the TORC2-specific proteins AVO1/hSIN1 and AVO3/Rictor seem to be lost in algae and plants, it remains unknown whether TORC2 is also structurally conserved in photosynthetic organisms (Figure 2A and B) (Dobrenel et al., 2011; Pérez-Pérez and Crespo, 2017; Brunkard, 2020). However, it is possible that algae and plants may have a TOR complex functionally similar to TORC2 constituted by highly divergent proteins not seen in other eukaryotes (Díaz-Troya et al., 2011; Burkart and Brandizzi, 2021).

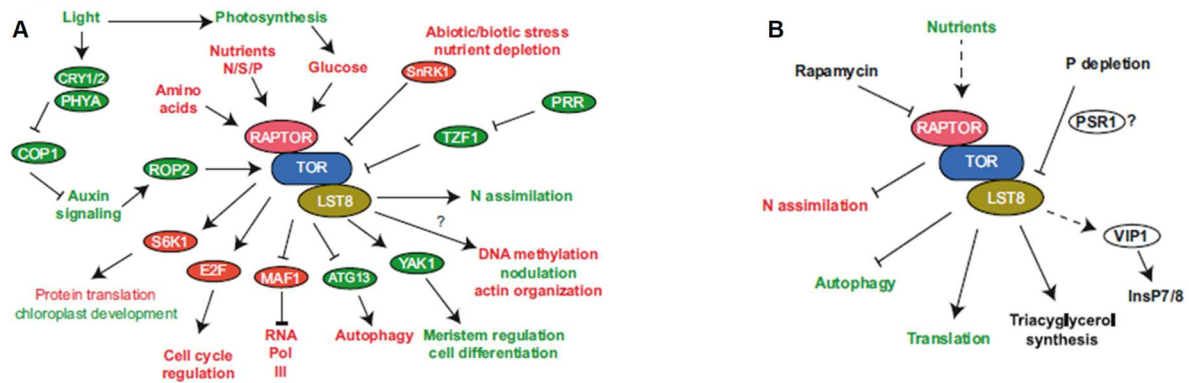


Figure 2. Summary of Plant Target of Rapamycin (TOR) Signaling in *Arabidopsis thaliana* and *Chlamydomonas reinhardtii*. **(A)** Inputs and mechanisms for the activation/inhibition of TOR signaling and the downstream processes regulated by TOR in *A. thaliana*. Activators/inhibitors, effectors, and cellular processes in red are conserved with mammalian TOR signaling. Those in green are plant specific. **(B)** Inputs and mechanisms for the activation/inhibition of TOR signaling and the downstream processes regulated by TOR in *C. reinhardtii*. Activators/inhibitors, effectors, and cellular processes in green are conserved with arabidopsis TOR signaling. Nitrogen assimilation in *C. reinhardtii* is highlighted in red because TOR appears to have the opposite regulation on this process compared with arabidopsis. Abbreviations: ATG, autophagy-related protein; COP1, CONSTITUTIVE PHOTOMORPHOGENESIS 1; LST8, lethal with sec13 protein 8; N, nitrogen; P, phosphorus; PRR, pseudo response regulators; PSR1, phosphate starvation regulator protein 1; RAPTOR, regulatory-associated protein of mTOR; ROP2, RHO OF PLANTS 2; S, sulfur; S6K1, S6 KINASE β -1; YAK1, yet another kinase 1 (Burkart and Brandizzi, 2021).

3 TOR COMPLEXES – CELULAR LOCALIZATION

Yeast and mammalian TORs have been detected in different cellular compartments, including plasma, vacuolar, and ER membranes, as well as in the nucleus, the Golgi apparatus and the mitochondria, and despite significant discrepancies, these studies indicate that TOR complexes are primarily membrane associated (Wedaman et al., 2003; Walther, 2009; Gaubitz et al., 2016). Biochemical fractionation and immunofluorescence studies of *Chlamydomonas* cells have revealed that CrTOR and CrLST8 are peripherally associated to internal membranes, suggesting that TOR complexes may localize on these membranous sites (Díaz-Troya et al., 2008a).

Both CrTOR and CrLST8, in *Chlamydomonas* cells, have a common localization at the peribasal body region, which is enriched in membranes (Díaz-Troya et al., 2008a). However, CrTOR is also detected in discrete punctae that are abundant in regions adjacent to the plasma membrane, while CrLST8 is more abundant around the nucleus (Pérez-Pérez and Crespo, 2010b; Pérez-Pérez et al., 2017). Like in other evolutionarily distant eukaryotes (Drenan et al., 2004; Barquilla et al., 2008), the link of TORC proteins to ER membranes in *Chlamydomonas* indicates the important role that this cellular compartment may play in TOR signaling.

4 EFFECTS OF RAPAMYCIN ON METABOLISM

The sensitivity of *Chlamydomonas* to rapamycin has been considered an experimental advantage to explore the function of TOR in a photosynthetic organism (Dobrenel et al., 2016a; Upadhyaya et al., 2018; Mubeen et al., 2019; Prioretti et al., 2019). The mechanism by which TOR regulates transcription is still poorly understood not only in microalgae but also in land plants and is a topic to be addressed in future research.

Light, sugar, and brassinosteroid signaling through TOR maintain the balance between hormone-promoted growth and carbon availability in plants (Xiong et al., 2013; Dong et al., 2015; Zhang et al., 2016; Kajikawa and Fukuzawa, 2020). During photosynthesis, light energy is captured to convert the carbon intake into sugars, that can be used as material for plant growth or stored as starch for long-term reserves (Ingargiola et al., 2020; Pancha et al., 2020). Photosynthesis, the primary source of energy for plants, also appears to be under the control of the TOR pathway (Ren et al., 2013a; Burkart and Brandizzi, 2021). Plants deficient in TOR signaling exhibit abnormalities in thylakoid grana architecture and normal photosynthetic ability (Zhang et al., 2016; Schepetilnikov and Ryabova, 2018; Bakshi et al., 2021).

In terms of metabolomic approaches, analysis conducted using *C. reinhardtii* cells revealed that the TCA cycle intermediates, malate, succinate and citrate, were significantly increased in cells after exposure to 24 h of rapamycin treatment compared to the control culture (Lee and Fiehn, 2013; Jüppner et al., 2018). The negative effect on the TCA cycle is accompanied by the simultaneous down-regulation of some amino acids such as phenylalanine, glutamic acid, aspartic acid, asparagine, tyrosine, or glutamine (Mubeen et al., 2019).

Remarkably, metabolomics data also indicated that cysteine and methionine pools are strongly affected in *Chlamydomonas* cells treated with rapamycin (Kleessen et al., 2015; Ford et al., 2019). A cysteine and methionine metabolism is needed for the assimilation of sulfur and the synthesis of glutathione, a highly abundant free soluble thiol that maintains the intracellular redox balance in the cell (Foyer and Noctor, 2011). Recent studies using synchronized *C. reinhardtii* cultures indicate that the levels of primary metabolites and carbon storage molecules are higher in rapamycin-treated cultures (Jüppner et al., 2018). A study by Mubeen et al., (2018) on *C. reinhardtii* indicated that in few minutes of rapamycin treatment, the cells accumulate a very high amount of almost all amino acids. When cells were simultaneously exposed to rapamycin and either translation inhibitor cycloheximide or proteasome inhibitor MG132, the amount of amino acids also increased, indicating that translation and proteasome-dependent proteolysis are not major events in this phenomenon. Instead, it was confirmed that the *de novo*

amino acid synthesis mainly depends upon the carbon and nitrogen pull availability (Jüppner et al., 2018; Mubeen et al., 2018). Studies also indicate that the amounts of isomaltotriose and hexose phosphate obtained from the Calvin-Benson cycle are significantly higher during rapamycin treatment in the early-nightphase (Jüppner et al., 2018).

Transcriptomic studies performed on inhibition of TOR signaling, in *Chlamydomonas* cells treated with rapamycin, demonstrated a profound effect on the expression of several genes (Ramundo et al., 2014; Kleessen et al., 2015; Werth et al., 2019; Busche et al., 2021). Up-regulated genes are implicated in amino acid metabolism, vacuolar function, tetrapyrrole metabolism, autophagy, and the transport of metabolites (Kim and Guan, 2011; Couso et al., 2018; Pancha et al., 2019). Most highly induced genes include small heat shock proteins and chaperones, proteases, proteins involved in autophagy and thylakoid membrane biogenesis, protein kinases, and transporters (Ramundo et al., 2014; Prioretti et al., 2020). Down regulated genes upon rapamycin treatment are involved in cell cycle, DNA replication and repair, nucleotide metabolism, and photosynthesis (Shimobayashi and Hall, 2014; Imamura et al., 2018; Jüppner et al., 2018). Together, these transcriptomic and metabolomic data highlight the central role of TOR in cell growth control by regulating anabolic and catabolic processes in *Chlamydomonas*.

5 TOR SIGNALING IN THE ACCUMULATION OF ENERGY STORAGE MOLECULES

There is usually in microalgae an inverse relationship between growth and accumulation of energy storage molecules (Jüppner et al., 2018; Covell et al., 2020). Starch and triacylglycerols (TAGs) are accumulated in relatively low amounts under favorable growth conditions and in high amounts under the influence of various stress, such as nitrogen depletion (Siaut et al., 2011; Rocha et al., 2019; Zhu et al., 2019; Covell et al., 2020). Stress-related responses, e.g. inhibition of cell growth, accumulation of starch/TAGS, are also generally observed under rapamycin-induced TOR inactivation (Jüppner et al., 2018; Pancha et al., 2019; Werth et al., 2019), indicating that algal TOR is involved in sensing the nutrient and energy status of cells.

The inhibition of TOR signaling by rapamycin in *Chlamydomonas* and the distant red alga *Cyanidioschyzon merolae* resulted in the accumulation of lipid bodies containing TAGs and the up-regulation of genes involved in TAG synthesis such as glycerol-3-phosphate acyltransferase and acyl-CoA:diacylglycerol acyltransferase (DGAT) (Imamura et al., 2015; Imamura et al.,

2016). In the green alga *E. gracilis* treated with rapamycin has also been demonstrated a similar effect on lipid body accumulation (Mukaida et al., 2016). However, as the genome sequence of *E. gracilis* is not publicly available, it is not possible to identify the molecular mechanism by which rapamycin affects TAG metabolism in this alga (Mukaida et al., 2016). In the diatom *P. tricornutum* TOR inhibition by AZD8055 also results in a dose-dependent increase in TAG accumulation and inhibition of cell proliferation (Prioretti et al., 2017). The biochemical activity of certain enzymes, e.g. glyceraldehyde 3-phosphate dehydrogenase and glucose-6-phosphate dehydrogenase, increased significantly upon AZD8055 treatment. Since these enzymes are important for intracellular levels of ATP and pyruvate, which are involved in lipid production, this indicate a mechanism by which TOR signaling regulates TAG accumulation in diatoms (Prioretti et al., 2017).

During the screening of a *C. reinhardtii* insertion mutant library, it has been identified rapamycin-hypersensitive VIP1 loss-of-function mutant cells (Couso et al., 2016). Even under normal growth conditions, these mutants accumulate a large amount of TAGs. The *vip1* gene encodes an inositol polyphosphate kinase, which phosphorylates inositol phosphate (InsP) to produce the signaling metabolites InsP7 and InsP8 (Couso et al., 2016). In addition, *vip1-1* mutant has decreased InsP7 and InsP8 levels and increased TAG levels under normal growth conditions. These observations demonstrate that TOR signaling regulates the amount of InsPs in cells and that InsP levels determine intracellular TAG levels (Couso et al., 2016; Prioretti et al., 2020). Based on these observations, it is clear that algal TOR signaling is also involved in TAG accumulation in divergent microalgae, this signaling pathway might also be a biotechnological target to improve TAG productivity in algae.

Apart from TAGs, starch is another important carbon storage molecule in microalgae (Juergens et al., 2016; Zhao and Wang, 2020). Microalgae generally accumulate starch under the same growth conditions that lead to TAG accumulation (Himanshu et al., 2016; Mubeen et al., 2018), but starch accumulation is also induced by TOR inactivation (Fan et al., 2012; Johnson and Alric, 2013). Starch accumulation after TOR inactivation has been observed in *C. reinhardtii* (Pérez-Pérez and Crespo, 2017; Jüppner et al., 2018; Mubeen et al., 2019), indicating that TOR signaling is also involved in starch accumulation in microalgae. Microalgae are a potential feedstock for the production of biofuels (Chisti, 2007), so the enhancement of TAG/starch content in microalgae is necessary for the commercialization of microalgae-based biofuel. Thus, modulation of the TOR signaling pathway(s) and its regulator(s) appear to be a potential method by which the accumulation of TAGs/starch can be enhanced without

compromising the growth of microalgae. Furthermore, accumulation of TAGs and starch after TOR inactivation was also observed in *A. thaliana* (Caldana et al., 2013), indicating that the role of TOR signaling in the accumulation of these energy storage molecules seems to be conserved in plant lineages. Therefore, further research on the effects of TOR on the accumulation of energy storage molecules will be helpful for the improvement of biomass production not only in microalgae but also in plants (Prioretti et al., 2019).

6 CONTROL OF AUTOPHAGY BY TOR

Eukaryotic cells have developed specialized mechanisms to respond and adapt to stresses in the extracellular environment (Couso et al., 2018). Autophagy is a major catabolic pathway by which eukaryotic cells remove damaged or unnecessary cytoplasmic material to the vacuole for degradation and recycling in order to maintain cellular homeostasis (Marshall and Vierstra, 2018; Barros et al., 2020). During this degradative process, cytosolic components, including proteins, membranes, and entire organelles, are engulfed in bulk or selectively within a double-membrane vesicle known as an autophagosome and delivered to the vacuole (Liu and Bassham, 2012; Zeng et al., 2019). Generally, autophagy occurs as a result of stress, such as carbon and/or nitrogen depletion, pathogen attack and senescence (Liu and Bassham, 2012; Marshall and Vierstra, 2018). Autophagy is also carried out, albeit to a lesser extent, under normal growth conditions in all cells to remove waste materials (Mizushima et al., 2011; Ohsumi, 2014; Avin-Wittenberg, 2019).

The genes encoding proteins functioning in the autophagy machinery (autophagy-related genes - ATG genes), which were originally identified in yeast and subsequently in mammals (Elander et al., 2018), have also been identified in photosynthetic eukaryotes, including land plants and various microalgae (Liu and Bassham, 2012; Pérez-Pérez and Crespo, 2017; Couso et al., 2018; Marshall and Vierstra, 2018). In plants, autophagy has been described in the model plant *A. thaliana* as well as the model algae *C. reinhardtii* (Doelling et al., 2002; Pérez-Pérez et al., 2012; Barros et al., 2020).

Autophagy induction can be initiated by multiple signaling pathways, one of which is the negative regulator of TOR protein (Mizushima et al., 2011; Couso et al., 2018). Autophagy is triggered when the cell senses a reduction in the availability of nutrients (Kajikawa and Fukuzawa, 2020). TORC1 has been identified as an essential component in the molecular mechanism that transmits this starvation signal to the autophagic machinery (Elander et al., 2018; Marshall and Vierstra, 2018). TORC1 inhibits autophagy by negatively regulating the

association between the Ser/Thr kinase ATG1 with ATG13, a regulatory subunit of ATG1 (Couso et al., 2018; Pugkaew et al., 2018). Under nutrient-rich conditions, TORC1 promotes phosphorylation of ATG1 and ATG13. When phosphorylated, these proteins cannot interact and consequently, ATG1 kinase remains inactive (Zeng et al., 2019; Barros et al., 2020).

TOR inactivation via RNAi-mediated downregulation, chemical inhibitors such as rapamycin and AZD8055, or genetic elimination of RAPTOR or LST8, causes rapid dephosphorylation of ATG1 and ATG13 (Couso et al., 2018; Zeng et al., 2019), which results in ATG1 activation and autophagy induction (Couso et al., 2018; Avin-Wittenberg, 2019).

Whole-genome analysis of *C. reinhardtii* revealed that its nucleus encodes a single copy of almost all ATGs (Díaz-Troya et al., 2008b; Pérez-Pérez and Crespo, 2017). Structural analysis indicates that the structure of CrATG8 is very similar to that of *A. thaliana* ATG8. Both CrATG8 and AtATG8 proteins possess a long C-terminal extension after a conserved glycine residue (Pérez-Martín et al., 2015; Couso et al., 2018). It is already known that ATG8 is conjugated to phosphatidylethanolamine (PE), in which the glycine residue plays a key role, and this process is required autophagosome formation (Nakatogawa et al., 2007; Avin-Wittenberg, 2019; Barros et al., 2020). In *C. reinhardtii* cells, CrATG8 is present as punctate structures with rapamycin treatment or under other stresses, such as nitrogen depletion or oxidative stress, suggesting that TOR plays an important role in signaling nutritional to proteins involved in autophagy activation and autophagosome formation (Pérez-Pérez and Crespo, 2010a; Couso et al., 2018; Kajikawa and Fukuzawa, 2020).

Overall, the mechanism underlying the TOR-dependent regulation of autophagy in green microalgae is still poorly understood and further research on this topic is needed for clarification.

7 ROLE OF TOR IN PROTEIN SYNTHESIS

When energy or amino acids become limiting, protein production needs to be downregulated, so that cells can use their limited resources to survive (Ma and Blenis, 2009; Guerra et al., 2013; Liang et al., 2019). Protein synthesis is an intricate, energy-demanding, and strictly controlled process that plays a fundamental role in cell growth, proliferation, and differentiation. The control of protein synthesis is one of the best-characterized processes downstream of TOR which regulates various catabolic and anabolic processes in cells. Protein synthesis is one such process and must be tightly regulated according to cell growth to maintain cellular homeostasis (Schepetilnikov and Ryabova, 2018).

In mammalian and yeast cells, ribosomal S6 kinases (S6Ks, SCH9 in yeast) and eIF4E-binding proteins (4E-BPs) are major downstream targets of TOR that are involved in the translation process (Albert and Hall, 2015; Dobrenel et al., 2016b). TORC1 promotes the synthesis of proteins through phosphorylation of two main substrates namely ribosomal protein S6kinase – (S6K/Sch9 the functional homolog in yeast) and 4E-BP1 (translation initiation factor 4E-binding protein-1) (Ma and Blenis, 2009; Schepetilnikov and Ryabova, 2018). S6K (Sch9) phosphorylation by TORC1 activates the S6K as well as multiple other substrates including eIF4B (elongation initiation factor-4B). The eIF4B protein regulates cap-dependent translation by forming an active complex with eIF4A (Hay and Sonenberg, 2004; Holz et al., 2005; Dorrello et al., 2006). The 4E-BP1 inhibits the assembly of eIF-4E complex for cap-dependent translation. When the TORC1 is active it negatively regulates 4E-BP1 by phosphorylating at multiple sites to inhibit its interaction with eIF4E (Brunn et al., 1997; Gingras et al., 1999; Howell et al., 2013). As in yeasts and mammals, S6K is well conserved in photosynthetic eukaryotes, although no 4E-BP-related proteins have been identified in plants or algae (Schepetilnikov and Ryabova, 2018).

The Arabidopsis genome encodes two S6K homologs, S6K1 and S6K2 (Zhang et al., 1994), and it has been demonstrated that TOR regulates S6K1 and S6 phosphorylation in Arabidopsis (Schepetilnikov et al., 2011; Dobrenel et al., 2016b). It has been reported that S6Ks play an essential role in the control of the translation process through the phosphorylation of ribosomal protein S6 and eukaryotic elongation factor-2 kinase (Schepetilnikov and Ryabova, 2018). The recent development of S6K antibody, which can be used to detect the specific phosphorylation residue of endogenous *A. thaliana* S6K as well as for phosphoproteomic analysis, has resulted in the discovery that Ser240 of S6K is phosphorylated by TOR (Dobrenel et al., 2016b).

Recently, it was identified a single copy of CrS6K in *C. reinhardtii* and confirmed the presence of the well conserved TOR phosphorylation motif FLGFTYVAP at the C-terminal of the protein (Upadhyaya et al., 2018). It still has not been clear whether this protein is a canonical S6K, although the C-terminus of the protein contains the TOR phosphorylation motif. Still according to Upadhyaya et al., (2018), CrS6K is involved in protein synthesis under light conditions. Therefore, it has been reported no direct evidence relating to the involvement of CrS6K in protein synthesis.

Díaz-Troya et al., (2011) showed that, the function of the ER chaperone BiP is regulated by its phosphorylation status and that its phosphorylation is accelerated by rapamycin-induced

TOR inactivation in *C. reinhardtii*. In addition, rapamycin treatment also results in translation inhibition in this alga. Under ER stress induced by heat shock or tunicamycin, both of which inhibit the glycosylation of protein in the ER, BiP was dephosphorylated. A recent study in *C. reinhardtii* showed that phosphorylation of Ser245, a conserved amino acid of RPS6 in the C-terminus region, is strongly decreased under the treatment of rapamycin, Torin 1 and AZD8055. These results also support that TOR inactivation results in translation inhibition in *C. reinhardtii* (Couso et al., 2020).

8 PHOTOSYNTHETIC ORGANISMS – TOR SIGNALING IN CHLOROPLAST PROCESSES

Chloroplasts are one of the most important cellular compartments of plant and algae cells, as they are responsible for the essential processes of photosynthesis (Couso et al., 2021). The availability of nutrients and other environmental conditions determine the size, number and activity of chloroplasts in plant cells (Li et al., 2013; Upadhyaya et al., 2018; Ingargiola et al., 2020). How the regulation of chloroplast processes occurs via TOR remains largely unknown. The mechanism by which TOR regulates the transcription of chloroplast ribosomal RNA (rRNA) was revealed in *C. merolae* (Imamura et al., 2018). TOR inactivation increased the expression of a nuclear-encoded chloroplast RelA-SpoT homolog (RSH) gene, CmRSH4b, which encodes a homolog of the guanosine 30-diphosphate 50-diphosphate (ppGpp) synthetases. Biochemical analyses showed that ppGpp inhibits bacteria-type RNA polymerase-dependent chloroplast rRNA synthesis and chloroplast guanylate kinase (GK). The inhibition of GK reduces the GTP pool, inhibiting rRNA transcription, for which GTP is the initiating nucleotide (Imamura et al., 2018).

Recent proteomic and phosphoproteomic analyses using *C. reinhardtii* indicated that the levels of tetrapyrrole-related proteins are increased, while the levels of most of the proteins related to the Calvin-Benson cycle are decreased in cells under TOR inactivation (Roustan and Weckwerth, 2018; Couso et al., 2021). This suggests that TOR signaling regulates photosynthesis and other processes in the chloroplast (Couso et al., 2021). Furthermore, two metalloproteases, A8IL08 and A8J6C7, which localize in the thylakoid membrane, are decreased, while the serine protease A8IL21 is increased during rapamycin treatment (Roustan and Weckwerth, 2018). Thus, it seems likely that TOR signaling plays important role in cellular processes in chloroplast. Therefore, further analyses of the functions of TOR in these cellular

processes may better clarify the function of TOR pathway signaling and its association with photosynthetic performance in microalgae.

9 PERSPECTIVES

Compared to animals and yeasts, the current knowledge of TOR functions and signaling in microalgae is very limited. The recent development of rapamycin-sensitive strains and novel TOR inhibitors combined with various “omic” analyses have revealed that algal TOR is involved in many cellular processes in microalgae, as which the accumulation of energy storage molecules, autophagy, rRNA transcription in the chloroplast. However, still little is known about the molecular mechanisms by which TOR promotes photosynthetic cell growth. Efforts should concentrate in the identification of components of this signaling cascade that may act upstream or downstream of TOR, being able to provide valuable information about nutritional or stress inputs to this kinase. This knowledge will help us not only to understand TOR functions in plant and algae lineages but also to develop various tools for the sustainable development of biomass production using microalgae and algal biotechnology to benefits in industrial sectors like agriculture or biofuel production.

10 REFERENCES

- Albert V, Hall MN** (2015) mTOR signaling in cellular and organismal energetics. *Curr Opin Cell Biol* **33**: 55–66
- Avin-Wittenberg T** (2019) Autophagy and its role in plant abiotic stress management. *Plant Cell Environ* **42**: 1045–1053
- Bakshi A, Moin M, Madhav MS, Datla R, Kirti PB** (2021) Target of Rapamycin (TOR) negatively regulates chlorophyll degradation and lipid peroxidation and controls responses under abiotic stress in *Arabidopsis thaliana*. *Plant Stress* **2**: 100020
- Barquilla A, Crespo JL, Navarro M** (2008) Rapamycin inhibits trypanosome cell growth by preventing TOR complex 2 formation. *Proc Natl Acad Sci U S A* **105**: 14579–14584
- Barros JAS, Siqueira JAB, Cavalcanti JHF, Araújo WL, Avin-Wittenberg T** (2020) Multifaceted Roles of Plant Autophagy in Lipid and Energy Metabolism. *Trends Plant Sci* **25**: 1141–1153
- Brunkard JO** (2020) Exaptive Evolution of Target of Rapamycin Signaling in Multicellular Eukaryotes. *Dev Cell* **54**: 142–155

- Burkart GM, Brandizzi F** (2021) A Tour of TOR Complex Signaling in Plants. *Trends Biochem Sci* **46**: 417–428
- Busche M, Regina Scarpin M, Hnasko R, Brunkard JO** (2021) TOR coordinates nucleotide availability with ribosome biogenesis in plants. *Plant Cell* **33**: 1615–1632
- Caldana C, Li Y, Lisse A, Zhang Y, Bartholomaeus L, Fernie AR, Willmitzer L, Giavalisco P** (2013) Systemic analysis of inducible target of rapamycin mutants reveal a general metabolic switch controlling growth in *Arabidopsis thaliana*. *Plant J* **73**: 897–909
- Chantranupong L, Wolfson RL, Sabatini DM** (2015) Nutrient-sensing mechanisms across evolution. *Cell* **161**: 67–83
- Chisti Y** (2007) Biodiesel from microalgae. *Biotechnol Adv* **25**: 294–306
- Couso I, Evans BS, Li J, Liu Y, Ma F, Diamond S, Allen DK, Umen JG** (2016) Synergism between inositol polyphosphates and TOR kinase signaling in nutrient sensing, growth control, and lipid metabolism in *Chlamydomonas*. *Plant Cell* **28**: 2026–2042
- Couso I, Pérez-Pérez ME, Ford MM, Martínez-Force E, Hicks LM, Umen JG, Crespo JL** (2020) Phosphorus Availability Regulates TORC1 Signaling via LST8 in *Chlamydomonas*. *Plant Cell* **32**: 69–80
- Couso I, Pérez-Pérez ME, Martínez-Force E, Kim HS, He Y, Umen JG, Crespo JL** (2018) Autophagic flux is required for the synthesis of triacylglycerols and ribosomal protein turnover in *Chlamydomonas*. *J Exp Bot* **69**: 1355–1367
- Couso I, Smythers AL, Ford MM, Umen JG, Crespo JL, Hicks LM** (2021) Inositol polyphosphates and target of rapamycin kinase signalling govern photosystem II protein phosphorylation and photosynthetic function under light stress in *Chlamydomonas*. *New Phytol* **232**: 2011–2025
- Covell L, Machado M, Vaz MGMV, Soares J, Batista AD, Araújo WL, Martins MA, Nunes-Nesi A** (2020) Alternative fertilizer-based growth media support high lipid contents without growth impairment in *Scenedesmus obliquus* BR003. *Bioprocess Biosyst Eng* **43**: 1123–1131
- Crespo JL, Díaz-Troya S, Florencio FJ** (2005) Inhibition of target of rapamycin signaling by rapamycin in the unicellular green alga *Chlamydomonas reinhardtii*. *Plant Physiol* **139**: 1736–1749
- Crespo JL, Hall MN** (2002) Elucidating TOR Signaling and Rapamycin Action: Lessons from *Saccharomyces cerevisiae*. *Microbiol Mol Biol Rev* **66**: 579–591
- Cross FR, Umen JG** (2015) The *Chlamydomonas* cell cycle. *Plant J* **82**: 370–392

- Díaz-Troya S, Florencio FJ, Crespo JL** (2008a) Target of rapamycin and LST8 proteins associate with membranes from the endoplasmic reticulum in the unicellular green alga *Chlamydomonas reinhardtii*. *Eukaryot Cell* **7**: 212–222
- Díaz-Troya S, Pérez-Pérez ME, Florencio FJ, Crespo JL** (2008b) The role of TOR in autophagy regulation from yeast to plants and mammals. *Autophagy* **4**: 851–865
- Díaz-Troya S, Pérez-Pérez ME, Pérez-Martín M, Moes S, Jenó P, Florencio FJ, Crespo JL** (2011) Inhibition of protein synthesis by TOR inactivation revealed a conserved regulatory mechanism of the BiP chaperone in *Chlamydomonas*. *Plant Physiol* **157**: 730–741
- Dibble CC, Manning BD** (2013) Signal integration by mTORC1 coordinates nutrient input with biosynthetic output. *Nat Cell Biol* **15**: 555–564
- Dobrenel T, Caldana C, Hanson J, Robaglia C, Vincentz M, Veit B, Meyer C** (2016a) TOR Signaling and Nutrient Sensing. *Annu Rev Plant Biol* **67**: 261–285
- Dobrenel T, Mancera-Martínez E, Forzani C, Azzopardi M, Davanture M, Moreau M, Schepetilnikov M, Chicher J, Langella O, Zivy M, et al** (2016b) The arabidopsis TOR kinase specifically regulates the expression of nuclear genes coding for plastidic ribosomal proteins and the phosphorylation of the cytosolic ribosomal protein S6. *Front Plant Sci* **7**: 1–16
- Dobrenel T, Marchive C, Azzopardi M, Clément G, Moreau M, Sormani R, Robaglia C, Meyer C** (2013) Sugar metabolism and the plant target of rapamycin kinase: A sweet operaTOR? *Front Plant Sci* **4**: 1–6
- Dobrenel T, Marchive C, Sormani R, Moreau M, Mozzo M, Montané MH, Menand B, Robaglia C, Meyer C** (2011) Regulation of plant growth and metabolism by the TOR kinase. *Biochem Soc Trans* **39**: 477–481
- Doelling JH, Walker JM, Friedman EM, Thompson AR, Vierstra RD** (2002) The APG8/12-activating enzyme APG7 is required for proper nutrient recycling and senescence in *Arabidopsis thaliana*. *J Biol Chem* **277**: 33105–33114
- Dong P, Xiong F, Que Y, Wang K, Yu L, Li Z, Ren M** (2015) Expression profiling and functional analysis reveals that TOR is a key player in regulating photosynthesis and phytohormone signaling pathways in *Arabidopsis*. *Front Plant Sci* **6**: 1–15
- Dorrello NV, Peschiaroli A, Guardavaccaro D, Colburn NH, Sherman NE, Pagano M** (2006) S6k1- and β TRCP-mediated degradation of PDCD4 promotes protein translation and cell growth. *Science* (80-) **314**: 467–471

- Drenan RM, Liu X, Bertram PG, Zheng XFS** (2004) FKBP12-Rapamycin-associated Protein or Mammalian Target of Rapamycin (FRAP/mTOR) Localization in the Endoplasmic Reticulum and the Golgi Apparatus. *J Biol Chem* **279**: 772–778
- Efeyan A, Comb WC, Sabatini DM** (2015) Nutrient-sensing mechanisms and pathways. *Nature* **517**: 302–310
- Elander PH, Minina EA, Bozhkov P V.** (2018) Autophagy in turnover of lipid stores: Trans-kingdom comparison. *J Exp Bot* **69**: 1301–1311
- Fan J, Yan C, Andre C, Shanklin J, Schwender J, Xu C** (2012) Oil accumulation is controlled by carbon precursor supply for fatty acid synthesis in *Chlamydomonas reinhardtii*. *Plant Cell Physiol* **53**: 1380–1390
- Ford MM, Smythers AL, McConnell EW, Lowery SC, Kolling DRJ, Hicks LM** (2019) Inhibition of TOR in *Chlamydomonas reinhardtii* Leads to Rapid Cysteine Oxidation Reflecting Sustained Physiological Changes. *Cells*. doi: 10.3390/cells8101171
- Foyer CH, Noctor G** (2011) Ascorbate and glutathione: The heart of the redox hub. *Plant Physiol* **155**: 2–18
- Gaubitz C, Oliveira TM, Prouteau M, Leitner A, Karuppasamy M, Konstantinidou G, Rispal D, Eltschinger S, Robinson GC, Thore S, et al** (2015) Molecular Basis of the Rapamycin Insensitivity of Target Of Rapamycin Complex 2. *Mol Cell* **58**: 977–988
- Gaubitz C, Prouteau M, Kusmider B, Loewith R** (2016) TORC2 Structure and Function. *Trends Biochem Sci* **41**: 532–545
- Gingras A, Gygi SP, Raught B, Polakiewicz RD, Abraham RT, Hoekstra MF, Aebersold R, Sonenberg N** (1999) Regulation of 4E-BP1 phosphorylation : a novel two-step mechanism. 1422–1437
- Hall MN** (2016) TOR and paradigm change: Cell growth is controlled. *Mol Biol Cell* **27**: 2804–2806
- Hara K, Maruki Y, Long X, Yoshino K ichi, Oshiro N, Hidayat S, Tokunaga C, Avruch J, Yonezawa K** (2002) Raptor, a binding partner of target of rapamycin (TOR), mediates TOR action. *Cell* **110**: 177–189
- Hayashi T, Hatanaka M, Nagao K, Nakaseko Y, Kanoh J, Kokubu A, Ebe M, Yanagida M** (2007) Rapamycin sensitivity of the *Schizosaccharomyces pombe* tor2 mutant and organization of two highly phosphorylated TOR complexes by specific and common subunits. *Genes to Cells* **12**: 1357–1370

- Heitman J, Movva NR, Hall MN** (1991) Targets for cell cycle arrest by the immunosuppressant rapamycin in yeast. *Science* (80-) **253**: 905–909
- Helliwell SB, Wagner P, Kunz J, Deuter-Reinhard M, Henriquez R, Hall MN** (1994) TOR1 and TOR2 are structurally and functionally similar but not identical phosphatidylinositol kinase homologues in yeast. *Mol Biol Cell* **5**: 105–118
- Himanshu S, Manish RS, Basuthkar JR, Kandala VRC** (2016) Regulation of starch, lipids and amino acids upon nitrogen sensing in *Chlamydomonas reinhardtii*. *Algal Res* **18**: 33–44
- Holz MK, Ballif BA, Gygi SP, Blenis J** (2005) mTOR and S6K1 mediate assembly of the translation preinitiation complex through dynamic protein interchange and ordered phosphorylation events. *Cell* **123**: 569–580
- Howell JJ, Ricoult SJH, Ben-Sahra I, Manning BD** (2013) A growing role for mTOR in promoting anabolic metabolism. *Biochem Soc Trans* **41**: 906–912
- Imamura S, Kawase Y, Kobayashi I, Shimojima M, Ohta H, Tanaka K** (2016) TOR (target of rapamycin) is a key regulator of triacylglycerol accumulation in microalgae. *Plant Signal Behav.* doi: 10.1080/15592324.2016.1149285
- Imamura S, Kawase Y, Kobayashi I, Sone T, Era A, Miyagishima S ya, Shimojima M, Ohta H, Tanaka K** (2015) Target of rapamycin (TOR) plays a critical role in triacylglycerol accumulation in microalgae. *Plant Mol Biol* **89**: 309–318
- Imamura S, Nomura Y, Takemura T, Pancha I, Taki K, Toguchi K, Tozawa Y, Tanaka K** (2018) The checkpoint kinase TOR (target of rapamycin) regulates expression of a nuclear-encoded chloroplast RelA-SpoT homolog (RSH) and modulates chloroplast ribosomal RNA synthesis in a unicellular red alga. *Plant J* **94**: 327–339
- Ingargiola C, Duarte GT, Robaglia C, Leprince A-S, Meyer C** (2020) The Plant Target of Rapamycin: A Conduc TOR of Nutrition and Metabolism in Photosynthetic Organisms. doi: doi.org/10.3390/genes11111285
- Jewell JL, Guan KL** (2013) Nutrient signaling to mTOR and cell growth. *Trends Biochem Sci* **38**: 233–242
- Johnson X, Alric J** (2013) Central carbon metabolism and electron transport in *Chlamydomonas reinhardtii*: Metabolic constraints for carbon partitioning between oil and starch. *Eukaryot Cell* **12**: 776–793
- Juergens MT, Disbrow B, Shachar-Hill Y** (2016) The relationship of triacylglycerol and starch accumulation to carbon and energy flows during nutrient deprivation in *Chlamydomonas reinhardtii*. *Plant Physiol* **171**: 2445–2457

- Jüppner J, Mubeen U, Leisse A, Caldana C, Wiszniewski A, Steinhauser D, Giavalisco P** (2018) The target of rapamycin kinase affects biomass accumulation and cell cycle progression by altering carbon/nitrogen balance in synchronized *Chlamydomonas reinhardtii* cells. *Plant J* **93**: 355–376
- Kajikawa M, Fukuzawa H** (2020) Algal Autophagy Is Necessary for the Regulation of Carbon Metabolism Under Nutrient Deficiency. *Front Plant Sci* **11**: 1–6
- Kim D, Sarbassov DD, Ali SM, Latek RR, Guntur KVP, Erdjument-bromage H, Tempst P, Sabatini DM** (2003) <1-s2.0-S109727650300114X-main.pdf>. **11**: 895–904
- Kim SG, Buel GR, Blenis J** (2013) Nutrient regulation of the mTOR complex 1 signaling pathway. *Mol Cells* **35**: 463–473
- Kleessen S, Irgang S, Klie S, Giavalisco P, Nikoloski Z** (2015) Integration of transcriptomics and metabolomics data specifies the metabolic response of *Chlamydomonas* to rapamycin treatment. *Plant J* **81**: 822–835
- Laplante M, Sabatini DM** (2012) MTOR signaling in growth control and disease. *Cell* **149**: 274–293
- Li J, Kim SG, Blenis J** (2014) Rapamycin: One drug, many effects. *Cell Metab* **19**: 373–379
- Liang Y, Kong F, Torres-Romero I, Burlacot A, Cuine S, Légeret B, Billon E, Brotman Y, Alseekh S, Fernie AR, et al** (2019) Branched-chain amino acid catabolism impacts triacylglycerol homeostasis in *Chlamydomonas reinhardtii*. *Plant Physiol* **179**: 1502–1514
- Liu Y, Bassham DC** (2012) Autophagy: Pathways for self-eating in plant cells. *Annu Rev Plant Biol* **63**: 215–237
- Loewith R, Jacinto E, Wullschleger S, Lorberg A, Crespo JL, Bonenfant D, Oppliger W, Jenoe P, Hall MN** (2002) Two TOR complexes, only one of which is rapamycin sensitive, have distinct roles in cell growth control. *Mol Cell* **10**: 457–468
- Ma XM, Blenis J** (2009) Molecular mechanisms of mTOR-mediated translational control. *Nat Rev Mol Cell Biol* **10**: 307–318
- Marshall RS, Vierstra RD** (2018) Autophagy: The Master of Bulk and Selective Recycling. *Annu Rev Plant Biol* **69**: 173–208
- Matsuo T, Otsubo Y, Urano J, Tamanoi F, Yamamoto M** (2007) Loss of the TOR Kinase Tor2 Mimics Nitrogen Starvation and Activates the Sexual Development Pathway in Fission Yeast. *Mol Cell Biol* **27**: 3154–3164
- McCready K, Spencer V, Kim M** (2020) The Importance of TOR Kinase in Plant Development. *Front Plant Sci* **11**: 1–7

- Menand B, Desnos T, Nussaume L, Bergert F, Bouchez D, Meyer C, Robaglia C** (2002) Expression and disruption of the Arabidopsis TOR (target of rapamycin) gene. *Proc Natl Acad Sci U S A* **99**: 6422–6427
- Mizushima N, Yoshimori T, Ohsumi Y** (2011) The role of atg proteins in autophagosome formation. *Annu Rev Cell Dev Biol* **27**: 107–132
- Moreau M, Azzopardi M, Clément G, Dobrenel T, Marchive C, Renne C, Martin-Magniette ML, Taconnat L, Renou JP, Robaglia C, et al** (2012) Mutations in the Arabidopsis homolog of LST8/GβL, a partner of the target of Rapamycin kinase, impair plant growth, flowering, and metabolic adaptation to long days. *Plant Cell* **24**: 463–481
- Mubeen U, Giavalisco P, Caldana C** (2019) TOR inhibition interrupts the metabolic homeostasis by shifting the carbon-nitrogen balance in *Chlamydomonas reinhardtii*. *Plant Signal Behav* **14**: 1670595
- Mubeen U, Jüppner J, Alpers J, Hinch DK, Giavalisco P** (2018) Target of rapamycin inhibition in *Chlamydomonas reinhardtii* triggers de novo amino acid synthesis by enhancing nitrogen assimilation[open]. *Plant Cell* **30**: 2240–2254
- Mukaida S, Ogawa T, Ohishi K, Tanizawa Y, Ohta D, Arita M** (2016) The effect of rapamycin on biodiesel-producing protist euglena gracilis. *Biosci Biotechnol Biochem* **80**: 1223–1229
- Ohsumi Y** (2014) Historical landmarks of autophagy research. *Cell Res* **24**: 9–23
- Pancha I, Chokshi K, Tanaka K, Imamura S** (2020) Microalgal Target of Rapamycin (TOR): A Central Regulatory Hub for Growth, Stress Response and Biomass Production. *Plant Cell Physiol* **61**: 675–684
- Pancha I, Shima H, Higashitani N, Igarashi K, Higashitani A, Tanaka K, Imamura S** (2019) Target of rapamycin-signaling modulates starch accumulation via glycogenin phosphorylation status in the unicellular red alga *Cyanidioschyzon merolae*. *Plant J* **97**: 485–499
- Pérez-Martín M, Blaby-Haas CE, Pérez-Pérez ME, Andrés-Garrido A, Blaby IK, Merchant SS, Crespo JL** (2015) Activation of autophagy by metals in *Chlamydomonas reinhardtii*. *Eukaryot Cell* **14**: 964–973
- Pérez-Pérez ME, Couso I, Crespo JL** (2017) The TOR signaling network in the model unicellular green alga *Chlamydomonas reinhardtii*. *Biomolecules* **7**: 1–13

- Pérez-Pérez ME, Crespo JL** (2010a) Autophagy in the model alga *Chlamydomonas reinhardtii*. *Autophagy* **6**: 562–563
- Pérez-Pérez ME, Crespo JL** (2017) Monitoring Autophagy in the Model Green Microalga *Chlamydomonas reinhardtii*. *Cells* **6**: 36
- Pérez-Pérez ME, Crespo JL** (2010b) Elucidating TOR signaling in *Chlamydomonas reinhardtii*. *Enzymes* **28**: 245–261
- Pérez-Pérez ME, Lemaire SD, Crespo JL** (2012) Reactive oxygen species and autophagy in plants and algae. *Plant Physiol* **160**: 156–164
- Porstmann T, Santos CR, Griffiths B, Cully M, Wu M, Leever S, Griffiths JR, Chung YL, Schulze A** (2008) SREBP Activity Is Regulated by mTORC1 and Contributes to Akt-Dependent Cell Growth. *Cell Metab* **8**: 224–236
- Prioretti L, Avilan L, Carrière F, Montané MH, Field B, Grégori G, Menand B, Gontero B** (2017) The inhibition of TOR in the model diatom *Phaeodactylum tricornutum* promotes a get-fat growth regime. *Algal Res* **26**: 265–274
- Prioretti L, Carriere F, Field B, Avilan L, Montané M, Menand B, Gontero B** (2019) SC.
- Prioretti L, Carriere F, Field B, Avilan L, Montané MH, Menand B, Gontero B** (2020) Targeting TOR signaling for enhanced lipid productivity in algae. *Biochimie* **169**: 12–17
- Pugkaew W, Meetam M, Ponpuak M, Yokthongwattana K, Pokethitiyook P** (2018) Role of autophagy in triacylglycerol biosynthesis in *Chlamydomonas reinhardtii* revealed by chemical inducer and inhibitors. *J Appl Phycol* **30**: 15–22
- Ramundo S, Casero D, Mühlhaus T, Hemme D, Sommer F, Crèvecoeur M, Rahire M, Schroda M, Rusch J, Goodenough U, et al** (2014) Conditional depletion of the *Chlamydomonas* chloroplast ClpP protease activates nuclear genes involved in autophagy and plastid protein quality control. *Plant Cell* **26**: 2201–2222
- Ren M, Venglat P, Qiu S, Feng L, Cao Y, Wang E, Xiang D, Wang J, Alexander D, Chalivendra S, et al** (2013a) Target of rapamycin signaling regulates metabolism, growth, and life span in arabidopsis. *Plant Cell* **24**: 4850–4874
- Ren M, Venglat P, Qiu S, Feng L, Cao Y, Wang E, Xiang D, Wang J, Alexander D, Chalivendra S, et al** (2013b) Target of rapamycin signaling regulates metabolism, growth, and life span in arabidopsis. *Plant Cell* **24**: 4850–4874
- Rocha DN, Martins MA, Soares J, Vaz MGMV, de Oliveira Leite M, Covell L, Mendes LBB** (2019) Combination of trace elements and salt stress in different cultivation modes

improves the lipid productivity of *Scenedesmus* spp. Bioresour Technol. doi: 10.1016/j.biortech.2019.121644

Rory J. Flinn,* Ying Yan SG, Peter J. Parker and JMB, *Department (2009) The Late Endosome is Essential for mTORC1 Signaling. *Mol Biol Cell* **21**: 833–841

Roustan V, Weckwerth W (2018) Quantitative phosphoproteomic and system-level analysis of TOR inhibition unravel distinct organellar acclimation in *Chlamydomonas reinhardtii*. *Front Plant Sci* **871**: 1–21

Saxton RA, Sabatini DM (2017) mTOR Signaling in Growth, Metabolism, and Disease. *Cell* **168**: 960–976

Schepetilnikov M, Kobayashi K, Geldreich A, Caranta C, Robaglia C, Keller M, Ryabova LA (2011) Viral factor TAV recruits TOR/S6K1 signalling to activate reinitiation after long ORF translation. *EMBO J* **30**: 1343–1356

Schepetilnikov M, Ryabova LA (2018) Recent discoveries on the role of tor (Target of rapamycin) signaling in translation in plants. *Plant Physiol* **176**: 1095–1105

Schmelzle T, Beck T, Martin DE, Hall MN (2004) Activation of the RAS/Cyclic AMP Pathway Suppresses a TOR Deficiency in Yeast. *Mol Cell Biol* **24**: 338–351

Shemi A, Ben-Dor S, Vardi A (2015) Elucidating the composition and conservation of the autophagy pathway in photosynthetic eukaryotes. *Autophagy* **11**: 701–715

Shimobayashi M, Hall MN (2014) Making new contacts: The mTOR network in metabolism and signalling crosstalk. *Nat Rev Mol Cell Biol* **15**: 155–162

Tulin F, Zhang Z, Wang ZY (2021) Activation of TOR signaling by diverse nitrogen signals in plants. *Dev Cell* **56**: 1213–1214

Upadhyaya S, Agrawal S, Gorakshakar A, Rao BJ (2018) Modulation of TOR kinase activity in *Chlamydomonas reinhardtii*: Effect of N-starvation and changing carbon pool. *bioRxiv*. doi: 10.1101/312942

Vézina C, Kudelski A (1975) Rapamycin (AY-22,989), a new antifungal antibiotic. I. taxonomy of the producing streptomycete and isolation of the active principle. *J Antibiot (Tokyo)* **28**: 721–726

Walther DB and TC (2009) TORC2 Plasma Membrane Localization Is Essential for Cell Viability and Restricted to a Distinct Domain. *Mol Biol Cell* **20**: 1565–1575

Wedaman karen P, Reinke A, Anderson S, Yates J, McCaffery JM, Powers T (2003) Tor Kinases Are in Distinct Membrane-associated Protein Complexes in *Saccharomyces cerevisiae*. *Mol Biol Cell* **14**: 1204–1220

- Werth EG, McConnell EW, Couso Lianez I, Perrine Z, Crespo JL, Umen JG, Hicks LM** (2019) Investigating the effect of target of rapamycin kinase inhibition on the *Chlamydomonas reinhardtii* phosphoproteome: from known homologs to new targets. *New Phytol* **221**: 247–260
- Wullschleger S** (2006) TOR signaling in growth and metabolism. *Cell*. doi: 10.1016/j.cell.2006.01.016
- Xiong Y, Sheen J** (2014) The Role of Target of Rapamycin Signaling Networks in Plant Growth and Metabolism. *PLANT Physiol* **164**: 499–512
- Xiong Y, Sheen J** (2012) Rapamycin and glucose-target of rapamycin (TOR) protein signaling in plants. *J Biol Chem* **287**: 2836–2842
- Xu Q, Liang S, Kudla J, Luan S** (1998) Molecular characterization of a plant FKBP12 that does not mediate action of FK506 and rapamycin. *Plant J* **15**: 511–519
- Yuan HX, Xiong Y, Guan KL** (2013) Nutrient Sensing, Metabolism, and Cell Growth Control. *Mol Cell* **49**: 379–387
- Zeng Y, Li B, Lin Y, Jiang L** (2019) The interplay between endomembranes and autophagy in plants. *Curr Opin Plant Biol* **52**: 14–22
- Zhang SH, Lawton MA, Hunter T, Lamb CJ** (1994) atpk1, a novel ribosomal protein kinase gene from Arabidopsis. I. Isolation, characterization, and expression. *J Biol Chem* **269**: 17586–17592
- Zhang Z, Zhu JY, Roh J, Marchive C, Kim SK, Meyer C, Sun Y, Wang W, Wang ZY** (2016) TOR Signaling Promotes Accumulation of BZR1 to Balance Growth with Carbon Availability in Arabidopsis. *Curr Biol* **26**: 1854–1860
- Zhao Y, Wang XQ** (2020) The hot issue: TOR signalling network in plants. *Funct Plant Biol* **48**: 1–7
- Zhu L, Li S, Hu T, Nugroho YK, Yin Z, Hu D, Chu R, Mo F, Liu C, Hiltunen E** (2019) Effects of nitrogen source heterogeneity on nutrient removal and biodiesel production of mono- and mix-cultured microalgae. *Energy Convers Manag*. doi: 10.1016/j.enconman.2019.112144
- Biophys Acta - Mol Cell Biol Lipids* **1861**: 1269–1281

GENERAL CONSIDERATIONS

Under non-stress conditions, microalgae are genetically programmed to synthesize and store starch to support growth and cell division, as they are evolved to be highly specialized for carbon capture and carbohydrate synthesis. On the other hand, when microalgae are subjected to stress conditions, they tend to accumulate higher amounts of storage lipids at the expense of growth.

Nitrogen starvation led to a severe inhibition of cell growth in *C. reinhardtii* CC503, *S. obliquus* BR003, *C. vulgaris* BR017, *Chlamydomonas* sp. BR020 and *Monoraphidium* sp. BR023 (Chapter 1). In addition, metabolomic and physiological analysis of these strains grown in N-starvation, N-replete and N-saturated conditions indicated that N starvation lead to typical stress-related responses such as reduction of chlorophyll and protein levels. Hence, they also markedly differ in accumulation in membrane lipid composition FA saturation and increase in TAGs.

It seems reasonable to suggest that some microalgae are programmed to accumulate lipids while others accumulate starch during the stationary phase under nutritional stress like N deplete, reinforcing the importance of evolutionary and ecological constraints in the final phenotype of a strain. Thus, it reveals a complementary finding which attributes the storage of reserve compounds not only to species type, but also to environment conditions.

The impact of rapamycin addition clearly shows that TOR inhibition causes a severely reduced growth, leading to a reduction by 50% on the cell growth (Chapter 2). The present data therefore reveals that TOR is involved in the regulation of cell growth in different strains. Next to the direct cell growth related results our data reveals that the obtained growth-phenotype was accompanied by strong accumulation of C-storage compounds, such as starch and TAGs). Changes in amino acid contents demonstrated the diverse expression pattern in relationship to the strains that will aid in specifying the role and mechanism of individual compounds in the response to the rapamycin treatment. Taken together, our findings reveal strong and different changes in carbon and nitrogen portioning in response to TOR inhibition for each strain. Further analyses using *C. reinhardtii*, together with other algae, will provide important information on the regulatory mechanism of reserve compounds accumulation and TOR signaling pathway. Furthermore, such data will be useful for the construction of algae being targeted to specific goals.

Compared to animals and yeasts, the current knowledge of TOR functions and signaling in microalgae is still limited (Chapter 3). The recent development of rapamycin-sensitive strains

and novel TOR inhibitors combined with various “omic” analyses have revealed that algal TOR is involved in many cellular processes in microalgae, as which the accumulation of energy storage molecules, autophagy, rRNA transcription in the chloroplast. However, there is still a lack of knowledge about the molecular mechanisms by which TOR promotes photosynthetic cell growth. Efforts should focus on the identification of components of this signaling cascade that may act upstream or downstream of TOR, being able to provide valuable information about nutritional or stress inputs to this kinase. This information will help us not only to understand TOR functions in plant and algae lineages but also to develop various tools for the sustainable development of biomass production using microalgae and algal biotechnology to benefits in industrial sectors like agriculture or biofuel production.

SUPPLEMENTARY DATA

SI Table 1. P-values for significant main effects and interactions between the factors (strain, concentration and time) of five strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, *S. obliquus* BR003, *C. vulgaris* BR017 and *Monoraphidium* sp. BR023) cultivated under tree different nitrogen (N) concentration (0mM, 3.5mM and 7mM)

	AFDW	μ	Chl <i>a</i>	Chl <i>b</i>	Chl <i>a/b</i>	Protein	Starch	Lipids
Main effects								
Strain	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**
Concentration	0.000**	0.000**	0.000**	0.001**	0.000**	0.000**	0.000**	0.000**
Time	0.000**	0.000**	0.000**	0.001**	0.011**	0.000**	0.000**	0.000**
Interaction effects								
Strain x Concentration	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**
Strain x Time	0.000**	0.000**	0.000**	0.013**	0.533 ^{NS}	0.000**	0.000**	0.000**
Concentration x Time	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**
Strain x Dosage x Time	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**
R²	0.9899	0.9918	0.8808	0.7342	0.8298	0.9162	0.9496	0.9596

** indicate that effect and interaction are significant at p -value < 0.05;

NS = not significant;

SI Table 2. Relative abundance of primary metabolites of *C. reinhardtii* CC503 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Amino acid	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
Alanine	0.33 Ca	0.59 Ab	0.46 Bb	0.29 Ba	1.08 Aa	1.22 Aa	0.28 Ba	0.88 Aa	0.98 Aa	0.16 Cb	0.32 Bc	0.58 Ab
Arginine	0.39 Cb	1.66 Aa	1.03 Bab	0.71 Bab	1.49 Aab	1.35 Aa	0.88 Aa	1.34 Aab	0.94 Aa	0.69 Aab	0.88 Ab	0.50 Ab
Asparagine	1.08 Aa	0.80 Aa	0.94 Aa	0.75 Aa	1.18 Aa	0.96 Aa	0.77 Aa	1.58 Aa	1.13 Aa	0.66 Aa	1.76 Aa	1.70 Aa
Aspartate	0.53 Bb	0.75 Aa	0.65 ABb	0.34 Bb	0.71 Aab	0.68 Ab	0.29 Cbc	0.57 Bbc	1.13 Aa	0.24 Cc	0.47 Bc	0.66 Ab
b-Alanine	0.48 Ba	0.96 Aa	0.72 ABb	0.48 Aa	0.65 Aa	0.71 Ab	0.39 Ba	0.82 Aa	1.00 Aab	0.33 Ca	0.88 Ba	1.59 Aa
Citrulline	1.46 Aa	1.50 Aa	1.48 Aab	0.83 Ab	0.99 Aa	0.86 Ac	0.86 Ab	1.01 Aa	0.89 Abc	0.84 Bb	0.33 Cb	1.58 Aa
Glutamate	0.65 Bb	1.49 Ab	1.07 Ab	0.94 Ba	1.72 Aa	1.61 Aa	0.85 Ba	1.55 Aa	1.75 Aa	0.77 Bb	1.21 Ab	1.23 Ab
Glutamine_2	0.14 Cab	1.21 Ab	0.68 Bb	0.16 Bab	3.08 Aa	2.40 Aa	0.09 Bb	0.26 Ac	0.55 Ab	0.31 Ba	0.90 Ab	0.81 Ab
Glycine	1.30 Ba	1.57 ABa	1.44 Aa	0.88 Bab	1.01 ABab	1.37 Aab	0.96 Bab	1.22 ABab	1.18 Aab	0.47 Bb	0.63 ABb	1.01 Ab
Isoleucine	0.72 Ab	0.44 Cc	0.59 Bbc	1.12 Aa	0.54 Bc	0.48 Bc	0.91 Aab	0.79 ABb	0.71 Bb	0.22 Cc	1.14 Ba	2.02 Aa
Leucine	1.36 Aa	0.91 Cb	1.14 Bb	1.35 Aa	0.90 Bb	0.85 Bc	0.94 Bb	1.52 Aa	1.00 Bbc	0.30 Cc	1.03 Bb	1.84 Aa
Lysine	1.32 Aa	1.21 Aa	1.26 Ab	0.67 Bb	0.90 ABab	1.12 Ab	0.48 Bb	1.07 Aa	1.51 Ab	0.40 Bb	0.63 Bb	2.96 Aa
Methionine	1.09 Ad	1.09 Abc	1.09 Ac	1.72 Ac	0.97 Cc	1.33 Bb	2.12 Ab	1.17 Cb	1.69 Ba	2.93 Aa	2.20 Ba	1.48 Cab
Ornithine	0.77 Ba	1.68 Aa	1.23 ABb	0.63 Bab	0.92 ABb	1.15 Ab	0.45 Bb	0.99 Ab	1.14 Ab	0.40 Bb	0.40 Bc	1.80 Aa
Phenylalanine	0.92 Ab	0.57 Bb	0.75 ABb	1.34 Aa	0.80 Bb	0.66 Bb	0.83 Ab	1.28 Ba	0.83 Bb	0.29 Ac	1.13 Ba	2.04 Ca
Proline	0.76 Aa	0.84 Aa	0.80 Aab	0.83 Aa	0.49 Bb	0.64 Ab	0.88 Aa	0.82 Aa	0.84 Aa	0.89 Aa	0.95 Aa	0.97 Aa
Serine	0.38 Aa	0.28 Bb	0.33 ABb	0.25 Bb	0.54 Aa	0.46 Aa	0.18 Ac	0.17 Ac	0.18 Ac	0.06 Cd	0.13 Bd	0.47 Aa
Threonine	0.50 Ab	0.51 Ac	0.51 Ac	1.15 Aa	0.81 Bb	0.78 Bb	1.14 Aa	0.67 Bbc	0.67 Bbc	0.57 Cb	1.26 Ba	1.86 Aa
Tryptophan	0.97 Ac	0.57 Bc	0.77 ABb	6.00 Aa	0.74 Bbc	0.72 Bb	4.95 Aa	0.96 Bb	0.89 Bb	2.39 Bb	5.75 Aa	4.39 Aa
Tyrosine	1.07 Aa	0.74 Bb	0.91 ABb	1.01 Aa	0.47 Bc	0.44 Bc	0.89 Aa	1.12 Aa	0.84 Ab	0.48 Cb	1.25 Ba	2.08 Aa
Valine	0.89 Aa	0.67 Bb	0.79 ABb	0.94 Aa	0.74 Bb	0.67 Bb	0.79 Ba	1.08 Aa	0.83 Bb	0.33 Cb	0.81 Bb	1.13 Aa
5-Oxoproline	0.35 Ca	0.94 Aab	0.65 Bc	0.49 Ba	1.07 Aa	0.99 Aab	0.45 Ba	0.86 Aab	1.03 Aa	0.41 Ba	0.66 Ab	0.69 Abc

SI Table 2. (continuation) Relative abundance of primary metabolites of *C. reinhardtii* CC503 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Organic acid	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
Benzoate	3.92 Ab	3.44 Bb	3.68 Bb	5.27 Ab	3.67 Bb	3.27 Bb	6.68 Aa	4.43 Ba	4.38 Ba	6.27 Aa	5.06 Ba	5.80 Ba
Citramalate	2.09 Ac	2.13 Ab	2.11 Aa	4.51 Aa	2.91 Ba	2.59 Ba	3.25 Ab	1.57 Cc	2.11 Ba	2.28 Ac	1.02 Bd	0.95 Bb
Citrate	0.13 Aa	0.08 Bab	0.11 ABa	0.07 Ab	0.08 Ab	0.07 Ab	0.12 Aa	0.11 Aa	0.08 Aab	0.13 Aa	0.06 Bb	0.07 Bb
Dehydroascorbate	1.30 Ab	0.99 Aab	1.15 Abc	0.92 Ac	0.87 Ab	0.95 Ac	1.06 Bbc	1.18 ABab	1.46 Ab	2.41 Aa	1.29 Ba	2.00 Aa
Fumarate	3.22 Aa	2.60 Aa	2.91 Aa	3.82 Aa	2.77 Aa	2.71 Aa	3.84 Aa	3.22 Aa	3.28 Aa	3.60 Aa	4.14 Aa	3.26 Aa
Gluconate	4.20 Aa	2.20 Aa	3.20 Aa	1.37 Ab	0.82 Bb	0.64 Bb	1.14 Ab	0.46 Bbc	0.32 Bbc	1.51 Ab	0.32 Bc	0.29 Bc
Glycerate	0.62 Aa	0.57 Aa	0.59 Aa	0.34 Ab	0.25 Ab	0.28 Ab	0.31 Ab	0.27 Ab	0.29 Ab	0.42 Ab	0.38 Ab	0.37 Ab
Ketoglutarate	1.34 Aa	1.26 Ab	1.30 Aab	1.15 Aa	1.20 Ab	1.04 Ab	1.14 Aa	1.41 Ab	1.37 Aa	1.24 Ba	2.07 Aa	1.44 Ba
Lactate	0.71 Ab	0.56 Ab	0.63 Ab	0.93 Aa	1.13 Aa	1.02 Aa	0.49 Ab	0.50 Ab	0.58 Ab	0.63 Ab	0.67 Ab	0.63 Ab
Malate	0.56 Ab	0.61 Ab	0.59 Ab	0.82 Aa	0.63 Bb	0.51 Bb	0.54 Cb	0.77 Bab	0.99 Aa	0.57 Bb	0.99 Aa	1.16 Aa
Nicotinate	1.31 Aa	1.21 Aab	1.26 Ab	0.90 Bb	1.22 Aab	1.13 Ab	0.93 Cb	1.37 Ba	1.70 Aa	0.81 Cb	1.06 Bb	1.73 Aa
Pyruvate	0.84 Ad	0.86 Ac	0.85 Ac	1.99 Ab	1.95 Ab	1.22 Bc	3.14 Aa	3.85 Aa	3.56 Ab	1.37 Cc	3.76 Ba	6.62 Aa
Succinate	0.76 Ab	0.81 Ac	0.79 Ab	0.75 Bb	0.91 ABbc	1.11 Aa	1.20 Aa	1.21 Aab	1.01 Aab	1.48 Aa	1.31 Aa	1.01 Bab
Sugar	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
Cellobiose	2.14 Ac	1.39 Bb	1.77 ABa	5.21 Ab	0.53 Bc	0.37 Cb	7.16 Aab	2.05 Ba	0.26 Cb	7.64 Aa	2.09 Ba	0.35 Cb
Fructose	1.67 Aa	1.14 Ba	1.41 ABa	0.85 Ab	1.12 Aa	0.93 Ab	0.87 Ab	0.62 ABb	0.57 Bc	0.95 Ab	0.56 Bb	0.55 Bc
Fucose	2.67 Aa	1.32 Ba	2.00 Ba	0.81 Ab	0.31 Bb	0.30 Bb	0.73 Ab	0.38 Bb	0.41 Bb	0.91 Ab	0.37 Bb	0.32 Bb
Glucose_1	2.08 Aa	1.32 Ba	1.70 ABa	0.88 Ab	0.90 Ab	1.02 Ab	0.86 Ab	0.53 Bc	0.41 Bc	0.88 Ab	0.29 Bd	0.32 Bc
Maltose	1.62 Ac	1.04 Bb	1.33 ABa	3.93 Ab	0.40 Bc	0.28 Cb	5.39 Aab	1.54 Ba	0.20 Cb	5.76 Aa	1.57 Ba	0.26 Cb
Sucrose	0.01 Ab	0.01 Ab	0.01 Ab	0.04 Aab	0.26 Aab	0.04 Aab	0.03 Aab	0.01 Aab	0.01 Aab	0.09 Aa	0.01 Aa	0.08 Aa
Trehalose	3.10 Ac	2.01 Bb	2.56 ABa	7.84 Ab	0.72 Bc	0.51 Cb	10.87 Aab	2.96 Ba	0.38 Cb	11.52 Aa	2.97 Ba	0.49 Cb
Xylose	2.73 Ab	2.52 Ac	2.62 Abc	5.06 Aa	2.58 Bc	2.31 Bc	6.21 Aa	3.73 Bb	3.46 Bab	4.95 ABa	6.29 Aa	4.04 Ba
Glycerol	1.70 Ab	1.41 Bb	1.56 ABa	1.80 Ab	1.05 Bc	1.05 Bb	1.94 Aab	1.28 Bb	1.07 Cb	2.21 Aa	1.95 Aa	1.00 Bb
Glycerol 3-P	1.39 Ba	1.83 Aa	1.61 ABc	1.34 Ba	1.70 Aa	1.76 Abc	1.34 Ba	2.14 Aa	2.07 Aab	1.19 Ca	1.81 Ba	2.30 Aa

SI Table 2. (continuation) Relative abundance of primary metabolites of *C. reinhardtii* CC503 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Others	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
Putrescine	8.47 Aa	10.81 Aa	9.64 Aa	6.29 Ba	10.41 Aa	11.83 Aa	5.70 Ba	9.88 Aa	12.73 Aa	4.99 Ba	5.64 Bb	14.50 Aa
Spermidine	2.95 Aa	3.18 Aab	3.06 Ac	1.79 Ba	5.68 Aab	5.24 Abc	1.41 Ba	6.41 Aa	11.09 Aab	1.30 Ba	2.95 Bb	11.75 Aa
Adenine	2.79 Aa	2.13 Aa	2.46 Aa	1.19 Ab	1.09 Ab	1.38 Ab	1.19 Ab	1.13 Ab	1.15 Ab	1.40 Ab	1.24 Ab	1.53 Ab
Uracil	4.22 Aa	2.69 Ba	3.46 Ba	1.25 Ab	1.10 Bb	1.12 Bb	1.15 Abc	0.90 Bbc	0.83 Bbc	1.22 Ac	0.50 Bc	0.69 Bc
2-Hydroxypyridine	2.85 Ab	2.43 Ab	2.64 Ab	3.44 Ab	2.55 Ab	2.19 Ab	3.15 Aab	2.79 Aab	2.91 Aab	3.43 Aa	3.69 Aa	3.58 Aa
4-Aminobutanoate	2.60 Aa	1.60 Ba	2.10 ABa	0.41 Ab	0.40 Bb	0.51 ABb	0.33 Ac	0.24 Bc	0.27 ABc	0.41 Ac	0.16 Bc	0.16 ABc
Galactinol	3.32 Aa	1.83 Aa	2.58 Aa	1.98 Aab	0.98 Bb	1.20 ABb	1.92 Aab	0.95 Bb	0.68 Bbc	1.65 Ab	0.36 Bc	0.41 Bc
Myo-Inositol	4.19 Aa	2.94 Aa	3.57 Aa	1.73 Ab	1.22 Ab	1.22 Ab	1.75 Ab	0.93 Bbc	0.73 Bc	1.91 Ab	0.74 Bc	1.03 Bbc
Orthophosphate	1.70 Ac	1.54 Ac	1.62 Ac	2.01 Ac	1.70 Ac	1.64 Ac	2.11 Ab	2.02 Ab	2.02 Ab	2.38 Aa	2.52 Aa	2.21 Aa

SI Table 3. Relative abundance of primary metabolites of *Chlamydomonas* sp. BR020 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Amino acid	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
Alanine	1.14 Aa	1.15 Ab	1.13 Ab	0.63 Bb	1.23 Aab	1.31 Aab	0.50 Bc	1.40 Aa	1.47 Aa	0.39 Cd	0.89 Bc	1.30 Aab
Arginine	1.38 Aa	1.46 Ab	1.28 Ab	0.18 Bb	2.67 Aa	2.07 Aab	0.12 Bbc	3.33 Aa	2.47 Aa	0.11 Cc	0.26 Bc	2.78 Aa
Asparagine	1.61 Aa	1.63 Ab	1.67 Ac	0.34 Bb	2.22 Aa	2.07 Ac	0.36 Bb	2.96 Aa	3.03 Ab	0.28 Cb	0.65 Bc	6.57 Aa
Aspartate	1.18 Aa	1.17 Ab	1.14 Ab	0.46 Cb	2.08 Aa	1.73 Ba	0.33 Cc	2.37 Aa	1.97 Ba	0.33 Bc	0.32 Bc	1.93 Aa
b-Alanine	1.08 Aa	1.08 Aa	1.10 Aa	0.77 Ab	0.80 Ab	0.61 Bb	0.60 Bc	0.80 Ab	0.79 Ab	0.98 Aab	0.39 Bc	1.21 Aa
Citrulline	1.41 Aa	1.41 Aab	1.31 Aa	0.96 Ba	1.97 Aa	1.53 ABa	1.01 Ba	2.16 Aa	1.64 ABa	0.93 Ba	1.05 Bb	1.92 Aa
Glutamate	0.81 Ab	0.81 Abc	0.98 Ab	0.91 Aab	0.79 Bc	0.86 ABab	0.96 Aa	0.91 Ab	0.94 Aa	0.83 Bb	1.04 Aa	0.86 BAb
Glutamine_2	6.41 Aa	6.41 Aa	6.61 Ab	0.44 Bb	8.33 Aa	10.13 Aa	0.48 Bb	3.50 Ab	4.14 Ac	0.30 Cc	0.40 Bc	9.68 Aa
Glycine	0.80 Aa	0.80 Aab	0.88 Ac	0.47 Bb	0.87 Aa	0.85 Ac	0.57 Bb	1.07 Aa	1.29 Ab	0.43 Cb	0.64 Bb	3.17 Aa
Isoleucine	0.81 Ab	0.81 Ac	0.85 Ac	0.98 Ba	1.13 Ab	1.07 ABb	1.08 Aa	1.16 Ab	1.11 Ab	1.00 Ca	1.93 Ba	2.35 Aa
Leucine	0.53 Ac	0.63 Ac	0.51 Ab	1.13 Aa	0.58 Bbc	0.58 Bb	0.89 Ab	0.67 Bb	0.59 Bb	0.85 Cb	1.72 Ba	2.23 Aa
Lysine	0.55 Aa	0.75 Ac	0.61 Ac	0.54 Ba	1.33 Ab	0.72 Bc	0.59 Ca	1.94 Aa	1.10 Bb	0.49 Ba	0.59 Bc	2.42 Aa

SI Table 3. (continuation) Relative abundance of primary metabolites of *Chlamydomonas* sp. BR020 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Amino acid	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Methionine	0.57 Ac	0.68 Ac	0.61 Ac	0.68 Ab	0.75 Ab	0.73 Ab	0.93 Aab	0.68 Aab	0.83 Aab	0.87 Aa	0.79 Aa	1.08 Aa
Ornithine	1.60 Aa	1.71 Ab	1.66 Aa	0.62 Cbc	2.48 Aa	1.55 Ba	0.46 Cc	3.10 Aa	1.86 Ba	0.65 Bb	0.38 Cc	1.70 Aa
Phenylalanine	1.07 Abc	1.13 Ab	1.10 Ab	1.68 Aa	1.01 Bb	0.93 Bbc	0.98 Ac	0.99 Ab	0.81 Bc	1.20 Bb	2.26 Aa	1.98 Aa
Proline	1.84 Aa	1.95 Aa	1.89 Aa	2.87 Aa	2.15 Aa	2.61 Aa	2.84 Aa	2.36 Aa	2.54 Aa	2.22 Aa	2.39 Aa	1.93 Aa
Serine	1.34 Aa	1.41 Ab	1.44 Ac	1.18 Bbc	1.38 Ab	1.13 Bd	1.25 Bab	1.76 Aa	1.65 Ab	1.11 Cc	1.24 Bb	2.57 Aa
Threonine	1.03 Aa	1.11 Ac	1.10 Ac	0.83 Bb	1.42 Ab	1.23 Ab	1.00 Ba	1.38 Ab	1.23 Ab	0.77 Cb	1.71 Ba	2.75 Aa
Tryptophan	0.24 Ac	0.32 Ac	0.24 Ac	1.07 Aa	0.48 Bb	0.43 Bb	0.52 Ab	0.42 ABb	0.36 Bb	0.59 Cb	0.97 Ba	1.48 Aa
Tyrosine	0.57 Ac	0.66 Ac	0.58 Ab	1.35 Aa	0.69 Bbc	0.56 Cb	0.92 Ab	0.76 Bb	0.53 Cb	1.16 Ba	1.35 ABa	1.50 Aa
Valine	0.98 Aa	0.10 Ac	0.98 Ac	0.99 Aa	1.12 Ac	0.99 Ac	1.03 Ba	1.30 Ab	1.15 ABb	0.88 Ca	1.52 Ba	1.92 Aa
5-Oxoproline	0.96 Aa	0.15 Ab	0.98 Ab	0.70 Bb	1.34 Aa	1.29 Aa	0.55 Bc	1.38 Aa	1.34 Aa	0.40 Cd	0.78 Bb	1.42 Aa
Organic acid	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Benzoate	0.77 Ab	0.79 Ab	0.80 Aa	0.84 Ab	0.80 Ab	0.88 Aa	1.41 Aa	1.29 Aa	0.84 Ba	0.89 Ab	0.72 Ab	0.98 Aa
Citramalate	0.39 Ac	0.33 Ad	0.43 Ab	0.60 Ab	0.54 ABc	0.47 Bb	1.00 Aa	1.09 Aa	0.77 Ba	0.89 Aa	0.82 Ab	0.24 Bc
Citrate	4.21 Aa	4.28 Aa	4.29 Aa	1.85 Bb	4.80 Aa	4.29 Aa	1.06 Bc	3.23 Ab	3.16 Ab	0.93 Ac	0.37 Cc	0.65 Bc
Dehydroascorbate	0.47 Ab	0.37 Ab	0.55 Ac	0.58 Ab	0.59 Ab	0.44 Bc	0.56 Bb	0.89 Aa	0.76 Ab	0.86 Ba	1.00 ABa	1.08 Aa
Fumarate	0.86 Aa	0.79 Aa	0.91 Aa	0.72 Aa	0.84 Aa	0.75 Aa	0.91 Aa	0.95 Aa	0.94 Aa	1.01 Aa	0.90 Aa	0.98 Aa
Gluconate	3.18 Aa	3.23 Aa	3.15 Aa	3.85 Aa	1.16 Bb	0.99 Bb	3.57 Aa	0.46 Bc	0.34 Cc	3.15 Aa	1.35 Bb	0.14 Cd
Glycerate	0.95 Ab	1.00 Ab	0.85 Ab	0.95 Cb	1.41 Aa	1.17 Ba	1.12 Aab	1.00 ABb	0.92 Bb	1.33 Aa	0.95 Bb	1.34 Aa
Ketoglutarate	0.73 Aa	0.82 Ac	0.86 Ab	0.61 Bb	0.95 Ab	0.93 Aa	0.73 Bab	0.85 Abc	0.74 ABa	0.52 Cc	1.13 Aa	0.64 Ba
Lactate	1.37 Aa	1.47 Ab	1.45 Aa	1.43 Aa	1.38 Ab	1.47 Aa	1.50 Aa	1.25 Bb	1.42 Aa	1.53 Aa	1.56 Aa	0.95 Bb
Malate	0.58 Ab	0.66 Ad	0.69 Ad	0.58 Bb	0.96 Ac	0.96 Ac	0.89 Ba	1.46 Aa	1.47 Ab	0.79 Ca	1.20 Bb	2.10 Aa
Nicotinate	0.43 Aa	0.53 Ab	0.50 Abc	0.37 Bb	0.43 Ab	0.43 ABc	0.40 Bab	0.55 Aa	0.51 Aab	0.25 Cc	0.34 Bc	0.53 Aa
Pyruvate	0.65 Aa	0.69 Ab	0.60 Ac	0.32 Cb	0.53 Bb	0.70 Ac	0.30 Bb	0.95 Aa	1.00 Ab	0.15 Cc	0.41 Bc	2.56 Aa
Succinate	0.61 Aa	0.70 Abc	0.67 Ab	0.64 Aa	0.70 Aab	0.71 Ab	0.57 Ba	0.82 Aa	0.86 Aa	0.63 ABa	0.58 Bc	0.71 Ab
Sugar	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Cellobiose	0.80 Ab	0.83 Aa	0.90 Aa	1.22 Aa	0.35 Bb	0.29 Bb	1.25 Aa	0.19 Bc	0.21 Bc	1.09 Aab	0.67 Ba	0.16 Cc
Fructose	5.34 Aa	5.44 Aa	5.39 Aa	5.10 Aa	3.50 Bb	3.12 Bb	4.33 Aa	1.03 Bd	0.98 Bc	6.17 Aa	1.92 Bc	0.64 Cd
Fucose	1.76 Ac	1.86 Aa	1.83 Aa	1.94 Abc	1.18 Bb	0.84 Cb	2.46 Ab	1.02 Bb	0.90 Bb	3.75 Aa	2.36 Ba	0.15 Cc

SI Table 3. (continuation) Relative abundance of primary metabolites of *Chlamydomonas* sp. BR020 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Sugar	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Glucose_1	1.85 Ab	1.90 Aa	1.93 Aa	2.17 Aab	1.46 Bb	1.30 Bb	1.81 Ab	0.95 Bc	0.99 Bc	2.52 Aa	1.85 Ba	0.86 Cc
Maltose	1.19 Aa	1.26 Aa	1.27 Aa	1.48 Aa	1.03 Aa	0.21 Bb	0.94 Aa	0.14 Bb	0.15 Bb	1.56 Aa	1.33 Aa	0.12 Bb
Sucrose	1.00 Ac	1.15 Ab	1.08 Aa	1.13 Ab	0.89 Cc	1.01 Ba	1.27 Ab	1.03 Bb	1.05 Ba	1.46 Aa	1.32 Aa	0.95 Ba
Trehalose	1.17 Ab	1.12 Aa	1.22 Aa	1.80 Aa	0.49 Bb	0.41 Bb	1.82 Aa	0.26 Bc	0.30 Bc	1.59 Aab	0.94 Ba	0.24 Cc
Xylose	0.67 Bb	0.60 Ab	0.73 Ab	0.68 Ba	0.75 Aa	0.81 Aa	0.69 Ba	0.84 Aa	0.82 Aa	0.74 Ba	0.80 Aa	0.82 Aa
Glycerol	0.67 Ab	0.72 Ab	0.65 Aa	0.70 Ab	0.62 Bb	0.64 ABa	0.83 Aa	0.68 Bb	0.65 Ba	0.88 Aa	0.91 Aa	0.60 Ba
Glycerol 3-P	0.49 Aa	0.41 Ab	0.50 Ac	0.46 Aa	0.57 Aab	0.53 Abc	0.55 Aa	0.67 Aa	0.64 Ab	0.50 Ca	0.66 Ba	0.82 Aa
Others	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Putrescine	0.66 Aa	0.67 Ab	0.70 Aa	0.26 Bb	1.01 Aa	0.83 Aa	0.29 Cb	1.12 Aa	0.78 Ba	0.18 Cc	0.25 Bc	0.38 Ab
Spermidine	1.28 Aa	1.35 Ab	1.38 Abc	0.73 Aab	0.81 Ab	1.00 Ac	0.71 Bab	2.74 Aa	4.25 Aa	0.64 Bb	1.00 Bb	2.02 Ab
Adenine	0.96 Aa	0.92 Ab	0.97 Aab	0.74 Ba	1.57 Aa	1.20 Aa	0.79 Ba	1.50 Aa	1.16 Aa	0.84 Aa	0.91 Ab	0.70 Ab
Uracil	0.99 Aa	1.00 Aa	0.95 Aa	0.85 Aab	1.19 Aa	1.10 Aa	1.07 Aa	1.10 Aa	0.82 Aa	0.65 Ab	0.55 ABb	0.40 Bb
2-Hydroxypyridine	0.90 Aab	0.90 Aab	0.81 Aab	0.73 Ab	0.86 Ab	0.83 Ab	0.96 Aab	0.96 Aab	0.86 Aab	1.05 Aa	1.03 Aa	1.08 Aa
4-Aminobutanoate	2.85 Aa	2.86 Aa	2.87 Aa	2.77 Aa	1.76 Bb	1.35 Bb	2.71 Aa	1.02 Bc	0.85 Bc	2.99 Aa	0.41 Bd	0.26 Bd
Galactinol	2.73 Ac	2.56 Aa	2.53 Aa	4.98 Aab	0.95 Bb	1.03 Bb	5.25 Aa	0.67 Bb	0.80 Bb	3.53 Abc	3.97 Aa	0.30 Bc
Myo-Inositol	0.98 Ab	1.00 Ab	0.92 Aa	1.16 Ab	0.78 Bc	0.76 Bb	1.06 Ab	0.65 Bd	0.56 Bc	1.77 Aa	1.19 Ba	0.60 Cc
Orthophosphate	0.71 Ac	0.67 Ac	0.81 Ab	0.76 Ac	0.72 Ac	0.74 Ab	0.88 Ab	0.80 Bb	0.84 ABa	0.99 Aa	0.92 Aa	0.74 Bb

SI Table 4. Relative abundance of primary metabolites of *Scenedesmus obliquus* BR003 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Amino acid	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
Alanine	2.1 Aa	2.09 Aa	2.05 Aa	0.46 Bb	2.06 Aa	2.10 Aa	0.38 Cb	1.05 Bb	2.01 Aa	0.37 Cb	0.74 Bb	1.80 Aa
Arginine	1.6 Aa	1.33 Aa	1.94 Aa	0.27 Bb	1.45 Aa	1.63 Aab	0.21 Bb	0.71 Ab	1.05 Ab	0.17 Cb	0.33 Bc	0.64 Ac
Asparagine	2.3 Aa	2.20 Aa	2.38 Aa	0.35 Bb	1.21 Ab	0.89 Ab	0.27 Bb	0.73 Ac	0.93 Ab	0.29 Cb	0.92 Bbc	2.33 Aa
Aspartate	1.8 Aa	1.80 Aa	1.70 Ab	0.33 Bb	1.14 Ab	1.27 Ac	0.32 Cb	0.98 Bb	2.10 Aab	0.22 Cc	0.94 Bb	2.29 Aa
b-Alanine	2.6 Aa	2.86 Aa	2.40 Aa	1.24 Ab	1.04 Abc	1.19 Ac	0.82 Bb	1.18 ABb	1.45 Abc	0.46 Cc	0.75 Bc	1.90 Aab
Citrulline	0.7 Aa	0.56 Aa	0.79 Aa	0.71 Aa	0.68 Aa	0.76 Aa	0.69 Aa	0.45 Aa	0.67 Aa	0.66 Aa	2.17 Aa	0.69 Aa
Glutamate	1.7 Aa	1.73 Aa	1.58 Aa	1.51 Aa	1.68 Aa	1.56 Aa	1.66 Aa	1.64 Aa	1.70 Aa	1.57 Aa	1.65 Aa	1.50 Aa
Glutamine_2	4.1 ABa	2.42 Ba	5.79 Aa	0.49 Bb	2.47 Aa	2.32 Ab	0.49 Bb	1.95 Aa	1.93 Ab	0.39 Cb	2.56 Ba	4.35 Aa
Glycine	0.9 Aa	0.95 Aa	0.77 Ab	0.75 Ba	1.15 Aa	1.13 Aa	0.69 Ba	0.93 Aa	1.12 Aa	0.51 Bb	0.67 Bb	1.15 Aa
Isoleucine	0.5 Ab	0.51 Ab	0.43 Ab	0.88 Aa	0.64 ABb	0.53 Bb	0.85 Aa	0.73 Aab	0.65 Ab	0.74 Aa	1.09 Aa	1.00 Aa
Leucine	0.8 Ab	0.87 Aa	0.77 Ab	1.50 Aa	1.09 ABa	0.88 Bb	1.43 Aa	1.21 ABa	0.94 Bb	1.16 Aab	1.35 Aa	1.47 Aa
Lysine	1.1 Aa	1.04 Aa	1.12 Aa	0.56 Bb	1.05 Aa	1.14 Aa	0.61 Cb	0.90 Bab	1.36 Aa	0.49 Cb	0.68 Bb	1.37 Aa
Methionine	1 Aa	1.04 Ab	0.97 Ab	1.30 Aa	1.53 Aa	1.29 Aab	1.27 ABa	1.04 Bb	1.51 Aa	1.49 Aa	0.78 Bb	1.72 Aa
Ornithine	5.4 ABa	4.36 Ba	6.35 Aa	0.25 Bb	1.11 Ab	1.24 Ab	0.24 Cb	0.71 Bc	1.23 Ab	0.18 Cb	0.31 Bd	0.81 Ac
Phenylalanine	0.5 Ab	0.48 Ac	0.49 Ac	0.78 Aa	0.95 Ab	0.81 Ab	0.64 Ca	1.25 Aa	0.83 Bb	0.73 Ca	1.42 Ba	1.97 Aa
Proline	0.5 Ab	0.48 Ac	0.56 Aa	0.72 Aa	0.56 Bbc	0.60 ABa	0.75 Ba	2.10 Aa	0.57 Ca	0.70 Aa	0.66 Ab	0.60 Aa
Serine	0.4 Aa	0.42 Aa	0.42 Ab	0.27 Bb	0.36 Aab	0.36 Ab	0.25 Bb	0.29 Bb	0.56 Aa	0.25 Cb	0.44 Ba	0.60 Aa
Threonine	1 Aa	0.99 Aa	1.00 Ab	0.56 Bb	0.72 Ab	0.69 Abc	0.58 Bb	0.71 Bb	0.90 Ab	0.53 Cb	0.87 Bab	1.52 Aa
Tryptophan	0.4 Ab	0.39 Ab	0.35 Ac	2.26 Aa	2.37 Aa	1.83 Aa	2.95 Aa	2.23 Aa	0.99 Bb	2.34 Aa	2.06 Aa	2.01 Aa
Tyrosine	0.4 Ab	0.37 Ab	0.34 Ac	0.64 Ba	1.21 Aa	1.07 Ab	0.61 Ca	1.23 Aa	0.98 Bb	0.61 Ca	1.05 Ba	1.60 Aa
Valine	0.8 Aa	0.91 Aa	0.72 Aa	0.90 Aa	1.05 Aa	0.85 Aa	0.87 Aa	1.03 Aa	1.18 Aa	0.71 Aa	0.92 Aa	0.88 Aa
5-Oxoproline	1.4 Ba	1.36 ABa	1.46 Aa	0.87 Bb	1.09 ABb	1.08 Ab	1.12 Bb	0.98 ABb	1.23 Ab	0.93 Bb	1.02 ABb	1.12 Ab

SI Table 4. (continuation) Relative abundance of primary metabolites of *Scenedesmus obliquus* BR003 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Organic acid	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
Benzoate	0.9 Aa	0.89 Aa	0.85 Aa	1.18 Aa	1.19 Aa	0.97 Aa	1.14 Aa	1.22 Aa	1.04 Aa	1.24 Aa	1.31 Aa	0.95 Aa
Citramalate	0.9 Ab	0.98 Ab	0.78 Ac	1.39 Aa	1.39 Aa	1.11 Ab	1.39 Ba	1.09 Bab	2.80 Aa	1.57 Aa	0.56 Bc	0.30 Cd
Citrate	3.6 ABd	3.91 Aa	3.25 Ba	5.26 Ac	2.69 Cb	3.30 Ba	6.59 Ab	2.19 Bc	2.45 Bb	8.59 Aa	2.67 Bb	1.07 Cc
Dehydroascorbate	1.3 Aa	1.06 Ca	1.48 Ba	1.52 Aa	0.97 Ca	0.96 Ba	1.75 Aa	0.90 Ca	1.18 Ba	1.36 Aa	0.74 Ca	1.02 Ba
Fumarate	1.2 Aa	1.34 Aa	0.97 Aa	1.00 Aa	1.24 Aa	0.84 Aa	1.29 Aa	1.16 Aa	0.94 Aa	1.11 Aa	1.21 Aa	0.91 Aa
Gluconate	1.4 Ab	1.09 Aa	1.61 Aa	3.44 Aa	0.28 Bb	0.49 Bb	1.97 Aab	0.24 Bb	0.26 Bb	1.28 Ab	0.33 Bb	0.30 Bb
Glycerate	1.2 Aa	1.34 Ba	1.16 Ba	1.25 Ab	0.49 Bb	0.65 Bb	1.28 Ab	0.55 Bb	0.69 Bb	1.28 Ab	1.37 Bb	0.52 Bb
Ketoglutarate	0.6 Ac	0.54 Ac	0.56 Ac	0.83 Ab	1.04 Ab	0.76 Ab	1.10 Aa	1.45 Aa	1.12 Aa	0.87 Ab	0.95 Ab	0.86 Ab
Lactate	0.2 Aa	0.25 Aa	0.19 Ba	0.30 Aa	0.28 Aa	0.20 Ba	0.22 Aa	0.29 Aa	0.14 Ba	0.28 Aa	0.26 Aa	0.23 Ba
Malate	2.6 Ab	2.93 Aa	2.23 Aa	3.98 Aa	2.73 Ba	2.32 Ba	4.04 Aa	3.53 Aa	2.13 Ba	3.41 Aab	3.07 Aa	2.73 Aa
Nicotinate	2.2 Ca	1.99 Ba	2.33 Aa	1.98 Ca	3.06 Ba	3.15 Aa	1.82 Ca	2.85 Ba	3.56 Aa	1.45 Ca	1.91 Ba	3.11 Aa
Pyruvate	0.7 Aa	0.70 Ac	0.61 Ac	0.51 Ca	3.68 Aa	2.03 Bb	0.80 Ba	4.02 Aa	3.73 Aa	0.60 Ca	1.67 Bb	5.31 Aa
Succinate	1.1 Aab	1.22 Aa	1.04 Ab	1.15 Ba	1.43 Aa	1.32 ABa	1.28 Aa	1.45 Aa	1.50 Aa	0.91 Ab	0.75 Bb	0.86 ABb
Sugar	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
Cellobiose	0.7 Ab	0.66 Ac	0.72 Ac	1.71 Aa	1.47 Aab	1.26 Ab	1.58 Aa	1.98 Aa	0.93 Bbc	1.63 Ba	1.32 Bb	2.89 Aa
Fructose	0.7 Ab	0.60 Ab	0.82 Ab	1.49 Aab	0.69 Aab	0.66 Aab	1.00 Ab	0.71 Ab	0.42 Ab	0.98 Aa	3.58 Aa	1.08 Aa
Fucose	1.6 Ab	1.43 Aa	1.86 Aa	2.91 Aa	0.25 Bc	0.48 Bb	2.87 Aab	0.71 Bb	0.63 Bb	3.79 Aa	0.56 Bb	0.18 Cc
Glucose_1	0.7 Ab	0.56 Ab	0.77 Ab	2.10 Aa	0.92 Bab	0.83 Bab	1.04 Ab	0.91 ABab	0.53 Bb	0.99 Ab	2.25 Aa	1.38 Aa
Maltose	0.7 Ab	0.76 Ab	0.69 Ac	5.08 Aa	1.11 Bab	4.21 Aab	1.55 Aab	2.81 Aa	1.95 Abc	1.88 Bab	4.65 ABa	9.02 Aa
Sucrose	0.2 Ab	0.22 Ac	0.20 Ac	1.45 Aa	0.25 Bc	0.24 Bbc	1.64 Aa	0.80 Bb	0.29 Cb	1.95 Aa	1.62 Aa	0.63 Ba
Trehalose	1 Ab	0.91 Aab	1.02 Aa	2.09 Aa	0.62 Bb	0.59 Bb	2.14 Aa	0.93 Bab	0.45 Cb	2.17 Aa	1.05 Ba	1.12 Ba
Xylose	1.4 Aa	1.42 Aa	1.48 Aa	1.29 Aa	1.40 Aa	1.44 Aa	1.59 Aa	1.38 Aa	1.57 Aa	1.37 Aa	1.67 Aa	1.87 Aa
Glycerol	1 Ab	1.02 Ab	1.06 Aa	1.44 Aa	1.23 Aa	1.24 Aa	1.55 Aa	1.33 ABa	1.20 Ba	1.57 Aa	1.31 Ba	1.05 Ca
Glycerol 3-P	0.5 Ab	0.44 Ab	0.61 Ab	0.71 Aa	0.83 Aa	0.93 Aa	0.71 Aa	0.74 Aa	0.75 Aa	0.72 Aa	0.78 Aa	0.93 Aa

SI Table 4. (continuation) Relative abundance of primary metabolites of *Scenedesmus obliquus* BR003 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Others	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Putrescine	2.4 Aa	2.50 Aa	2.40 Ab	1.25 Bb	2.97 Aa	2.92 Aab	0.97 Bbc	2.91 Aa	3.24 Aa	0.86 Bc	0.92 Bb	2.90 Aab
Spermidine	0.4 Ac	0.38 Ac	0.45 Ac	0.89 Ab	0.76 Ab	0.53 Ab	0.81 Aab	0.81 Aab	0.67 Aab	0.93 Aa	1.03 Aa	1.01 Aa
Adenine	1.3 Aa	1.16 Aa	1.48 Aa	1.03 Ab	0.72 Ab	0.69 Ab	0.85 Ab	0.74 Ab	0.83 Ab	0.82 Aab	1.17 Aab	0.96 Aab
Uracil	1.5 Aa	1.23 Ba	1.69 Aa	1.36 Aab	0.90 Bab	1.17 Aab	1.14 Abc	0.70 Bbc	1.00 Abc	0.67 Ac	0.53 Bc	0.90 Ac
2-Hydroxypyridine	1.2 Aa	1.29 Aa	1.01 Ba	1.08 Aa	1.09 Aa	0.99 Ba	1.23 Aa	1.31 Aa	0.95 Ba	1.46 Aa	1.18 Aa	1.06 Ba
4-Aminobutanoate	2.6 Aa	2.44 Aa	2.81 Aa	1.47 Aab	0.34 Bb	0.62 Bb	1.36 Aab	0.23 Bb	0.42 Bb	0.77 Ab	0.58 Bb	0.17 Bc
Galactinol	0.5 Ab	0.42 Ab	0.65 Aa	4.94 Aa	0.51 Bb	0.99 Ba	4.28 Aa	0.71 Bab	0.43 Ba	4.92 Aa	1.28 Ba	0.51 Ca
Myo-Inositol	0.5 Ab	0.45 Abc	0.57 Aa	1.07 Aa	0.34 Bc	0.49 Ba	1.29 Aa	0.63 Bab	0.56 Ba	1.36 Aa	1.30 Aa	0.43 Ba
Orthophosphate	1.4 Aa	1.49 Aa	1.30 Aa	1.52 Aa	1.52 Aa	1.43 Aa	1.56 Aa	1.66 Aa	1.57 Aa	1.59 Aa	1.53 Aa	1.33 Aa

SI Table 5. Relative abundance of primary metabolites of *Chlorella vulgaris* BR017 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Amino acid	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Alanine	0.65 Ca	1.01 Bb	1.13 Ac	0.59 Bb	1.29 Aa	1.24 Abc	0.52 Bc	1.34 Aa	1.35 Aab	0.56 Cbc	1.01 Bb	1.44 Aa
Arginine	0.82 Ba	2.31 Aa	2.58 Aa	0.16 Bb	2.92 Aa	2.33 Aa	0.14 Bb	2.81 Aa	2.18 Aab	0.13 Cb	0.37 Bb	1.54 Ab
Asparagine	0.63 Ba	1.03 Aa	1.39 Ac	0.37 Bb	1.18 Aa	1.57 Ac	0.46 Cab	1.46 Ba	2.54 Ab	0.53 Ba	0.64 Bb	6.64 Aa
Aspartate	1.82 Ba	2.41 Aa	2.55 Ab	0.70 Bb	2.44 Aa	2.43 Ab	0.43 Cd	2.66 Ba	3.37 Aa	0.58 Cc	0.79 Bb	3.00 Aa
b-Alanine	1.57 Aa	1.36 Aa	1.35 Aa	1.31 Aa	1.06 Aab	0.93 Aab	0.56 Bb	0.99 Aab	0.85 ABb	0.54 Bb	0.70 Bb	1.68 Aa
Citrulline	1.02 Ba	1.28 Aba	1.41 Aa	1.11 Ba	1.47 Aa	1.15 Bab	1.15 Aba	1.32 Aa	1.07 Bb	0.95 Ba	0.81 Bb	1.32 Aab
Glutamate	0.72 Bb	0.76 Abc	0.80 Ab	0.78 Ab	0.81 Abc	0.80 Ab	1.05 Aa	0.88 Bb	0.87 Bb	1.00 Aa	1.06 Aa	1.00 Aa
Glutamine_2	0.22 Ba	1.75 Aa	1.99 Aa	0.15 Ba	1.85 Aa	1.70 Aa	0.22 Ba	0.92 Ab	1.05 Ab	0.21 Ca	0.50 Bb	2.37 Aa
Glycine	0.88 Ba	1.09 Abb	1.15 Ab	0.76 Ba	1.60 Aa	1.69 Aa	0.71 Ba	1.61 Aa	1.67 Aa	0.72 Ca	0.92 Bb	1.27 Ab
Isoleucine	1.14 Aa	0.87 Bd	0.96 Bc	1.00 Aab	1.08 Ac	1.05 Abc	0.89 Bb	1.29 Ab	1.18 Ab	0.89 Cb	1.56 Ba	2.38 Aa
Leucine	0.89 Aa	0.59 Bd	0.67 Bb	0.94 Aa	0.81 Abc	0.74 Bb	0.88 Aba	1.00 Ab	0.79 Bb	0.81 Ca	1.54 Ba	2.06 Aa
Lysine	0.65 Aab	0.64 Ab	0.64 Ac	0.58 Bab	1.82 Aa	1.51 Ab	0.76 Ca	1.92 Aa	1.44 Bb	0.52 Cb	0.84 Bb	2.41 Aa

SI Table 5. (continuation) Relative abundance of primary metabolites of *Chlorella vulgaris* BR017 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Amino acid	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Methionine	0.38 Bb	0.58 Aab	0.66 Ab	0.50 Ab	0.44 Ab	0.42 Ac	0.77 Aa	0.53 Bb	0.60 ABb	0.83 Ba	0.77 Ba	1.79 Aa
Ornithine	0.84 Ba	2.68 Aa	2.01 Aa	0.25 Bb	2.48 Aa	1.81 Aa	0.17 Bc	2.29 Aa	1.65 Aa	0.24 Bbc	0.27 Bb	1.09 Ab
Phenylalanine	0.97 Ab	0.93 Ac	1.04 Ab	1.42 Aa	0.94 Bc	0.97 Bb	1.33 Aa	1.38 Ab	0.95 Bb	1.21 Ba	2.29 Aa	2.51 Aa
Proline	1.58 Ba	1.78 Bb	2.19 Ab	1.56 Ba	2.45 Aa	2.54 Aab	1.27 Bb	2.61 Aa	2.67 Aa	0.97 Ac	0.73 Bc	0.91 Ac
Serine	1.58 Aa	1.31 Bc	1.40 Bd	1.05 Bb	1.55 Ab	1.60 Ac	1.14 Bb	1.90 Aa	2.06 Ab	1.14 Cb	1.26 Bc	2.52 Aa
Threonine	1.38 Aa	1.02 Bc	1.06 Bd	0.78 Bb	1.32 Ab	1.39 Ac	0.81 Bb	1.60 Aa	1.73 Ab	0.80 Cb	1.05 Bc	2.53 Aa
Tryptophan	0.69 Ac	0.37 Bc	0.40 Bc	1.39 Aa	0.55 Bb	0.66 Bb	1.01 Ab	0.61 Bb	0.66 Bb	1.25 Bab	1.67 Aa	1.83 Aa
Tyrosine	1.43 Aa	0.98 Bc	1.05 Bb	1.76 Aa	0.99 Bc	1.15 Bb	1.45 Aa	1.28 Ab	1.01 Bb	1.58 Aa	1.70 Aa	1.87 Aa
Valine	1.06 Aa	0.92 Ac	1.06 Ac	0.86 Bb	1.21 Ab	1.09 Ac	1.02 Ca	1.54 Aa	1.34 Bb	0.72 Cc	1.43 Ba	1.91 Aa
5-Oxoproline	0.8 Ba	1.17 Aa	1.26 Aa	0.54 Bc	1.22 Aa	1.32 Aa	0.68 Bab	1.12 Aa	1.19 Aa	0.60 Cbc	0.94 Bb	1.42 Aa
Organic acid	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Benzoate	0.87 Aa	0.81 Aa	1.01 Aa	1.01 Aa	1.00 Aa	0.80 Aa	1.47 Aa	0.90 Aa	0.72 Aa	1.03 Aa	1.00 Aa	1.19 Aa
Citramalate	0.52 Ac	0.49 Ab	0.43 Aa	1.21 Ab	0.63 Bb	0.53 Ba	1.14 Ab	0.56 Bb	0.49 Ba	4.18 Aa	1.94 Ba	0.26 Cb
Citrate	2.53 Ba	4.74 Aa	5.31 Aa	1.17 Bb	4.41 Aa	4.29 Aa	1.02 Bbc	2.27 Ab	2.52 Ab	0.80 Ac	0.86 Ac	0.16 Bc
Dehydroascorbate	1.61 Aa	0.96 Ba	0.90 Bb	1.11 Abc	0.85 Ba	0.71 Cc	1.07 Ac	0.90 Aa	0.70 Bc	1.34 Aab	0.93 Ba	1.14 Aa
Fumarate	0.7 Bc	0.68 Bc	0.76 Ab	0.81 Ab	0.77 ABb	0.75 Bb	1.08 Aa	0.79 Bb	0.80 Bb	1.10 Aa	1.00 Ba	0.92 Ca
Gluconate	12.8 Aa	8.00 ABa	6.87 Ba	8.92 Aa	2.00 Bb	1.94 Bb	4.56 Ab	0.78 Bc	0.46 Cc	4.18 Ab	1.32 Bb	0.19 Cd
Glycerate	1.86 Aa	1.20 Ba	1.19 Ba	1.52 Aa	1.06 Ba	1.16 Ba	1.03 Ab	0.74 Bb	0.65 Bb	1.09 Ab	0.68 Bb	0.79 Bb
Ketoglutarate	0.99 ABbc	1.05 Abc	0.75 Bbc	0.89 ABc	0.81 Ac	0.79 Bc	1.14 ABab	1.01 Aab	0.96 Bab	1.05 Aab	1.37 Aa	1.10 Ba
Lactate	0.68 Cc	0.83 Bc	1.00 Ab	1.36 Ab	1.34 Ab	1.36 Aa	1.74 Aa	1.21 Bb	1.31 Ba	1.75 Ba	1.95 Aa	1.03 Cb
Malate	0.56 Bb	0.64 ABb	0.70 Ac	0.60 Bb	0.74 Ab	0.70 Ac	0.91 Ba	1.02 ABa	1.15 Ab	0.67 Bb	0.71 Bb	1.71 Aa
Nicotinate	1.01 Aa	0.80 Bb	0.77 Bc	0.73 Bb	0.93 Aab	0.90 Ab	0.71 Bb	1.07 Aa	0.98 Ab	0.59 Cc	0.85 Bb	1.15 Aa
Pyruvate	0.34 Bb	0.34 ABc	0.51 Ac	0.26 Bb	1.00 Ab	0.75 Ac	0.54 Ba	2.00 Aa	2.53 Ab	0.56 Ca	1.09 Bb	5.38 Aa
Succinate	0.97 Aa	0.65 Bb	0.75 Bb	0.81 Ba	0.92 ABa	1.08 Aa	0.85 Ba	0.99 ABa	1.15 Aa	0.86 Ba	0.93 ABa	1.06 Aa
Sugar	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Cellobiose	0.98 Ab	0.73 Aa	0.79 Aa	1.38 Aa	0.26 Bc	0.27 Bb	1.65 Aa	0.34 Bbc	0.13 Cc	1.61 Aa	0.42 Bb	0.09 Cc
Fructose	7.61 Aa	4.71 Ba	2.94 Ca	6.69 Aa	0.93 Bc	0.95 Bb	3.08 Ab	0.62 Bd	0.65 Bc	3.02 Ab	1.33 Bb	0.62 Cc
Fucose	1.23 Ab	1.01 Ab	1.04 Aa	1.79 Aab	0.99 Bb	1.26 ABa	1.57 Aab	1.27 Ab	1.15 Aa	2.03 Aa	2.16 Aa	0.19 Bb

SI Table 5. (continuation) Relative abundance of primary metabolites of *Chlorella vulgaris* BR017 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Sugar	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Glucose_1	2.21 Aa	1.20 Ba	0.85 Cab	2.43 Aa	0.88 Bb	1.02 Ba	2.03 Aab	0.81 Bb	0.87 Bab	1.69 Ab	1.43 Aa	0.78 Bb
Maltose	1.07 Aa	0.70 Aa	0.99 Aa	1.04 Aa	0.58 Aa	0.51 Aab	1.25 Aa	0.67 ABa	0.37 Bbc	2.91 Aa	1.03 Aa	0.16 Bc
Sucrose	1.04 Ac	1.08 Ab	1.11 Aa	1.22 Ab	1.07 Bb	1.04 Ba	1.66 Aa	1.10 Bb	1.10 Ba	1.77 Aa	1.53 Ba	1.11 Ca
Trehalose	1.42 Ab	1.05 Aa	1.15 Aa	2.03 Aa	0.37 Bc	0.38 Bb	2.41 Aa	0.49 Bbc	0.17 Cc	2.35 Aa	0.58 Bb	0.13 Cc
Xylose	0.65 Bc	0.79 Ab	0.85 Ab	0.66 Bc	0.92 Aa	0.91 Aab	0.99 Aa	0.86 Bab	0.89 ABab	0.78 Cb	0.90 Bab	1.02 Aa
Glycerol	0.82 Ab	0.78 Ab	0.78 Aa	0.89 Ab	0.76 Abc	0.75 Aab	1.16 Aa	0.71 Bc	0.71 Bb	1.22 Aa	1.09 Ba	0.79 Ca
Glycerol 3-P	0.99 Aab	0.90 Ab	0.78 Bc	0.92 Ab	0.98 Ab	0.96 Ab	0.94 Aab	0.93 Ab	0.91 Ab	1.04 Ca	1.27 Ba	1.45 Aa
Others	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Putrescine	0.34 Ba	0.70 Aab	0.85 Aa	0.47 Ba	0.79 Aab	0.66 ABab	0.33 Ca	1.05 Aa	0.64 Bab	0.52 Aa	0.58 Ab	0.51 Ab
Spermidine	1.98 Aa	1.30 Ac	1.06 Ac	0.77 Bb	4.05 Aab	3.44 Ab	0.83 Bb	5.14 Aa	5.06 Aab	1.81 Cab	2.75 Bb	8.18 Aa
Adenine	0.53 Ab	0.52 Ab	0.52 Ab	0.83 Aa	0.69 Aa	0.89 Aa	0.54 Ab	0.51 Ab	0.56 Ab	0.45 Ab	0.59 Ab	0.67 Ab
Uracil	1.85 Aa	1.34 Ba	1.36 Ba	1.24 Ab	1.32 Aa	1.11 Aa	1.18 Abc	0.88 Bb	0.63 Cb	0.92 Ac	0.73 Ab	0.53 Bb
2-Hydroxypyridine	0.7 ABb	0.64 Bc	0.76 Abc	0.77 Ab	0.72 Abc	0.71 Ac	0.98 Aa	0.75 Cb	0.83 Bb	0.97 Aa	1.05 Aa	1.08 Aa
4-Aminobutanoate	4.61 Aa	4.15 Aa	3.15 Aa	4.09 Aa	1.35 Bb	1.61 Bb	1.92 Ab	0.56 Bc	0.58 Bc	2.42 Ab	0.73 Bc	0.44 Cc
Galactinol	3.07 Aa	2.64 Aa	1.30 Ba	3.68 Aa	0.67 Bb	0.65 Bb	3.51 Aa	0.43 Bb	0.34 Bc	2.85 Aa	1.74 Aa	0.26 Bc
Myo-Inositol	1.64 Aab	1.14 Ba	1.04 Ba	1.34 Ac	0.80 Bc	0.78 Bc	1.43 Abc	0.97 Bb	1.01 Bab	1.81 Aa	1.27 Ba	0.90 Cbc
Orthophosphate	0.63 Bc	0.69 Ac	0.72 Ab	0.74 Ab	0.72 Abc	0.72 Ab	0.99 Aa	0.78 Bb	0.77 Bb	1.06 Aa	0.99 Aa	0.87 Ba

SI Table 6. Relative abundance of primary metabolites of *Monoraphidium* sp. BR023 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Amino acid	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
Alanine	0.5 Ba	0.93 Ab	0.96 Ab	0.40 Bb	1.34 Aa	1.39 Aa	0.45 Cab	1.19 Ba	1.45 Aa	0.39 Cb	0.68 Bc	1.46 Aa
Arginine	0.4 Ba	1.65 Ab	1.57 Aa	0.18 Bb	3.41 Aa	2.61 Aa	0.21 Bab	2.00 Aab	2.59 Aa	0.18 Bb	0.30 Bc	1.48 Aa
Asparagine	0.5 Ba	1.01 Aa	1.17 Ac	0.33 Bab	1.25 Aa	1.41 Ac	0.28 Cb	1.39 Ba	2.20 Ab	0.35 Bab	0.51 Bb	5.60 Aa
Aspartate	0.7 Ba	1.36 Ab	1.20 Ac	0.39 Bb	2.01 Aa	1.75 Ab	0.42 Cb	1.47 Bb	2.64 Aa	0.32 Cc	0.43 Bc	2.95 Aa
b-Alanine	1.7 Ba	2.00 Aa	1.63 ABa	2.09 Ba	2.53 Aa	1.96 ABa	1.59 Ba	2.50 Aa	2.06 ABa	1.30 Bb	1.39 Ab	1.60 ABb
Citrulline	1.1 Aa	1.01 Aab	1.05 Aa	1.06 Aa	1.66 Aa	1.54 Aa	0.67 Bb	1.05 Aab	1.57 Aa	0.71 Bab	0.76 Bb	1.18 Aa
Glutamate	0.8 Ac	0.78 Ac	0.81 Ac	0.91 Ab	0.90 Ab	0.88 Ab	0.99 Aa	1.02 Aa	0.94 Aa	0.97 Aa	1.08 Aa	1.05 Aa
Glutamine_2	0.3 Ba	2.15 Ab	2.05 Ab	0.23 Ba	4.30 Aa	3.81 Aa	0.24 Ca	0.60 Bc	1.34 Ac	0.23 Ca	0.65 Bc	3.10 Aab
Glycine	1.2 Aa	1.36 Aa	1.11 Ac	0.73 Bb	1.26 Aab	1.45 Abc	0.76 Bb	1.44 Aa	1.76 Aab	0.64 Cb	0.97 Bb	1.88 Aa
Isoleucine	1 Aab	0.87 ABd	0.77 Bd	0.91 Bb	1.07 Ac	1.06 Ac	1.08 Ba	1.25 Ab	1.34 Ab	0.95 Cab	1.46 Ba	2.61 Aa
Leucine	1.4 Aab	1.12 Bb	0.97 Cc	1.31 Aab	0.95 Bc	0.90 Bc	1.46 Aa	1.20 Bb	1.12 Bb	1.22 Cb	1.68 Ba	2.42 Aa
Lysine	0.5 Bb	0.76 Ab	0.80 Ac	0.66 Bb	1.83 Aa	1.47 Ab	0.89 Ba	1.65 Aa	1.45 Ab	0.95 Ba	1.06 Bb	2.13 Aa
Methionine	0.8 Ab	0.89 Abc	0.81 Ab	0.79 Bb	1.17 Aa	1.00 ABab	1.23 Aa	1.12 Aab	1.15 Aa	1.45 Aa	0.68 Bc	1.28 Aa
Ornithine	0.6 Ba	2.35 Aab	2.24 Aa	0.36 Cb	2.84 Aa	1.81 Ba	0.30 Bb	1.91 Ab	1.81 Aa	0.26 Bb	0.29 Bc	1.20 Ab
Phenylalanine	0.9 Ab	0.80 Ac	0.82 Ab	1.44 Aa	0.87 Bc	0.87 Bb	1.36 Aa	1.08 Bb	0.88 Cb	1.46 Ba	2.53 Aa	2.42 Aa
Proline	1.9 Aa	1.96 Ac	2.08 Ab	1.45 Bb	2.24 Ab	2.41 Aa	1.14 Bc	2.73 Aa	2.54 Aa	0.78 Ad	0.64 Bd	0.84 Ac
Serine	1.3 Aa	1.22 Ab	1.21 Ac	0.85 Bb	1.34 Ab	1.32 Ac	0.87 Cb	1.66 Ba	2.01 Ab	0.93 Bb	0.82 Cc	2.58 Aa
Threonine	1 Aa	1.02 Abc	0.99 Ac	0.69 Bb	1.16 Aab	1.21 Ac	0.85 Cab	1.32 Ba	1.62 Ab	0.70 Cb	0.92 Bc	2.69 Aa
Tryptophan	0.7 Ab	0.39 Bc	0.42 Bc	1.43 Aa	0.65 Bb	0.65 Bb	1.45 Aa	0.81 Bb	0.71 Bb	1.76 Aa	2.09 Aa	1.72 Aa
Tyrosine	0.7 Ac	0.58 Bc	0.64 ABb	0.94 Ab	0.68 Bc	0.67 Bb	1.18 Aa	0.87 Bb	0.69 Cb	1.19 Ba	1.61 Aa	1.64 Aa
Valine	0.9 Aa	1.00 Ac	0.87 Ad	0.90 Ba	1.21 Ab	1.08 Ac	1.04 Ba	1.60 Aa	1.52 Ab	0.96 Ca	1.40 Bab	2.01 Aa
5-Oxoproline	0.6 Ba	0.88 Ab	0.79 Ab	0.60 Ba	1.31 Aa	1.31 Aa	0.64 Ba	1.16 Aa	1.40 Aa	0.54 Ca	0.88 Bb	1.55 Aa

SI Table 6. (continuation) Relative abundance of primary metabolites of *Monoraphidium* sp. BR023 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Organic acid	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Benzoate	1 Aa	0.93 ABa	0.73 Bb	0.86 Aa	0.96 Aa	0.83 Ab	1.05 Aa	0.85 ABa	0.83 Bb	0.94 Ba	0.88 Ba	1.28 Aa
Citramalate	0.4 Ad	0.38 Ad	0.30 Ab	0.97 Ac	0.93 ABb	0.80 Ba	1.45 Ab	0.61 Cc	0.97 Ba	6.66 Aa	3.55 Ba	0.38 Cb
Citrate	0.3 Cb	1.06 Bb	1.54 Aa	0.53 Ba	1.63 Aa	1.51 Aa	0.39 Ba	0.45 Bc	0.69 Ab	0.51 Aa	0.40 Ac	0.26 Bc
Dehydroascorbate	1.6 Aa	1.19 Ba	1.13 Ba	1.34 Ab	0.86 Bb	0.76 Bb	1.68 Ab	0.80 Bb	0.73 Bb	2.07 Aa	1.20 Ba	1.01 Ba
Fumarate	0.8 Aa	0.78 ABa	0.80 Ba	1.01 Aa	0.93 ABa	0.89 Ba	1.14 Aa	0.84 ABa	0.76 Ba	1.23 Aa	1.10 ABa	0.85 Ba
Gluconate	6.6 Aa	5.01 ABa	3.81 Ba	3.82 Ab	0.79 Bbc	0.76 Bb	2.89 Ab	0.55 Bc	0.35 Cc	2.54 Ab	1.13 Bb	0.25 Cc
Glycerate	1.5 Aab	1.21 Bab	1.11 Bab	1.50 Aa	1.39 Ba	1.42 Ba	1.56 Ab	1.13 Bb	1.01 Bb	1.76 Aab	1.13 Bab	1.26 Bab
Ketoglutarate	0.9 Ac	0.95 Ab	0.82 Aab	0.97 Abc	1.01 Ab	0.98 Aa	1.12 Aab	1.00 Ab	0.79 Bb	1.22 Ba	1.58 Aa	0.87 Cab
Lactate	0.7 Ab	0.76 Ac	0.75 Ac	1.32 Aa	1.28 Ab	1.39 Aa	1.61 Aa	0.92 Bc	0.95 Bb	1.51 Ba	1.91 Aa	0.78 Cbc
Malate	0.5 Ab	0.53 ABc	0.41 Bd	0.76 Ba	1.25 Aa	1.11 Ac	0.68 Ca	1.23 Ba	1.77 Ab	0.71 Ca	0.97 Bb	2.74 Aa
Nicotinate	1.1 Aa	1.13 Aa	0.95 Aab	0.77 Bb	1.04 Aa	0.91 Ab	0.74 Bb	1.04 Aa	0.95 Aab	0.63 Cc	0.87 Bb	1.09 Aa
Pyruvate	0.6 Ba	1.33 Aa	1.06 Ab	0.21 Bc	1.12 Aab	0.96 Ab	0.41 Cab	0.79 Bbc	1.26 Ab	0.28 Cbc	0.57 Bc	2.35 Aa
Succinate	1.3 Aa	1.22 ABb	0.99 Bc	0.87 Bb	1.24 Aab	1.33 Ab	1.29 Ba	1.46 ABa	1.66 Aa	1.20 Aa	1.08 Ab	0.76 Bd
Sugar	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Cellobiose	1.4 Ab	0.99 Bb	0.97 Ba	3.79 Aa	0.35 Bc	0.35 Bb	4.69 Aa	1.13 Bb	0.32 Cb	4.99 Aa	1.97 Ba	0.27 Cb
Fructose	8.1 Aa	6.13 Aa	7.02 Aa	5.61 Ab	1.01 Bc	1.02 Bb	3.87 Abc	0.89 Bc	0.51 Cc	3.58 Ac	2.12 Bb	0.68 Cc
Fucose	2.6 Aa	2.15 Aa	2.25 Aa	2.79 Aa	0.80 Bc	0.69 Bb	2.43 Aa	1.42 Bb	0.68 Cb	3.22 Aa	1.97 Ba	0.24 Cc
Glucose_1	2.5 Aa	1.81 Ba	2.20 Aa	2.51 Aa	0.70 Bc	0.73 Bbc	1.77 Ab	0.62 Bc	0.59 Bc	1.85 Ab	1.36 Bb	0.87 Cb
Maltose	1 Ab	0.75 Ab	0.73 Aa	2.86 Aa	0.27 Bc	0.26 Bb	3.54 Aa	0.95 Bb	0.39 Cb	3.76 Aa	1.78 Ba	0.27 Cb
Sucrose	1.1 Ac	1.02 Ab	1.10 Aa	1.45 Ab	0.80 Bc	0.83 Bb	1.54 Aab	1.13 Bb	0.83 Cb	1.75 Aa	1.61 Aa	0.79 Bb
Trehalose	2 Ab	1.43 Bb	1.40 Ba	5.57 Aa	0.48 Bc	0.49 Bb	6.93 Aa	1.59 Bb	0.31 Cc	7.33 Aa	2.90 Ba	0.38 Cbc
Xylose	0.7 Bb	0.75 Ab	0.74 Ab	0.78 Ba	1.00 Aa	1.03 Aa	0.88 Ba	0.90 Aa	0.98 Aa	0.79 Ba	0.95 Aa	1.01 Aa
Glycerol	0.8 Ac	0.73 Bc	0.69 Bb	0.99 Ab	0.78 Bbc	0.76 Bab	1.01 Ab	0.82 Bb	0.75 Bab	1.16 Aa	1.15 Aa	0.78 Ba
Glycerol 3-P	1 Ab	1.11 Ab	1.07 Abc	1.24 Aa	1.21 Aab	1.17 Aab	1.18 Aa	1.06 ABb	0.96 Bc	1.28 Aa	1.37 Aa	1.31 Aa

SI Table 6. (continuation) Relative abundance of primary metabolites of *Monoraphidium* sp. BR023 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Others	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
Putrescine	1 Ba	1.60 Aa	1.73 Aa	0.79 Bab	1.61 Aa	1.27 Aa	0.59 Cbc	2.13 Aa	1.23 Ba	0.45 Bc	0.66 Ab	0.76 Ab
Spermidine	0.8 Aab	0.59 Ba	0.54 Bb	0.50 Ac	0.39 Bb	0.39 Bc	0.61 Abc	0.59 Aa	0.50 Abc	0.80 Ba	0.52 Ca	1.14 Aa
Adenine	1.7 Aa	1.82 Aa	1.92 Aa	1.40 Aab	1.47 Aa	1.64 Aab	1.11 Bb	1.72 Aa	1.41 ABb	1.01 Ab	0.99 ABb	0.76 Bc
Uracil	2 Aa	2.12 Aa	1.52 Aa	1.20 Bb	1.67 Aab	1.44 ABa	1.15 Abc	1.26 Ab	0.95 Ab	0.85 Ac	0.91 Ac	0.50 Bc
2-Hydroxypyridine	0.8 Ab	0.81 Ab	0.80 Ab	0.91 Ab	0.79 Ab	0.84 Ab	0.85 Ab	0.81 Ab	0.80 Ab	0.95 Aa	1.03 Aa	1.02 Aa
4-Aminobutanoate	5.2 Aa	4.99 Aa	4.21 Aa	3.17 Ab	2.14 Ab	2.17 Ab	2.29 Ab	1.16 Bc	1.23 Bc	2.10 Ab	0.73 Bc	0.42 Cd
Galactinol	2.2 Aa	1.17 Aa	1.11 Aa	2.10 Aa	0.56 Bb	0.40 Bb	2.22 Aa	0.44 Bb	0.22 Bb	2.17 Aa	1.79 Aa	0.21 Bb
Myo-Inositol	1.4 Ab	1.12 Bb	1.00 Ba	1.22 Ab	0.49 Bd	0.49 Bd	1.32 Ab	0.77 Bc	0.71 Bc	1.72 Aa	1.35 Ba	0.84 Cb
Orthophosphate	0.7 Ad	0.69 Bd	0.67 Bd	0.92 Ac	0.79 Bc	0.79 Bc	1.00 Ab	0.88 Bb	0.85 Bb	1.11 Aa	1.01 Ba	0.92 Ba

SI Table 7. Relative abundance of lipid of *C. reinhardtii* CC503 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N		0h_3.5N		0h_7N		10h_0N		10h_3.5N		10h_7N		18h_0N		18h_3.5N		18h_7N		36h_0N		36h_3.5N		36h_7N	
DAG 34:1	NA	Aa	NA	Aa	NA	Ab	NA	Ba	NA	Ba	5754.5	Aa	NA	Aa	NA	Aa	NA	Ab	NA	Ba	NA	Ba	3924.2	Aa
DAG 34:2	5969.5	Ac	5341.6	Ab	5726.0	Aa	40084.2	Ab	3369.1	Bb	6408.5	Ba	65620.6	Ab	3227.3	Bb	2377.2	Ba	194660.9	Aa	78232.3	Ba	1262.3	Ca
DAG 34:3	11217.4	Ac	10144.0	Ab	11748.8	Aa	74840.5	Ab	7887.2	Bb	15624.6	Ba	94895.5	Ab	6936.7	Bb	4716.4	Ba	274342.9	Aa	134029.0	Ba	6350.7	Ca
DAG 34:4	NA	Ac	NA	Ab	NA	Aa	17957.2	Ab	NA	Bb	NA	Ba	25516.7	Ab	NA	Bb	NA	Ba	108613.1	Aa	26506.5	Ba	NA	Ca
DAG 34:5	2866.2	Ab	3438.6	Ab	3049.0	Aa	15586.4	Ab	4192.1	Ab	6164.6	Aa	18182.4	Ab	NA	Bb	NA	Ba	99860.0	Aa	20032.6	Ba	NA	Ca
DAG 34:6	3389.3	Ab	2720.4	Aa	2775.1	Aa	6574.5	Ab	NA	Aa	NA	Aa	10098.9	Ab	NA	Ba	NA	Ba	50049.6	Aa	9594.0	Ba	NA	Ca
DAG 36:1	NA	Ab	NA	Aa	NA	Aa	1217.4	Aa	NA	Ba	NA	Ba	1081.5	Aa	NA	Ba	NA	Ba	NA	Ab	NA	Aa	NA	Aa
DAG 36:2	11342.5	Ac	9253.9	Ab	8551.8	Aa	15514.7	Abc	4570.6	Bb	8214.5	Bab	17344.4	Ab	6161.9	Bb	3479.9	Bc	30835.9	Aa	14420.9	Ba	3749.6	Cbc
DAG 36:3	17462.7	Aa	12117.3	Aa	12606.6	Aa	21859.3	Aa	5307.4	Bab	9333.8	Bab	24230.3	Aa	4376.0	Bb	2595.5	Bbc	NA	Ab	NA	Ab	NA	Ac
DAG 36:4	NA	Aa	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Aa	NA	Ba	34471.4	Aa	NA	Ba
DAG 36:5	12254.5	Ac	7669.2	ABb	4294.4	Bab	0.0	Bd	3806.6	ABb	10410.6	Aa	32791.9	Ab	NA	Bb	NA	Bb	83655.6	Aa	24496.9	Ba	NA	Cb
DAG 36:6	16092.8	Ab	11827.9	Aab	9848.2	Aa	20996.9	Ab	6878.9	Bb	11336.7	Ba	23006.2	Ab	4223.1	Bb	NA	Bb	49670.7	Aa	15520.8	Ba	NA	Cb
DGDG 32:0	410904.9	Aa	420934.2	Aa	457653.9	Aa	363484.9	Aab	198320.0	Bb	255743.9	Bb	291307.4	Abc	186589.1	Bb	150301.6	Bc	223263.2	Bc	208252.2	Bb	498723.8	Aa
DGDG 32:1	90080.4	Ba	116429.1	Aa	115422.6	ABb	85881.1	Aa	57205.3	Bb	76113.7	ABc	72084.1	Aa	56426.8	Ab	48159.9	Ac	39068.0	Bb	57572.1	Bb	149080.2	Aa
DGDG 32:2	45994.0	Aa	58821.9	Aa	55764.3	Ab	36994.4	Bab	39062.8	Bb	57703.4	Ab	27314.7	Ab	28483.7	Ab	25451.1	Ac	25478.5	Bb	25179.6	Bb	94728.9	Aa
DGDG 32:3	41176.4	Aa	56268.7	Aa	50714.9	Ac	NA	Cb	62636.3	Ba	87672.6	Ab	35015.1	Aa	51304.2	Aab	48290.7	Ac	38784.1	Ba	35054.9	Bb	161819.0	Aa
DGDG 32:3.1	96727.6	Aa	132756.8	Aa	121450.2	Ac	123523.7	Ba	144742.5	Ba	194724.5	Ab	129339.3	Aa	119302.0	Aa	92846.0	Ac	112201.6	Ba	134865.2	Ba	292475.8	Aa
DGDG 34:0	929370.0	Ba	1140019.3	Aa	1188645.1	Aa	410439.2	Bb	490672.0	Ab	629023.2	Ab	295194.7	Bc	408580.7	Ac	406970.6	Ac	196453.6	Bd	249758.5	Ad	278547.3	Ad
DGDG 34:1	6615217.3	Aa	6129760.5	Aa	5669417.1	Aa	4356504.5	Ab	3252506.7	Bb	4169022.5	ABb	3359294.6	ABbc	3461781.9	Ab	2309245.4	Bc	2202529.2	Ac	2802149.0	Ab	2826361.8	Ac
DGDG 34:2	6673997.0	Aa	6618319.1	Aa	6012700.1	Aa	6397609.7	Aa	4568798.0	Bb	5909850.8	ABa	5292291.9	Aa	4495130.0	Ab	2766719.4	Bb	3256301.1	Ab	4215253.6	Ab	3592936.4	Ab
DGDG 34:3	5179112.1	Aab	5420345.5	Aa	5032823.4	Aab	6080469.9	Aa	5004207.1	Aa	6561815.9	Aa	5319548.7	Aab	4733889.6	ABa	3277090.1	Bc	3969506.0	Ab	4390603.8	Aa	4258311.7	Abc
DGDG 34:4	2391349.4	Aa	3005105.4	Aa	2750166.1	Ab	2430566.2	Ba	2793756.6	Ba	3782564.1	Aa	1944773.3	ABab	2649080.5	Aa	1830626.6	Bc	1450428.9	Bb	2430702.4	Aa	2484776.1	Abc
DGDG 34:5	2574618.6	Aa	3421810.5	Aa	3014167.0	Ab	3080843.0	Ba	3542052.6	Ba	4660695.2	Aa	2894091.3	ABa	3550009.3	Aa	2420821.0	Bb	2233074.9	Aa	3054227.9	Aa	3174171.8	Ab
DGDG 34:6	1518722.5	Bb	2382038.0	Ab	2134252.3	ABb	2550214.0	Ba	2822265.1	Bab	3678317.6	Aa	2564551.2	Ba	3276426.6	Aa	2162472.7	Bb	2427810.4	Ba	2732741.5	ABab	3337867.2	Aa
DGDG 36:2	51955.7	Ba	91694.1	Aa	89667.9	Aa	40107.3	Bab	52853.1	Bb	68873.2	Ab	32434.5	Abc	44899.8	Ab	43539.6	Ac	19127.9	Ac	26092.9	Ac	26076.9	Ad
DGDG 36:3	36429.7	Ba	55111.8	Aa	48857.8	Aa	49469.4	Ba	47941.4	Aa	51564.3	Aa	NA	Bb	34484.4	Ab	33155.5	Ab	NA	Bc	NA	Ac	NA	Ac
DGDG 36:4	51086.1	Ba	81103.6	Aab	72994.8	ABc	53759.2	Ca	94082.1	Ba	130060.5	Ab	52302.8	Ba	77215.4	Aab	58264.5	ABc	22664.2	Cb	61619.8	Bb	190797.4	Aa
DGDG 36:5	51291.0	Aa	78575.0	Aab	70088.3	Ab	44001.1	Ca	96698.3	Ba	136956.4	Aa	37440.5	Bab	78232.2	Aab	71125.9	Ab	13293.9	Cb	62159.1	Bb	143432.6	Aa
DGDG 36:6	185223.6	Ba	288694.5	Aa	264021.9	ABbc	196719.6	Ba	245881.4	Bab	339592.6	Ab	166603.4	Aab	215937.5	Aab	183298.5	Ac	87261.7	Cb	182863.2	Bb	706126.6	Aa

SI Table 7. (continuation) Relative abundance of lipid of *C. reinhardtii* CC503 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N		0h_3.5N		0h_7N		10h_0N		10h_3.5N		10h_7N		18h_0N		18h_3.5N		18h_7N		36h_0N		36h_3.5N		36h_7N	
LysoPC 16:0	34134.5	Ba	73521.0	Aa	65160.9	Aa	44718.7	Aa	24909.7	Bb	31492.3	ABb	47867.6	Aa	38098.5	Ab	16095.8	Bbc	46368.5	Aa	21546.2	Bb	13299.0	Bc
LysoPC 18:3	NA	Ba	3570.9	Aa	NA	Ba	NA	Aa	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Aa
MGDG 34:1	738486.9	Ba	1101458.7	Aa	993272.0	ABa	289327.1	Ab	340707.4	Ab	502121.9	Ab	660644.6	Aa	317465.4	Bb	506227.8	ABb	138899.6	Bb	436070.4	Ab	261008.3	ABb
MGDG 34:2	463860.7	Ba	729176.6	Aa	661861.5	ABab	93577.2	Cb	471081.5	Bab	843318.0	Aa	72387.8	Bb	359170.9	Ab	458779.2	Ab	55873.5	Ab	NA	Ac	169189.4	Ac
MGDG 34:2.1	298356.9	Ab	414289.2	Aa	388497.2	Aa	319528.8	Ab	227152.0	Ab	322615.7	Aab	571845.8	Aa	169018.2	Bb	187050.8	Bbc	118956.9	Bc	394991.1	Aa	153429.8	Bc
MGDG 34:3	21576.9	Aa	31925.7	Aa	30526.2	Aab	16582.3	Cab	30208.7	Ba	41097.9	Aa	16389.0	Bab	31317.7	Aa	27492.2	Ab	7896.2	Bb	9818.1	ABb	19658.5	Ab
MGDG 34:4	381285.4	Ab	647946.2	Ab	636677.9	Ab	1165790.0	Ba	1465736.7	Ba	2200362.7	Aa	587712.3	Ab	1087164.1	Aab	992620.3	Ab	494453.8	Bb	1072745.9	Aab	884598.8	ABb
MGDG 34:5	354958.5	Ac	601952.6	Ab	579713.3	Ac	1977985.1	Ba	1941321.2	Ba	2879283.3	Aa	1547048.8	Aab	1626423.1	Aa	1452512.9	Ab	978593.3	Bbc	1814158.0	Aa	1384336.4	ABb
MGDG 34:6	NA	Ab	NA	Ab	NA	Aa	NA	Bb	1490384.3	Aa	NA	Ba	1542464.0	Aa	1604227.1	Aa	NA	Ba	NA	Ab	NA	Ab	NA	Aa
MGDG 36:6	15708.2	Aa	23072.6	Aab	21627.6	Ac	9917.6	Ca	34206.4	Ba	52789.1	Ab	10016.1	Aa	18036.3	Abc	22674.0	Ac	2368.5	Ba	8547.3	Bc	74554.5	Aa
PC 32:0	5192.8	Aa	NA	Ba	NA	Ba	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Aa	NA	Aa
PC 32:1.1	10602.9	Aa	10190.6	Aa	11579.9	Aa	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab
PC 34:1	NA	Ca	182994.7	Aa	164956.4	Ba	NA	Ba	NA	Bb	177793.5	Aa	NA	Aa	NA	Ab	NA	Ab	NA	Aa	NA	Ab	NA	Ab
PC 34:3	15172.0	Aa	16150.4	Aa	14904.9	Aa	12876.1	Aa	12743.8	Aa	17989.4	Aa	10949.3	Aa	13631.1	Aa	11016.3	Aa	7511.6	Aa	11685.9	Aa	NA	Bb
PC 34:4	NA	Ac	NA	Aa	NA	Aa	3381.1	Ab	NA	Ba	NA	Ba	4241.1	Aa	NA	Ba	NA	Ba	NA	Ac	NA	Aa	NA	Aa
PC 36:1	125583.6	Bc	356415.7	Ab	321727.1	Aa	288319.6	Bb	455164.9	Ab	370886.2	ABa	395660.0	Aab	423902.0	Ab	294220.9	Aa	449527.1	Ba	786434.8	Aa	NA	Cb
PC 36:2	1917986.3	Bb	8089571.4	Ac	7813703.6	Ac	8000228.2	Ba	12925730.1	Ab	11375169.6	ABbc	10836674.5	Ba	15635365.5	Ab	12933043.0	ABb	9572776.3	Ba	20485387.1	Aa	21885026.2	Aa
PC 36:3	NA	Aa	NA	Ab	NA	Ab	NA	Aa	NA	Ab	NA	Ab	NA	Aa	NA	Ab	NA	Ab	NA	Ca	49559.8	Aa	43259.5	Ba
PC 36:3.1	84204.8	Aa	272756.7	Ad	260317.7	Ad	261625.0	Ba	708139.5	Ac	677372.3	Ac	329816.0	Ba	1709558.7	Ab	1414002.0	Ab	240014.5	Ba	2910605.2	Aa	2779678.1	Aa
PC 36:5	4469.3	Aa	3244.6	Aa	4145.2	Aa	2322.8	Ba	NA	Bb	5903.8	Aa	3007.9	Aa	3566.7	Aa	4102.2	Aa	2114.9	ABa	3436.2	Aa	NA	Bb
PC 36:6	NA	Ab	NA	Ab	NA	Ab	2717.5	Aa	1683.7	Aa	2845.8	Aa	NA	Bb	2114.1	Aa	1672.3	Aa	2766.9	Aa	1225.1	Bab	2813.7	Aa
PC 38:2	26750.9	Bb	89341.0	Ab	83336.4	Ac	80182.9	Ba	174927.5	Aa	147377.7	Ab	94991.1	Ba	140826.2	Aa	114456.9	ABbc	77613.4	Ca	144717.9	Ba	205696.3	Aa
PC 38:3.1	2022.2	Aa	NA	Ad	NA	Ac	3035.1	Ba	9075.4	Ac	8185.0	Ab	3620.7	Ba	13765.0	Ab	16082.9	Aa	3206.5	Ca	22943.6	Aa	15220.4	Ba

SI Table 7. (continuation) Relative abundance of lipid of *C. reinhardtii* CC503 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N		0h_3.5N		0h_7N		10h_0N		10h_3.5N		10h_7N		18h_0N		18h_3.5N		18h_7N		36h_0N		36h_3.5N		36h_7N	
PE 32:1	NA	Bc	10781.7	ABb	12395.3	Ac	15308.5	Bb	30680.3	Aa	20829.4	ABbc	25596.7	Bab	25663.8	Ba	42182.7	Aa	32961.2	Aa	23173.6	Aa	29066.9	Ab
PE 32:2	NA	Aa	NA	Ab	NA	Ab	NA	Aa	NA	Ab	NA	Ab	NA	Ba	3816.8	Aa	4496.0	Aa	NA	Aa	NA	Ab	NA	Ab
PE 34:1	23497.8	Ab	81212.4	Ab	70264.5	Ac	112975.2	Ba	212926.1	Aa	146884.0	Bb	172081.0	Aa	176248.6	Aa	228616.4	Aa	180278.1	Aa	150300.6	Aa	154840.6	Ab
PE 34:2	20213.7	Ab	63475.4	Ac	66834.1	Ac	111571.9	Bab	304284.6	Aa	215374.1	Ab	176900.5	Ba	261037.3	Bab	428702.2	Aa	163283.7	Ba	185386.2	Bb	294262.2	Ab
PE 34:3	NA	Ab	3921.3	Ab	3992.7	Ab	7312.4	Ba	13123.6	Aa	11098.5	ABa	10235.4	Ba	11829.9	ABa	14895.5	Aa	8549.9	Aa	12020.8	Aa	NA	Bb
PE 34:4	NA	Ab	NA	Ab	NA	Ac	NA	Bb	1934.2	Aa	1917.1	Ab	1323.5	Ba	2094.7	ABa	3012.5	Aa	NA	Bb	NA	Bb	2809.5	Aab
PE 34:5	NA	Aa	NA	Aa	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Ba	NA	Ba	5174.0	Aa	NA	Aa	NA	Aa	NA	Ab
PE 34:6	6042.8	Ba	10747.3	Ab	9060.1	Ab	3640.0	Bab	15620.5	Aa	16015.0	Aa	3373.7	Bab	6708.7	Ac	5176.8	ABc	1786.0	Bb	NA	Bd	8899.7	Ab
PE 36:1	18320.3	Bb	45069.1	Ab	33971.3	Ab	58186.6	Ba	124174.6	Aa	78825.7	Aa	75255.0	Ba	102775.8	Aa	116439.2	Aa	62541.5	Ba	79216.9	Aa	89642.6	Aa
PE 36:2	386046.4	Ab	1271316.7	Ab	1282271.1	Ab	1382791.5	Bab	4164931.7	Aa	3257907.8	Aa	1812601.5	Ba	3214509.5	Aa	4037547.3	Aa	1060849.5	Bab	1861462.1	Bb	3091429.0	Aa
PE 36:3	NA	Aa	27745.2	Ac	25728.4	Ac	35767.4	Ba	987206.6	Aa	756487.8	Aa	37635.0	Ba	690310.7	Ab	848395.4	Aa	22643.7	Ba	257718.5	ABc	393522.4	Ab
PE 36:3.1	1313.2	Bc	4985.3	Ac	3579.8	Ac	8325.2	Ba	14679.3	Aa	16582.7	Aa	8896.5	Ba	14749.8	Aa	14791.1	Aa	7454.7	Bb	11965.0	Ab	10069.5	Ab
PE 36:4.1	4634.0	Bc	11456.0	Ab	11564.7	Ac	15905.6	Cab	27417.4	Ba	35290.3	Aa	17762.5	Ba	29020.1	Aa	30371.1	Aa	10674.1	Bbc	17350.7	Ab	21385.3	Ab
PE 38:2	117737.6	Ba	427817.1	Abc	387641.5	Ab	200251.8	Ba	829380.1	Aa	754471.9	Aa	238492.8	Ba	536569.1	Ab	696781.4	Aa	116361.4	Ca	290291.6	Bc	619752.1	Aa
PE 38:3	8805.7	Aa	17521.6	Ab	17545.4	Ac	12723.3	Ba	147593.7	Aa	150589.2	Aab	10786.9	Ba	143439.9	Aa	171164.7	Aa	4945.9	Ca	52624.7	Bb	112583.0	Ab
PE 40:1	NA	Bb	23024.6	Aa	NA	Bc	10885.1	Ba	15285.8	Ab	15346.7	Aa	12273.3	Aa	12101.7	Ab	10689.7	Ab	8762.8	Ba	15797.0	Ab	16400.4	Aa
PE 40:2	90963.2	Bb	283290.5	Ab	267134.2	Ab	290126.4	Aa	336806.5	Ab	290504.0	Ab	397160.3	Aa	350755.2	Ab	350837.0	Ab	390261.4	Ba	527059.9	Aa	554993.9	Aa
PE 40:3	14079.8	Aa	16409.3	Aab	17823.9	Ab	6372.9	Cab	24449.9	Ba	39031.2	Aa	6060.6	Bab	13643.4	ABb	19129.6	Ab	3690.3	Bb	NA	Bc	13195.8	Ab
PG 32:0	45228.6	Ac	60859.5	Ab	48493.5	Aab	130954.8	Aa	38023.9	Bb	28812.7	Bb	108061.8	Aab	56822.5	Bb	49429.1	Bab	95308.2	Ab	106674.9	Aa	78375.2	Aa
PG 32:1	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	2707.8	Ba	NA	Cb	4077.7	Aa	4048.4	Aa	2497.6	Bb	NA	Ab
PG 34:2	19951.8	Ac	36611.1	Ac	34132.7	Ac	71722.7	Ab	88442.3	Ab	79326.9	Ac	123752.5	Ba	136226.3	Bab	216754.8	Aa	63698.7	Bbc	148384.0	Aa	148040.7	Ab
PG 34:3	5212.5	Ab	8076.2	Ab	7281.8	Ab	8415.3	Bb	14783.8	Aa	NA	Cc	13846.2	Ba	15363.2	Ba	20952.4	Aa	7467.8	Ab	11588.4	Aab	10855.9	Ab
PG 34:4	38810.0	Aa	88850.6	Aa	71025.1	Ac	92949.9	Aa	166102.8	Aa	184443.9	Abc	66754.4	Ba	162494.5	ABa	236733.9	Ab	53371.4	Ca	162192.5	Ba	790469.3	Aa
PG 36:1	14580.4	Bc	40143.9	Ac	30648.7	Ac	53669.9	Bb	86609.9	Ab	60114.3	Ab	74297.2	Ba	119738.4	Aa	132078.4	Aa	68820.3	Bb	95006.6	Ab	70838.8	Ab
PG 36:2	103971.8	Ab	293320.2	Ac	238703.1	Ac	319428.1	Cab	905185.7	Aab	613740.9	Bb	411599.5	Ba	1054457.2	Aa	1304598.2	Aa	299998.0	Bab	661330.5	Ab	853917.0	Ab
SQDG 32:0	17876129.2	Aa	16360206.3	Aa	16283770.1	Aa	12005000.4	Ab	8752447.8	Bb	10878940.1	ABb	10420566.1	Abc	8000311.4	Bb	6225713.6	Bc	8917879.0	Ac	8421257.9	Ab	9437115.2	Ab
SQDG 32:1	336794.5	Aa	373446.5	Aa	368173.5	Aa	186931.2	Ab	145187.7	Ab	181998.4	Ab	134345.7	Abc	99068.8	Ab	88525.0	Ac	73116.8	Bc	78371.9	Bb	236649.1	Ab
SQDG 32:2	115652.2	Aa	121243.1	ABa	122420.1	Ba	66301.1	Ab	50605.8	ABb	57416.0	Bb	54799.2	Ac	36738.8	ABc	27965.4	Bc	32354.1	Ad	26183.1	ABd	NA	Bd
SQDG 34:0	1002318.3	Aa	1045286.0	Aa	1012088.6	Aa	515413.7	Bb	803684.1	Ab	882470.1	Aab	384550.7	Bbc	691076.9	Ab	699561.0	Ab	248745.8	Ac	401042.9	Ac	367290.7	Ac

SI Table 7. (continuation) Relative abundance of lipid of *C. reinhardtii* CC503 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N		0h_3.5N		0h_7N		10h_0N		10h_3.5N		10h_7N		18h_0N		18h_3.5N		18h_7N		36h_0N		36h_3.5N		36h_7N	
SQDG 34:1	NA	Aa	NA	Aa	NA	Ac	NA	Ba	NA	Ba	2156475.4	Aa	NA	Ba	NA	Ba	1370235.0	Ab	NA	Aa	NA	Aa	NA	Ac
SQDG 34:2	1500374.7	Ba	2025423.1	Aab	1975344.0	Ab	1312220.1	Cab	2397189.8	Ba	3056343.0	Aa	993850.9	Bb	1762206.3	Ab	1503682.0	Ab	445650.9	Cc	1707744.4	Ab	923408.2	Bc
SQDG 34:3	4293796.4	Ba	5505243.9	Aa	5217432.8	ABa	2993091.9	Bb	3264257.7	ABb	4128431.0	Ab	2217176.7	Ab	2542011.0	Ab	2127983.2	Ac	1071683.4	Cc	2203186.2	Bb	4724686.7	Aab
SQDG 34:4	63699.7	Ba	86655.5	Aa	82805.9	ABa	43636.4	Bab	52610.5	Bb	78013.5	Aab	30319.0	Bbc	52805.6	Ab	57690.4	Ab	9292.0	Cc	37227.8	Bb	78096.6	Aab
SQDG 34:5	90562.4	Ba	117277.5	Aa	113486.7	Aa	54143.5	Bb	58334.9	ABb	76770.6	Ab	33210.0	Abc	50192.2	Abc	52594.9	Ac	9327.2	Cc	32507.0	Bc	85887.2	Ab
SQDG 34:6	53475.5	Ba	70636.9	Aa	68698.5	Ab	32305.8	Bb	36295.4	ABb	48006.6	Ac	20051.1	Bb	32783.0	ABb	41123.8	Ac	4911.9	Cc	18410.2	Bc	94924.8	Aa
TAG 42:0	21527.8	Aa	18023.5	Aa	19507.2	Aa	12657.7	Ab	9634.6	Ab	13259.8	Ab	11057.7	Ab	11025.6	Ab	6819.2	Ac	22861.1	Aa	8691.7	Bb	7410.2	Bc
TAG 42:1	26214.0	Aa	19767.1	Aa	21092.3	Aa	17016.6	Ab	11688.0	Ab	16923.9	Aa	16365.6	Ab	12401.6	ABab	7363.5	Bb	30602.6	Aa	12032.3	Bb	8247.4	Bb
TAG 42:2	5155.8	Ab	3814.2	ABa	3295.7	Ba	3053.0	Ac	2339.7	Aab	2128.4	Aab	2371.3	Ac	2310.2	Aab	1440.0	Ab	7730.4	Aa	2086.6	Bb	1509.4	Bb
TAG 44:0	98719.1	Ab	79384.6	Aa	83000.0	Aa	64272.9	Ac	37881.7	Bb	52437.9	ABb	66563.8	Ac	40872.1	Bb	26200.8	Bc	153598.9	Aa	53957.7	Bb	30389.1	Cbc
TAG 44:1	54456.5	Ab	45069.9	Aa	45035.7	Aa	48546.2	Ab	27961.5	Aa	37210.2	Aab	62654.5	Ab	32922.3	Ba	19358.4	Bb	184194.7	Aa	36506.9	Ba	28559.4	Bab
TAG 44:2	37473.6	Aa	30860.1	Aa	29135.5	Aa	20652.2	Ab	14477.0	Ab	22001.1	Aa	19873.6	Ab	15136.2	Ab	9301.2	Ab	45260.1	Aa	14770.2	Bb	10156.4	Bb
TAG 46:0	510899.5	Aa	441152.2	Aa	420053.1	Aa	329683.9	Ab	207505.1	Bb	286579.9	ABb	302935.7	Ab	228151.0	ABb	142463.5	Bc	548158.4	Aa	214141.6	Bb	166522.9	Bc
TAG 46:1	265494.8	Ab	234820.1	Aa	228319.0	Aa	254666.4	Ab	101768.3	Ba	138404.3	ABab	361368.3	Ab	136865.6	Ba	63278.2	Bb	1218569.3	Aa	182009.9	Ba	65351.5	Bb
TAG 46:2	45274.7	Ab	39806.6	Aab	37473.3	Aa	44173.4	Ab	NA	Ab	26367.0	Aa	65046.9	Ab	21927.5	Bab	NA	Ba	450825.7	Aa	65626.8	Ba	14920.9	Ca
TAG 46:2.1	46247.7	Aa	45987.1	Aa	43731.2	Aab	35835.7	ABa	34058.2	Ba	50486.9	Aa	NA	Bb	36321.1	Aa	26485.6	Ac	NA	Bb	28130.5	Aa	27834.9	Abc
TAG 46:3	13870.7	Ab	12166.6	Aa	11474.7	Aa	11359.7	Ab	5275.1	Aa	7762.5	Aa	13388.5	Ab	5413.3	Aa	NA	Aa	152701.2	Aa	15118.2	Ba	2876.8	Ba
TAG 46:3.1	7839.6	Ab	5516.9	Aa	5848.8	Aa	6141.9	Ab	3034.3	Aa	4500.6	Aa	4544.8	Ab	2704.9	Aa	2004.6	Aa	36249.2	Aa	7034.2	Ba	1617.3	Ca
TAG 46:4	NA	Ab	NA	Aa	NA	Aa	1314.5	Ab	NA	Aa	NA	Aa	1519.4	Ab	NA	Aa	NA	Aa	10747.1	Ab	1426.1	Ba	NA	Ba
TAG 48:0	2404175.7	Ab	2101606.1	Aa	1999714.9	Aa	2702692.8	Ab	1081809.9	Bb	1439723.7	Bab	2983159.5	Ab	1130772.7	Bb	720788.9	Bb	6919572.5	Aa	2247342.1	Ba	768472.4	Cb
TAG 48:1	1595155.3	Ab	1380595.4	Aa	1287700.2	Aa	1883833.0	Ab	786792.4	Ba	1118326.5	Ba	2291573.9	Ab	905544.6	Ba	534741.1	Ba	5516827.8	Aa	1295309.7	Ba	610374.2	Ba
TAG 48:2	376912.1	Aa	NA	Bc	NA	Bc	NA	Cb	190264.9	Bb	251672.9	Aa	350611.7	Aa	NA	Bc	NA	Bc	NA	Cb	284345.6	Aa	134351.4	Bb
TAG 48:3	NA	Ab	NA	Ab	NA	Aa	NA	Ab	NA	Ab	NA	Aa	145982.3	Aa	NA	Bb	NA	Ba	NA	Bb	112794.0	Aa	NA	Ba
TAG 48:4	NA	Aa	NA	Aa	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Ba	NA	Ba	1117.4	Aa	NA	Ba	NA	Ba	1111.5	Aa
TAG 48:5	NA	Ad	NA	Ab	NA	Aa	1560.6	Ac	NA	Bb	NA	Ba	3050.2	Ab	NA	Bb	NA	Ba	27188.3	Aa	2253.6	Ba	NA	Ca
TAG 48:6	NA	Ac	NA	Aa	NA	Aa	NA	Ac	NA	Aa	NA	Aa	1251.6	Ab	NA	Ba	NA	Ba	10664.0	Aa	NA	Ba	NA	Ba
TAG 48:7	NA	Ac	NA	Aa	NA	Aa	NA	Ac	NA	Aa	NA	Aa	1816.5	Ab	NA	Ba	NA	Ba	5110.7	Aa	NA	Ba	NA	Ba
TAG 50:0	4541793.1	Aa	3804987.5	ABa	3650994.6	Ba	3223058.0	Ab	2152347.7	Bb	2819326.8	ABa	2973449.9	Ab	2237162.1	ABb	1426064.5	Bb	3502091.4	Ab	1968546.7	ABb	1634235.9	Bb
TAG 50:1	8512754.8	Ac	7222758.8	Ab	6906568.4	Aa	15697932.2	Ab	4237448.5	Bb	5429747.2	Ba	20911116.5	Ab	4753778.1	Bb	2710726.2	Ba	69454664.1	Aa	16481514.0	Ba	3110969.1	Ca

SI Table 7. (continuation) Relative abundance of lipid of *C. reinhardtii* CC503 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
TAG 50:2	3520776.7 Ac	3017658.5 Ab	2873683.1 Aa	6420261.5 Abc	1879863.0 Ab	2542259.2 Aa	10283477.5Ab	2025538.6 Bb	1213082.3 Ba	58109002.7Aa	8671310.8 Ba	1403458.4 Ca
TAG 50:3	NA Ac	351799.7 Aa	NA Aa	1867764.9 Abc	NA Aa	NA Aa	3777098.5 Ab	NA Ba	116688.5 Ba	36263918.7Aa	3733264.9 Ba	0.0 Ca
TAG 50:4	NA Ab	NA Aa	NA Aa	370062.2 Ab	NA Aa	NA Aa	1055632.0 Ab	NA Aa	NA Aa	19889610.3Aa	1137964.6 Ba	0.0 Ba
TAG 50:5	9042.7 Ab	7616.7 Aa	8540.6 Aa	85672.8 Ab	3630.3 Aa	6865.5 Aa	228075.1 Ab	4515.9 Aa	2298.4 Aa	6764486.6 Aa	249178.4 Ba	2145.6 Ba
TAG 50:6.1	4857.3 Ab	3357.0 Aa	4293.1 Aa	22884.3 Ab	2415.4 Aa	3317.3 Aa	53173.8 Ab	2088.4 Aa	1039.1 Aa	1850130.9 Aa	47686.3 Ba	1034.3 Ba
TAG 50:7	NA Ab	NA Aa	NA Aa	2749.1 Ab	NA Aa	NA Aa	5920.0 Ab	NA Aa	NA Aa	93829.2 Aa	3761.9 Ba	0.0 Ba
TAG 50:8	NA Ab	NA Aa	NA Aa	1454.4 Ab	NA Aa	NA Aa	2898.6 Ab	NA Aa	NA Aa	34643.7 Aa	1958.4 Ba	NA Ba
TAG 50:9	NA Ab	NA Aa	NA Aa	NA Ab	NA Aa	NA Aa	NA Ab	NA Aa	NA Aa	12366.6 Aa	NA Ba	NA Ba
TAG 52:0	4095332.8 Aa	3384494.5 Ba	3175951.1 Ba	2590011.3 Ab	2080909.7 Bb	2640001.0 Bb	2208371.8 Ac	2060938.3 Bc	1305978.6 Bc	1976069.2 Ac	1623267.6 Bc	1509985.8 Bc
TAG 52:1	11772850.3Ab	9842391.0 Aa	9483122.8 Aa	10815901.2Ab	5726456.9 Bb	7716457.1 ABab	12186790.4Ab	6501865.4 Bab	3854790.2 Bc	22488178.3Aa	6599602.5 Bab	4423322.9 Bbc
TAG 52:2	17801553.2Ab	14622574.9Aa	14047293.8Aa	18685626.0Ab	9328425.9 Ba	12029177.2Bab	20751788.9Ab	10091213.3Ba	6115149.3 Bb	60816760.6Aa	15193486.5Ba	6987378.5 Cb
TAG 52:3	4128804.0 Ac	3462381.6 Ab	3417929.1 Aa	7833197.7 Abc	2176314.4 Bb	2977256.8 Ba	11808270.2Ab	2265163.3 Bb	1443334.3 Ba	59156415.7Aa	8776396.1 Bb	1612815.1 Ca
TAG 52:4	2010270.5 Ab	1583432.9 Aa	1547266.8 Aa	4880189.4 Ab	1008846.1 Aa	1403909.8 Aa	7487030.1 Ab	1060886.8 Ba	656976.9 Ba	49710176.8Aa	5593150.9 Ba	754155.2 Ba
TAG 52:5.1	66045.1 Ab	49026.8 Aa	49604.4 Aa	412595.8 Ab	21762.0 Aa	38394.4 Aa	963241.9 Ab	20454.6 Aa	10291.9 Aa	14168121.8Aa	1098312.0 Ba	NA Ba
TAG 52:6	41159.9 Ab	NA Aa	35394.3 Aa	220386.7 Ab	15170.2 Aa	27720.1 Aa	452060.6 Ab	13517.5 Aa	6422.5 Aa	9704978.9 Aa	333569.9 Ba	7687.9 Ba
TAG 52:6.1	29019.8 Ab	22339.7 Aa	22810.6 Aa	202387.0 Ab	10089.1 Aa	17454.6 Aa	476961.8 Ab	9385.4 Aa	4353.0 Aa	8775173.2 Aa	517012.5 Ba	6073.1 Ba
TAG 52:7	6916.8 Ab	6927.6 Aa	7925.8 Aa	37700.4 Ab	3907.4 Aa	6308.9 Aa	78997.7 Ab	3716.6 Aa	2224.2 Aa	2557698.9 Aa	60914.5 Ba	2357.0 Ba
TAG 52:8	4042.1 Ab	1862.1 Aa	2344.0 Aa	10271.9 Ab	1729.1 Aa	2839.8 Aa	21484.5 Ab	1548.2 Aa	959.0 Aa	625327.5 Aa	13822.4 Ba	NA Ba
TAG 52:9	3032.6 Ab	3146.7 Aa	2918.3 Aa	2436.4 Ab	2189.9 Aa	2851.3 Aa	4004.7 Ab	1965.3 Aa	NA Aa	107962.3 Aa	2179.7 Ba	NA Ba
TAG 54:0	1213854.7 Aa	1027911.1 ABa	958074.3 Ba	771977.0 Ab	649907.5 ABb	785931.7 Bb	625291.8 Ac	637178.4 ABc	404825.7 Bc	482574.1 Ac	478347.5 ABc	459562.6 Bc
TAG 54:1	5146660.1 Aa	4328964.1 Ba	4013610.9 Ba	3495873.1 Ab	2648183.4 Bb	3430016.7 Bb	3128460.7 Ab	2825266.5 Bb	1795592.2 Bb	3588668.7 Ab	2313759.5 Bb	2110739.0 Bb
TAG 54:2	9199894.3 Aa	7731148.7 ABa	7198463.9 Ba	6438124.7 Ab	4764322.3 Ab	6267172.9 Aa	5556935.3 Ab	5051845.1 ABb	3314953.4 Bb	7247613.7 Aab	4535635.1 Bb	3778297.1 Bb
TAG 54:3	8719225.3 Aa	6714229.0 Ba	6847032.4 Ba	5838901.3 Ab	4208515.4 Ab	5584338.7 Aa	4766702.0 Ab	4546618.3 Ab	2932317.9 Ab	6662350.6 Ab	4092327.1 Bb	3356483.3 Bb
TAG 54:4	5024212.1 Aa	3963792.3 Aa	3946562.2 Aa	3711224.0 Ab	2504368.6 Bb	3371619.3 ABa	3295928.3 Ab	2710466.0 ABb	1722608.0 Bb	6056640.6 Aa	2727899.1 Bb	1981165.3 Bb
TAG 54:5	3280300.1 Ab	2643358.5 Aa	2551488.2 Aa	2989076.6 Ab	1773748.9 Ba	2391987.0 ABa	2798567.2 Ab	1857561.0 Ba	1150212.0 Bb	5567632.6 Aa	2151043.3 Ba	1348062.1 Bb
TAG 54:6	1830880.1 Ab	1471584.9 Aa	1386018.2 Aa	1372439.2 Ab	952140.3 Aa	1226466.5 Aab	1493260.2 Ab	981622.9 Ba	633091.5 Bc	3413108.1 Aa	1148507.3 Ba	754272.5 Bbc
TAG 54:7	124389.1 Ab	97759.2 Aa	92978.8 Aa	148469.4 Ab	58149.7 Aa	86189.2 Aa	178650.1 Ab	58449.9 Aa	35732.5 Aa	1168465.5 Aa	123830.8 Ba	42342.5 Ba
TAG 54:8	24417.0 Ab	16607.5 Aa	16432.3 Aa	29365.7 Ab	9789.0 Aa	15191.3 Aa	38180.5 Ab	8889.9 Aa	4477.4 Aa	290609.4 Aa	23179.0 Ba	4871.3 Ba
TAG 54:9	10429.8 Ab	7912.8 Aa	7080.5 Aa	7486.0 Ab	3313.2 Aab	4957.2 Aab	8949.7 Ab	2625.2 Bb	1087.8 Bb	42701.3 Aa	NA Bb	1366.5 Bb

SI Table 7. (continuation) Relative abundance of lipid of *C. reinhardtii* CC503 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
TAG 56:0	79335.9 Aa	64823.9 Ba	63485.3 Ba	55720.9 Ab	40578.5 Bb	54018.4 Bb	49198.0 Ab	40682.6 Bb	28470.1 Bb	53918.3 Ab	35788.6 Bb	29947.6 Bb
TAG 56:1	183759.3 Ab	152856.2 Aa	153726.8 Aa	154074.9 Ab	91703.1 Bb	119732.1 ABa	174590.4 Ab	96577.9 Bb	60932.4 Bb	356144.2 Aa	108612.6 Bab	68709.5 Bb
TAG 56:2	441394.7 Aa	347296.1 Aa	337559.8 Aa	311699.7 Ab	208704.2 Ab	285373.0 Aa	310143.7 Ab	238193.0 ABab	145952.1 Bb	490870.8 Aa	214503.7 Bb	158043.5 Bb
TAG 56:3	367566.4 Aa	283849.5 Ba	274355.3 Ba	254987.4 Ab	184982.4 Bb	252880.6 Bb	231041.1 Ab	188993.2 Bb	121032.6 Bb	302322.4 Ab	184619.3 Bb	142505.3 Bb
TAG 56:4	275806.7 Aa	213483.6 Aa	209720.6 Aa	191763.0 Abc	138575.9 Aa	189871.2 Aa	170794.4 Ac	143834.0 ABa	90559.9 Bb	263291.6 Aab	140776.8 Ba	110737.0 Bb
TAG 56:5	93558.6 Ab	69136.8 Aa	70308.1 Aa	80627.1 Ab	44639.3 Ba	67253.4 ABa	78676.0 Ab	48588.0 ABa	29543.5 Bb	215822.9 Aa	73038.4 Ba	34782.6 Cab
TAG 56:6	21888.9 Ab	13896.6 Aa	14548.2 Aa	17868.1 Ab	8666.1 Aa	15539.2 Aa	22312.0 Ab	9428.9 ABa	5839.0 Ba	106329.2 Aa	23804.3 Ba	7662.1 Ca
TAG 56:7	6053.8 Ab	4705.4 Aa	4600.3 Aa	4999.8 Ab	1875.4 Aab	4070.5 Aab	5531.4 Ab	NA Bb	NA Bb	29051.6 Aa	5479.5 Ba	1595.6 Cab
TAG 58:0	28585.9 Ab	23204.7 Aa	22342.0 Aa	21329.7 Ab	15518.7 Ab	20549.0 Aa	22927.2 Ab	15665.1 Bb	10053.6 Bb	39656.0 Aa	16311.2 Bab	11360.3 Bb
TAG 58:1	57701.1 Aa	43109.3 Aab	44283.5 Aa	69260.9 Abc	27215.4 Bb	39064.8 Ba	96363.6 Ab	31088.1 Bab	20597.3 Ba	268043.3 Aa	59838.8 Ba	22472.8 Ca
TAG 58:2	139704.1 Ab	106695.9 Aa	99784.9 Aa	110550.3 Ab	71502.3 Aa	96635.0 Aab	130333.5 Ab	75774.6 Ba	48559.0 Bc	268771.3 Aa	81196.3 Ba	52096.0 Bbc
TAG 58:3	146377.3 Aa	119085.8 ABa	105389.8 Ba	101966.8 Ab	77568.6 Ab	100926.9 Aa	87056.1 Ab	80401.9 ABb	51738.5 Bb	157877.2 Aa	66746.1 Bb	58761.3 Bb
TAG 58:4	160756.6 Aa	125389.6 Ba	115907.8 Ba	108522.4 Ab	87108.2 Bb	115609.9 Bb	92928.2 Abc	92435.3 Bbc	60413.6 Bbc	87690.6 Ac	72323.7 Bc	64813.4 Bc
TAG 58:5	NA Ac	NA Aa	NA Aa	13801.5 Ab	NA Ba	NA Ba	NA Ac	NA Aa	NA Aa	64050.2 Aa	NA Ba	NA Ba
TAG 58:6	NA Ac	NA Aa	NA Ab	NA Bc	NA Ba	12997.3 Aa	8891.3 Ab	NA Ba	NA Bb	28422.0 Aa	NA Ba	NA Bb
TAG 60:0	10387.3 Aa	8100.6 Ba	10975.0 Aa	6296.7 Ab	4949.8 Ab	7134.9 Ab	5564.3 Ab	5268.9 Ab	3422.7 Ac	6163.8 Ab	4172.2 Ab	3926.0 Ac
TAG 60:1	19860.7 Ac	15426.6 Ab	15673.2 Aa	37740.8 Ac	9869.2 Ab	15338.5 Aa	74089.8 Ab	11144.5 Bb	6549.3 Ba	336539.0 Aa	50025.7 Ba	7940.2 Ca
TAG 60:2	48570.9 Ab	36976.6 Aa	36066.1 Aa	49381.8 Ab	25832.9 Aa	35032.6 Aa	78156.0 Ab	27203.4 Ba	17354.9 Ba	340553.8 Aa	48478.9 Ba	19284.7 Ba
TAG 60:3	43677.7 Ab	36004.4 Aa	33489.5 Aa	37105.0 Ab	25173.9 Aa	30940.2 Aa	43990.2 Ab	25441.4 ABa	16372.3 Ba	201032.9 Aa	29668.3 Ba	18169.8 Ba
TAG 60:4	49805.3 Aa	40221.3 ABa	35703.5 Ba	35247.4 Ab	27875.8 Aab	34528.0 Aa	29332.2 Ab	29355.3 Aab	18533.9 Ab	NA Bc	23260.4 Ab	20155.7 Ab
TAG 60:5	5594.1 Aa	4501.1 Aa	4348.7 Aa	4586.6 Aa	2766.5 Bb	3618.3 ABab	5145.4 Aa	3163.3 Bab	1904.2 Bb	NA Bb	2874.2 Aab	1925.3 Ab
TAG 60:5.1	NA Ab	NA Aa	NA Aa	3089.4 Ab	NA Aa	NA Aa	4971.7 Ab	NA Aa	NA Aa	56917.5 Aa	3280.6 Ba	NA Ba
TAG 60:6	14026.5 Ac	20060.9 Ab	17584.9 Ab	48079.3 Aab	19328.0 Bb	26819.1 ABb	67333.6 Aa	60609.6 Aa	22978.9 Bb	26445.6 Bbc	33568.0 Bab	85480.4 Aa
FA 16:0	23890500.7Aa	17714052.0Ba	17161412.5Ba	20934553.4Aa	8192391.0 Bb	10973252.7Bb	18461051.8Aab	10322784.3Bb	4699738.6 Cc	14572431.8Ab	11769561.6Aab	5573305.7 Bbc
FA 16:1	1991151.2 Aa	NA Bc	NA Bb	2020068.0 Aa	595380.4 Bb	837219.2 Ba	1687284.0 Aa	691492.3 Bab	295318.8 Bab	1491348.2 Aa	1248882.1 Aa	163365.6 Bb
FA 16:2	2879934.0 Aa	2510230.9 Aa	2336779.1 Aa	2444348.6 Aab	1929013.0 Aab	2454426.9 Aa	2043788.6 Aab	1044704.3 Bc	443907.6 Bb	1819515.5 Ab	1319192.2 Abc	304508.7 Bb
FA 16:3	1511169.0 Aa	1220286.3 Aab	1183045.4 Ab	2084414.9 Aa	1762256.6 Aa	2159545.6 Aa	2157636.2 Aa	1548467.1 Aab	780843.4 Bbc	2041842.8 Aa	966091.6 Bb	388644.5 Bc
FA 16:4	52597.4 Aa	39762.9 Aa	41753.5 Aa	49523.1 Aa	17500.3 Bb	25928.5 Bb	42352.1 Aa	16581.3 Bb	7195.7 Bc	53157.8 Aa	14715.3 Bb	4475.2 Bc
FA 16:4.1	3882263.6 Bab	6687494.9 Aab	6534915.3 Ab	4573746.1 Ba	6215936.4 Bab	9126578.7 Aa	4102283.7 Bab	6747232.2 Aa	4947691.2 ABb	1796769.7 Cb	4192151.6 Bb	9168353.8 Aa

SI Table 7. (continuation) Relative abundance of lipid of *C. reinhardtii* CC503 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
FA 18:0	14788595.0Aa	11563701.0Ba	12536164.5Ba	8630916.2 Ab	5740262.3 Bb	7768917.2 Bb	7335283.9 Ac	6261083.9 Bc	3159366.5 Bc	5858367.0 Ad	3036257.3 Bd	2773854.0 Bd
FA 18:1	84501152.5Aa	64370972.8Ba	61062507.9Ba	41869863.6Ab	25752883.6Bb	35893372.5ABb	31730444.8Abc	29305750.3Ab	12741830.5Bc	26566481.4Ac	19669789.2ABb	11478436.1Bc
FA 18:2	39679594.8Aa	34361947.0Aa	33342348.4Aa	34299582.4Aab	28967485.1Aab	39711733.9Aa	30736064.3Aab	24918587.2Aab	12242241.3Bb	23534650.1Ab	19309349.4ABa	9524973.8 Bb
FA 18:3	70480000.3Aa	66576558.3Aa	62832350.5Aa	43117087.3Bb	45913497.4ABb	60856534.3Aa	37195546.2ABbc	40525626.2Ab	21664465.1Bb	25131477.5Ac	21583346.6Ac	35513660.0Ab
FA 20:0	326725.1 Aa	286173.2 Aa	298301.2 Aa	347130.2 Aa	187937.3 Bab	207828.2 Ba	370747.0 Aa	157791.6 Bb	67231.1 Bb	349856.8 Aa	170743.2 Bb	38270.7 Cb
FA 20:1	1346428.3 Aa	1017039.4 Ba	997263.3 Ba	862495.8 ABb	654280.7 Bb	971576.1 Aa	720116.7 Abc	679080.8 Ab	328422.7 Bb	450623.8 ABc	621725.2 Ab	225712.9 Bb
FA 20:3	84036.9 Aa	81271.4 Aa	75895.5 Aa	58644.8 Ab	44977.0 Ab	62239.2 Aa	56797.5 Abc	46513.6 Ab	21009.4 Bb	35554.2 Bc	35229.2 Bb	57440.8 Aa
FA 22:0	86512.6 Ab	98510.6 Aa	120701.4 Aa	119930.9 Aab	65506.5 Ba	86412.4 ABa	132283.6 Aa	65889.8 Ba	28173.2 Bb	125592.4 Aab	73989.8 Ba	28397.9 Cb
FA 22:1	80941.0 Aa	63293.2 Ba	59911.0 Ba	38971.4 Ab	30444.7 Ab	41781.8 Ab	31704.2 Ab	32991.2 Ab	19726.2 Ac	15455.9 Ac	25149.5 Ab	17702.3 Ac
FA 24:1	7897.9 Aa	6498.3 Aa	5824.6 Aab	7399.5 Aa	5827.1 Aab	7899.7 Aa	7090.5 Aa	6473.1 Aa	3627.1 Bbc	3512.2 Ab	3652.1 Ab	2563.7 Ac
FA 26:0	349147.0 Aa	311776.6 Ba	312163.4 Ba	174487.6 Abc	128317.3 Bbc	145749.7 Bbc	218112.5 Ab	182589.3 Bb	96424.9 Bb	155931.1 Ac	107598.0 Bc	94556.4 Bc
FA 28:0	58690.8 Ca	120425.7 Ba	183539.4 Aa	31862.9 Bab	31451.0 Bb	72948.6 Ab	18829.4 Ab	34368.3 Ab	21425.6 Ac	34167.3 Aab	13490.6 Ab	20827.7 Ac
FA 30:0	10053.5 Bb	22550.7 Ba	45406.7 Aa	15223.9 ABab	10404.1 Ba	27554.4 Ab	4502.5 Ab	14538.8 Aa	12259.9 Ab	27643.7 Aa	5855.8 Ba	11675.0 Bb
FA 30:1	3758.2 Aa	4357.1 Aa	4165.3 Aa	1551.6 Bb	1815.2 Bb	3807.3 Aa	1898.7 Ab	1615.7 ABb	774.2 Bb	1084.3 Ab	918.3 Ab	925.1 Ab

SI Table 8. Relative abundance of lipid of *Chlamydomonas* sp. BR020 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N		0h_3.5N		0h_7N		10h_0N		10h_3.5N		10h_7N		18h_0N		18h_3.5N		18h_7N		36h_0N		36h_3.5N		36h_7N	
DAG 34:1	59601.8	Ab	54124.4	Ab	65866.0	Abc	131629.6	Aa	143414.3	Aa	129867.2	Aa	129671.6	Aa	74057.7	Bb	85187.1	Bb	NA	Cc	169760.3	Aa	40916.6	Bc
DAG 34:2	61042.8	Bb	68380.4	Bb	116098.6	Aa	69180.2	Ca	157876.3	Aa	119359.6	Ba	75967.7	Aa	45076.7	Ab	47679.7	Ab	119830.4	Aa	64013.3	Bb	27721.0	Cb
DAG 34:3	119331.4	Bb	126204.5	Bbc	262585.7	Aa	191756.7	Ba	284928.0	Aa	NA	Cc	173343.6	Aab	73297.5	Bc	90293.5	Bb	204174.0	Aa	151841.4	Ab	26873.6	Bbc
DAG 34:4	NA	Ac	NA	Ad	NA	Ab	200270.5	Bb	450016.7	Aa	NA	Cb	220004.0	Aab	98618.7	Bc	119845.0	Ba	296935.2	Aa	213956.8	Ab	NA	Bb
DAG 34:5	288985.0	Ba	229177.7	Bb	547127.2	Aa	325534.9	Aa	NA	Bc	NA	Bb	NA	Bb	256551.5	Ab	NA	Bb	NA	Bb	398176.4	Aa	51903.3	Bb
DAG 34:6	148342.7	Ab	98392.9	Ab	341324.8	Ab	629119.2	Ba	1667651.6	Aa	1365924.3	Aa	725481.4	Aa	273194.8	Bb	417573.8	ABb	961456.5	Aa	418098.7	Bb	80007.6	Bb
DAG 36:1	8349.7	Aa	8146.9	Aa	8951.6	Aa	10130.8	Aa	7875.4	ABa	5262.8	Bb	8457.8	Aa	4666.2	Bb	4574.9	Bbc	11079.7	Aa	6056.1	Bab	2157.3	Cc
DAG 36:2	148239.3	Ac	132537.7	Ab	169195.0	Aab	278634.3	Ab	309806.2	Aa	253875.6	Aa	350636.3	Ab	188273.7	Bb	214445.9	Bab	501722.2	Aa	360584.7	Ba	137558.7	Cb
DAG 36:3	227471.3	Ab	176645.7	Ab	331661.0	Aab	419506.0	Aa	512928.9	Aa	429255.1	Aa	456886.6	Aa	229924.7	Bb	249313.4	Bbc	544281.9	Aa	582779.0	Aa	93633.3	Bc
DAG 36:4	NA	Ad	NA	Ac	NA	Ab	245512.5	Ac	NA	Bc	NA	Bb	370213.9	Ab	151276.0	Bb	162794.2	Ba	564057.0	Aa	385905.6	Ba	78799.1	Cab
DAG 36:5	261006.2	Bb	343757.3	Ba	451503.7	Aa	NA	Ac	NA	Ab	NA	Ac	304178.9	Aab	NA	Cb	190270.9	Bb	374295.1	Aa	288807.5	Aa	60016.9	Bc
DAG 36:6	90639.7	Bb	93301.7	Bb	262529.3	Ab	185294.4	Bab	619244.9	Aa	491127.4	Aa	215047.4	Aab	140191.7	Ab	180031.1	Abc	235240.2	Aa	176288.6	ABb	47867.9	Bc
DGDG 32:0	85291.6	Ba	83815.6	Ba	108305.0	Aa	60549.8	ABb	69735.6	Ab	54016.1	Bb	45502.2	Ac	37752.9	Ac	35270.6	Ac	59165.3	Ab	39538.5	Bc	29587.3	Bc
DGDG 32:1	39212.3	Ba	37055.9	Ba	45781.0	Aa	15478.4	Bb	24260.1	Ab	19661.0	Bb	7959.4	Bc	12938.1	Ac	11714.8	ABc	7822.2	ABc	4819.0	Bd	10269.5	Ac
DGDG 32:2	147545.9	Ba	142138.1	Ba	190815.4	Aa	61784.0	Bb	88355.6	Ab	70849.0	ABb	41223.2	Ac	36445.2	Ac	31890.0	Ac	34447.4	Ac	36617.5	Ac	45133.0	Ac
DGDG 32:3	NA	Bc	NA	Bb	383920.6	Aa	125665.2	Ba	158160.2	Aa	NA	Cc	NA	Ac	NA	Ab	NA	Ac	43061.0	Bb	NA	Cb	156842.8	Ab
DGDG 32:3.1	53016.2	Aab	46020.3	Ac	64040.6	Ab	70735.7	Ca	129507.9	Aa	102445.8	Ba	49345.5	Bb	69836.4	Ab	67023.7	ABb	56254.6	Aab	24620.5	Bd	73214.3	Ab
DGDG 34:0	135483.0	ABa	130883.9	Ba	148655.7	Aa	50510.5	Bb	72243.1	Ab	57534.0	Bb	24958.9	Bc	50751.2	Ac	44149.6	Abc	18771.8	ABc	10603.1	Bd	31007.6	Ac
DGDG 34:1	2776765.9	Aa	2939726.2	Aa	2903640.6	Aa	1514724.0	Cb	2357203.0	Ab	2096243.3	Bb	1132252.1	Bc	1862299.2	Ac	1768520.8	Ac	843259.1	Bd	982047.2	Bd	1423300.4	Ad
DGDG 34:2	4535439.2	Aa	4798274.0	Aa	4800668.7	Aa	2182533.3	Bb	3831575.4	Ab	3482459.7	Ab	1263199.6	Bc	2644475.8	Ac	2458962.8	Ac	779817.7	Bc	834627.3	Bd	1589194.7	Ad
DGDG 34:3	2024259.0	Aab	2030726.3	Ac	2317443.5	Ab	2169394.9	Ba	3803849.0	Aa	3496918.1	Aa	1620118.6	Bbc	2817823.0	Ab	2725719.3	Ab	1196144.0	Bc	965739.7	Bd	2431092.9	Ab
DGDG 34:4	4883891.3	Aa	5318388.9	Aa	5271385.3	Aa	2036648.7	Bb	3500500.2	Ab	3121836.5	Ab	703674.8	Bc	2064616.7	Ac	1896959.3	Ac	312629.2	Bc	703897.3	ABd	1111728.3	Ad
DGDG 34:5	5583170.1	Aa	5881012.6	Aa	6086048.1	Aa	3911570.7	Bb	6037475.8	Aa	5482973.4	Aa	2963763.0	Bc	4176059.4	Ab	4228664.9	Ab	1775799.7	Cd	2682717.9	Bc	4020250.8	Ab
DGDG 34:6	5899517.5	Aa	6024223.3	Aab	6296180.4	Aa	4352941.5	Bb	6677870.7	Aa	6268790.5	Aa	3837500.1	Bb	4960678.1	Abc	5031174.5	Ab	2648223.2	Cc	3943925.0	Bc	5706928.0	Aab
DGDG 36:2	205097.5	Ba	179470.3	Ca	269019.5	Aa	72806.0	Cb	133529.0	Ab	109147.4	Bb	32444.2	Bc	78561.8	Ac	71996.6	Ac	11906.2	Bc	16360.9	ABd	35996.3	Ad
DGDG 36:3	203201.2	Ba	172634.2	Ca	277840.8	Aa	52455.3	Bb	137251.9	Ab	116999.8	Ab	15684.3	Bc	110395.4	Ab	96315.9	Ab	NA	Bc	28787.5	Ac	NA	Bc
DGDG 36:4	1556609.2	Ba	1537496.8	Aa	1835664.2	Aa	256228.7	Bb	474587.3	Ab	358901.7	ABc	52127.2	Bc	263881.5	Ac	222935.3	Ad	NA	Bc	50998.2	Bd	577123.9	Ab
DGDG 36:5	2797137.8	Aa	2894936.0	Aa	2976634.4	Aa	1059209.4	Bb	2024629.4	Ab	1773261.8	Ab	354566.0	Bc	1175063.3	Ac	1073464.3	Ac	62785.7	Bc	212088.7	Bd	1375943.8	Ac
DGDG 36:6	2818138.9	Ba	2703786.0	Bb	3168652.6	Aa	1877100.3	Bb	3270548.9	Aa	3027284.4	Aa	1085359.4	Bc	2256781.7	Ac	2151720.6	Ab	381472.1	Bd	454003.4	Bd	2226940.6	Ab

SI Table 8. (continuation) Relative abundance of lipid of *Chlamydomonas* sp. BR020 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N												
LysoPC 16:0	33211.8	ABb	21228.7	Bc	50182.8	Aa	42444.1	Bb	86087.3	Aa	60627.4	Ba	57102.9	Ab	60330.4	Aab	50624.6	Aa	173949.0	Aa	57212.3	Bb	75521.1	Ba
LysoPC 16:0.1	2701.0	Bb	1969.5	Bc	5002.2	Aa	3547.2	Bb	8921.6	Aa	5573.3	Ba	4738.0	Ab	5509.5	Ab	4580.0	Aa	13348.5	Aa	5484.3	Bb	6219.0	Ba
LysoPC 16:2	16874.4	Aa	10025.6	Ac	37838.4	Ac	28087.8	Ba	98485.4	Ab	79545.9	Ab	41512.1	Ba	92540.9	Ab	93749.2	Ab	29785.1	Ca	153481.9	Ba	193075.2	Aa
LysoPC 16:3	7796.9	Aa	4367.5	Ac	18222.3	Ac	17593.7	Ba	73629.0	Ab	58420.9	ABbc	33467.0	Ba	88987.8	Ab	95030.8	Ab	22539.3	Ca	177442.8	Ba	294598.6	Aa
LysoPC 18:2	56903.9	Aa	31879.7	Ab	96608.5	Ac	111116.1	Ba	683432.6	Aa	521057.7	Ab	160645.4	Ba	569253.2	Aa	576993.9	Ab	115303.6	Ca	628113.3	Ba	1812148.7	Aa
LysoPC 18:3	23300.5	Aa	9961.4	Ab	42456.1	Ac	41055.5	Ba	240347.6	Aa	191777.5	ABbc	66490.6	Aa	240740.2	Aa	243323.1	Ab	48672.3	Ca	290542.9	Ba	989661.6	Aa
MGDG 34:1	424980.3	Ba	445793.8	ABa	494679.6	Aa	75442.0	Bb	347374.1	Ab	285212.4	Ab	47067.7	Bb	229045.8	Ac	224455.2	Abc	12807.1	Bb	44213.4	Bd	171506.8	Ac
MGDG 34:2	521578.6	Ba	553887.6	Aa	596274.1	Aa	26309.7	Bb	97455.2	Ab	77732.2	Ab	13806.6	Bb	78670.3	Ab	89670.4	Ab	4943.2	Bc	18218.5	Ac	43483.2	Ac
MGDG 34:2.1	396287.0	Aa	455476.6	Aa	462701.9	Aa	45676.2	Bb	528589.5	Aa	470569.0	Aa	40930.6	Bb	340416.0	Ab	371331.7	Aa	7269.8	Bb	52464.4	Bc	388023.9	Aa
MGDG 34:3	5767.8	Ba	6595.5	Ba	8785.5	Aa	NA	Cb	8678.8	Aa	6039.1	Bb	NA	Bb	6333.6	Aa	6523.0	Aab	NA	Bb	NA	Bb	7566.3	Aab
MGDG 34:4	1721801.6	Ba	2165609.6	Aa	1758982.7	Ba	91731.9	Bb	983245.9	Ab	939813.9	Ab	113224.3	Bb	1015216.0	Ab	1117089.7	Ab	16320.0	Bb	184596.5	Bc	1895818.8	Aa
MGDG 34:5	1581538.6	Aa	1938060.6	Aa	1643056.5	Ab	216301.3	Bb	1635914.8	Aa	1595646.5	Ab	191173.2	Bb	1538836.6	Aa	1688022.5	Ab	30842.0	Bb	353677.0	Bb	3106367.1	Aa
MGDG 36:5	233851.1	Aa	283888.3	Aa	280027.1	Ab	NA	Bb	223304.4	Aa	182293.7	Ab	0.0	Bb	242111.2	Aa	249558.3	Ab	NA	Bb	NA	Bb	1098709.1	Aa
MGDG 36:6	181343.0	Aa	228454.6	Aa	222222.7	Ab	14659.1	Ba	197248.0	Aab	185505.0	Ab	19577.3	Ba	238877.1	Aa	288154.7	Ab	1342.5	Ba	16197.5	Bb	1802619.4	Aa
PC 32:0	8286.9	Bb	8077.0	Bab	12029.2	Aa	10955.4	Aa	8929.4	Ba	7922.0	Bb	7844.4	Ab	6671.9	Ab	7068.2	Abc	12815.2	Aa	7429.1	Bab	5474.2	Cc
PC 32:1	35225.6	Bb	30595.1	Bb	45638.3	Aa	38819.3	Bb	48520.8	Aa	48264.8	ABa	31971.4	Ab	32727.1	Ab	34463.0	Ab	55121.5	Aa	36022.3	Bb	50443.5	Aa
PC 32:1.1	23583.3	Ab	21942.8	Ab	25804.7	Ab	24260.2	Bb	35672.5	Aa	29363.3	ABb	22310.0	Ab	22798.1	Ab	22097.7	Ab	38409.7	Aa	20831.7	Bb	44942.1	Aa
PC 32:2	126783.6	Ab	64723.7	Ac	190808.2	Ac	216048.1	Bb	546630.5	Aa	439760.0	Ab	230771.8	Aab	361088.4	Ab	364149.4	Ab	385548.5	Ba	318773.5	Bb	825508.1	Aa
PC 32:3	118861.1	Aa	61828.9	Ac	187712.6	Ac	133754.4	Ba	494211.2	Aa	399637.6	Ab	143474.3	Ba	320965.7	Ab	346402.0	Abc	216652.7	Ca	386769.5	Bab	1151604.9	Aa
PC 32:4	NA	Bb	NA	Bb	7430.3	Ab	7292.7	Ba	12679.5	Aa	10325.4	Abb	2603.5	Bab	9558.3	Aa	11056.3	Ab	2422.3	Cab	11790.0	Ba	35881.4	Aa
PC 34:1	NA	Ba	NA	Bc	235299.0	Ab	NA	Aa	NA	Ac	NA	Ac	NA	Ba	506002.8	Aa	491964.8	Aa	NA	Ba	196813.2	Ab	NA	Bc
PC 34:2	NA	Ab	NA	Ab	NA	Ac	711987.0	Ba	1304404.1	Aa	1045497.7	ABb	399845.7	Bab	1183609.9	Aa	1157840.5	Ab	624616.5	Ba	NA	Cb	3434174.0	Aa
PC 34:3	196772.6	Aa	141975.4	Ab	291713.4	Ac	155214.8	Ba	624654.3	Aa	490156.0	Abc	162584.2	Ba	621764.6	Aa	598106.8	Ab	313685.9	Ba	390681.1	Bab	2116066.2	Aa
PC 34:4	52486.9	Aa	36151.7	Ab	86117.7	Ac	47719.2	Ba	241521.8	Aa	208417.2	Ab	36139.0	Ba	221456.9	Aa	226401.9	Ab	42391.8	Ca	157627.4	Ba	805215.4	Aa
PC 34:5	34926.2	Aa	23343.2	Ab	60708.6	Ac	54352.2	Aa	299113.7	Aab	256350.0	Abc	44844.3	Ba	356367.0	Aa	384721.5	Ab	35684.4	Ba	209564.3	Bab	1657105.5	Aa
PC 34:6	13269.9	Aa	7761.9	Aa	20893.7	Ac	24311.0	Aa	143038.6	Aa	120160.8	Abc	28170.7	Ba	286689.7	Aa	347806.8	Ab	15858.1	Ba	157248.1	Ba	1577583.1	Aa
PC 36:1	231241.2	Bb	146987.1	Cc	310159.7	Ab	328641.8	Aa	369553.9	Ab	356324.4	Ab	245459.1	Bb	396533.5	Ab	453790.2	Aa	208469.8	Bb	467552.8	Aa	185711.2	Bc
PC 36:2	3214453.0	ABa	1817153.4	Bc	4381735.8	Ab	3957864.3	Aa	4748681.7	Ab	5136352.3	Ab	3435201.4	Ba	9144370.3	Aa	10566180.3	Aa	3148950.2	Ba	10326954.0	Aa	9490229.1	Aa
PC 36:3	155112.5	ABb	82837.2	Bd	240471.5	Ad	384682.9	Ba	821453.9	Aa	691059.2	Ab	199766.7	Bb	465521.5	Ac	445742.8	Ac	295279.2	Cab	635529.0	Bb	1638545.8	Aa

SI Table 8. (continuation) Relative abundance of lipid of *Chlamydomonas* sp. BR020 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test ($P < 0.05$). Metabolite not detected is represented by NA.

Lipids	0h_0N		0h_3.5N		0h_7N		10h_0N		10h_3.5N		10h_7N		18h_0N		18h_3.5N		18h_7N		36h_0N		36h_3.5N		36h_7N	
PC 36:3.1	19357.3	Aa	17121.8	Ac	22549.8	Ac	16024.8	Aa	54629.8	Ac	75942.6	Ac	8922.3	Ca	398224.9	Bb	508428.1	Aa	9687.2	Ca	581014.0	Aa	396627.3	Bb
PC 36:5	83334.4	Aa	48702.6	Ab	169015.4	Ac	207906.5	Ba	1337939.7	Aa	1202097.9	Ab	189336.8	Ba	1109232.8	Aa	1439296.5	Ab	248624.0	Ba	869903.0	Bab	5941379.5	Aa
PC 36:6	33504.9	Aa	24165.4	Aa	55882.1	Ab	75838.0	Aa	591913.4	Aa	508648.5	Ab	64012.8	Aa	576509.0	Aa	649142.5	Ab	79263.4	Ba	362267.2	Ba	4222914.1	Aa
PC 38:2	77623.2	Ba	57250.8	Ce	102382.5	Ab	78667.3	Ba	98185.1	Ab	109674.4	Ab	46444.0	Cb	122676.0	Ba	141407.4	Aa	54911.2	Cb	80392.7	Bb	138141.7	Aa
PC 38:3	4982.5	Ba	2446.5	Bd	10480.7	Ac	3955.8	Ba	18691.2	Aa	16650.4	Ab	4293.9	Ba	14858.4	Ab	15292.3	Ab	3672.2	Ba	6928.5	Bc	28433.2	Aa
PC 38:3.1	1546.7	Ab	1282.8	Ac	1752.2	Ac	2686.0	Ba	3556.6	ABb	3915.3	Ab	2950.0	Ba	5737.7	Aa	6671.9	Aa	2946.1	Ca	5831.3	Aa	4219.5	Bb
PE 32:1	74749.8	Aa	70106.0	Ac	102230.9	Ac	81483.1	Ba	130693.2	Ab	157031.3	Ab	59457.5	Ca	271519.4	Ba	336670.0	Aa	84894.1	Aa	82696.2	Ac	79585.5	Ac
PE 32:2	24754.2	Aa	21866.0	Ac	34555.8	Ac	36210.6	Ba	72388.0	Ab	87406.8	Ab	25432.6	Ca	128622.3	Ba	151980.5	Aa	30513.0	Aa	NA	Bd	22556.2	Ac
PE 34:1	89906.9	Ba	75825.1	Bc	152689.4	Ac	139350.4	Ba	208984.4	Ab	219007.2	Ab	112082.9	Ba	267639.7	Aa	294845.3	Aa	109370.6	Ba	159076.1	Ab	167016.1	Ac
PE 34:2	532195.9	Aa	446878.7	Ac	786876.7	Ad	635232.1	Ba	1342024.4	Ab	1588647.7	Ac	423771.0	Ba	2750568.5	Aa	3049963.9	Aa	481225.0	Ca	1596230.6	Bb	2201545.4	Ab
PE 34:3	10126.3	Aa	6635.0	Aa	24537.4	Ab	10524.8	Aa	24079.7	Aa	21681.1	Ab	6148.1	Ba	26100.0	ABa	42482.6	Ab	8885.9	Ba	11340.6	Ba	84249.3	Aa
PE 34:4	2876.8	Aa	2744.2	Aa	4013.0	Ab	2612.5	Aa	8988.2	Aa	7868.1	Ab	938.8	Ba	8239.8	ABa	12834.9	Ab	1531.2	Ba	2769.4	Ba	33792.7	Aa
PE 34:5	1984.0	Aa	1674.5	Aa	3054.5	Ac	2609.2	Aa	9622.5	Aa	9381.2	Abc	3243.5	Ba	11524.1	ABa	17991.5	Ab	NA	Ba	2874.8	Ba	42225.7	Aa
PE 34:6	NA	Aa	NA	Aa	1834.6	Ab	1319.3	Aa	5946.3	Aa	5369.3	Ab	NA	Ba	5884.8	ABa	8825.1	Ab	NA	Ba	2177.8	Ba	25469.4	Aa
PE 36:1	27348.1	Aa	28724.2	Ab	54606.8	Ac	29924.2	Ba	146888.3	Aa	168672.1	Aa	25190.9	Ba	128343.7	Aa	141061.7	Aa	11523.6	Ca	50965.8	Bb	94194.0	Ab
PE 36:2	860470.2	Aa	879272.8	Ac	1485356.0	Ad	1218948.0	Ba	4308257.5	Aa	4559571.7	Ab	1110166.3	Ba	5106036.8	Aa	5505162.3	Aa	512941.3	Ba	2726482.1	Ab	3089702.9	Ac
PE 36:3	NA	Aa	NA	Ad	NA	Ad	NA	Ca	314649.1	Bb	388822.9	Ab	NA	Ba	482012.9	Aa	529214.0	Aa	NA	Ba	140167.7	Ac	162122.2	Ac
PE 36:3.1	12876.0	Aa	9943.7	Ab	25071.1	Ac	19044.5	Aa	40735.8	Aa	42220.3	Abc	10629.2	Ba	38005.3	Aa	51767.7	Ab	15776.8	Ba	22201.3	Bab	111649.4	Aa
PE 36:4	22002.6	ABb	14820.2	Bb	32894.3	Ac	31458.9	Bab	77146.1	Aa	83870.2	Ab	21070.7	Cb	72631.7	Ba	102954.5	Aa	40004.4	Ba	82717.3	Aa	77085.3	Ab
PE 36:4.1	23743.5	Aa	11335.1	Aa	47652.4	Ab	24526.8	Aa	59033.6	Aa	66459.6	Ab	15771.1	Ba	66307.7	ABa	107171.9	Ab	22253.2	Ba	34733.6	Ba	251497.4	Aa
PE 36:5	7979.3	Aa	6259.6	Aa	16514.4	Ab	8430.2	Aa	39974.2	Aa	43613.0	Ab	5681.6	Ba	53880.9	ABa	92547.4	Ab	4279.6	Ba	23039.5	Ba	278959.0	Aa
PE 36:6	3122.5	Aa	3067.4	Aa	5322.8	Ab	2039.1	Aa	10674.5	Aa	10805.8	Ab	1513.6	Ba	15480.1	ABa	27721.0	Bb	1583.6	Ba	5319.1	Ba	80154.6	Aa
PE 38:2	4530953.9	Ba	3464152.9	Ce	6115181.6	Aa	4459625.9	Aa	4897814.3	Ab	5077599.8	Abc	2659294.0	Bb	3771661.6	Ac	4579005.1	Ac	2358305.8	Bb	6642412.1	Aa	5767399.6	Aab
PE 38:3	NA	Aa	NA	Ac	NA	Ac	NA	Ba	30563.2	Ab	39754.7	Ab	1753.8	Ca	83648.8	Ba	105278.0	Aa	NA	Ba	38449.8	Ab	36228.7	Ab
PE 40:1	NA	Bb	NA	Bc	5568.1	Aab	NA	Bb	NA	Bc	5589.5	Aab	5585.7	Aa	6053.1	Aa	5989.0	Aa	5536.5	Aa	4803.9	Ab	4728.7	Ab
PE 40:2	49500.9	ABb	29860.3	Bd	69387.8	Ab	64466.0	Aab	65691.5	Ac	68931.8	Ab	58301.3	Bb	112773.8	Ab	125038.5	Aa	86138.7	Ca	148689.3	Aa	109170.7	Ba
PG 32:0	28221.2	Ba	34163.0	Aa	27836.2	Ba	8330.0	Bb	13737.1	Ab	11075.1	ABb	9647.2	Ab	11602.9	Abc	11381.5	Ab	9838.9	Bb	6734.3	Bc	15734.0	Ab
PG 32:1	13473.0	Aa	13711.2	Ab	15883.5	Ab	10647.2	Aa	14722.3	Ab	15298.0	Ab	9504.2	Ba	27960.8	Aa	32634.4	Aa	12475.3	Aa	5926.5	Bc	7944.5	ABc
PG 34:2	284158.4	Aa	336252.5	Ab	289089.6	Ab	147573.1	Bb	356288.7	Ab	363509.7	Ab	94973.7	Bb	531750.9	Aa	584305.7	Aa	110650.9	Cb	207301.7	Bc	505531.9	Aa

SI Table 8. (continuation) Relative abundance of lipid of *Chlamydomonas* sp. BR020 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N		0h_3.5N		0h_7N		10h_0N		10h_3.5N		10h_7N		18h_0N		18h_3.5N		18h_7N		36h_0N		36h_3.5N		36h_7N	
PG 34:3	66549.1	Aa	74382.2	Abc	80195.0	Ac	35142.9	Ba	174419.5	Aab	152562.7	Abc	15937.8	Ba	214645.9	Aa	225743.1	Ab	12780.5	Ba	21451.8	Bc	617799.1	Aa
PG 34:4	15740.2	Aa	16738.1	Aa	19145.9	Ab	20980.4	Aa	48484.0	Aa	40535.3	Ab	7819.7	Aa	41390.2	Aa	42264.4	Ab	11067.0	Ba	7723.6	Ba	151393.9	Aa
PG 36:1	25626.2	Aa	24611.5	Ac	29874.5	Ac	31115.4	Ba	69709.4	Ab	74939.9	Ab	24035.5	Ba	105624.7	Aa	120720.8	Aa	27247.9	Ba	51244.4	Ab	55857.5	Ab
PG 36:2	332243.0	Aa	296639.9	Ac	386428.9	Ac	385687.4	Ba	923862.3	Ab	982482.9	Ab	255424.0	Ba	1618946.7	Aa	1747619.2	Aa	318276.6	Ba	882106.5	Ab	1058410.6	Ab
SQDG 32:0	2959146.5	Ba	3341828.9	Aa	3431755.1	Aa	1209701.5	Bb	1773062.0	Ab	1471412.6	ABb	944181.9	Ab	1125894.4	Ac	1097442.3	Ac	1231352.3	Ab	1028316.8	Ac	1239169.8	Abc
SQDG 32:1	72918.7	Ba	78504.1	Ba	89861.7	Aa	26566.6	Bb	42408.8	Ab	31726.7	Bbc	16045.2	Ac	23191.3	Ac	22627.4	Ac	15173.1	Bc	10607.4	Bd	38633.2	Ab
SQDG 32:2	84539.7	Ba	89844.6	Ba	97884.4	Aa	26849.9	Bb	37819.5	Ab	30766.6	ABc	NA	Bc	25121.4	Ac	24768.2	Ac	NA	Bc	NA	Bd	42260.6	Ab
SQDG 32:3	151915.7	Ba	164814.1	ABa	175322.6	Aa	61727.7	Bb	88197.4	Ab	71792.5	ABc	39259.8	Bc	65903.3	Ac	70966.1	Ac	26683.5	Bc	34528.3	Bd	95129.2	Ab
SQDG 34:0	673063.6	Ba	728616.7	Ba	821366.2	Aa	290280.5	Bb	412798.1	Ab	330768.1	ABb	168091.8	Ac	231562.5	Ac	225395.0	Ac	135260.7	Ac	85395.9	Ad	139419.8	Ac
SQDG 34:1	1346802.0	Ba	1469626.3	ABa	1577086.6	Aa	NA	Cb	776942.9	Ab	620376.8	Bb	NA	Bb	445450.4	Ac	436202.0	Ac	NA	Cb	323454.7	Bc	602366.1	Ab
SQDG 34:2	4197522.1	Ba	4792963.5	Aa	4928817.3	Aa	1088806.3	Bb	2278238.7	Ab	1860299.1	Abc	605882.2	Bbc	1390599.4	Ac	1373204.0	Ac	525690.0	Bc	934314.1	Bc	1918286.6	Ab
SQDG 34:3	2496651.0	Ba	2884779.4	Ba	3504580.0	Aa	1794870.3	Bb	3291608.0	Aa	2842997.9	Ab	1239649.2	Bb	2284594.4	Ab	2242424.7	Ac	1660711.1	Bb	1314107.2	Bc	3159481.0	Aab
SQDG 34:4	66016.7	Ba	69626.3	Ba	78006.9	Aa	18679.5	Bb	26814.3	Ab	24247.7	ABc	9653.6	Bc	21536.6	Ab	20861.4	Ac	6154.4	Bc	11156.9	Bc	35556.5	Ab
SQDG 34:5	49274.1	Ba	53500.0	ABa	59084.1	Aa	18385.5	Bb	28568.4	Ab	26568.4	Ac	9284.5	Bc	24609.5	Ab	24578.7	Ac	5418.9	Cc	12781.3	Bc	41175.1	Ab
SQDG 34:6	38198.6	Ba	41254.2	ABa	46392.6	Ab	14471.5	Bb	25883.3	Ab	23960.5	Ac	6878.0	Bc	26459.0	Ab	28057.8	Ac	4837.3	Cc	13627.7	Bc	53653.2	Aa
TAG 42:0	28981.1	Aa	33767.8	Aa	29069.7	Aab	24628.7	Aa	28453.5	Aa	29801.9	Aa	22906.3	Aa	19589.8	Ab	22635.7	Ab	NA	Cb	30515.5	Aa	15236.9	Bc
TAG 42:1	30838.8	Ab	32225.2	Aa	33186.3	Aa	34057.2	Aab	33883.0	Aa	31678.9	Aab	37030.6	Aab	21309.7	Bb	22103.8	Bbc	44045.7	Aa	40503.7	Aa	16392.7	Bc
TAG 42:2	5400.7	Ab	5607.9	Abc	5944.9	Aab	11170.4	Aa	7410.4	Bb	6392.4	Ba	10065.7	Aa	3549.3	Bc	4406.0	Bab	9876.7	Aa	10929.4	Aa	3282.4	Bb
TAG 44:0	105605.3	Aa	117231.9	Aa	108053.4	Aa	88903.0	Aab	85912.6	Ab	86863.9	Aa	98507.9	Aab	53151.4	Bc	56745.6	Bb	77029.5	Ab	92053.1	Ab	44092.0	Bb
TAG 44:1	69283.3	Ac	72659.8	Ab	71505.5	Aa	91002.5	Abc	62802.1	Bb	54832.9	Bab	103839.6	Aab	33862.4	Bc	37970.7	Bb	122178.3	Aa	102089.2	Aa	38488.5	Bb
TAG 44:2	33130.8	Ac	36361.0	Aa	35703.5	Aa	43694.6	Ab	36244.0	ABa	29379.5	Bab	48348.0	Ab	20002.3	Bb	20164.2	Bbc	62505.9	Aa	41206.7	Ba	14618.6	Cc
TAG 46:0	454616.5	Aa	502010.8	Aa	450679.5	Aa	381716.6	Aab	375101.8	Ab	395200.2	Aa	392524.5	Aab	264702.6	Bc	303729.8	Bb	326895.4	Ab	390722.8	Ab	225033.3	Bb
TAG 46:1	390291.4	Ac	361006.2	Ab	453626.0	Aa	551621.7	Ab	414327.0	Bb	361771.3	Ba	667282.7	Aab	178471.3	Bc	207140.0	Bb	746436.0	Aa	677161.4	Aa	103212.6	Bb
TAG 46:2	84433.4	Ac	83538.2	Abc	101587.5	Aa	146268.4	Ab	104628.8	Bb	82824.2	Bab	166056.3	Ab	46336.9	Bc	50760.6	Bb	238586.4	Aa	183352.5	Ba	NA	Cc
TAG 46:2.1	73619.9	Aa	86313.9	Aa	83269.9	Aa	63089.8	Aab	55268.0	Ab	64072.1	Ab	68690.9	Aa	39768.7	Bb	44172.3	Bc	36537.1	Ab	NA	Bc	34536.0	Ac
TAG 46:3	39477.8	Ac	35469.7	Abc	51906.7	Aa	85349.6	Ab	60650.0	ABb	48837.9	Ba	102881.1	Ab	21678.1	Bc	25943.4	Bab	178751.6	Aa	135773.0	Ba	7479.8	Cb
TAG 46:3.1	13352.7	Aa	14169.7	Aa	16070.5	Aa	NA	Bb	11564.5	Aa	12483.7	Aa	NA	Bb	6715.0	Ab	7910.1	Ab	NA	Cb	13549.5	Aa	4250.0	Bb
TAG 46:4	15611.9	Ac	17722.3	Ab	19000.0	Aa	24215.5	Abc	16090.9	ABbc	13571.0	Bab	28217.1	Ab	6660.6	Bc	8589.1	Bbc	41667.6	Aa	32519.6	Ba	1957.6	Cc
TAG 48:0	1878310.2	Aa	2069776.1	Aa	1861266.0	Aa	1388429.8	Ab	1443088.5	Ab	1412176.3	Ab	1279227.0	Ab	1058261.6	Ac	1105675.5	Ac	1279103.6	ABb	1525413.1	Ab	1075407.2	Bc

SI Table 8. (continuation) Relative abundance of lipid of *Chlamydomonas* sp. BR020 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
TAG 48:1	2580390.8 Ac	2606663.0 Ab	2948438.2 Aa	4264684.5 Ab	2829548.1 Bb	2597513.4 Ba	5604381.1 Ab	1410873.3 Bb	1539942.9 Bab	8219934.7 Aa	4904361.5 Ba	1080090.1 Cb
TAG 48:2	2752401.5 Ac	2569657.6 Abc	3362814.3 Aab	4281700.1 Abc	3966173.3 Ab	3525570.5 Aa	4508514.8 Ab	1484882.9 Bc	1783469.9 Bbc	7569232.9 Aa	8300616.7 Aa	546047.1 Bc
TAG 48:3	2531105.8 Ac	2329525.9 Ab	3093841.2 Aab	4186256.6 Abc	4210514.0 Ab	3818544.8 Aa	5388960.4 Ab	1791940.3 Bb	2161676.8 Bab	11739948.3 Aa	11370502.2 Aa	927182.7 Bb
TAG 48:4	522970.2 Ab	433240.1 Ac	692972.5 Aab	1031947.6 Aa	947400.5 Ab	813484.5 Aa	983798.6 Aa	259623.4 Bc	326587.3 Bbc	1316917.7 Ba	2037126.8 Aa	76717.7 Cc
TAG 48:5	450838.5 Ac	389541.5 Ac	596819.3 Aa	964487.7 Ab	824512.7 Ab	671871.8 Aa	1054055.8 Ab	251513.5 Bc	319911.4 Bab	1596939.2 Aa	1914800.5 Aa	68284.8 Bb
TAG 48:6	125366.7 Ac	107000.0 Abc	163388.6 Aab	343274.0 Ab	293273.6 Ab	250616.8 Aa	434844.5 Ab	92031.0 Bc	111333.5 Bab	755168.8 Ba	929752.3 Aa	32605.1 Cb
TAG 48:7	39808.2 Ab	32517.9 Ac	53227.9 Aab	101158.9 Aa	77215.9 ABb	58823.5 Ba	98525.6 Aa	20764.4 Bc	22667.4 Bbc	88495.3 Ba	153628.3 Aa	5050.6 Cc
TAG 48:8	14019.1 Ac	11957.8 Ac	19997.2 Aab	47242.1 Ab	45505.1 Ab	35514.0 Aa	56088.2 Aab	12629.7 Bc	15475.9 Bb	67983.7 Ba	88196.6 Aa	4506.9 Cb
TAG 48:9	2679.9 Ac	2355.5 Ac	3459.9 Ab	8929.3 Ab	11224.5 Ab	9953.8 Aa	12627.8 Ab	4062.7 Bc	5535.9 Bab	19625.1 Aa	18901.9 Aa	2329.2 Bb
TAG 50:0	2957181.4 Ba	3403698.7 Aa	2867207.7 ABa	2174615.2 Bb	2373572.0 Ab	2183718.4 ABb	1982520.1 Bc	1716822.5 Ac	1859730.4 ABc	1644191.1 Bc	2208651.5 Ac	1929407.7 ABc
TAG 50:1	50922653.4 Ac	48381188.6 Ac	56587300.2 Aab	86667510.4 Ab	71773241.7 ABb	63730557.6 Ba	103781138.0Ab	31280574.1Bc	36697957.4Bbc	136819922.2Aa	115684097.3Ba	17359312.7Cc
TAG 50:2	17846104.7 Ac	17868760.5 Abc	22334493.9 Aa	29185745.6 Ab	22911472.2 Ab	19693564.9 Aab	35727394.2 Ac	9598139.3 Bc	10721269.8Bbc	55514607.0 Aa	43742228.2 Ba	5642313.2 Cc
TAG 50:3	14179013.1 Ac	13184517.0 Ac	17244035.7 Aab	28354992.6 Ab	24251526.9 Ab	21511485.4 Aa	32944030.1 Ab	10575616.2Bc	12089983.9Bbc	44064126.0 Aa	42254980.8 Aa	3765087.3 Bc
TAG 50:4	13698435.9 Ac	12182317.0 Abc	16826141.9 Aa	31675709.5 Ab	23773043.5 Ab	21428508.8 Aa	40920978.4 Ab	9897415.7 Bc	11921038.0Bab	64939228.2 Aa	54463280.5 Aa	3410880.7 Bb
TAG 50:5	8571862.9 Ac	7442600.8 Abc	10821620.5 Aa	23599409.4 Ab	12118699.7 Bb	10427452.2 Ba	23548170.2 Ab	4130663.1 Bc	5031403.8 Bab	33374098.7 Aa	32282593.7 Aa	1159656.0 Bb
TAG 50:6	11711.7 Ac	13740.1 Ab	8544.4 Aa	149511.5 Aa	39794.5 Bab	29355.6 Ba	81923.2 Ab	9049.6 Bb	11871.2 Ba	190605.3 Aa	78184.0 Ba	1555.5 Ca
TAG 50:6.1	4701649.4 Ac	4000928.5 Ab	5937711.1 Aa	17620592.5 Ab	6916727.4 Bb	6332846.9 Ba	25324279.0 Ab	2633146.7 Bb	3259896.4 Ba	38713409.8 Aa	26593335.4 Ba	846181.9 Ca
TAG 50:7	577474.7 Ac	497627.4 Ab	749649.2 Aa	2397949.0 Ab	1168087.6 Bb	914289.9 Ba	2803855.1 Ab	351592.3 Bb	419556.7 Ba	4162254.5 Aa	3891784.4 Aa	88985.3 Ba
TAG 50:8	240733.8 Ac	195638.3 Ab	349925.0 Aa	1135520.2 Ab	694905.3 Ab	647509.3 Aa	1410128.3 Ab	237279.1 Bb	309838.4 Ba	2536588.9 Aa	2280598.5 Aa	75624.8 Ba
TAG 50:9	65672.0 Ad	53446.4 Ab	88278.5 Aa	460487.9 Ac	286957.3 Ab	250243.7 Aa	786871.5 Ab	115095.4 Bb	146804.2 Ba	1569741.6 Aa	930971.8 Ba	55139.1 Ca
TAG 52:0	2651355.6 Aa	2941912.2 Aa	2628531.6 Aa	1945383.6 Ab	2054215.4 Ab	1939100.1 Ab	1799135.2 Ac	1618324.0 Ac	1675584.0 Ac	1497763.7 Ac	1929907.5 Ac	1755596.5 Ac
TAG 52:1	39043405.6 Ab	38831259.3 Aa	43303066.7 Aa	42366057.2 Ab	36292322.0 ABa	31221308.7 Bb	49020253.4 Ab	18208695.3Bb	20178443.2Bc	64463033.6 Aa	38504999.9 Ba	9044862.1 Cd
TAG 52:2	102616699.3Ab	101086352.8Ac	116689122.8Aab	186301449.9Aa	163407842.5Ab	152667354.0Aa	209305650.5Aa	90185875.8Bc	98089165.5Bb	220523899.7Aa	216898535.7Aa	44035893.4Bc
TAG 52:3	53974806.9 Ac	50564473.3 Ac	61860458.3 Aab	111563158.1Ab	96809460.9 Ab	84264618.0 Aa	132139757.8Ab	41288750.0Bc	47736074.5Bb	167089320.8Aa	143896857.1Aa	17264395.2Bc
TAG 52:4	30446672.2 Ac	27742338.3 Ac	37194589.3 Aab	75496585.1 Ab	65063758.2 Ab	58167907.4 Aa	94176033.1 Ab	28258906.6Bc	32867134.2Bbc	139467359.3Aa	119343299.1Aa	11931178.7Bc
TAG 52:5	17248421.8 Ac	15517226.9 Ac	21706209.2 Aa	57053422.1 Ab	34775809.7 Bb	30877038.8 Ba	68333792.9 Ab	14540982.1Bc	17319522.0Bab	90278945.4 Aa	65910390.2 Ba	3855724.9 Cb
TAG 52:5.1	21560.8 Ab	15661.8 Ab	29763.8 Aa	97895.5 Ab	127929.4 Ab	145821.5 Aa	170146.5 Ab	23435.4 Ab	30410.8 Aa	514713.6 Aa	432579.8 Aa	7405.7 Ba
TAG 52:6	10101566.0 Ac	8611201.4 Ab	12842056.0 Aab	48363416.4 Ab	23157777.0 Bb	21652250.7 Ba	57335003.0 Ab	9346124.5 Bb	10957972.1Bab	80484503.2 Aa	56949691.3 Ba	2195586.2 Cb
TAG 52:6.1	4492.1 Ad	5247.8 Ab	11009.8 Aa	54062.6 Ac	17402.7 ABb	9774.0 Ba	857137.3 Aa	6441.1 Bb	4191.3 Ba	102953.9 Ab	72349.7 Aa	2987.1 Ba

SI Table 8. (continuation) Relative abundance of lipid of *Chlamydomonas* sp. BR020 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N	
TAG 52:7	4458210.2 Ac	3785192.2 Ab	5767775.8 Aa	35164670.9 Ab	12027574.9 Bb	11373386.3 Ba	49496584.4 Ab	4689970.7 Bb	5877826.2 Ba	76013889.5 Aa	44314379.2 Ba	1303301.2 Ca	
TAG 52:8	991766.0 Ac	769803.7 Ab	1317126.6 Aa	5974479.6 Ab	2885831.6 Bb	2702247.6 Ba	6418081.6 Ab	922732.0 Bb	1257175.9 Ba	10248831.9 Aa	8790298.4 Aa	295716.0 Ba	
TAG 52:9	257139.9 Ac	194264.9 Ab	341112.0 Aa	2304922.0 Ab	942973.7 Bb	911980.8 Ba	2897660.8 Ab	418682.2 Bb	545139.0 Ba	5051331.1 Aa	3835608.3 Ba	195624.8 Ca	
TAG 54:0	971323.3 Aa	1108111.8 Aa	956339.5 Aa	735671.4 Ab	786729.5 Ab	761392.1 Ab	687987.1 Ab	543943.4 Ac	588348.9 Abc	607233.9 Bb	799442.4 Ab	541715.8 Bc	
TAG 54:1	12134760.8 Aa	12265746.6 Aa	13735701.4 Aa	10263627.7 Ab	8708367.7 ABb	7551382.6 Bb	9905434.3 Ab	4479798.9 Bd	4849934.8 Bc	11610402.4 Aab	6757962.1 Bc	2829056.4 Cd	
TAG 54:2	45952269.9 Ac	45356315.5 Aa	52147286.1 Aa	62102441.1 Ab	55349417.9 ABa	47241876.1 Ba	73303708.3 Ab	29144511.6Bb	31716285.6Bb	87110117.6 Aa	50255388.6 Ba	11519739.7Cc	
TAG 54:3	75129272.5 Ab	70514552.7 Ac	90055843.4 Ab	187234012.4Aa	157040487.4ABb	138420530.2Ba	217593851.4Aa	84407348.6Bc	93120809.6Bb	216753212.4Aa	198225439.1Aa	33299954.0Bc	
TAG 54:4	51096306.5 Ac	46385423.1 Ac	60002300.1 Ab	131891049.4Ab	106528297.7ABb	99089964.3 Ba	158357743.4Aab	49598862.4Bc	58350075.4Bb	189529276.6Aa	146441801.7Ba	16683962.0Cc	
TAG 54:5	32383480.3 Ad	29249686.9 Ac	39220978.6 Abc	100973664.8Ac	86953568.0 Ab	76313517.1 Aa	134576541.1Ab	39643457.2Bc	46029634.4Bb	180292351.5Aa	139855539.3Ba	13643393.4Cc	
TAG 54:6	10378633.2 Ac	9511411.6 Ac	12861104.0 Ab	28213264.5 Ab	26455593.7 Ab	25164419.9 Aa	33828009.6 Ab	10944290.4Bc	13262905.7Bb	51109938.2 Aa	48168943.6 Aa	4322861.4 Bb	
TAG 54:7	2824678.7 Ac	2384806.9 Ac	3625229.9 Ab	9904003.1 Ab	9215938.7 Ab	8779930.4 Aa	13086923.6 Ab	3656667.0 Bc	4473300.8 Bab	22593105.8 Aa	21006474.8 Aa	1123067.2 Bb	
TAG 54:8	459283.4 Ac	377081.7 Ac	652764.0 Abc	1085174.5 Ab	1275046.2 Ab	1225603.6 Aa	1221740.2 Ab	717181.5 Bc	875247.2 ABab	1843344.1 Ba	2859874.8 Aa	212275.0 Cc	
TAG 54:9	66766.4 Ac	53042.1 Ac	99348.8 Aab	175523.2 Ab	182984.2 Ab	161506.0 Aa	198689.1 Ab	103829.0 Bc	132767.3 ABa	331528.8 Aa	327032.6 Aa	39423.5 Bb	
TAG 56:0	104122.2 Aa	105410.3 Aa	111406.6 Aa	86576.5 Aa	73971.6 Ab	73497.7 Ab	103419.2 Aa	48330.3 Bc	49258.8 Bc	91118.9 Aa	97874.6 Aa	48835.6 Bc	
TAG 56:1	804845.8 Ac	791734.4 Aab	929941.1 Aa	1424621.6 Ab	927411.1 Ba	751735.8 Ba	1726831.6 Ab	395915.4 Bb	443726.4 Bab	2809939.2 Aa	1199611.0 Ba	155431.8 Cb	
TAG 56:2	3067739.4 Ad	2888950.1 Abc	3683852.2 Aa	5922339.4 Ac	4862057.2 ABa	3819861.2 Ba	7928783.0 Ab	2125438.3 Bc	2327599.9 Bab	10489290.6 Aa	4617846.2 Bab	672346.1 Cb	
TAG 56:3	4242900.9 Ac	4197747.1 Ab	5619079.9 Ab	10528129.8 Ab	11226113.9 Aa	9930783.6 Aa	13240081.0 Ab	5539541.4 Bb	6192521.1 Bb	17059293.4 Aa	11629898.1 Ba	1953508.9 Cc	
TAG 56:4	2216655.0 Ab	2120748.7 Ab	2732274.2 Aab	3186536.0 Aa	3865500.2 Aa	3374505.2 Aa	3296047.2 Aa	1864343.5 Bb	2125177.4 Bb	3141953.4 Aa	3484104.4 Aa	833722.0 Bc	
TAG 56:5	1338873.0 Ac	1151034.5 Ab	1692776.1 Ab	2632131.0 Ab	3392798.7 Aa	2945195.3 Aa	3165180.5 Aab	1539449.3 Bb	1734550.6 Bb	3976329.9 Aa	3696841.2 Aa	516312.5 Bc	
TAG 56:6	413621.4 Ab	386270.7 Ab	527257.0 Ab	683012.6 Aa	821198.4 Aa	753596.0 Aa	619806.0 Aa	356154.2 Bb	410458.3 Bb	647779.2 Ba	873928.1 Aa	138694.4 Cc	
TAG 56:7	114200.1 ABa	99902.0 Bc	153511.5 Ab	152476.2 Ba	255500.8 Ab	241935.0 Aa	154901.1 Aa	116989.3 Ac	136807.9 Ab	NA	Bb	341968.3 Aa	29943.1 Bc
TAG 58:0	43659.3 Aa	46872.9 Aa	45132.3 Aa	29838.6 Ab	25106.1 Abc	26207.8 Ab	31515.5 Ab	18511.8 Bc	19548.9 Bbc	31891.9 Ab	27748.8 Ab	16689.1 Bc	
TAG 58:1	695870.2 Ac	622142.0 Ab	816958.0 Aa	1455733.7 Ab	735268.2 Bb	568517.5 Bab	1728082.1 Ab	319162.1 Bb	343449.0 Bab	3448253.0 Aa	1375641.3 Ba	127658.7 Cb	
TAG 58:2	911292.7 Ad	857892.2 Ab	1094160.2 Aa	1979842.4 Ac	1371177.8 ABab	1144878.2 Ba	2755290.1 Ab	649711.9 Bb	672509.9 Bab	4107180.9 Aa	1688359.5 Ba	198298.7 Cb	
TAG 58:3	540330.9 Ac	504234.3 Abc	660551.1 Aa	848000.6 Ab	719453.2 ABab	622020.0 Bab	935575.9 Ab	364260.5 Bc	397427.0 Bbc	1207793.7 Aa	787709.1 Ba	165454.7 Cc	
TAG 58:4	308621.7 Ac	323533.6 Abc	349971.4 Aa	480514.5 Abc	415553.9 Ab	354425.1 Aa	622057.5 Ab	211442.6 Bc	225608.6 Bab	952400.6 Aa	620385.0 Ba	133150.0 Cb	
TAG 58:5	208282.6 Ac	187593.5 Ab	234667.3 Aa	347481.9 Aab	121709.9 Bc	109697.6 Bb	312196.3 Ab	74189.7 Bc	90199.1 Bb	383190.2 Aa	288978.5 Ba	22218.7 Cc	
TAG 58:6	148716.3 Ac	130014.0 Ab	167912.0 Aa	357775.5 Ab	104345.9 Bb	79872.6 Ba	459209.3 Ab	67783.2 Bb	75238.4 Ba	764232.7 Aa	325101.1 Ba	19604.6 Ca	
TAG 60:0	11139.1 Aa	12430.3 Aa	10580.7 Aa	8497.2 Ab	7208.2 ABb	5552.1 Bb	6293.9 Ac	4267.0 Bc	4498.3 ABb	5054.3 Ac	6237.3 Abc	4946.1 Ab	

SI Table 8. (continuation) Relative abundance of lipid of *Chlamydomonas* sp. BR020 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N		0h_3.5N		0h_7N		10h_0N		10h_3.5N		10h_7N		18h_0N		18h_3.5N		18h_7N		36h_0N		36h_3.5N		36h_7N	
TAG 60:1	470168.8	Ab	435798.8	Aab	540988.1	Aa	485153.1	Ab	300106.0	Bbc	237635.1	Bb	615464.9	Ab	166262.4	Bc	186910.3	Bb	1143005.8	Aa	580912.8	Ba	119241.6	Cb
TAG 60:2	1112211.3	Ac	975947.2	Ab	1362294.0	Aa	2307702.1	Ab	1277560.2	Bab	1005914.0	Bab	2964578.8	Ab	632728.6	Bb	732382.4	Bab	4773944.1	Aa	1839373.8	Ba	208056.7	Cb
TAG 60:3	594939.6	Ac	548561.0	Aab	685733.0	Aa	839312.8	Abc	558007.3	ABab	475771.9	Bab	1025672.7	Ab	260363.8	Bb	289669.7	Bbc	1649037.6	Aa	827639.8	Ba	89958.1	Cc
TAG 60:4	342568.4	Ac	323590.6	Ab	407071.9	Aa	519036.4	Abc	367534.7	ABb	307953.9	Ba	637944.5	Ab	199523.8	Bb	230447.2	Bab	1085268.9	Aa	668821.5	Ba	75692.3	Cb
TAG 60:5	117439.5	Ab	80901.8	Bab	134301.0	Aa	78762.9	Ac	79457.1	Ab	66993.1	Ab	77665.9	Ac	53535.1	Ab	58640.7	Ab	154612.6	Aa	116217.7	Ba	16681.6	Cc
TAG 60:5.1	162958.1	ABa	151705.3	Ba	198443.0	Aa	157427.4	Aa	69863.3	Bb	61930.6	Bb	153655.2	Aa	42645.5	Bb	52297.8	Bb	186891.3	Aa	182841.1	Aa	19777.8	Bb
TAG 60:6	124436.2	Ac	105607.9	Ab	147876.7	Aa	129245.0	Abc	51036.5	Bc	42076.7	Bb	174021.1	Ab	38307.0	Bc	48247.5	Bb	236443.3	Aa	180198.2	Ba	20377.6	Cb
FA 16:0	16409037.8	Aa	16401123.2	Aa	16112227.8	Aa	13237803.7	Ab	11629473.0	ABb	9275082.5	Bb	13826261.3	Aab	7010990.8	Bc	6386398.0	Bbc	11039875.0	Ab	14916713.1	Ba	5257071.3	Cc
FA 16:1	3582455.7	Ba	3393014.9	Ba	3817315.8	Aa	985837.2	ABb	1059946.6	Ab	788173.1	Bb	1092636.9	Ab	545838.5	Bc	514184.4	Bc	NA	Bc	1105906.4	Ab	NA	Bd
FA 16:2	21087231.1	Aa	20640021.0	Aa	22308069.4	Aa	12699031.8	Ab	12471901.4	Ab	10223858.2	Ab	9568985.6	Ac	6758084.9	Bc	6562711.2	Bc	5096861.1	Bd	13021236.3	Ab	3919362.9	Bc
FA 16:3	11434355.1	Aa	11177304.1	Ab	12506387.4	Aa	13177225.1	Aa	13116771.0	Aab	10969714.0	Aab	11257487.4	Aa	7895542.7	Bc	7894412.8	Bb	6513933.5	Bb	14340604.7	Aa	8552358.1	Bb
FA 16:4	65158.4	Ab	65660.2	Aa	68731.3	Aa	117478.7	Aa	72046.3	Ba	34774.4	Cb	134350.6	Aa	27601.0	Bb	23692.7	Bb	72017.5	Ab	69365.3	Aa	23214.9	Bb
FA 16:4.1	18252.8	Aa	17680.2	Aa	18997.8	Aa	14771.4	Aa	11442.9	Aab	10010.3	Ab	13015.2	Aab	5327.3	Bb	6618.9	Bb	7324.6	Ab	10868.8	Ab	5548.9	Ab
FA 18:0	3056622.4	ABa	3359515.3	Aa	2673021.0	Ba	2395989.9	Ab	1940209.7	ABb	1555460.7	Bb	2060584.5	Ab	1445528.5	Bb	1282383.2	Bb	1396697.5	Ac	1791255.0	Ab	682290.0	Bc
FA 18:1	39825596.5	Aab	41688413.5	Aa	38103453.3	Aa	36474640.0	Aab	34373433.2	Aa	23190768.0	Bb	42533822.9	Aa	19178154.0	Bb	18468524.2	Bbc	30456098.4	Bb	42233612.1	Aa	12762091.1	Cc
FA 18:2	59149335.7	Aa	58531511.5	Aa	63277251.7	Aa	36557043.6	Ab	38166657.8	Ab	31473844.3	Ab	31425304.9	Ab	20812580.3	Bc	20352139.0	Bc	21428685.7	Bc	38648513.5	Ab	17324300.0	Bc
FA 18:3	53250187.5	Aa	52138049.6	Aa	59133448.5	Aa	49729454.6	Aa	52628312.4	Aa	42278918.4	Ab	45596756.7	Aa	30804743.3	Bb	31019220.3	Bb	31344404.4	Bb	56854786.2	Aa	35231499.7	Bb
FA 18:4	29751.8	ABa	28367.4	Ba	33162.5	Aa	24130.4	Ab	24418.7	Aa	18119.4	Bb	18868.5	Ac	12583.2	Bc	11628.6	Bc	7988.3	Bd	18621.3	Ab	12465.5	Bc
FA 20:0	119289.1	Aa	124608.9	Aa	118244.7	Aa	111904.1	Aa	97931.5	Aa	71911.4	Bb	97268.2	Aab	63217.8	Bb	54782.5	Bbc	73928.8	Bb	100514.7	Aa	37745.9	Cc
FA 20:1	NA	Ac	NA	Ac	NA	Ab	338739.9	ABa	415790.7	Aa	258193.8	Ba	371445.2	Aa	207682.7	Bb	188763.1	Ba	177101.6	Bb	268464.4	Ab	160140.3	Ba
FA 20:3	133819.2	Ba	125293.6	Ba	159420.7	Aa	77983.5	Bb	116963.8	Aa	80875.9	Bb	63048.6	Ab	57667.4	Ab	52782.5	Ac	30525.8	Bc	73367.9	Ab	56282.5	Abc
FA 22:0	53749.9	Aa	56037.8	Ab	65473.9	Aa	49479.9	Ba	77063.6	Aa	51829.8	Bab	47868.9	Aa	39290.7	Ab	43540.8	Ab	38615.2	Aa	46160.0	Ab	43401.3	Ab
FA 22:1	56110.9	Ba	77435.6	Aa	45396.9	Ca	31569.6	Ab	30320.9	Ab	24069.7	Ab	26775.8	Abc	16109.0	Bc	15496.6	Bb	17512.6	Ac	12740.5	Ac	19379.2	Ab
FA 24:1	6039.4	Ba	8074.9	Aa	4790.6	Ca	3333.2	Ab	3377.2	Ab	2835.3	Abc	2655.4	Abc	2207.0	Ac	2076.7	Ac	1912.4	Bc	1753.4	Bc	3125.7	Ab
FA 26:0	666283.1	Ba	547234.5	Ca	904797.3	Aa	195371.5	Ab	175675.8	ABb	119709.5	Bb	99962.7	Ac	96865.8	Ab	103085.7	Ab	60618.3	Ac	121669.8	Ab	130063.3	Ab
FA 28:0	110278.0	Aa	103878.1	Aa	141394.7	Aa	116787.2	Aa	206716.9	Aa	94102.4	Aa	45567.6	Ab	45683.0	Ab	80037.2	Ab	49446.5	Ab	51462.2	Ab	49283.9	Ab
FA 30:0	18480.7	Aa	20337.5	Ab	33624.1	Aa	37379.8	Ba	66621.6	Aa	27592.6	Ba	10761.3	Aa	14553.8	Ab	27671.4	Aa	30833.7	Aa	14760.8	Ab	18659.4	Aa
FA 30:1	3174.4	Aa	3057.4	Aa	2930.7	Ba	3595.9	Aa	3005.7	Aa	2350.8	Ba	2961.1	Ab	1858.6	Ab	1844.2	Bb	2427.7	Ab	2790.7	Ab	1460.8	Bb

SI Table 9. Relative abundance of lipid of *Scenedesmus obliquus* BR003 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N So	0h 3.5N So	0h 7N So	10h 0N So	10h 3.5N So	10h 7N So	18h 0N So	18h 3.5N So	18h 7N So	36h 0N So	36h 3.5N So	36h 7N So
DAG 34:1	34926.9 Ac	20287.4 Aa	18494.9 Aa	30069.7 Ac	25568.7 Aa	28156.6 Aa	77255.4 Ab	21234.5 Ba	16537.1 Ba	112932.3 Aa	23550.6 Ba	10914.1 Ba
DAG 34:2	85890.0 Aa	17300.3 Ba	15168.4 Ba	31155.0 Aa	14703.2 Ba	15401.5 Ba	71853.4 Aa	NA Ba	11908.1 Ba	117671.8 Aa	24810.5 Ba	12043.2 Ba
DAG 34:3	29581.2 Ac	20094.5 Ab	18783.3 Aa	51463.7 Ac	24256.8 Bb	25305.4 Ba	121282.9 Ab	29260.5 Bab	21410.9 Ba	216984.9 Aa	52026.4 Ba	19902.7 Ca
DAG 34:4	12391.4 Ab	6392.6 ABa	4803.9 Bab	16396.2 Ab	NA Ca	7400.1 Ba	NA Ac	NA Aa	NA Ab	70367.2 Aa	NA Ba	4454.2 Bab
DAG 34:5	8873.7 Ac	5525.6 Aab	4936.0 Aa	12684.8 Ac	NA Bb	NA Ba	28959.6 Ab	6958.0 Ba	5040.3 Ba	54332.1 Aa	8401.9 Ba	4145.1 Ba
DAG 34:6	5562.3 Ac	4218.8 Aa	3862.9 Aa	9863.6 Ac	4926.5 Aa	5179.2 Aa	25280.5 Ab	8012.6 Ba	5861.3 Ba	41374.4 Aa	7958.2 Ba	5049.8 Ba
DAG 36:1	2103.5 Ac	2428.0 Aa	1928.3 Aab	3192.3 Ac	2986.0 Aa	3263.7 Aa	7399.8 Ab	1823.6 Ba	1216.8 Bbc	9808.7 Aa	1149.0 Ba	NA Bc
DAG 36:2	239023.9 Aa	39242.3 Ba	38250.9 Ba	94155.9 Aa	103759.9 Ba	100673.8 Ba	175097.0 Aa	70539.4 Ba	71486.9 Ba	260151.4 Aa	75672.3 Ba	40482.4 Ba
DAG 36:3	173021.2 Aa	36390.8 Ba	35674.5 Ba	65339.8 Aa	52530.1 Ba	54687.2 Ba	142228.0 Aa	44107.4 Ba	37519.6 Ba	197597.7 Aa	55283.4 Ba	25044.3 Ba
DAG 36:4	44886.2 Ac	29988.2 Ab	30963.6 Aa	61239.0 Ac	53638.2 Aab	52934.3 Aa	128193.5 Ab	55288.0 Bab	46101.9 B	231360.2 Aa	65862.8 Ba	59618.1 Ba
DAG 36:5	32762.1 Ac	23636.3 Aa	23112.8 Aa	33581.6 Ac	22482.4 Aa	24896.2 Aa	85410.1 Ab	33378.2 Ba	24665.0 Ba	138605.8 Aa	33531.6 Ba	37837.3 Ba
DAG 36:6	19038.3 Ac	16262.9 Ac	18290.6 Ab	32720.4 Ac	31389.1 Abc	32914.8 Ab	77018.7 Ab	55316.3 Ba	35214.4 Cb	100974.2 Aa	37674.5 Cab	71276.9 Ba
DGDG 32:0	221370.0 Ac	203496.2 Aab	212958.6 Ab	272004.5 Aab	182602.0 Bb	188433.2 Bbc	309658.8 Aa	184485.9 Bb	150513.6 Bc	241652.9 Abc	239161.7 Aa	261136.2 Aa
DGDG 32:1	68018.2 Aa	51515.6 Ba	52569.7 Ba	21929.2 Ab	25110.2 Ab	26768.2 Ab	24530.4 Ab	22190.6 Ab	18025.9 Ab	20777.7 Bb	24619.2 Bb	59769.4 Aa
DGDG 32:2	72026.6 Aa	47919.8 Ba	40885.3 Ba	30104.3 Ab	35844.9 Aab	36343.4 Aab	30742.3 Ab	26837.8 Ab	23166.6 Ab	26738.3 Bb	23325.4 Bb	43065.6 Aa
DGDG 32:3	71588.2 Aa	51263.1 ABb	41623.1 Bc	40792.2 Bb	78381.2 Aa	72264.9 Ab	47639.1 Bab	78990.2 Aa	66626.6 ABb	37738.0 Bb	58788.5 Bab	152829.6 Aa
DGDG 32:3.1	22083.2 Aa	20230.3 Ac	18809.5 Ac	25071.1 Ba	90631.7 Aa	80200.8 Ab	36641.7 Ba	78081.3 Aab	77898.8 Ab	49392.2 Ba	50319.7 Bbc	171849.1 Aa
DGDG 34:0	612443.4 ABa	532586.0 Ba	643455.6 Aa	322512.5 Ab	222566.7 Bb	221751.5 Bb	295063.0 Ab	194009.7 Bb	151005.7 Bb	245425.5 Ab	160487.9 ABb	143784.5 Bb
DGDG 34:1	2555996.3 Aa	2506799.6 Aa	2596965.8 Aa	1830896.3 Ab	1844437.4 Ab	1935525.8 Ab	1969270.6 Ab	1814174.3 Ab	1640732.1 Ab	1823395.8 Ab	1989709.1 Ab	2026765.6 Ab
DGDG 34:2	1487656.6 Ab	1417853.1 Ab	1360782.2 Ac	1849813.3 Bab	2394648.6 Aa	2533929.4 Aa	1952498.2 Aa	2126533.4 Aa	2053647.7 Ab	1850352.1 Bab	2138525.2 ABa	2322421.0 Aab
DGDG 34:3	565658.9 Ab	557725.4 Ab	456114.9 Ab	1392950.6 Ba	2593232.7 Aa	2740558.2 Aa	1596075.4 Ba	2596579.9 Aa	2440187.2 Aa	1640718.2 Ca	2234407.5 Ba	2811278.3 Aa
DGDG 34:4	1077565.4 Aa	747240.2 Ba	628887.1 Bb	786216.2 Ab	706921.4 Aa	760978.9 Aab	827760.1 Aab	684134.9 Aa	594499.2 Ab	670904.0 Bb	692440.4 Ba	986577.7 Aa
DGDG 34:5	1268418.7 Aa	1275237.1 Ab	1093556.3 Ab	1322614.1 Ba	1814394.6 Aa	1844966.8 Aa	1537567.8 Aa	1773359.1 Aa	1650950.7 Aa	1530779.1 Ba	1614071.7 Bab	2062059.4 Aa
DGDG 34:6	1035707.7 Ac	937906.9 Ab	806229.6 Ab	1594282.7 Bbc	2675137.8 Aa	2695872.9 Aa	2017300.9 Bab	2844685.3 Aa	2704310.3 Aa	2165238.7 Ba	2440549.5 Ba	3034656.3 Aa
DGDG 36:3	53189.4 Aa	43652.4 Aa	35790.1 Ab	41044.7 Aab	51037.5 Aa	56918.2 Ab	35906.4 Bab	59612.9 Aa	51265.3 ABb	24088.9 Bb	60282.3 Aa	79292.3 Aa
DGDG 36:4	66541.0 Aa	51461.7 Ba	NA Ca	31482.1 Ab	NA Bb	NA Ba	33928.4 Ab	NA Bb	NA Ba	23965.9 Ab	NA Bb	NA Ba
DGDG 36:5	220253.2 Aa	168550.0 Bab	131800.6 Bb	74007.4 Bb	135218.7 Ab	135870.4 Ab	78662.4 Bb	127144.7 Ab	111670.7 ABb	56592.0 Cb	192537.8 Ba	531978.3 Aa
DGDG 36:6	352845.3 Aa	245726.1 Ba	196136.8 Bb	132139.4 Bb	315579.7 Aa	284876.8 Ab	134495.0 Bb	309922.1 Aa	260621.7 Ab	97360.6 Cb	361995.5 Ba	1343396.5 Aa

SI Table 9. (continuation) Relative abundance of lipid of *Scenedesmus obliquus* BR003 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N So	0h 3.5N So	0h 7N So	10h 0N So	10h 3.5N So	10h 7N So	18h 0N So	18h 3.5N So	18h 7N So	36h 0N So	36h 3.5N So	36h 7N So
LysoPC 16:0	27481.1 Aa	27079.9 Aa	28171.7 Aa	15233.5 Ab	15758.9 Ab	13347.9 Ab	18668.7 Ab	14334.9 Ab	14253.6 Ab	19429.2 Bb	11651.9 Cb	29388.9 Aa
LysoPC 16:0.1	1969.8 Aa	1994.6 Aa	1973.5 Aa	1173.9 Aa	1167.4 Ab	966.2 Ab	1545.1 Aa	835.8 Ab	955.9 Ab	1580.5 Ba	NA Cc	2333.1 Aa
LysoPC 16:2	1860.9 Aa	2530.4 Aa	NA Bc	NA Bb	1459.9 Ab	NA Bc	NA Bb	994.2 Ab	1040.0 Ab	NA Bb	NA Bc	3631.4 Aa
LysoPC 16:3	2713.1 Aa	3277.9 Aa	793.5 Bb	NA Ab	1553.9 Aab	NA Ab	NA Ab	1380.2 Ab	1568.1 Ab	NA Bb	NA Bb	5849.9 Aa
LysoPC 18:2	25288.0 Aa	37197.0 Aa	17561.8 Ab	5694.4 Aa	19574.3 Aa	14250.8 Ab	7867.7 Aa	21835.0 Aa	18102.5 Ab	8055.9 Ba	25226.0 Ba	94306.6 Aa
LysoPC 18:3	24069.9 Aa	41069.4 Aa	17898.6 Ab	7892.3 Aa	58148.9 Aa	37623.8 Ab	10325.0 Aa	49981.4 Aa	48639.3 Ab	8938.0 Ba	33878.7 Ba	239921.3 Aa
MGDG 34:1	352999.9 Aa	359752.2 Aa	306101.9 Aa	108979.2 Bb	342445.2 Aa	257858.4 Aab	202932.3 Ab	176162.3 Ab	151728.5 Ab	131062.8 Bb	163735.1 ABb	254022.7 Aab
MGDG 34:2	778679.8 Aa	392061.3 Ba	414340.3 Ba	43278.4 Bb	149737.1 Abc	122922.9 ABb	75849.2 Bb	213968.7 Ab	123257.3 ABb	54675.4 Bb	56395.5 Bc	419637.9 Aa
MGDG 34:2.1	77198.2 Aa	112538.5 Ab	80580.1 Ab	48639.7 Ba	245420.2 Aa	202706.2 Aa	64380.8 Aa	61601.5 Ab	75277.3 Ab	61209.1 Aa	65006.2 Ab	87508.3 Ab
MGDG 34:3	32558.7 Aa	13051.3 Aa	9993.3 Aa	2429.5 Aab	14839.0 Aab	11706.1 Aab	3014.6 Aab	8471.4 Aab	6634.4 Aab	2384.8 Ab	3473.6 Ab	5666.4 Ab
MGDG 34:4	1396832.1 Aa	974785.8 Ba	675483.0 Bb	146855.4 Bb	766255.7 Aab	634167.0 Ab	216362.3 Bb	472910.5 ABbc	543644.1 Ab	151107.2 Bb	338907.5 Bc	1131802.3 Aa
MGDG 34:5	3441846.7 Aa	2488098.6 Ba	1867885.7 Bb	917382.3 Bb	2079202.7 Aa	1882041.5 Ab	1492898.8 Ab	1978569.3 Aa	1842429.0 Ab	1213341.7 Bb	1657094.2 Ba	3382334.6 Aa
MGDG 34:6	1491626.2 Aa	1101496.8 ABbc	774258.4 Bb	325246.9 Bb	2043599.5 Aa	1646786.6 Aa	671486.1 Bb	1642072.9 Aab	1950432.5 Aa	328644.1 Bb	882170.5 Bc	1685035.3 Aa
MGDG 36:5	NA Ba	134553.0 Aa	NA Bb	NA Ba	93711.0 Ab	NA Bb	NA Ba	97845.4 Ab	NA Bb	NA Ba	NA Bc	242632.8 Aa
MGDG 36:6	96308.4 Aa	103211.2 Aa	75179.0 Ab	14283.9 Bb	80720.5 Aa	60871.0 ABb	18230.9 Bb	84266.5 Aa	83824.9 Ab	12341.2 Cb	81619.5 Ba	751130.3 Aa
PC 32:0	24169.3 Aa	22990.0 Aa	25567.1 Aa	13650.4 Ab	11787.9 ABb	10420.9 Bb	13070.3 Ab	8611.7 Bb	10930.9 ABb	21542.5 Aa	9546.2 Bb	11496.1 Bb
PC 32:1	60010.8 ABa	68525.5 Aa	55314.9 Ba	37076.6 Ab	42019.8 Abc	36595.1 Ac	34733.4 ABb	30699.6 Bc	43158.7 Abc	58067.3 Aa	49154.8 Ab	50377.2 Aab
PC 32:1.1	35311.8 Aa	39415.8 Aab	25384.2 Ab	10471.1 Bb	50653.8 Aa	32670.0 Ab	12295.6 Bb	33017.6 Aab	31485.8 ABb	NA Cb	26011.9 Bb	66404.4 Aa
PC 32:2	12473.9 ABa	19457.4 Aab	NA Bc	2225.9 Ba	31512.7 Aa	17826.8 Ab	3337.3 Aa	16862.4 Aab	16627.8 Ab	NA Ba	9823.5 Bb	42531.8 Aa
PC 32:3	14819.9 Aa	22258.8 Aa	6841.3 Ab	2555.7 Ba	25184.5 Aa	15096.0 ABb	3787.3 Aa	18239.3 Aa	17412.7 Ab	2873.5 Ba	10764.2 Ba	48213.2 Aa
PC 34:1	NA Ab	NA Aa	NA Aa	10108.8 Aa	NA Ba	NA Ba	NA Ab	NA Aa	NA Aa	NA Ab	NA Aa	NA Aa
PC 34:3	147289.9 Aa	205344.7 Aa	88983.6 Ab	40496.0 Ba	481604.4 Aa	265886.3 ABb	47747.7 Aa	335520.8 Aa	320935.0 Ab	45878.1 Ba	199954.6 Ba	1350004.1 Aa
PC 34:4	99435.3 Aa	145448.9 Aa	51705.4 Ab	23993.7 Aa	153013.6 Aa	95395.5 Ab	33907.5 Aa	121848.3 Aa	96305.7 Ab	29654.6 Ba	91256.5 Ba	646597.8 Aa
PC 34:5	31668.3 Aa	48306.4 Aa	17737.8 Ab	6612.7 Aa	52954.9 Aa	30315.1 Ab	7471.7 Aa	46184.2 Aa	39233.9 Ab	5826.1 Ba	24084.3 Ba	158514.3 Aa
PC 34:6	21403.1 Aa	35093.2 Aa	10993.3 Ab	5139.2 Aa	53954.5 Aa	30847.7 Ab	6261.1 Aa	55517.8 Aa	48573.7 Ab	4435.9 Ba	25137.4 Ba	206579.8 Aa
PC 36:1	478722.8 Ba	615454.8 Aa	435676.6 Ba	344935.1 Ab	430796.1 Ab	415715.5 Aa	293669.9 Bb	429300.5 Ab	459819.0 Aa	367784.3 Bb	571962.8 Aa	402786.3 Ba
PC 36:2	10925226.0 Ba	13830934.5 Aa	10075490.8 Bb	6403139.5 Bb	10397523.1 Ac	9033402.6 Ab	5483528.3 Bb	10766733.7 Abc	11136063.3 Aab	7360846.6 Bb	13476082.3 Aab	13032454.9 Aa
PC 36:3	NA Bc	NA Ba	68678.8 Aa	47034.1 Ab	NA Ba	NA Bb	NA Ac	NA Aa	NA Ab	58692.0 Aa	NA Ba	NA Bb
PC 36:3.1	684868.0 ABa	822987.5 Aab	580784.8 Ba	375002.4 Bb	660460.3 Ab	529605.6 ABa	277966.3 Bb	690531.0 Aab	630967.4 Aa	352708.2 Cb	885007.6 Aa	674094.7 Ba

SI Table 9. (continuation) Relative abundance of lipid of *Scenedesmus obliquus* BR003 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N So	0h 3.5N So	0h 7N So	10h 0N So	10h 3.5N So	10h 7N So	18h 0N So	18h 3.5N So	18h 7N So	36h 0N So	36h 3.5N So	36h 7N So
PC 36:5	193545.9 Aa	283073.2 Aa	99563.4 Ab	36804.1 Aa	382738.8 Aa	222950.3 Ab	47988.3 Aa	389521.0 Aa	287297.9 Ab	43420.3 Ba	309551.7 Ba	2127094.6 Aa
PC 36:6	135205.9 Aa	207824.2 Aa	87418.8 Ab	25629.7 Aa	1108955.0 Aa	494364.5 Ab	40058.8 Aa	851729.5 Aa	716290.9 Ab	27641.1 Ba	402114.1 Ba	4679244.8 Aa
PC 38:2	122997.7 Ba	160537.0 Aa	106886.8 Ba	83071.8 Bb	135707.5 Aab	119513.0 Aa	65682.7 Bb	113415.2 Ab	122119.0 Aa	81083.3 Bb	116418.5 Ab	130318.6 Aa
PC 38:3	3722.9 Aa	4374.9 Aa	3147.0 Ab	NA Aa	1696.5 Aa	NA Ab	NA Aa	2283.0 Aa	2266.7 Ab	NA Ba	2871.5 Ba	14987.5 Aa
PC 38:3.1	8170.6 ABa	8978.9 Aa	6886.1 Ba	4938.9 Bb	7864.3 Aa	6743.7 Aa	4753.5 Bb	7658.5 Aa	6688.2 Aa	4746.4 Bb	8078.2 Aa	6996.0 Aa
PE 32:1	181006.0 Aa	214188.2 Ac	185031.1 Ab	112627.8 Ca	548933.3 Aa	443943.4 Ba	102598.6 Ca	331289.4 Bb	451768.5 Aa	164670.3 ABa	218084.7 Ac	97994.3 Bc
PE 34:1	277134.8 Aa	320709.4 Ab	305217.9 Ab	182861.8 Cb	578010.4 Aa	481856.9 Ba	162445.6 Cb	320361.4 Bb	424053.7 Aa	239187.4 Aab	251861.9 Ab	242333.4 Ab
PE 34:2	1069825.8 Aa	1261406.4 Ac	1093879.0 Ab	675265.0 Cab	2969242.2 Aa	2366274.0 Ba	535838.9 Bb	2044119.4 Ab	2314037.4 Aa	757637.7 Bab	2002332.7 Ab	2230663.3 Aa
PE 34:3	39696.7 Aa	54717.8 Ab	43972.7 Ac	26614.6 Ca	99076.2 Aa	72556.9 Bb	29286.4 Ba	65669.3 Ab	85858.5 Ab	41608.9 Ba	43741.1 Bb	135116.3 Aa
PE 34:4	5670.6 ABa	NA Bc	6402.3 Ab	3144.0 Ba	17398.0 Aa	14128.4 Aa	4683.1 Ba	10616.4 Ab	13667.3 Aa	4119.4 Ba	6098.2 Bbc	15554.7 Aa
PE 34:5	5172.1 Aa	8832.5 Ab	4173.2 Ab	2171.3 Ba	22221.4 Aa	14355.0 Aab	3358.4 Ba	14595.1 ABab	19226.3 Aa	1921.3 Ba	5640.5 Bb	21077.2 Aa
PE 34:6	2685.7 Aa	4600.1 Ab	NA Ab	NA Ba	18450.6 Aa	13123.8 Aa	2219.6 Ba	13397.6 Aab	20018.8 Aa	NA Ba	3027.6 Bb	22111.6 Aa
PE 36:2	2741013.6 Aa	3364562.0 Abc	2826953.7 Ac	1492321.8 Cb	7218189.2 Aa	6034886.0 Ba	1146038.6 Bb	3999922.9 Ab	4300242.5 Ab	1205362.4 Bb	2677047.3 Ac	3475750.5 Abc
PE 36:3	51499.2 Aa	66606.7 Ac	48658.9 Ac	23820.3 Ba	596309.0 Aa	583133.1 Aa	14776.6 Ba	295874.4 Ab	265520.1 Ab	8975.8 Ba	128381.9 Ac	136276.3 Ac
PE 36:3.1	151719.9 Aa	173045.1 Aa	146879.0 Aa	87172.2 Ab	NA Bb	NA Bb	70871.4 Ab	NA Bb	NA Bb	106740.9 Ab	NA Bb	NA Bb
PE 36:4	44099.1 Aa	52410.3 Ab	45438.0 Ac	29890.4 Ba	116776.6 Aa	110751.1 Ab	29185.3 Ca	105436.6 Ba	181898.3 Aa	43097.0 Ca	124004.4 Aa	68849.1 Bc
PE 36:4.1	220613.3 Aa	271409.8 Aa	237388.5 Aa	117370.9 Ba	NA Bb	267776.8 Aa	98061.9 Ba	250491.8 Aa	300453.6 Aa	137242.3 Ba	267676.2 Aa	NA Cb
PE 36:5	94368.6 Aa	155278.2 Ab	60462.5 Ab	22577.7 Ba	599046.6 Aa	406186.2 Aa	40063.5 Ba	328229.7 Aab	430114.1 Aa	24481.0 Ba	149470.0 Bb	688981.5 Aa
PE 36:6	53629.0 Aa	83001.6 Ab	34302.1 Ac	14308.5 Ba	684265.1 Aa	437487.2 ABbc	24754.1 Ba	448757.5 ABab	611958.1 Ab	12053.2 Ba	102430.5 Bb	1185973.7 Aa
PE 38:2	6236041.3 Aa	6756510.0 Aa	6622333.3 Ab	3235740.3 Bb	5725711.8 Aab	5283593.7 Ab	2488441.7 Cb	3908675.5 Bc	5525349.2 Ab	2731272.6 Cb	4814100.3 Bbc	8560484.1 Aa
PE 38:3	12517.3 Aa	16579.4 Ac	10769.5 Ad	4188.3 Ba	75693.4 Aa	66824.2 Aa	3468.6 Ba	46788.5 Ab	52379.1 Ab	NA Ca	17103.5 Bc	28512.7 Ac
PE 40:1	20122.2 Ba	21038.5 Aa	18942.8 Aa	8855.7 Bb	13211.1 Ab	14790.3 Ab	8087.7 Bb	11003.8 Ab	12904.1 Ab	8548.1 Bb	10547.2 Ab	10293.4 Ab
PE 40:2	440047.5 Ba	495117.8 Aa	378480.0 ABa	284508.0 Bb	368054.1 Ab	315704.3 ABb	261798.6 Bb	324586.0 Ab	401456.5 ABb	384894.5 Ba	443136.0 Aa	376959.5 ABa
PE 40:3	7816.7 Aa	NA Bb	7448.2 Aa	NA Bc	10016.0 Aa	NA Bb	2673.0 Ab	NA Bb	NA Bb	NA Ac	NA Ab	NA Ab
PG 32:0	45951.2 Aa	53389.5 Aa	45628.6 Aa	20470.4 Bb	49862.3 Aa	29714.0 Bab	19071.7 Ab	26003.5 Ab	28325.6 Ab	22173.5 Bb	18998.9 Bb	43831.2 Aab
PG 32:1	17245.2 Aa	20446.5 Ab	16000.0 Ab	8435.6 Bb	27185.4 Aa	23259.6 Aa	6670.7 Cb	13896.2 Bc	27426.9 Aa	10299.9 Ab	5088.1 ABd	4396.3 Bc
PG 34:2	166981.0 Ba	231846.4 Ab	179397.7 Bc	NA Cb	316093.6 Aa	254717.1 Bb	NA Cb	217374.4 Bb	304330.4 Aab	NA Bb	NA Bc	309889.9 Aa
PG 34:3	17270.1 Aa	21741.2 Aab	11490.2 Ab	4408.5 Ba	44171.3 Aa	25954.6 ABb	4924.1 Ba	25134.3 ABab	29214.5 Ab	NA Ba	12786.2 Bb	63288.0 Aa
PG 34:4	31418.8 Aa	42721.8 Aa	24492.8 Ab	6916.1 Ba	143367.1 Aa	88440.8 ABb	8777.2 Aa	75504.4 Aa	86704.2 Ab	4918.1 Ba	33702.2 Ba	386644.7 Aa

SI Table 9. (continuation) Relative abundance of lipid of *Scenedesmus obliquus* BR003 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N So	0h 3.5N So	0h 7N So	10h 0N So	10h 3.5N So	10h 7N So	18h 0N So	18h 3.5N So	18h 7N So	36h 0N So	36h 3.5N So	36h 7N So
PG 36:1	105255.8 Aa	111475.4 Abc	110344.3 Ab	71563.5 Bb	186868.8 Aa	168158.1 Aa	55752.4 Cb	130214.9 Bb	161005.2 Aa	62500.9 Bb	97684.8 Ac	80692.6 ABb
PG 36:2	1104754.8 Aa	1176600.3 Abc	1125037.5 Ab	647076.8 Bb	1775498.1 Aa	1587492.2 Aa	494230.2 Bb	1387826.4 Ab	1555661.4 Aa	499753.2 Bb	1095928.5 Ac	1058196.6 Ab
SQDG 32:0	5160100.7 Aa	4887323.8 Aa	5062432.2 Aa	3001919.0 Ab	2415083.8 Ab	2442353.5 Ab	3050068.1 Ab	2908015.0 Ab	2503348.2 Ab	2997191.3 Ab	3030098.9 Ab	3613859.9 Ab
SQDG 32:1	231702.7 Aa	217508.3 Aa	204529.3 Aa	58546.2 Ab	86057.9 Ab	81544.0 Ab	56171.4 Ab	76615.0 Ab	68945.1 Ab	37083.4 Bb	51036.3 Bb	176008.3 Aa
SQDG 32:2	19788.2 Aa	19284.2 ABa	17957.6 Ba	NA Ab	NA Ab	NA Ab	3497.6 Ab	NA Bb	NA Bb	2341.3 Ab	NA Bb	NA Bb
SQDG 32:3	13638.5 Aa	12794.5 Aa	12314.1 Aa	NA Bb	2751.4 Ab	3048.5 Ab	NA Ab	2188.3 Ab	2391.9 Ab	NA Bb	2621.6 Ab	4690.9 Ab
SQDG 34:0	430540.4 Aa	389628.0 Ba	438946.9 ABa	193469.7 Ab	171490.2 Bb	187093.5 ABb	214246.9 Ab	187056.7 Bb	145262.0 ABb	177810.7 Ab	118599.2 Bb	128442.3 ABb
SQDG 34:1	2229234.4 Aa	1940372.1 Aa	2084238.1 Aa	577317.6 Bb	1607547.5 Aa	1638386.6 Abc	779744.3 Bb	1555256.3 Aa	1256590.3 Ac	NA Cc	944983.9 Bb	1892026.3 Aab
SQDG 34:2	1941765.2 Aa	1864199.2 Aa	1719938.4 Aab	1130157.5 Bb	1915119.0 Aa	2019682.0 Aab	1131074.8 Bb	1533017.7 ABab	1612368.5 Ab	1030195.9 Bb	1319010.7 Bb	2115626.5 Aa
SQDG 34:3	3043717.3 Aa	3049968.8 Ab	2789384.4 Ac	1756361.9 Bb	4472025.5 Aa	4336485.2 Ab	1947107.8 Bb	4471805.3 Aa	4113282.9 Ab	1494145.5 Cb	2840512.7 Bb	6670922.1 Aa
SQDG 34:4	40998.0 Aa	41578.9 Aa	35442.7 Ab	15880.9 Bb	27000.5 Ab	28137.8 Abc	15418.3 Ab	21426.9 Ab	20747.4 Ac	8916.4 Cb	18566.1 Bb	47243.7 Aa
SQDG 34:5	22195.5 Aa	22270.8 Aa	17987.6 Aab	6958.9 Bb	12866.4 Ab	14291.6 Ab	6668.2 Bb	10302.8 ABbc	13659.0 Ab	3475.8 Bb	7216.7 Bc	21368.9 Aa
SQDG 34:6	18751.6 Aa	19344.2 Aa	16774.7 Ab	4892.5 Bb	13623.1 Ab	14474.4 Ab	4748.2 Cb	10975.2 Bbc	17281.4 Ab	1942.9 Cb	6700.3 Bc	28591.4 Aa
TAG 42:0	18590.4 Ab	17511.1 Aa	18341.2 Aa	15860.0 Ab	10808.4 Aa	14970.3 Aa	21131.0 Aab	13285.8 Ba	12111.3 Ba	27245.1 Aa	13422.1 Ba	12343.3 Ba
TAG 42:1	15131.7 Ac	15442.2 Aa	18717.3 Aa	17828.4 Abc	9153.7 Ba	11956.7 Bb	22910.1 Ab	9603.0 Ba	NA Cc	30981.7 Aa	11072.9 Ba	9406.5 Bb
TAG 42:2	2134.9 Ac	NA Bb	NA Bb	2721.4 Ac	NA Bb	2254.7 Aa	4916.5 Ab	NA Cb	1660.4 Ba	7331.8 Aa	1654.1 Ba	1972.5 Ba
TAG 44:0	58188.0 Aab	54389.2 Aa	60108.0 Aa	48443.4 Ab	34502.5 Aa	43664.9 Aab	57902.7 Aab	36528.2 Ba	37287.8 Bb	77896.2 Aa	39831.7 Ba	36526.7 Bb
TAG 44:1	37802.4 Ab	39188.2 Aa	36427.4 Aa	37072.5 Ab	25835.1 Aa	30248.4 Aa	50126.0 Ab	26778.5 Ba	25691.7 Ba	87581.6 Aa	28761.6 Ba	32583.2 Ba
TAG 44:2	22451.7 Ab	20674.5 Aa	22395.6 Aa	22378.2 Ab	13707.2 Ba	15117.9 ABab	28974.2 Ab	13281.9 Ba	13273.7 Bb	39560.4 Aa	15325.4 Ba	13553.9 Bb
TAG 46:0	182369.6 Ab	157776.5 Aa	193448.2 Aa	174224.0 Ab	110065.1 Aa	136779.2 Aab	226769.0 Ab	107161.4 Ba	112726.2 Bb	365745.3 Aa	119306.2 Ba	116982.2 Bb
TAG 46:1	NA Ac	NA Ab	NA Aa	NA Ac	NA Ab	NA Aa	169356.3 Ab	NA Bb	NA Ba	297515.9 Aa	78854.0 Ba	NA Ca
TAG 46:2	NA Ad	NA Ab	NA Aa	31322.4 Ac	NA Bb	NA Ba	57296.4 Ab	NA Bb	NA Ba	112388.8 Aa	23921.1 Ba	NA Ca
TAG 46:2.1	37420.0 Aa	37176.0 Aa	37180.5 Aa	25158.2 Bb	28126.7 ABab	37671.3 Aa	NA Bc	26482.8 Aab	30764.8 Aa	NA Bc	24318.4 Ab	33307.1 Aa
TAG 46:3	5216.0 Ac	5066.5 Aa	4901.3 Aa	11077.1 Ac	4243.8 Aa	4759.0 Aa	25265.6 Ab	7315.8 Ba	6306.5 Ba	54458.5 Aa	7600.0 Ba	3480.2 Ba
TAG 46:3.1	6176.2 Ab	5448.5 Aa	5556.7 Aa	6520.0 Ab	3055.4 Bb	4304.2 Ba	6173.4 Ab	2940.7 Bb	3450.7 Ba	8984.4 Aa	3239.2 Bab	3564.4 Ba
TAG 46:4	NA Ad	NA Aa	NA Aa	1756.6 Ac	NA Ba	NA Ba	4684.5 Ab	1316.3 Ba	904.7 Ba	10933.0 Aa	NA Ba	NA Ba
TAG 48:0	877361.9 Ad	753938.9 Aa	876857.2 Aa	4050115.8 Ac	494802.4 Ba	585454.9 Ba	8594256.3 Ab	641261.8 Ba	436574.2 Ba	16684849.4 Aa	1592627.3 Ba	415994.7 Ba
TAG 48:1	356761.7 Ac	432913.8 Aa	306843.5 Aa	1017402.1 Ac	303735.4 Ba	360267.3 Ba	2123296.8 Ab	358557.1 Ba	286304.4 Ba	4931052.2 Aa	616857.0 Ba	242920.6 Ba
TAG 48:2	88447.0 Ad	102966.4 Aa	NA Aa	291428.5 Ac	71096.6 Ba	85666.7 Ba	670283.9 Ab	92345.2 Ba	71425.3 Ba	1614262.1 Aa	171379.4 Ba	50249.7 Ba

SI Table 9. (continuation) Relative abundance of lipid of *Scenedesmus obliquus* BR003 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N So		0h 3.5N So		0h 7N So		10h 0N So		10h 3.5N So		10h 7N So		18h 0N So		18h 3.5N So		18h 7N So		36h 0N So		36h 3.5N So		36h 7N So	
TAG 48:3	25114.3	Ad	25818.9	Aa	21590.0	Aa	168992.5	Ac	25707.4	Ba	27971.1	Ba	429407.2	Ab	42026.5	Ba	28873.0	Ba	1122505.4	Aa	97869.6	Ba	15710.7	Ba
TAG 48:4	4747.6	Ad	4851.0	Aa	3512.0	Aa	24919.3	Ac	2769.3	Ba	2648.9	Ba	49631.9	Ab	4824.6	Ba	3544.4	Ba	121519.4	Aa	9971.6	Ba	1453.9	Ba
TAG 48:5	764.5	Ad	NA	Aa	NA	Aa	7458.6	Ac	NA	Ba	NA	Ba	17340.2	Ab	1799.8	Ba	NA	Ba	52354.6	Aa	2529.1	Ba	NA	Ba
TAG 48:6	NA	Ad	NA	Aa	NA	Aa	3764.9	Ac	NA	Ba	NA	Ba	10138.9	Ab	1324.2	Ba	NA	Ba	27685.4	Aa	NA	Ba	NA	Ba
TAG 48:7	NA	Ab	NA	Ab	NA	Aa	NA	Ab	NA	Ab	NA	Aa	NA	Ab	NA	Ab	NA	Aa	2943.6	Aa	758.3	Ba	NA	Ca
TAG 50:0	1193989.1	Ac	979182.5	Aa	1225418.9	Aa	2245144.2	Ac	605427.2	Ba	668504.7	Ba	4501948.4	Ab	601597.8	Ba	541759.2	Ba	7988425.6	Aa	761525.3	Ba	561094.5	Ba
TAG 50:1	6899376.7	Ad	6106301.7	Ab	5518185.0	Aa	39803128.6	Ac	7157808.0	Bb	7931794.0	Ba	82500723.2	Ab	8150809.4	Bab	5059264.9	Ba	131626461.9	Aa	23644273.2	Ba	2075442.8	Ca
TAG 50:2	1143042.9	Ad	1371345.6	Aa	1371855.3	Aa	13335930.9	Ac	1466090.7	Ba	1684813.7	Ba	34095668.7	Ab	1927382.1	Ba	1232327.5	Ba	68727966.0	Aa	7574957.7	Ba	670635.2	Ba
TAG 50:3	705456.0	Ad	678205.6	Ab	516300.6	Aa	9618439.3	Ac	897184.5	Bb	980706.6	Ba	27459842.1	Ab	1698145.4	Bab	815816.6	Ba	64996866.2	Aa	8087449.7	Ba	240692.1	Ca
TAG 50:4	194278.9	Ad	166647.5	Aa	124750.7	Aa	2590850.9	Ac	256600.2	Ba	266791.0	Ba	6949156.2	Ab	510479.6	Ba	248037.6	Ba	17323860.0	Aa	1369718.9	Ba	64508.8	Ba
TAG 50:5	51390.9	Ad	174367.8	Aa	35430.5	Aa	794380.4	Ac	54252.7	Ba	56994.4	Ba	2082693.2	Ab	111801.4	Ba	60342.6	Ba	5549670.0	Aa	347249.3	Ba	15230.9	Ba
TAG 50:6.1	18633.4	Ac	19714.8	Aa	14597.3	Aa	283650.9	Ac	27840.4	Aa	27304.9	Aa	880704.9	Ab	74235.5	Ba	39151.1	Ba	2554601.8	Aa	168879.8	Ba	9044.2	Ba
TAG 50:7	3389.4	Ac	4162.5	Aa	2754.3	Aa	26120.8	Ac	3215.5	Aa	4168.0	Aa	74152.0	Ab	9266.3	Ba	NA	Ba	225738.8	Aa	15963.5	Ba	NA	Ba
TAG 50:8	1648.4	Ac	2170.7	Aa	NA	Aa	18307.7	Ac	1120.5	Aa	1572.3	Aa	47404.2	Ab	4604.9	Ba	2595.9	Ba	165427.6	Aa	7580.6	Ba	NA	Ba
TAG 50:9	NA	Ac	NA	Aa	NA	Aa	13521.7	Ac	NA	Aa	NA	Aa	42157.1	Ab	3278.4	Ba	1737.0	Ba	142985.4	Aa	5102.7	Ba	NA	Ba
TAG 52:0	895704.8	Ab	820758.1	Aa	932795.1	Aa	664455.1	Ab	505399.2	Aa	538343.1	Ab	964949.9	Ab	494699.1	Ba	489095.7	Bb	1385056.8	Aa	462425.1	Ba	526489.9	Bb
TAG 52:1	4293230.5	Ad	4036415.3	Aa	3818622.3	Aa	12325581.7	Ac	3327402.4	Ba	3942922.5	Ba	25756092.7	Ab	3040185.6	Ba	2160362.2	Ba	44525360.0	Aa	4702711.1	Ba	1377995.3	Ba
TAG 52:2	12747897.3	Ad	11680518.2	Ab	9383274.7	Aab	65518373.8	Ac	21327826.2	Bb	22348388.3	Ba	110092597.1	Ab	21123567.3	Bb	14728543.8	Bab	164416202.3	Aa	40836427.7	Ba	5572904.6	Cb
TAG 52:3	3002694.6	Ad	2806192.9	Aa	2427444.8	Aa	22508344.2	Ac	4282750.9	Ba	4684329.7	Ba	49468128.8	Ab	4694167.1	Ba	3093652.8	Ba	98109037.5	Aa	13765619.5	Ba	1224535.9	Ca
TAG 52:4	1887557.0	Ad	1702043.4	Ab	1612960.1	Aa	14568630.8	Ac	3035996.6	Bb	3387102.7	Ba	37106491.8	Ab	4330000.6	Bab	2539580.2	Ba	78681822.1	Aa	12902566.7	Ba	938555.2	Ca
TAG 52:5	264355.7	Ad	253064.7	Aa	238359.5	Aa	3133951.5	Ac	572858.9	Ba	651896.2	Ba	8071115.4	Ab	878221.2	Ba	530799.4	Ba	18703968.4	Aa	1724262.1	Ba	133133.4	Ba
TAG 52:5.1	117311.7	Aa	157594.7	Aa	102028.7	Aa	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab
TAG 52:6	154030.0	Ad	133917.4	Aa	123186.4	Aa	1222879.2	Ac	195590.6	Ba	230872.2	Ba	3279637.3	Ab	473333.8	Ba	236009.3	Ba	7654020.6	Aa	890330.9	Ba	75213.4	Ba
TAG 52:6.1	64409.5	Aa	78728.5	Aa	55611.9	Aa	43302.2	ABa	41280.0	Bbc	68215.4	Aa	NA	Bb	50348.2	Ab	49435.0	Aa	64620.5	Aa	18079.8	Bc	14222.6	Bb
TAG 52:7	53272.7	Ac	54932.1	Aa	41817.4	Aa	448894.5	Ac	71206.5	Aa	84927.3	Aa	1345254.2	Ab	180812.7	Ba	94468.5	Ba	3295222.7	Aa	295311.3	Ba	23784.5	Ba
TAG 52:8	17890.9	Ac	19802.1	Aa	14674.9	Aa	80070.1	Ac	16255.1	Aa	21235.8	Aa	217120.6	Ab	40006.6	Ba	24197.8	Ba	537312.6	Aa	47677.7	Ba	7639.9	Ba
TAG 52:9	6933.3	Ac	12234.1	Aa	5601.1	Aa	33549.3	Ac	9168.0	Aa	12102.3	Aa	87586.6	Ab	30063.7	Ba	16522.2	Ba	220749.4	Aa	26805.0	Ba	4829.5	Ba
TAG 54:0	314720.9	Aa	272266.7	Ba	325044.0	Ba	217976.7	Ab	189989.8	Bb	207364.3	Bb	264747.4	Ab	185337.6	Bb	183658.9	Bb	317681.2	Ab	195466.4	Bb	191786.3	Bb
TAG 54:1	1331662.5	Ac	1101949.0	Aa	1287124.8	Aa	1399392.5	Ac	877512.1	Aa	1027476.8	Aa	2143707.2	Ab	783355.3	Ba	716498.5	Ba	3633242.1	Aa	816013.9	Ba	672637.8	Ba

SI Table 9. (continuation) Relative abundance of lipid of *Scenedesmus obliquus* BR003 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N So	0h 3.5N So	0h 7N So	10h 0N So	10h 3.5N So	10h 7N So	18h 0N So	18h 3.5N So	18h 7N So	36h 0N So	36h 3.5N So	36h 7N So								
TAG 54:2	4311575.5 Ad	4185194.5 Aa	3639678.2 Aa	13252819.0Ac	5977913.4 Ba	7008794.1 Ba	24573238.3 Ab	5060081.1 Ba	3736043.5 Ba	37298171.2 Aa	5997778.1 Ba	1780143.9 Ba								
TAG 54:3	8098768.0 Ad	7155154.3 Ab	6081840.0 Ab	40316247.9Ac	19176410.6Bab	21082501.9Ba	67104695.8 Ab	18355503.0Bab	13963100.5Bab	100949843.3Aa	24979493.6Ba	4686598.1 Cb								
TAG 54:4	2820411.8 Ad	2499528.9 Aa	2466116.4 Aa	13022337.1Ac	4930161.0 Ba	5428366.9 Ba	25616809.9 Ab	4816480.8 Ba	3540665.5 Ba	47569065.9 Aa	8533198.7 Ba	1529027.9 Ca								
TAG 54:5	1903439.3 Ad	1832505.2 Ab	1775322.4 Aa	7080661.9 Ac	3663401.3 Aab	4116068.8 Aa	14705066.3 Ab	4399747.0 Bab	3052447.9 Ba	29690897.4 Aa	7051365.2 Ba	1254702.6 Ca								
TAG 54:6	922905.6 Ac	877836.0 Aa	925898.9 Aa	1919568.5 Ac	887700.5 Aa	1021827.0 Aa	3905861.8 Ab	1193114.9 Ba	889805.8 Ba	9424129.3 Aa	2091831.2 Ba	433995.0 Ca								
TAG 54:7	316477.5 Ac	293224.4 Ab	289910.2 Aa	822862.8 Ac	405910.2 Ab	503888.4 Aa	1648243.5 Ab	834412.4 Bab	495838.9 Ba	4072258.3 Aa	1156744.1 Ba	183540.2 Ca								
TAG 54:8	106488.6 Ac	110568.9 Aa	94950.3 Aa	218606.2 Ac	85393.3 Ba	126063.3 ABa	363896.9 Ab	177848.0 Ba	120121.9 Ba	767056.1 Aa	186274.4 Ba	40991.5 Ca								
TAG 54:9	29354.1 Ac	31898.9 Ac	27199.7 Ab	74698.4 Ac	45339.6 Abc	64500.2 Aab	126296.7 Ab	121807.4 Ba	74022.7 Ba	218794.2 Aa	82398.7 Bab	29198.7 Cab								
TAG 56:0	71176.7 Ab	64891.7 Aa	74512.0 Aa	71367.5 Ab	51561.8 Aa	59193.8 Aab	85472.2 Ab	58972.8 Ba	47949.3 Bb	116346.9 Aa	71215.1 Ba	49563.6 Bab								
TAG 56:1	226059.7 Ad	200197.4 Aa	190969.0 Aa	402937.9 Ac	246363.3 Ba	273948.6 ABa	602398.1 Ab	211650.2 Ba	149705.4 Ba	1112784.1 Aa	343495.9 Ba	138817.3 Ca								
TAG 56:2	426488.5 Ad	408472.5 Aa	383459.7 Aab	1094498.0 Ac	693262.5 Ba	748192.3 ABa	1725747.8 Ab	613874.9 Ba	426218.3 Bab	2924803.4 Aa	779043.9 Ba	313127.5 Cb								
TAG 56:3	533808.3 Ad	418756.4 Ab	594390.8 Aab	2504091.8 Ac	1495428.3 Ba	1560708.6 Ba	4153288.8 Ab	1612232.5 Ba	983565.4 Bab	6525434.9 Aa	2016494.7 Ba	489535.3 Cb								
TAG 56:4	332986.3 Ac	169475.1 Ab	570987.8 Aa	689500.6 Abc	437651.5 Aab	402140.5 Aa	1113596.3 Ab	443465.7 Bab	273966.1 Ba	1743979.5 Aa	668846.8 Ba	169008.9 Ca								
TAG 56:5	334702.8 ABb	111620.3 Ba	688278.4 Aa	442297.5 Ab	294276.6 Aa	251629.9 Aa	755879.5 Ab	364239.8 ABa	198713.2 Ba	1421727.5 Aa	576175.6 Ba	153452.7 Ba								
TAG 56:6	228734.2 Aa	59685.1 Aa	512537.0 Aa	121949.1 Aa	99021.3 Aa	63153.9 Aa	199244.3 Aa	103471.1 Aa	58081.5 Aa	402182.1 Aa	171947.4 Aa	49145.5 Aa								
TAG 56:7	84524.7 ABa	23017.2 Ba	186153.7 Aa	57101.6 Aa	42743.6 Aa	31651.5 Ab	92041.0 Aa	78413.1 Aa	36435.4 Aab	196040.6 Aa	111289.6 ABa	32295.9 Bb								
TAG 58:0	37310.6 Ac	33717.0 Aab	37747.6 Aa	44177.2 Ac	27399.3 Bb	30559.9 Ba	59882.6 Ab	31498.7 Bab	25785.8 Ba	77881.5 Aa	42364.7 Ba	27834.5 Ca								
TAG 58:1	95995.6 Ad	89753.0 Aa	84231.0 Aab	151860.0 Ac	111925.7 Aa	130322.3 Aa	210623.1 Ab	107392.4 Ba	73112.2 Bb	347240.0 Aa	133838.8 Ba	61114.8 Cb								
TAG 58:2	503068.8 Ad	454429.5 Ab	352899.7 Ab	1026936.4 Ac	790249.5 Aab	894203.3 Aa	1461687.4 Ab	682520.9 Bab	482479.4 Bb	2342361.1 Aa	876201.7 Ba	398581.5 Cb								
TAG 58:3	244791.6 Ad	205026.9 Ab	269560.1 Aa	727587.2 Ac	478809.3 Aab	486575.9 Aa	1130831.4 Ab	535848.2 Ba	348688.5 Ba	1899829.4 Aa	672560.1 Ba	249055.5 Ca								
TAG 58:4	113134.7 Ad	132958.9 Ab	85531.1 Aa	247668.1 Ac	181497.0 Ab	199871.1 Aa	393815.6 Ab	191680.0 Bb	127926.1 Ba	773479.3 Aa	325249.5 Ba	107893.1 Ca								
TAG 58:5	10635.0 Aa	12928.3 Aa	NA	Bb	NA	Ab	NA	Ab	NA	Ab	NA	Bb	NA	Bb	8189.0 Aa					
TAG 58:6	NA	Bc	7944.3 Ab	NA	Ba	NA	Ac	NA	Ac	NA	Aa	26158.4 Ab	NA	Bc	NA	Ba	46371.9 Aa	17521.7 Ba	NA	Ca
TAG 60:0	66187.6 Aa	66065.3 Aa	62585.0 Aa	75234.7 Aa	43076.5 Bb	47255.3 Bab	79158.2 Aa	53603.6 Bab	39814.5 Bb	78298.6 Aa	60087.4 Bab	48239.3 Bab								
TAG 60:1	179796.6 Ad	163978.3 Ab	159601.0 Ab	270105.6 Ac	253618.8 Aa	298311.9 Aa	358252.1 Ab	229673.9 Bab	150156.6 Cb	487659.6 Aa	289841.8 Ba	161176.4 Cb								
TAG 60:2	167869.8 Ad	164843.0 Ab	124666.5 Ab	323547.4 Ac	313936.1 Aa	368233.6 Aa	457725.6 Ab	284500.8 Ba	196207.5 Bb	675770.0 Aa	306053.5 Ba	153811.4 Cb								
TAG 60:3	65069.9 Ad	62418.9 Ab	66611.1 Ac	214779.0 Ac	203445.4 Aa	209897.9 Aa	342497.8 Ab	247704.1 Ba	161948.5 Cab	538686.1 Aa	225922.2 Ba	100129.9 Cbc								
TAG 60:4	37948.4 Aa	42197.8 Ac	32850.3 Ab	NA	Bb	63698.5 Ab	73264.9 Aa	NA	Cb	73829.1 Ab	48149.4 Bb	NA	Cb	101900.3 Aa	35812.3 Bb					
TAG 60:5	11414.1 Ac	14684.2 Ac	9757.9 Ab	29711.7 Ab	35580.1 Ab	30715.4 Aa	NA	Cc	53098.2 Aa	28227.7 Ba	98641.8 Aa	46662.7 Bab	21171.6 Cab							

SI Table 9. (continuation) Relative abundance of lipid of *Scenedesmus obliquus* BR003 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N So	0h 3.5N So	0h 7N So	10h 0N So	10h 3.5N So	10h 7N So	18h 0N So	18h 3.5N So	18h 7N So	36h 0N So	36h 3.5N So	36h 7N So
TAG 60:5.1	8007.2 Ad	11568.3 Ab	8302.3 Aa	48177.6 Ac	22884.0 Bab	27905.0 Ba	92051.9 Ab	28527.0 Bab	20093.1 Ba	143547.0 Aa	41371.5 Ba	12461.8 Ca
TAG 60:6	8873.2 Ac	12408.7 Ab	7193.5 Ab	24014.1 Ac	18330.7 Ab	21001.9 Aab	55575.3 Ab	41349.6 ABa	28185.9 Ba	88146.4 Aa	40921.2 Ba	32528.1 Ba
FA 16:0	8043628.3 Ac	7366681.2 Aa	8450180.7 Aa	10452974.5Ab	4686789.1 Bb	5979066.3 Bb	11757800.6 Ab	4521616.3 Bb	4370813.3 Bb	15351890.6 Aa	6234721.5 Bab	4125602.0 Bb
FA 16:1	1521808.8 Ab	1571535.4 Aa	1620831.0 Aa	1187932.7 Ab	489299.9 Bb	702301.2 Bb	1455739.1 Ab	596674.1 Bb	552693.1 Bb	2053248.2 Aa	686199.1 Bb	455319.9 Bb
FA 16:2	1773099.1 Ab	1904104.1 Aa	1888659.6 Aa	2011871.6 Ab	442423.6 Bb	780833.9 Bb	1883264.1 Ab	407494.1 Bb	442138.6 Bb	3383208.0 Aa	605069.4 Bb	355534.4 Bb
FA 16:3	2245471.3 Ab	2566960.0 Aa	2296031.9 Aa	3526015.3 Aa	1148704.0 Bb	2056802.5 Ba	3712577.2 Aa	1220362.9 Bb	1318615.8 Bab	4412122.1 Aa	1401089.3 Bab	586061.9 Bb
FA 16:4	62050.9 ABa	50223.9 Ba	70861.5 Aa	74086.5 Aa	6322.1 Bb	13914.9 Bb	69103.2 Aa	9388.0 Bb	8696.9 Bb	63309.4 Aa	11304.3 Bb	2583.0 Bb
FA 16:4.1	1080643.8 Aa	1469826.0 Aa	860371.3 Ab	118360.5 Bb	1551209.6 Aa	1352856.5 Ab	249794.6 Bb	1468252.9 Aa	1409739.9 Ab	159174.0 Cb	1226729.9 Ba	2795097.9 Aa
FA 18:0	2360900.4 Cb	2969076.6 Ba	3527074.8 Aa	2359620.2 Ab	1317958.9 Bb	NA Cc	3363101.1 Aa	1127314.4 Bb	1003479.6 Bb	NA Bc	1285824.0 Ab	785551.5 Ab
FA 18:1	25849773.4Ac	25214059.7Aa	25601258.6Aa	33205835.6Abc	20240570.3Ba	24705724.5Bab	37847387.8 Ab	19472832.4Ba	19552193.3Bab	54180840.7 Aa	22745985.7Ba	16181771.8Bb
FA 18:2	14529287.8Ab	17407175.1Aa	15648810.6Aa	12623201.4Ab	7300857.2 Bb	11442711.0ABab	16661742.4 Ab	8072681.9 Bb	8739817.0 Bb	22398343.5 Aa	10230946.3Bb	7917981.6 Bb
FA 18:3	17555771.7Aa	18918432.8Aa	17417222.5Aa	19198164.7Aa	16971867.9Aa	22317173.5Aa	20938564.8 Aa	19098397.3Aa	18232878.6Aa	27723021.7 Aa	17948903.0Aa	18356949.9Aa
FA 20:0	NA Ba	218648.8 Aa	NA Ba	NA Aa	NA Ab	NA Aa	NA Aa	NA Ab	NA Aa	NA Aa	NA Ab	NA Aa
FA 20:1	624658.0 Ab	613988.3 Aa	634829.7 Aa	819417.5 Aab	462958.8 Ba	581370.2 Ba	888534.7 Aa	628097.7 Ba	556775.9 Ba	1043978.5 Aa	671065.3 Ba	630767.1 Ba
FA 20:3	96993.1 Aa	110563.2 Aa	96388.3 Aa	73311.3 Ac	52668.5 Ac	67106.0 Ac	78810.5 Abc	87225.0 Abc	73897.4 Abc	107378.2 Aab	92235.1 Aab	97062.9 Aab
FA 22:1	107712.1 Ab	102028.7 Ac	99297.3 Ac	NA Bc	134481.4 Abc	141928.2 Ab	141947.9 Ba	181195.2 Aa	164435.5 ABb	156965.8 Ba	162342.7 Bab	250563.0 Aa
FA 24:1	32746.3 Ba	NA Cc	70146.2 Ac	NA Bb	91269.9 Ab	97323.4 Ab	NA Cb	123778.9 Aa	108564.4 Bb	NA Cb	87875.7 Bb	134882.2 Aa

SI Table 10. Relative abundance of lipid of *Chlorella vulgaris* BR017 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N		0h_3.5N		0h_7N		10h_0N		10h_3.5N		10h_7N		18h_0N		18h_3.5N		18h_7N		36h_0N		36h_3.5N		36h_7N	
DAG 34:1	48488.3	Ab	37588.8	Ab	51033.0	Aa	63592.9	Ab	42885.3	Ab	42430.9	Aa	106679.4	Aa	21346.5	Bb	26424.8	Bab	NA	Bc	131024.4	Aa	2823.3	Bb
DAG 34:2	57490.6	Ab	48688.6	Aa	57626.3	Aa	42328.2	Ab	49767.3	Aa	48518.2	Aa	50640.8	Ab	19248.1	Bb	23345.7	Bb	103802.4	Aa	62299.9	Ba	7299.6	Cb
DAG 34:3	140600.4	Ab	108155.8	Aa	124162.1	Aa	112360.0	Ab	91808.0	Aa	100301.9	Aa	116859.4	Ab	32647.4	Bb	40701.2	Bb	227945.1	Aa	82558.2	Ba	8775.9	Cb
DAG 34:4	125414.5	Ab	98216.4	Aa	123085.0	Aa	112275.5	Ab	87026.4	Aa	104215.6	Aa	149103.4	Ab	41331.4	Bb	56946.8	Bb	291466.4	Aa	109048.5	Ba	9050.8	Cc
DAG 34:5	207524.4	Ab	170640.3	Aa	214811.3	Aa	NA	Bc	205521.3	Aa	230681.5	Aa	228023.6	Ab	78911.9	Bb	86892.6	Bb	454228.1	Aa	169847.0	Ba	21434.2	Cb
DAG 34:6	160015.6	Ac	133786.3	Aab	171062.5	Aab	227833.8	Abc	204695.8	Aa	234842.4	Aa	279907.0	Ab	75806.9	Bb	92720.1	Bbc	659744.4	Aa	164997.7	Bab	24440.3	Cc
DAG 36:1	5587.1	Ac	4167.0	Aa	5340.6	Aa	7869.9	Ac	5878.9	Aa	5226.3	Aa	15753.6	Ab	5418.4	Ba	5248.6	Bab	25100.5	Aa	7350.4	Ba	NA	Cb
DAG 36:2	87320.7	Ad	86978.7	Ab	101835.5	Aa	167557.2	Ac	111963.2	Bb	101844.9	Ba	258105.0	Ab	69015.9	Bb	83661.2	Ba	501261.0	Aa	240425.3	Ba	7100.3	Cb
DAG 36:3	168384.2	Ac	125515.6	Ab	149946.5	Aa	190655.8	Ac	150413.0	Ab	131080.3	Aa	374023.1	Ab	63910.2	Bb	85115.0	Bab	797487.2	Aa	402678.0	Ba	8196.9	Cb
DAG 36:4	159808.7	Ac	127756.5	Ab	144784.7	Aa	212959.1	Ac	138829.1	Bb	129691.4	Bab	324082.4	Ab	49145.0	Bc	63756.7	Bbc	668101.2	Aa	279943.6	Ba	NA	Cc
DAG 36:5	176694.5	Ab	144385.0	Aa	151675.4	Aa	118284.7	Ab	138359.6	Aa	154439.2	Aa	140014.2	Ab	44870.3	Bb	54878.9	Bb	284226.6	Aa	118696.6	Ba	19603.0	Cb
DAG 36:6	121766.5	Ab	85963.4	Aab	116799.5	Aa	98054.2	Ab	126826.2	Aa	134329.3	Aa	108102.7	Ab	34758.5	Bc	47391.8	Bb	222456.7	Aa	58570.2	Bbc	12835.4	Cb
DGDG 32:0	111343.8	Aa	107704.4	Aa	100654.9	Aa	70707.1	Ac	72515.7	Ab	72916.6	Ab	77380.0	Abc	58108.8	Bb	62422.9	Bb	86428.8	Ab	62628.4	Bb	75193.2	ABb
DGDG 32:1	35796.4	Aa	35885.7	Aa	34156.1	Aa	7871.3	Bb	22515.1	Ab	23085.9	Ab	11164.5	Bb	17035.1	Ac	16865.6	Ac	10992.4	Bb	13111.7	ABc	17426.4	Ac
DGDG 32:2	129021.8	Aa	105823.2	Ba	101127.0	Ba	35627.1	Bb	64664.2	Ab	69958.6	Ab	33508.2	Bb	53404.6	Ab	54495.9	Ab	39769.9	Cb	54622.3	Bb	99107.5	Aa
DGDG 32:3	237532.5	Aa	197886.4	Aa	208371.6	Ab	53932.4	Bb	181349.0	Aab	188235.2	Abc	53916.0	Bb	147260.5	Abc	148921.2	Ac	71233.2	Cb	127212.4	Bc	311614.7	Aa
DGDG 32:3.1	28170.4	Bb	31933.4	ABc	38692.5	Ac	12062.7	Bc	60808.9	Aa	62786.0	Aa	22756.8	Bbc	45454.3	Ab	50282.7	Ab	55534.7	Ba	31314.9	Cc	68792.9	Aa
DGDG 34:0	65348.5	Aa	65725.2	Ab	67012.5	Ab	36941.7	Ba	142427.2	Aa	159832.6	Aa	37264.7	Ba	177626.1	Aa	191941.5	Aa	27503.0	Ba	57609.0	Bb	100632.0	Ab
DGDG 34:1	2071068.1	Ba	2184602.3	ABa	2500024.3	Aa	720343.3	Bb	1967730.1	Aa	1715656.0	Ab	1065203.3	Bb	1576366.2	Ab	1630860.7	Ab	1021402.7	Bb	1551715.0	Ab	1467276.4	Ab
DGDG 34:2	2736961.4	Aa	2816745.2	Aa	3081179.1	Aa	631568.0	Bc	2775960.5	Aa	2454446.3	Ab	964421.9	Bbc	2017574.0	Ab	2208796.9	Ab	1121828.2	Cb	1818367.6	Bb	2301074.2	Ab
DGDG 34:3	1231033.3	Aab	1300374.1	Ac	1495793.7	Ab	579772.4	Bc	2548513.5	Aa	2247591.7	Aa	971863.1	Bb	1861225.0	Ab	2039271.5	Aa	1450861.2	Ba	1358052.8	Bc	2078230.7	Aa
DGDG 34:4	3215081.7	Ba	3270020.9	Ba	3713968.4	Aa	470138.7	Bb	2546278.4	Ab	2367253.3	Ab	532765.5	Bb	1990814.9	Ac	2169599.1	Ab	531234.2	Cb	1693605.8	Bc	2234715.8	Ab
DGDG 34:5	3831406.0	Ba	3914190.2	Ba	4551955.6	Aa	1078277.1	Bc	4125810.3	Aa	3658621.3	Ab	1480772.2	Bbc	3083774.0	Ab	3334828.1	Ab	1805567.5	Cb	2991410.0	Bb	3822093.1	Ab
DGDG 34:6	4415164.0	Ba	4550077.9	Bab	5637679.8	Aa	1423329.0	Bc	5161564.9	Aa	4368288.2	Ab	2248417.6	Bbc	3846658.8	Ab	4264026.1	Ab	2927590.6	Bb	3908408.2	ABb	4793585.6	Aab
DGDG 36:2	41891.6	Aa	43015.3	Ac	48236.5	Ac	10179.2	Cb	74862.0	Bb	98940.8	Ab	11506.8	Cb	102350.3	Ba	129433.0	Aa	6819.4	Cb	56256.7	Bbc	91232.7	Ab
DGDG 36:3	49869.1	Aa	49286.4	Ac	55957.4	Ab	5861.2	Bb	66117.4	Ab	70404.4	Aa	6090.3	Bb	79129.9	Aa	74126.7	Aa	3379.3	Bb	78277.4	Aa	82031.8	Aa
DGDG 36:4	334604.4	Aa	349462.4	Aa	364734.3	Ab	23009.5	Bb	237430.9	Ab	242546.6	Ac	20443.1	Bb	245964.0	Ab	237777.7	Ac	NA	Cb	230065.4	Bb	698035.8	Aa
DGDG 36:5	830960.0	Ba	835249.9	Ba	950694.6	Ab	75047.6	Bb	801263.6	Aa	765716.0	Ac	79559.0	Bb	680172.6	Ab	687907.1	Ac	37009.1	Cb	460071.8	Bc	1070265.4	Aa
DGDG 36:6	1133821.7	Ba	1200583.0	ABb	1358580.0	Aab	187509.3	Bb	1594014.7	Aa	1514795.1	Aa	277205.0	Bb	1213471.5	Ab	1254635.8	Ab	231518.9	Cb	632783.2	Bc	1532103.6	Aa

SI Table 10. (continuation) Relative abundance of lipid of *Chlorella vulgaris* BR017 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N		0h_3.5N		0h_7N		10h_0N		10h_3.5N		10h_7N		18h_0N		18h_3.5N		18h_7N		36h_0N		36h_3.5N		36h_7N	
LysoPC 16:0	52209.8	Cb	166891.8	Ba	216845.7	Aa	35415.8	Bb	82229.1	Ab	80194.8	Abc	45305.3	Bb	79820.8	Abc	70633.7	ABc	103768.5	Aa	49161.5	Bc	109893.8	Ab
LysoPC 16:0.1	3880.9	Cb	15479.9	Ba	19949.9	Aa	2843.1	Bb	7154.9	Ab	7238.2	Abc	3231.7	Bb	6950.3	Ab	6568.0	Ac	8861.5	Aa	4533.9	Bb	9734.9	Ab
LysoPC 16:2	27572.0	Ba	74503.2	Ab	111423.9	Ac	14651.8	Ba	114061.3	Aab	100619.8	Ac	31527.7	Ba	155371.9	Aa	160925.8	Ab	43496.0	Ba	83375.7	Bb	475638.1	Aa
LysoPC 16:3	15737.7	Ba	51606.4	ABc	85183.0	Ac	11016.8	Ba	116060.6	Aab	109219.6	Ac	29866.5	Ba	170611.3	Aa	178515.6	Ab	37827.5	Ba	80563.8	Bbc	685116.3	Aa
LysoPC 18:2	46728.4	Ba	196897.7	ABc	316764.1	Ac	41434.1	Ba	513475.1	Aab	420511.6	Abc	139458.5	Ba	766154.3	Aa	584144.5	Ab	218529.6	Ca	458120.8	Bbc	3170119.8	Aa
LysoPC 18:3	26355.9	Ba	106090.6	ABc	174835.5	Ac	19537.6	Ba	304372.1	Aab	262732.0	Abc	68953.0	Ba	376432.8	Aa	368423.7	Ab	95376.9	Ba	218358.5	Bbc	1900874.6	Aa
MGDG 34:1	187851.1	Ba	240011.3	ABb	301290.8	Ab	40370.7	Bb	433191.3	Aa	386096.9	Aa	66322.9	Bb	258978.2	Ab	292792.5	Ab	NA	Bb	69167.5	Bc	153763.7	Ac
MGDG 34:2	168958.4	Ca	237076.3	Ba	279190.4	Aa	15255.8	Bb	179289.0	Ab	157358.7	Ab	22789.2	Bb	170644.8	Ab	170134.3	Ab	4392.0	Ab	30672.4	Ac	NA	Ac
MGDG 34:2.1	136092.1	Ba	166103.4	ABb	218732.2	Abc	18829.1	Bb	338167.0	Aa	281690.2	Ab	28677.3	Bb	144096.4	Ab	195236.2	Ac	9380.3	Bb	52829.0	Bc	407996.3	Aa
MGDG 34:3	2642.4	Ba	2854.0	Bc	5537.2	Ab	NA	Bb	9190.3	Aa	9282.6	Aa	NA	Bb	6351.2	Ab	7558.2	Aab	NA	Bb	NA	Bd	5442.0	Ab
MGDG 34:4	449246.6	Ba	742863.3	Aa	832887.6	Ac	26318.4	Bb	980309.3	Aa	873347.8	Ac	35196.6	Bb	1043067.9	Aa	1301158.8	Ab	23037.5	Cb	347063.4	Bb	2166782.2	Aa
MGDG 34:5	529970.1	Ba	812393.3	ABb	976802.7	Ac	43460.3	Bb	1341185.2	Aa	1233594.3	Abc	57418.0	Bb	1326896.9	Aa	1619978.8	Ab	39492.6	Cb	466027.7	Bb	3004791.1	Aa
MGDG 34:6	NA	Aa	NA	Ab	NA	Ac	NA	Ba	NA	Bb	1384767.3	Ab	NA	Ba	1465604.3	Aa	1691724.4	Ab	45899.2	Ba	NA	Bb	3548924.7	Aa
MGDG 36:5	78541.7	Aa	123131.6	Aa	120015.2	Ab	NA	Ba	155868.1	Aa	140863.6	Ab	NA	Ba	135780.7	Aa	160793.1	Ab	NA	Ba	61628.5	Ba	574085.5	Aa
MGDG 36:6	58602.7	Aa	90424.3	Abc	99001.1	Ac	4956.4	Ba	194169.6	Aab	182173.9	Abc	5444.9	Ba	200208.9	Aa	235944.4	Ab	2268.9	Ba	27880.2	Bc	908889.4	Aa
PC 32:0	4601.0	Bb	8038.5	Bab	11895.1	Aa	7317.2	Ab	6993.3	Ab	6947.1	Ab	8284.9	Ab	7659.7	Ab	8139.5	Aab	16057.1	Aa	11685.1	Ba	10711.4	Bab
PC 32:1	9597.7	Bb	18636.2	Bb	32339.3	Ab	9930.7	Bb	26545.1	Aab	28318.8	Ab	17186.4	Bb	33467.5	Aa	39471.5	Ab	47892.1	Ba	39879.1	Ba	65991.7	Aa
PC 32:1.1	14217.4	Cb	26230.3	Ba	37987.5	Ab	8149.7	Bb	30092.3	Aa	28333.3	Ac	12042.6	Bb	29922.4	Aa	33502.6	Abc	28735.8	Ba	24376.7	Ba	92714.4	Aa
PC 32:2	59964.1	Ca	179163.7	Bb	340690.8	Ab	32038.2	Ba	313488.9	Aa	289172.5	Ab	72394.0	Ba	333046.4	Aa	384769.6	Ab	138753.5	Ba	169847.3	Bb	981556.9	Aa
PC 32:3	62718.1	Ba	238042.1	ABbc	464332.6	Ab	26210.6	Ba	472052.6	Aab	437007.5	Ab	71545.5	Ba	528817.9	Aa	634749.5	Ab	124682.6	Ba	212855.2	Bc	1846028.6	Aa
PC 32:4	3338.2	Ba	12735.3	ABa	20717.2	Ab	NA	Ba	14694.5	Aa	13525.2	Ab	1653.6	Ba	17155.0	Aa	20752.4	Ab	2410.1	Ba	8365.6	Ba	81422.7	Aa
PC 34:1	NA	Aa	NA	Ab	NA	Aa	NA	Ba	388385.5	Aa	NA	Ba	NA	Aa	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Aa
PC 34:2	119100.2	Ba	368536.2	Bc	734540.0	Ac	NA	Ba	772983.4	Ab	698704.5	Ac	NA	Ba	1098338.7	Aa	1084247.9	Ab	NA	Ba	NA	Bd	3538294.6	Aa
PC 34:3	82485.8	Ba	291934.0	ABb	541443.6	Ac	37257.1	Ba	593756.0	Aa	557279.6	Ac	93755.6	Ba	770817.3	Aa	909184.2	Ab	195868.6	Ba	314650.5	Bb	2545890.8	Aa
PC 34:4	29341.2	Aa	85856.5	Aa	169904.1	Abc	9948.5	Aa	155988.2	Aa	146041.2	Ac	18912.9	Ba	255637.0	Aa	317593.7	Ab	27998.6	Ba	87923.5	Ba	1208301.6	Aa
PC 34:5	24717.5	Aa	97043.3	Aa	196801.4	Ab	11233.2	Aa	239175.1	Aa	226131.0	Ab	27001.5	Ba	429539.0	Aa	561528.4	Ab	36249.9	Ba	127380.6	Ba	2233983.6	Aa
PC 34:6	15222.6	Aa	54997.4	Ab	141693.9	Ac	6358.7	Aa	199359.8	Aab	188267.0	Ac	17584.2	Ba	472132.3	Aa	648875.8	Ab	23189.1	Ba	79421.4	Bb	2291920.3	Aa
PC 36:1	80192.1	Bb	146889.1	Bc	358845.2	Aa	131715.1	Bb	389400.1	Ab	474540.2	Aa	197373.0	Bb	380715.8	Ab	409848.9	Aa	347987.8	Ba	821213.8	Aa	NA	Cb
PC 36:2	1401149.1	Cb	3370475.1	Bc	8324610.6	Aab	1716879.1	Bb	5812624.4	Ab	6229927.3	Ac	2480633.0	Bab	7385764.8	Ab	7575685.5	Abc	4266669.0	Ba	10430358.2	Aa	10069783.7	Aa

SI Table 10. (continuation) Relative abundance of lipid of *Chlorella vulgaris* BR017 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N		0h_3.5N		0h_7N		10h_0N		10h_3.5N		10h_7N		18h_0N		18h_3.5N		18h_7N		36h_0N		36h_3.5N		36h_7N	
PC 36:3	25877.6	Ba	72841.1	ABbc	157965.1	Ab	23538.0	Ba	207662.1	Aa	181382.3	Ab	52590.4	Aa	NA	Ac	NA	Ac	113872.1	Ba	173510.3	Bab	928788.1	Aa
PC 36:3.1	43370.7	Bb	122330.5	Bc	372407.3	Aa	61257.0	Bb	253183.7	Ab	288757.4	Aa	123973.9	Bab	325107.4	Aab	304198.6	Aa	222635.2	Ba	376623.8	Aa	361170.7	Aa
PC 36:5	51362.8	Aa	219073.8	Aa	499061.3	Ab	31638.0	Aa	835136.6	Aa	741234.5	Ab	101524.8	Ba	1069431.2	Aa	1256235.9	Ab	198418.8	Ba	481527.8	Ba	6422661.9	Aa
PC 36:6	23582.4	Aa	99688.7	Aa	252022.7	Ab	14776.6	Aa	530592.8	Aa	485643.7	Ab	46726.1	Ba	621266.7	Aa	807406.3	Ab	80299.0	Ba	224059.2	Ba	3817578.1	Aa
PC 38:2	20625.0	Bb	37695.5	Bb	82432.4	Ab	25810.5	Bb	110299.9	Aa	113446.5	Aab	39996.6	Bab	110599.0	Aa	113917.6	Aab	68789.6	Ba	125409.5	Aa	143545.1	Aa
PC 38:3	2699.8	Ba	6644.8	ABb	8428.2	Ac	NA	Ba	14986.6	Aa	15626.3	Ab	2134.9	Ba	18197.8	Aa	19608.4	Ab	1886.6	Ba	4644.9	Bb	39221.3	Aa
PC 38:3.1	2403.0	Ba	2233.8	Bb	4244.2	Aa	2682.0	Ba	4572.1	Aa	4365.8	Aa	2836.0	Aa	3893.7	Aa	4031.5	Aa	2631.1	Aa	3789.5	Aa	3472.1	Aa
PE 32:1	7470.8	Ab	11935.9	Ab	24067.9	Ab	9015.5	Ab	47281.0	Ab	59728.7	Ab	18046.4	Bb	71044.4	ABb	97947.6	Aab	202481.8	Ba	303022.9	Aa	152956.0	Ba
PE 34:1	21360.2	Bb	38646.7	ABc	75215.2	Ac	27237.1	Bb	168633.3	Ab	197059.3	Aab	30127.8	Cb	170052.4	Bb	241643.9	Aa	134791.4	Ba	238227.1	Aa	173104.3	Bb
PE 34:2	51247.4	Bb	92243.8	ABc	213167.3	Ac	61869.4	Bb	422093.3	Ab	471074.7	Ab	85345.5	Cb	534832.4	Bab	717403.4	Aa	298027.4	Ba	664391.6	Aa	740050.1	Aa
PE 34:3	3830.3	Aa	6174.5	Ab	9326.9	Ab	3081.4	Ba	19330.0	Aab	24973.6	Ab	4466.6	Ca	32742.6	Ba	68911.9	Aa	8175.6	Ba	16206.0	Bab	86024.1	Aa
PE 34:4	NA	Aa	NA	Ab	NA	Ac	NA	Ba	7318.1	ABab	9209.6	Ac	NA	Ca	12491.9	Ba	23870.0	Ab	1020.8	Ba	4004.6	Bab	45540.4	Aa
PE 34:5	2226.3	Aa	1918.4	Aa	3661.4	Ac	NA	Aa	8064.1	Aa	10955.7	Ac	NA	Ca	18247.5	Ba	40321.2	Ab	NA	Ba	4574.3	Ba	64812.2	Aa
PE 34:6	NA	Aa	1225.5	Aa	2324.4	Ac	NA	Aa	6498.1	Aa	8610.7	Ac	NA	Ca	13478.4	Ba	30638.4	Ab	NA	Ba	3148.4	Ba	45709.7	Aa
PE 36:1	16746.7	Ba	24175.7	Bc	50959.9	Ac	12863.6	Ca	150380.8	Ba	176917.5	Aa	15592.6	Ca	138087.4	Ba	170015.4	Aa	16913.1	Ba	66975.3	Ab	82891.7	Ab
PE 36:2	236689.3	Ba	461360.0	Bc	1169401.5	Ac	235501.8	Ba	2823482.6	Aa	3081569.0	Aa	266726.3	Ca	2425396.8	Ba	2948359.0	Aa	300026.2	Ba	1522756.4	Ab	1861602.1	Ab
PE 36:3	NA	Ba	14867.4	ABc	30875.6	Ac	NA	Ba	138830.1	Aa	158785.8	Aa	NA	Ba	96973.3	Ab	107326.4	Ab	NA	Ba	33480.2	Ac	52714.6	Ac
PE 36:3.1	3067.6	Aa	4196.1	Ab	8741.0	Ac	4200.4	Ba	20317.1	Aa	22950.9	Ab	5676.9	Aa	NA	Ab	NA	Ac	9779.3	Ca	24296.8	Ba	83346.0	Aa
PE 36:4	NA	Ab	NA	Ac	NA	Ac	NA	Cb	9902.7	Bb	14129.5	Ab	2526.7	Cb	20394.1	Ba	27268.8	Aa	9060.5	Ca	19267.5	Aa	14930.5	Bb
PE 36:4.1	5803.8	Aa	8789.6	Aa	15861.0	Ac	6024.3	Aa	40419.9	Aa	47343.0	Ac	9249.8	Ba	58117.8	Aa	100382.7	Ab	17177.8	Ba	44746.6	Ba	252904.7	Aa
PE 36:5	3628.9	Aa	6417.2	Aa	15081.0	Ac	2482.5	Aa	39381.0	Aa	52803.1	Ac	5385.0	Ca	88436.1	Ba	172868.5	Ab	9241.6	Ba	34758.3	Ba	329735.6	Aa
PE 36:6	1921.6	Aa	3388.0	Ab	5011.6	Ab	NA	Aa	14609.6	Aab	19480.2	Ab	1855.0	Ca	36576.7	Ba	79132.2	Aa	2722.9	Ba	8273.6	Bab	104639.1	Aa
PE 38:2	910803.1	Ba	1182793.3	Ba	1680584.5	Ab	643183.7	Ba	1192753.2	Aa	1407862.2	Ab	608242.8	Ba	1238870.2	Aa	1477011.1	Ab	770497.7	Ca	1237644.4	Ba	2381357.6	Aa
PE 38:3	NA	Aa	NA	Ab	NA	Ab	NA	Ba	25175.7	Aa	26823.8	Aa	NA	Ba	23813.6	Aa	27079.1	Aa	NA	Aa	NA	Ab	NA	Ab
PE 40:1	NA	Aa	NA	Ac	NA	Ac	NA	Ba	6189.2	Ab	7289.8	Ab	NA	Ba	5783.3	Ab	6468.4	Ab	NA	Ba	10067.6	Aa	9718.5	Aa
PE 40:2	21713.7	Bb	25713.9	Bc	91559.3	Ac	32953.3	Bb	95233.9	Ab	106472.3	Ac	52772.1	Bb	134237.5	Ab	157045.0	Ab	95417.0	Ba	236571.8	Aa	208318.4	Aa
PE 40:3	NA	Aa	NA	Aa	NA	Ac	NA	Ba	NA	Ba	22436.0	Ab	NA	Ba	NA	Ba	40682.6	Aa	NA	Aa	NA	Aa	NA	Ac

SI Table 10. (continuation) Relative abundance of lipid of *Chlorella vulgaris* BR017 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N		0h_3.5N		0h_7N		10h_0N		10h_3.5N		10h_7N		18h_0N		18h_3.5N		18h_7N		36h_0N		36h_3.5N		36h_7N			
PG 32:0	NA	Ab	NA	Ab	NA	Aa	5090.1	Aa	NA	Bb	NA	Ba	NA	Ab	NA	Ab	NA	Aa	NA	Bb	9121.0	Aa	NA	Ba		
PG 32:1	2867.3	Ba	3001.5	Aa	2707.7	Ca	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab	NA	Ab
PG 34:2	85535.3	Aa	NA	Bb	NA	Ba	NA	Ac	NA	Ab	NA	Aa	NA	Ac	NA	Ab	NA	Aa	58847.3	Bb	111589.9	Aa	NA	Ca		
PG 34:3	50052.1	Ca	62311.5	Ba	70683.9	Aa	NA	Ac	NA	Ab	NA	Ab	NA	Ac	NA	Ab	NA	Ab	9271.4	Ab	NA	Bb	NA	Bb		
PG 34:4	NA	Ba	15797.3	Aab	18742.6	Ab	2996.5	Ba	27968.3	Aa	27551.8	Ab	NA	Ba	27042.7	Aa	NA	Bc	NA	Ba	5983.5	Bb	149104.2	Aa		
SQDG 32:0	2995195.4	Aa	NA	Ba	NA	Ba	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Aa	NA	Aa		
SQDG 32:1	65488.4	Aa	63423.2	Aa	50606.4	Ba	8281.4	Ab	NA	Bb	NA	Bb	9439.6	Ab	NA	Bb	NA	Bb	NA	Ac	NA	Ab	NA	Ab		
SQDG 32:2	65437.7	Aa	61396.1	Aa	59777.1	Aa	15385.9	Bb	30801.4	Ab	26476.8	Ab	11139.8	Bb	27780.0	Ab	30452.8	Ab	9445.1	Cb	19249.6	Bc	66630.0	Aa		
SQDG 32:3	118427.7	Aa	93249.7	Ba	89874.4	Ba	24077.8	Bb	63235.8	Ab	60457.7	Ab	19269.3	Bb	56982.5	Ab	64799.3	Ab	18341.8	Bb	34734.5	Ac	NA	Cc		
SQDG 34:1	1172130.9	Aa	1151463.3	Aa	1137111.3	Aa	NA	Bc	NA	Bb	849712.7	Ab	NA	Bc	NA	Bb	780236.9	Ab	292974.7	Ab	NA	Bb	NA	Bc		
SQDG 34:2	4241010.0	Aa	4169533.7	Aa	3235835.0	Ba	NA	Bb	2096655.0	Ab	2050479.4	Ab	456335.6	Bb	1716626.7	Ab	NA	Bc	NA	Ab	NA	Ac	NA	Ac		
SQDG 34:3	2974943.8	Aa	3161032.5	Aa	2610914.2	Aa	902186.9	Bb	2628065.8	Aa	2501841.1	Aa	793993.4	Ab	NA	Bc	NA	Bb	1255529.0	Ab	1146589.3	Ab	NA	Bb		
SQDG 34:4	56220.8	Aa	55471.0	ABa	50147.5	Ba	5983.1	Bb	25703.9	Ab	23630.7	Ab	NA	Bb	24315.0	Ab	25341.5	Ab	2923.6	Cb	15375.9	Bc	52720.8	Aa		
SQDG 34:5	55892.7	Aa	61265.3	Aa	53200.3	Ab	8071.4	Bb	40925.6	Ab	40840.6	Ac	6114.6	Bb	38126.4	Ab	42109.0	Abc	4173.8	Cb	17387.6	Bc	83111.9	Aa		
SQDG 34:6	50917.1	Aa	53842.4	Aa	50454.0	Aa	6935.3	Bb	44061.0	Aab	41319.7	Ab	5410.4	Bb	41228.0	Ab	45472.2	Ab	4342.6	Cb	15686.5	Bc	99001.3	Ab		
TAG 42:0	25359.3	Aa	30605.8	Aa	27302.0	Aa	25046.3	Aa	19764.9	Abc	18638.1	Aab	26072.4	Aa	13125.2	Bc	14611.0	Bb	26206.1	Aa	25564.7	Aab	12028.6	Bb		
TAG 42:1	27773.6	Aa	29675.9	Aa	31983.9	Aa	30262.8	Aa	19267.7	Bbc	16224.3	Bb	30215.6	Aa	12568.6	Bc	14405.8	Bb	28601.8	Aa	27016.5	Aab	10448.9	Bb		
TAG 42:2	5217.0	Ab	6051.0	Aa	6374.8	Aa	6129.5	Ab	3673.0	Bb	3749.6	Bb	7051.0	Ab	2569.5	Bb	2494.9	Bb	10147.9	Aa	6265.2	Ba	2578.0	Cb		
TAG 44:0	82549.3	Aa	85638.6	Aa	94336.1	Aa	72358.7	Aa	63094.0	Aab	54495.8	Ab	82015.9	Aa	40468.4	Bb	42543.6	Bb	86374.7	Aa	71797.3	Aa	37927.4	Bb		
TAG 44:1	56861.9	Ac	63332.9	Aa	68181.9	Aa	68989.7	Abc	41357.8	Bbc	36858.4	Bb	87146.3	Ab	29380.1	Bc	30553.4	Bb	148717.0	Aa	56964.0	Bab	38568.1	Cb		
TAG 44:2	39822.1	Aab	42233.5	Aa	35608.1	Aa	39077.6	Ab	21913.5	Bbc	20970.4	Bb	38215.6	Ab	14803.3	Bc	17093.3	Bb	51953.2	Aa	28362.1	Bb	13019.2	Cb		
TAG 46:0	289613.3	Aa	299672.0	Aa	359624.1	Aa	277178.9	Aa	250469.7	Aab	210064.4	Ab	307167.1	Aa	172085.8	Bb	188660.2	Bb	319796.0	Aa	286801.9	Aa	176730.7	Bb		
TAG 46:1	386832.3	Ad	347648.4	Aa	404544.2	Aa	641517.4	Ac	345304.2	Ba	334559.9	Bab	789915.8	Ab	202220.3	Bb	234309.5	Bb	1322922.8	Aa	441264.0	Ba	81263.0	Cc		
TAG 46:2	85543.5	Ac	73935.4	Aa	91084.4	Aa	110788.6	Abc	59670.9	Ba	59227.8	Bab	140396.2	Ab	NA	Cb	44330.2	Bb	273201.6	Aa	84800.1	Ba	NA	Cc		
TAG 46:2.1	54246.2	Aa	53667.5	Aa	50192.9	Aa	40731.6	Aa	NA	Bb	NA	Bb	NA	Ab	NA	Ab	NA	Ab	NA	Bb	49346.8	Aa	NA	Bb		
TAG 46:3	50615.2	Ac	39843.9	Aab	42992.4	Aa	93649.7	Ab	31591.5	Bb	30882.5	Bab	119225.4	Ab	16754.7	Bb	23406.0	Bab	271294.1	Aa	65858.9	Ba	3903.3	Cb		
TAG 46:3.1	11428.0	Aab	11934.2	Aa	9146.5	Aa	NA	Bc	5127.2	Ab	4130.3	Ab	8142.5	Ab	3294.4	Bb	3588.1	Bb	12448.8	Aa	9507.9	Aa	3476.5	Bb		
TAG 46:4	17355.2	Ac	11750.1	Aab	14501.5	Aa	26836.3	Ab	11921.9	Bab	13734.9	Ba	33105.1	Ab	7790.1	Bb	12058.8	Ba	71884.8	Aa	18696.6	Ba	NA	Cb		
TAG 48:0	1384296.8	Ba	1401341.0	Ba	1859239.9	Aa	1301987.5	Aa	1104752.5	Aab	925226.2	Ab	1442323.0	Aa	725708.2	Bb	830905.8	Bb	1727880.6	Aa	1493943.8	Aa	639559.9	Bb		

SI Table 10. (continuation) Relative abundance of lipid of *Chlorella vulgaris* BR017 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
TAG 48:1	1661599.2 Ad	1458606.6 Aab	2159684.2 Aa	2712376.8 Ac	1354152.3 Bb	1130951.4 Bb	3952472.2 Ab	830493.7 Bb	822372.5 Bb	8175172.0 Aa	2276707.7 Ba	567523.9 Cb
TAG 48:2	1803321.5 Ad	1476625.5 Ab	1737924.3 Aa	2829997.1 Ac	1230373.8 Bb	1056648.3 Bab	3836366.2 Ab	600156.3 Bb	727954.4 Bb	8419145.4 Aa	2636889.3 Ba	164389.7 Cb
TAG 48:3	2152427.2 Ad	1703743.3 Ab	2015374.4 Aa	3790933.3 Ac	1482467.5 Bb	1171647.2 Bab	5768578.7 Ab	623467.7 Bb	719372.5 Bab	14981131.7 Aa	3916047.4 Ba	51531.6 Cb
TAG 48:4	382142.4 Ac	306562.8 Ab	345653.3 Aa	681178.0 Ab	232217.8 Bb	200186.9 Bab	880711.2 Ab	80279.5 Bb	99866.3 Bb	2120964.5 Aa	760016.7 Ba	7447.9 Cb
TAG 48:5	347274.6 Ac	258511.2 Ab	291474.3 Aa	620469.8 Ab	215022.2 Bb	185219.0 Bab	881507.4 Ab	74887.0 Bb	97239.3 Bab	2249436.5 Aa	732307.4 Ba	8526.5 Cb
TAG 48:6	161563.6 Ad	111580.8 Ab	134170.2 Aa	358174.5 Ac	95499.6 Bb	82602.6 Ba	620509.7 Ab	32827.2 Bb	42616.3 Ba	1827725.0 Aa	477815.6 Ba	4430.5 Ca
TAG 48:7	44812.5 Ac	30053.3 Ab	34922.7 Aa	57472.8 Abc	20890.2 Bb	20415.0 Bab	77824.8 Ab	7842.3 Bb	10358.7 Bab	182949.7 Aa	95597.4 Ba	2111.8 Cb
TAG 48:8	19992.8 Ad	13720.7 Ab	17096.3 Aa	38951.7 Ac	15916.9 Bb	14934.4 Ba	55875.7 Ab	4521.4 Bb	6773.7 Ba	139725.2 Aa	51644.7 Ba	1364.6 Ca
TAG 48:9	4740.6 Ac	3199.0 Ab	4052.9 Aab	11486.1 Ab	6475.0 Bab	6410.3 Ba	14637.5 Ab	1539.2 Bb	2130.8 Bab	38173.8 Aa	11631.7 Ba	NA Cb
TAG 50:0	1816389.6 Ba	1795634.6 Ba	2596840.4 Aa	1699897.6 Aa	1606830.4 Aa	1399604.6 Ab	1753172.3 Aa	1144612.7 Aa	1295231.3 Ab	1738835.5 Aa	1475605.2 Aa	1179819.7 Ab
TAG 50:1	34193672.0Ad	32015956.6Ab	36497778.9Aa	65706794.3 Ac	25188616.4Bbc	20071784.1Bb	90306132.4 Ab	11623535.5Bc	12709845.0Bbc	135258887.8Aa	59149935.3 Ba	2536060.7 Ce
TAG 50:2	11109850.2Ad	9554659.2 Ab	11635714.5Aa	17256316.6 Ac	7434785.5 Bbc	6237063.8 Bab	26689252.2 Ab	3357905.6 Bc	3919674.0 Bb	54770461.3 Aa	19006206.3 Ba	1159019.8 Cb
TAG 50:3	8810658.4 Ac	7457007.3 Ab	8543942.3 Aa	17775298.4 Ab	6800774.6 Bb	6026498.0 Ba	23094386.4 Ab	2876538.9 Bb	3534872.5 Bab	40602222.1 Aa	18581199.4 Ba	187490.7 Cb
TAG 50:4	8178632.9 Ad	6328727.8 Ab	7169289.6 Aa	19798879.9 Ac	5733905.1 Bb	4754430.9 Bab	30296977.2 Ab	1996232.1 Bb	2670821.3 Bab	64306888.7 Aa	20985032.6 Ba	90641.1 Cb
TAG 50:5	6031626.8 Ad	4722250.5 Ab	5245273.9 Aa	13321850.1 Ac	2757622.6 Bb	2285962.0 Bab	19028032.1 Ab	934827.5 Bb	1232481.6 Bab	42234021.5 Aa	12001353.4 Ba	69908.1 Cb
TAG 50:6	13047.5 Ac	10733.8 Aab	9192.8 Aa	39571.9 Ab	6371.8 Bab	2851.2 Ba	41871.9 Ab	NA Bb	1875.9 Ba	143194.6 Aa	24918.1 Ba	NA Ca
TAG 50:6.1	4339596.7 Ad	3284941.7 Ab	3750182.8 Aa	12943799.7 Ac	2059147.4 Bb	1663754.0 Ba	20994223.9 Ab	731959.4 Bb	982729.6 Ba	47504249.6 Aa	10112401.2 Ba	59928.5 Ca
TAG 50:7	707272.6 Ad	526610.4 Ab	569378.8 Aa	1557457.5 Ac	318338.9 Bb	274588.0 Ba	2496217.2 Ab	108508.0 Bb	153388.0 Ba	6916455.5 Aa	1931041.7 Ba	23774.1 Ca
TAG 50:8	355370.2 Ad	246157.6 Ab	283655.8 Aa	970499.0 Ac	229111.1 Bb	206571.0 Ba	1446784.9 Ab	73906.9 Bb	111421.1 Ba	4236259.7 Aa	1130192.3 Ba	22923.9 Ca
TAG 50:9	135415.7 Ad	94229.1 Ab	109636.9 Aa	601771.1 Ac	124983.4 Bb	109002.9 Ba	987136.9 Ab	37788.1 Bb	56734.4 Ba	3090286.9 Aa	603695.6 Ba	15821.0 Ca
TAG 52:0	1337600.0 Aa	1393024.7 Aa	2063626.0 Aa	1413515.3 Aab	1419640.1 Aab	1073061.6 Aab	1370202.4 Ab	972916.4 Ab	1064937.6 Ab	1490583.4 Aab	1206873.5 Aab	1096909.5 Aab
TAG 52:1	19804556.1Ad	17619929.8Aab	22033559.9Aa	38365996.7 Ac	17630531.6Bab	15503692.2Bab	50788432.8 Ab	10642793.5Bb	11413381.1Bbc	76875298.0 Aa	20531882.5 Ba	3222720.9 Ce
TAG 52:2	59467416.6Ac	56494822.6Ab	67857532.1Aa	131165925.2Ab	57976750.3Bb	49067294.8Bab	157036067.4Ab	28887124.4Bb	34221198.9Bbc	198250176.9Aa	117986567.4Ba	5762468.1 Ce
TAG 52:3	31674098.9Ad	27234163.2Ab	32005155.5Aa	64753840.9 Ac	24198332.8Bb	20906912.1Bab	91941755.7 Ab	10003966.4Bb	12520009.8Bab	150723738.1Aa	68558960.3 Ba	1562897.6 Cb
TAG 52:4	23382526.0Ad	19111210.0Ab	21743741.3Aa	53787424.6 Ac	17704178.7Bb	14623735.6Bab	76119264.0 Ab	5448110.8 Bb	7028229.1 Bab	140798593.4Aa	56625081.0 Ba	945762.8 Cb
TAG 52:5	9178774.5 Ad	7254184.8 Ab	8061667.0 Aa	28220510.3 Ac	7645852.0 Bb	6453968.6 Ba	40500026.9 Ab	2650364.5 Bb	3545811.0 Ba	74650946.0 Aa	24649343.8 Ba	NA Ca
TAG 52:5.1	11534.0 Ac	11545.0 Ab	10070.6 Aa	30178.0 Abc	9896.1 Ab	8004.8 Aa	45409.4 Ab	3069.1 Bb	NA Ba	206341.2 Aa	56796.8 Ba	2145.5 Ca
TAG 52:6	6535523.7 Ad	5126840.0 Ab	5811218.7 Aa	23615822.2 Ac	4397033.3 Bb	3613385.5 Ba	34199125.5 Ab	1227388.8 Bb	1729493.3 Ba	68714333.9 Aa	21124266.0 Ba	76857.6 Ca
TAG 52:6.1	7233.2 Aa	5431.0 Aa	5584.4 Aa	NA Aa	7294.9 Aa	3990.6 Aa	NA Aa	2392.7 Aa	NA Aa	62192.3 Aa	6778.1 Aa	1681.3 Aa

SI Table 10. (continuation) Relative abundance of lipid of *Chlorella vulgaris* BR017 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
TAG 52:7	3839460.7 Ad	2848355.1 Ab	3342500.9 Aa	20492738.2 Ac	2580748.4 Bb	2076333.5 Ba	32055071.5 Ab	697431.2 Bb	978012.2 Ba	67468313.4 Aa	16417138.1 Ba	81343.9 Ca
TAG 52:8	1398039.8 Ad	935999.8 Ab	1074870.8 Aa	3534891.1 Ac	718824.0 Bb	667552.9 Ba	4928888.1 Ab	192155.5 Bb	294422.1 Ba	13156559.7 Aa	3711877.1 Ba	71203.8 Ca
TAG 52:9	497450.5 Ac	284869.4 Ab	349156.9 Aa	1832879.9 Ab	350693.3 Bb	313655.4 Ba	2387628.9 Ab	99766.6 Bb	150382.5 Ba	6855868.4 Aa	1489099.1 Ba	45223.0 Ca
TAG 54:0	503441.9 Ba	558862.3 Ba	847596.6 Aa	493716.4 Aa	532073.1 Aa	423215.0 Ab	524332.3 Aa	382027.3 Aa	422361.5 Ab	578843.3 Aa	468644.7 Aa	443243.3 Ab
TAG 54:1	3709227.8 Ac	3561555.2 Aa	5001958.1 Aa	8873826.7 Ab	5668852.7 Ba	4845678.4 Ba	11579459.0 Ab	3635071.8 Ba	3714112.4 Bab	15541297.2 Aa	3544617.1 Ba	1616719.3 Bb
TAG 54:2	17740917.9Ad	15997337.5Aa	20616523.9Aa	43190028.4 Ac	23542257.6Ba	22026415.7Ba	60771152.1 Ab	15740862.1 Ba	18252550.0Ba	88296987.2 Aa	23630665.2 Ba	3083361.6 Cb
TAG 54:3	36299528.2Ad	33609822.7Abc	40846117.4Aa	107568204.4Ac	45806671.3Bb	38658341.8Ba	140635558.2Ab	20329440.8Bc	24385322.9Bab	180690721.4Aa	90122582.2 Ba	3464413.1 Cb
TAG 54:4	25315481.3Ad	22036881.8Ab	26942843.0Aa	69181307.6 Ac	25195600.7Bb	21055770.5Ba	96620856.7 Ab	9097661.5 Bb	11754056.2Bab	151509823.3Aa	61491036.1 Ba	1867451.7 Cb
TAG 54:5	19552413.4Ad	16258965.0Ab	20051611.5Aa	60287624.5 Ac	20591883.6Bb	16727907.8Bab	85761404.6 Ab	6059117.0 Bb	8206976.1 Bab	149210793.5Aa	57669884.4 Ba	1397476.3 Cb
TAG 54:6	7140935.8 Ad	5475851.2 Ab	6434756.4 Aa	16328794.1 Ac	5340279.5 Bb	4246027.7 Ba	24168695.2 Ab	1556368.9 Bb	2147908.6 Ba	52419794.2 Aa	19621532.7 Ba	811393.9 Ca
TAG 54:7	2433494.7 Ad	1713174.7 Ab	2012022.1 Aa	7184022.4 Ac	1739616.6 Bb	1347273.8 Ba	10172305.0 Ab	343550.5 Bb	532705.9 Ba	26807372.1 Aa	8028893.2 Ba	92076.1 Ca
TAG 54:8	592505.1 Ac	392241.5 Ab	453694.0 Aa	759122.0 Abc	331049.5 Bb	274887.1 Ba	1134024.8 Ab	95504.2 Bb	159518.7 Ba	3016191.2 Aa	1205998.9 Ba	36477.7 Ca
TAG 54:9	118175.1 Ac	73917.6 Ab	86068.8 Aa	144536.4 Abc	77853.9 Bb	66762.6 Bab	197431.7 Ab	23296.8 Bb	42463.7 Bab	526566.6 Aa	145616.4 Ba	10851.3 Cb
TAG 56:0	67360.0 Ab	71197.8 Aa	74652.5 Aa	66273.2 Ab	58587.5 Aab	52219.6 Ab	84256.5 Aab	41189.9 Bb	46755.1 Bb	94392.2 Aa	62279.8 Ba	40073.5 Cb
TAG 56:1	309815.7 Ad	291253.1 Aa	385675.9 Aa	1182046.1 Ac	402264.4 Ba	335853.9 Bab	1628979.4 Ab	228537.4 Ba	236898.4 Bab	2793894.4 Aa	477795.3 Ba	70904.5 Cb
TAG 56:2	873864.6 Ad	783591.0 Aa	1042353.9 Aab	3625558.0 Ac	1751367.4 Ba	1594907.2 Ba	5379910.5 Ab	1092329.2 Ba	1238837.3 Ba	8067711.0 Aa	1663510.5 Ba	156414.7 Cb
TAG 56:3	1391172.6 Ad	1183395.8 Ac	1463979.6 Aab	4523077.9 Ac	2874528.5 Bab	2569080.3 Ba	6685213.6 Ab	1662966.7 Bbc	2123116.2 Ba	10845990.8 Aa	3783450.7 Ba	170960.1 Cb
TAG 56:4	878878.1 Ad	705594.3 Abc	799128.1 Aa	1717015.9 Ac	1197497.7 Bab	1100487.2 Ba	2311050.3 Ab	632139.1 Bc	873433.1 Ba	3345887.9 Aa	1568264.0 Ba	109969.3 Cb
TAG 56:5	618553.4 Ad	467374.2 Abc	520210.9 Aab	1302588.5 Ac	910071.0 ABab	764644.9 Ba	1961910.6 Ab	353350.3 Bc	481847.0 Bab	3679256.9 Aa	1374297.5 Ba	45854.7 Cb
TAG 56:6	259884.3 Ac	175140.6 Abc	175286.0 Aa	298734.6 Abc	224076.5 Ab	187057.5 Aa	413045.6 Ab	86626.4 Bc	123046.5 Bab	676446.3 Aa	371125.7 Ba	16124.3 Cb
TAG 56:7	91637.4 Ab	52639.9 Ab	52641.2 Aab	100760.4 Ab	68451.6 ABb	54848.1 Ba	131052.4 Ab	24418.6 Bb	33810.6 Bab	271268.0 Aa	121216.2 Ba	4677.6 Cb
TAG 58:0	26435.4 Ac	26795.7 Aa	29041.8 Aa	27578.8 Abc	24092.9 Aa	22349.3 Aab	37410.6 Aab	19371.5 Ba	21607.4 Bab	39003.6 Aa	24251.2 Ba	15004.5 Cb
TAG 58:1	357189.5 Ad	307135.6 Aab	375174.2 Aa	1108181.9 Ac	346099.8 Bab	299174.5 Ba	1490783.4 Ab	184385.8 Bb	193721.1 Ba	3516646.5 Aa	659514.4 Ba	27610.0 Ca
TAG 58:2	343999.1 Ad	317627.5 Aa	420722.4 Aa	1283982.9 Ac	522976.7 Ba	456276.7 Ba	1849341.8 Ab	287091.8 Ba	325001.5 Ba	3271521.4 Aa	578708.0 Ba	59803.1 Ca
TAG 58:3	210152.4 Ad	186644.7 Ab	248231.5 Aa	500653.7 Ac	311903.5 Bab	273802.8 Ba	689968.8 Ab	189967.6 Bb	225817.7 Ba	1074998.8 Aa	334608.2 Ba	64503.2 Cb
TAG 58:4	136280.3 Ad	130615.9 Aab	181090.3 Aa	376502.4 Ac	180374.3 Bab	144503.6 Bab	539429.9 Ab	96383.6 Bb	111329.3 Bab	947752.2 Aa	231286.9 Ba	63420.3 Cb
TAG 58:5	105904.2 Ac	76316.2 Aab	91645.9 Aa	268736.1 Ab	69024.2 Bb	58990.4 Bab	279043.3 Ab	35236.0 Bb	39674.5 Bab	452003.6 Aa	134809.7 Ba	7184.3 Cb
TAG 58:6	98342.5 Ad	66582.2 Aab	74915.3 Aa	310268.1 Ac	57915.3 Bb	51436.1 Ba	413016.8 Ab	30584.4 Bb	35983.7 Ba	1013484.3 Aa	140067.2 Ba	7546.2 Ca
TAG 60:0	7894.4 Aa	8560.5 Aa	8325.9 Aa	6506.5 Ab	5842.6 Ab	5357.8 Ab	6690.7 Ab	5076.3 Ab	5787.9 Ab	7770.4 Ab	6211.5 Ab	4862.5 Ab

SI Table 10. (continuation) Relative abundance of lipid of *Chlorella vulgaris* BR017 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
TAG 60:1	202851.3 Ad	161486.2 Aa	191758.0 Aab	412696.8 Ac	271373.5 Aa	247301.7 Aa	720581.7 Ab	186962.4 Ba	186865.7 Bab	1586685.2 Aa	329233.1 Ba	15429.0 Cb
TAG 60:2	410578.4 Ad	351665.8 Aa	427648.7 Aab	1272916.5 Ac	619628.2 Ba	578031.7 Ba	1851553.8 Ab	392423.4 Ba	438557.5 Bab	3926753.0 Aa	737289.8 Ba	28847.3 Cb
TAG 60:3	216803.7 Ad	179147.1 Aa	238028.4 Aa	478530.7 Ac	290662.7 Ba	266063.2 Ba	709249.4 Ab	165358.6 Ba	194663.3 Bab	1696891.7 Aa	332536.1 Ba	21529.1 Cb
TAG 60:4	172174.2 Ad	137517.7 Ab	174123.1 Aa	427842.7 Ac	171950.3 Bab	140289.0 Bab	570890.6 Ab	77805.8 Bb	93469.4 Bab	1350795.0 Aa	297610.4 Ba	22728.7 Cb
TAG 60:5	64578.3 Ac	44805.6 Aab	50788.0 Aa	77631.2 Ac	48979.5 Ba	39056.4 Bab	106010.9 Ab	23774.1 Bb	25687.5 Bbc	237999.8 Aa	56344.6 Ba	2989.2 Cc
TAG 60:5.1	72992.7 Ac	54033.2 Aab	56174.2 Aa	94859.8 Ac	54741.5 Bab	47408.3 Ba	151847.5 Ab	39145.5 Bb	42390.8 Ba	313095.2 Aa	84532.1 Ba	3178.0 Cb
TAG 60:6	66286.5 Ad	45809.5 Aab	53328.8 Aa	110806.9 Ac	50297.2 Bab	44252.7 Bab	216644.3 Ab	35445.9 Bb	40925.4 Bab	489450.4 Aa	87198.3 Ba	3393.3 Cb
FA 16:0	20636253.7Aa	17710665.5ABa	16331792.9Ba	12948602.5 Ab	8382244.5 Bc	6721828.4 Bb	13351159.2 Ab	5806816.6 Bc	5310828.5 Bb	13516054.2 Ab	13004349.4 Ab	5253280.1 Bb
FA 16:1	4997056.4 Aa	3698916.1 Ba	3554346.4 Ba	1811323.1 Abc	1266254.9 ABbc	1008963.9 Bb	1958664.5 Ab	785024.8 Bc	721746.1 Bbc	1205918.1 Ac	1497609.9 Ab	278634.8 Bc
FA 16:2	21972712.7Aa	17388833.9Ba	15503999.7Ba	7822142.2 Ab	7899901.6 Abc	6909944.1 Ab	6989481.8 Ab	5562229.2 Ac	5774220.0 Ab	6201160.9 Bb	9815503.4 Ab	5338532.3 Bb
FA 16:3	16379564.9Aa	12883778.5Ba	11514779.0Ba	9273510.2 Ab	8140565.3 Bb	6840959.4 Bb	8707017.5 Ab	5200187.2 Bb	5328047.1 Bb	8053318.4 Ab	8556370.0 Bb	5958048.3 Bb
FA 16:4	247396.8 ABa	282887.1 Aa	220483.2 Ba	158390.0 Ab	57391.7 Bb	52079.9 Bb	112374.8 Ab	31243.6 Bb	29123.4 Bb	62706.5 Ac	48731.1 Ab	29639.2 Ab
FA 16:4.1	27832.3 Aa	24880.0 Ba	19257.0 Ba	12813.3 Ab	6187.9 Bb	6555.4 Bb	7262.0 Ac	3243.1 Bc	4103.6 Bc	6758.8 Ac	5197.4 Bc	NA Bc
FA 18:0	4401820.6 Aa	4245789.5 Aa	3951164.7 Aa	3747288.4 Aa	3429269.0 ABab	2755200.5 Bb	3776147.4 Aa	2759415.2 Bb	2431093.9 Bb	3531775.1 Aa	2651764.4 Bb	831270.2 Cc
FA 18:1	56648140.8Aa	49556840.9Aa	35986808.3Ba	34434277.2 Ab	25063398.8ABc	20238401.4Bb	40335716.2 Ab	15386562.7Bc	14672220.6Bbc	42861977.9 Ab	37389010.7 Ab	6113248.3 Bc
FA 18:2	50829359.0Aa	48379398.7ABa	42392638.5Ba	22650486.9 Ab	23199884.9Ac	17563775.2Ab	24471377.8 Ab	15515773.9Bc	15878104.5Bb	23968424.4 Bb	31486900.9 Ab	18821488.3Bb
FA 18:3	61653932.3Aa	55121928.7Ba	50196068.1Ba	34345074.7 Abc	32387728.4Bbc	27389789.5Bbc	36828949.4 Ac	20710261.4Bc	21259256.0Bc	36780502.6 Ab	35820810.6 Bb	30387627.3Bb
FA 18:4	NA Bb	NA Bc	35649.7 Aa	16869.2 Aa	17945.4 Aa	NA Bd	17071.4 Aa	10402.8 Bb	10224.9 Bc	13817.8 Aa	14324.2 Aa	14389.9 Ab
FA 20:0	181813.5 Aa	186791.2 Aa	148994.7 Aa	153721.3 Aa	172745.6 Aa	129523.3 Aa	194524.3 Aa	122755.4 Bb	121329.3 Ba	170410.0 Aa	143973.2 Aab	41940.1 Bb
FA 20:1	1428134.9 Aa	1334376.8 Aa	718297.8 Ba	654563.1 Ab	539480.5 ABb	422904.1 Bb	495526.5 Abc	NA Bc	NA Bc	382013.4 Ac	NA Bc	NA Bc
FA 20:3	168218.6 Aa	138979.3 Ba	129785.3 Ba	49422.2 Bb	79564.3 Ab	69789.3 ABb	48801.4 Ab	52073.4 Ac	52701.7 Ab	42500.8 Bb	80945.4 Ab	68234.7 Ab
FA 22:0	82678.8 Aa	87288.6 Aa	61311.3 Ba	69048.6 Aa	69986.6 Aab	59642.6 Aa	70488.3 Aa	57749.8 ABbc	50111.0 Ba	63649.2 Aa	42999.6 Bc	23558.5 Cb
FA 22:1	127831.5 Ba	191412.3 Aa	113547.7 Ba	74512.0 Ab	66947.6 Ab	40681.1 Bb	44903.6 Ac	35032.7 Ac	32225.9 Ab	40743.8 Ac	27569.6 Ac	30012.5 Ab
FA 24:1	10213.5 Aa	10274.2 Aa	8986.5 Aa	5238.9 Ab	4143.2 Ab	3455.8 Ab	3112.1 Ac	2988.8 Ab	3422.3 Ab	2574.3 Bc	3092.5 ABb	4747.7 Ab
FA 26:0	583326.0 Aa	575573.3 Aa	335104.8 Ba	162204.7 Bbc	246521.6 Ab	206853.9 ABb	177548.2 Bb	252259.2 Ab	204429.1 ABb	104692.4 Bc	203389.5 Ab	125198.2 Bc
FA 28:0	225265.9 Aa	221953.2 Aa	65048.3 Bab	145813.1 Ab	107807.4 Ab	108706.7 Aa	72478.6 Ac	82300.3 Ab	NA Bc	123924.4 Abc	70509.2 ABb	31791.2 Bbc
FA 30:0	65153.7 Aa	63129.7 Aa	8771.9 Bab	58614.7 Aa	31547.4 Bb	34560.7 Ba	21597.4 Ab	28995.1 Ab	8578.6 Ab	46257.9 Aab	12394.9 Bb	3590.1 Bb
FA 30:1	4439.0 Aa	4389.5 Aa	5223.3 Aa	2498.9 Ab	2837.9 Ab	1981.9 Ab	3230.8 Ab	1744.4 Bb	1449.3 Bb	2823.5 Ab	2085.6 ABb	1351.5 Bb

SI Table 11. Relative abundance of lipid of *Monoraphidium* sp. BR023 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N		0h 3.5N		0h 7N		10h 0N		10h 3.5N		10h 7N		18h 0N		18h 3.5N		18h 7N		36h 0N		36h 3.5N		36h 7N	
DAG 34:1	NA	Bd	24344.3	Aa	25191.6	Aa	18790.9	Bc	18880.7	Bab	28273.9	Aa	39270.7	Ab	14309.5	Bb	13355.7	Bb	69659.8	Aa	NA	Bc	2419.8	Bc
DAG 34:2	19734.9	Bc	20103.1	Bb	26947.6	Aa	17450.4	ABc	14704.0	Bbc	22398.8	Aa	39019.8	Ab	11300.6	Bc	12938.5	Bb	70460.1	Aa	35432.5	Ba	5379.2	Cc
DAG 34:3	39741.5	Bc	39612.8	Bab	55915.5	Aa	24106.5	Bc	23997.2	Bbc	41271.7	Aa	73330.2	Ab	16711.6	Bc	19991.3	Bb	118279.7	Aa	55784.8	Ba	5476.7	Cb
DAG 34:4	45446.9	Bc	47125.0	Bab	69652.0	Aa	33044.3	Ac	26474.1	Abc	43193.1	Ab	76515.1	Ab	20216.7	Bc	22317.8	Bc	132022.3	Aa	63778.1	Ba	4948.3	Cc
DAG 34:5	51926.2	Ac	53663.4	Ab	83677.5	Aa	48552.4	Ac	45830.2	Ab	76760.6	Aab	129351.1	Ab	37925.7	Bb	41583.3	Bbc	194072.5	Aa	103033.6	Ba	14373.9	Cc
DAG 34:6	36686.8	Ac	37167.3	Ab	53100.1	Aab	46803.2	Ac	39062.1	Ab	67495.2	Aa	179756.4	Ab	35988.5	Bb	38653.1	Bab	261614.1	Aa	99807.2	Ba	20818.5	Cb
DAG 36:1	710.3	Ad	1134.7	Aab	926.8	Aab	1879.7	Ac	766.7	Bb	1357.6	ABa	3066.9	Ab	898.8	Bb	1111.9	Ba	7055.2	Aa	1923.7	Ba	NA	Cb
DAG 36:2	54547.3	Ac	48589.7	Ab	52798.3	Aa	82043.4	Ac	51738.1	Ab	75481.3	Aa	190687.6	Ab	28925.0	Bb	45497.4	Ba	323815.7	Aa	187122.9	Ba	5870.7	Cb
DAG 36:3	60497.3	Ac	56497.8	Ab	73323.0	Aa	75674.4	Ac	52909.4	Ab	82863.7	Aa	266580.3	Ab	28229.6	Bb	37920.9	Bab	328324.4	Aa	256583.1	Ba	6597.6	Cb
DAG 36:4	NA	Ad	NA	Ab	NA	Ab	60373.6	Ac	NA	Bb	57202.5	Aa	180559.8	Ab	22665.8	Bb	22386.2	Bb	310806.1	Aa	175609.3	Ba	NA	Cb
DAG 36:5	38156.8	Ac	44738.8	Aab	51566.2	Aab	41613.5	Ac	40622.0	Ab	58504.7	Aa	92251.8	Ab	26154.1	Bb	30565.0	Bbc	156327.4	Aa	70641.3	Ba	15740.2	Cc
DAG 36:6	15571.3	Ac	14448.5	Ab	24014.0	Aab	18424.0	Bc	22323.8	ABab	37597.4	Aa	53021.4	Ab	17233.3	Bb	21050.6	Bab	92128.4	Aa	35097.4	Ba	8961.5	Cb
DGDG 32:0	112482.2	Aa	111202.4	Aa	113578.7	Aa	92547.1	Ab	64544.7	Bc	65083.9	Bb	94891.9	Ab	67322.3	Bc	62214.1	Bb	113930.2	Aa	89025.0	Bb	70710.3	Cb
DGDG 32:1	24193.9	Ba	25179.2	Aa	26657.3	Aa	9842.5	Bb	19778.9	Ab	19705.8	Ab	14281.4	Bb	18340.5	Ab	18719.4	Ab	13650.9	Bb	17165.4	Ab	20488.4	Ab
DGDG 32:2	46921.2	Aa	49656.2	Aa	55042.2	Aab	15517.3	Bb	50610.0	Aa	46747.8	Abc	23412.0	Bb	35219.6	Ab	38735.4	Ac	19157.9	Cb	31851.0	Bb	62504.2	Aa
DGDG 32:3	60145.8	Aa	NA	Bb	84908.2	Ab	20929.2	Bb	NA	Bb	98094.4	Ab	39491.7	Bab	NA	Cb	78902.7	Ab	30323.9	Bab	53169.9	Ba	182683.1	Aa
DGDG 32:3.1	16484.0	Aab	19348.8	Ab	21731.7	Ac	9728.6	Bb	37568.6	Aa	41091.9	Ab	20915.3	Bab	32491.0	ABab	36861.0	Ab	27539.7	Ba	29701.0	Bab	61640.4	Aa
DGDG 34:0	114285.2	Aa	113700.1	Aa	129243.0	Aa	67344.3	Bb	81207.6	ABb	97304.2	Ab	64687.0	Bb	97001.2	Aab	102761.8	Ab	69499.7	Bb	54615.0	Bc	89587.7	Ab
DGDG 34:1	1727995.6	Ba	1735292.3	Aa	1983658.0	Aa	895842.1	Bb	1697280.3	Ab	1823910.0	Ab	1251740.8	Bab	1730526.5	Aab	1809117.4	Aab	1196551.3	Bb	1680544.7	Ab	1510060.9	Ab
DGDG 34:2	1757000.9	Aa	1815543.4	Aa	2065630.2	Aa	499717.3	Bb	1887310.5	Aa	1945742.3	Aa	861006.4	Bb	1656932.3	Aab	1778127.2	Aa	680822.5	Bb	1366042.5	Ab	1729209.7	Aa
DGDG 34:3	640471.9	Aab	755701.5	Ac	830144.4	Ab	392085.6	Bb	1826814.3	Aa	1920851.3	Aa	773462.2	Ba	1602682.7	Aab	1765520.2	Aa	820021.9	Ca	1254786.6	Bb	1952225.6	Aa
DGDG 34:4	1078677.9	Ba	1315267.6	ABa	1489562.7	Aa	177106.8	Bb	1553853.6	Aa	1690312.6	Aa	170190.9	Bb	1308905.6	Aa	1537520.3	Aa	109583.6	Cb	869101.9	Bb	1498860.9	Aa
DGDG 34:5	1283971.6	Aa	1445721.4	Ac	1768604.1	Ab	571595.4	Bb	2928173.1	Aa	3086039.8	Aa	916285.8	Bab	2548202.6	Aab	2885313.3	Aa	543897.9	Cb	2103782.7	Bb	3303541.4	Aa
DGDG 34:6	1386282.2	Aab	1546367.7	Ab	1942844.7	Ac	719919.9	Bb	3317940.8	Aa	3746241.1	Aab	1616634.7	Ba	3115804.1	Aa	3482189.6	Ab	1198690.5	Cab	2800703.9	Ba	4378153.4	Aa
DGDG 36:2	35233.0	Ba	48960.1	Aa	46630.3	ABab	10400.8	Bb	43499.6	Aa	48848.1	Aab	14874.0	Cb	46428.8	Ba	58355.9	Aa	12427.6	Bb	20885.8	Bb	37345.0	Ab
DGDG 36:3	62222.5	Ba	67981.6	ABab	82226.3	Aa	8633.8	Bb	71608.8	Aa	70571.9	Aab	13638.1	Bb	49382.8	Abc	50453.7	Ab	9375.6	Bb	30200.3	Ac	NA	Bc
DGDG 36:4	87998.9	Aa	108915.2	Aa	112024.8	Ab	NA	Bb	134863.2	Aa	136946.4	Ab	NA	Bb	111292.6	Aa	125930.2	Ab	NA	Cb	50463.0	Bb	257016.1	Aa
DGDG 36:5	137644.1	Aa	172689.3	Ab	195343.5	Ac	28311.3	Bb	430017.8	Aa	439344.3	Ab	42256.1	Bab	338254.6	Aa	386250.3	Ab	24392.6	Cb	158758.3	Bb	583108.1	Aa
DGDG 36:6	102468.2	Aa	134733.3	Ac	151540.9	Ac	45038.1	Ba	493136.7	Aa	496678.7	Ab	81100.6	Ca	423910.5	Ba	499043.9	Ab	56459.2	Ca	217871.3	Bb	998698.8	Aa

SI Table 11. (continuation) Relative abundance of lipid of *Monoraphidium* sp. BR023 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N		0h 3.5N		0h 7N		10h 0N		10h 3.5N		10h 7N		18h 0N		18h 3.5N		18h 7N		36h 0N		36h 3.5N		36h 7N	
LysoPC 16:0	56023.0	Bbc	76283.4	ABa	80968.9	Aa	53835.0	Bc	82157.2	Aa	89131.5	Aa	82427.6	Ab	97477.8	Aa	103355.7	Aa	129231.6	Aa	71970.3	Ba	105833.6	Aa
LysoPC 16:0.1	4727.9	Ab	6179.5	Aab	6066.2	Ab	4628.6	Bb	6612.2	ABab	7815.6	Aab	6646.7	Bb	8038.2	ABa	8760.0	Aa	10468.9	Ba	5376.6	Ab	9120.3	Aa
LysoPC 16:2	13449.9	Aa	26449.0	Ab	33993.9	Ad	20343.6	Ba	103166.2	Aa	91813.8	Ac	35818.0	Ba	131894.4	Aa	152002.9	Ab	35782.0	Ba	52138.8	Bb	418833.6	Aa
LysoPC 16:3	6011.3	Aa	12567.7	Ab	18075.3	Ac	13528.9	Ba	80693.7	Aab	76899.9	Ac	30778.1	Ba	131789.3	Aa	165136.1	Ab	29493.5	Ba	60797.2	Bb	702339.9	Aa
LysoPC 18:2	38108.9	Aa	66112.5	Ab	80888.0	Ac	72848.6	Ba	594513.2	Aa	433210.5	Ab	116951.8	Ba	634484.8	Aa	603003.0	Ab	137231.8	Ba	295462.7	Bb	2334589.2	Aa
LysoPC 18:3	17791.3	Aa	28122.9	Ab	36567.2	Ac	29336.6	Ba	237753.7	Aa	217022.6	Ab	63616.8	Ba	292780.3	Aa	376297.3	Ab	88287.1	Ba	177424.1	Bab	1716247.8	Aa
MGDG 34:1	133410.2	Ba	182953.5	Ab	199979.0	Ab	34828.2	Bb	258734.0	Aa	293102.1	Aa	NA	Cb	158849.7	Bb	231177.9	Ab	NA	Bb	94240.7	Ac	106560.5	Ac
MGDG 34:2	84123.2	Aa	106305.3	Aa	122971.2	Aa	5996.8	Bb	124092.8	Aa	161907.7	Aa	8611.8	Cb	92406.2	Ba	157623.4	Aa	8154.6	Bb	23298.4	Bb	64839.0	Ab
MGDG 34:2.1	81492.1	Ba	98367.1	ABb	128838.5	Ab	16091.4	Cb	219813.3	Ba	268131.1	Aa	29885.3	Cb	115491.1	Bb	173585.3	Ab	21498.6	Bb	42117.9	Bc	171111.0	Ab
MGDG 34:3	2155.4	Aa	2692.7	Ab	3097.5	Ab	NA	Cb	5390.5	Ba	6757.3	Aa	NA	Cb	5226.9	Ba	7501.0	Aa	NA	Bb	NA	Bc	4070.8	Ab
MGDG 34:4	165640.7	Aa	257371.3	Ab	303319.7	Ad	13914.6	Ba	632711.4	Aa	791254.9	Ac	22275.9	Ca	611571.2	Ba	1075986.2	Ab	21038.4	Ba	150291.3	Bb	1611472.4	Aa
MGDG 34:5	133120.7	Aa	217463.9	Ab	262701.7	Ad	20718.8	Ca	865954.5	Ba	1073759.4	Ac	36275.2	Ca	891039.9	Ba	1332932.0	Ab	32951.7	Ca	256096.6	Bb	2415936.3	Aa
MGDG 34:6	NA	Aa	NA	Aa	NA	Ac	17000.7	Aa	NA	Aa	NA	Ac	NA	Ba	NA	Ba	1481964.8	Ab	22133.3	Ba	NA	Ba	3164081.7	Aa
MGDG 36:5	NA	Aa	NA	Ab	NA	Ac	NA	Ba	98558.1	Aa	124310.8	Ab	NA	Ba	NA	Bb	109975.0	Ab	NA	Ba	NA	Bb	303630.7	Aa
MGDG 36:6	13313.2	Aa	21746.9	Aa	26797.3	Ac	3294.8	Ba	70220.9	Aa	87120.8	Abc	4989.5	Ba	60209.2	Ba	126542.2	Ab	3283.9	Ba	12705.0	Ba	616385.0	Aa
PC 32:0	27884.4	Ba	33228.7	Aa	33373.0	Aa	18829.4	Ac	14986.6	Ab	18691.7	Ab	20125.1	Abc	13975.4	Bb	14926.6	Bbc	25597.2	Aab	14456.8	Bb	11727.0	Bc
PC 32:1	37019.2	Cb	48996.0	Bb	47631.5	Ab	21145.6	Cc	32765.9	Bc	42177.9	Ac	30623.9	Cb	42601.6	Bb	51938.7	Ab	43737.5	Ca	50077.8	Ba	70931.1	Aa
PC 32:1.1	19640.3	Aa	23350.5	Ab	26956.0	Ac	13257.0	Ba	29784.5	Aab	33757.7	Ac	17363.3	Ba	36786.8	Aa	45621.5	Ab	21942.9	Ba	25686.9	Bab	89648.7	Aa
PC 32:2	36162.2	Aa	60144.5	Ab	80527.4	Ac	28031.2	Ba	206907.0	Aa	203240.7	Ab	51279.5	Ba	223860.9	Aa	311713.2	Ab	86150.6	Ba	116767.7	Bab	862977.5	Aa
PC 32:3	28309.1	Aa	51098.5	Aa	70093.4	Ab	19171.1	Aa	173576.6	Aa	170847.2	Ab	34725.1	Ba	206818.0	ABa	304590.6	Ab	58467.7	Ba	127115.5	Ba	1400996.5	Aa
PC 32:4	1475.1	Aa	3321.2	Aa	3960.3	Ac	1137.4	Aa	7899.4	Aa	8493.5	Abc	1285.1	Ba	10750.2	Aa	14495.6	Ab	938.6	Ba	3578.3	Ba	77157.1	Aa
PC 34:1	157716.3	Aa	NA	Ba	NA	Ba	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Aa	NA	Aa
PC 34:2	NA	Aa	NA	Ac	NA	Ac	NA	Ba	474158.4	Ab	NA	Bc	NA	Ba	731286.7	Aa	889451.0	Ab	NA	Ba	NA	Bc	2317233.4	Aa
PC 34:3	112093.4	Aa	152579.6	Ab	178609.7	Ac	55165.6	Ba	348940.2	Aab	370404.2	Ac	96870.5	Ba	441842.2	Aa	648680.8	Ab	145512.7	Ba	211706.2	Bab	1913221.4	Aa
PC 34:4	22843.8	Aa	38233.6	Ab	52463.4	Ac	10762.2	Ba	133196.5	Aab	129268.9	ABbc	16688.4	Ba	192855.4	Aa	261005.7	Ab	18021.0	Ba	53878.5	Bb	967318.1	Aa
PC 34:5	14725.0	Aa	23353.2	Aa	35820.0	Ab	11715.1	Aa	145439.2	Aa	147789.4	Ab	17685.5	Ba	242849.1	ABa	352547.6	Ab	17308.3	Ba	65592.9	Ba	1850434.6	Aa
PC 34:6	7388.3	Aa	11616.6	Aa	15522.5	Ab	NA	Aa	97877.4	Aa	105040.7	Ab	11257.4	Ba	249605.8	ABa	377081.9	Ab	10400.5	Ba	45869.9	Ba	2021642.8	Aa
PC 36:1	151921.9	Aab	200534.6	Ac	205906.7	Ab	89286.7	Bb	202994.0	Ac	254422.1	Aab	136472.3	Bab	295856.5	Ab	330892.2	Aa	172200.5	Ca	433731.7	Aa	254819.0	Bab
PC 36:2	2424013.6	Aa	3222168.7	Ac	3223319.3	Ac	1133915.9	Ba	3933832.4	Ac	4875504.8	Ac	2070216.4	Ba	6770862.7	Ab	7570075.4	Ab	2713487.8	Ba	10469420.0	Aa	10216540.5	Aa

SI Table 11. (continuation) Relative abundance of lipid of *Monoraphidium* sp. BR023 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
PC 36:3	82068.5 Aa	108467.1 Ac	144721.0 Ac	69071.4 Ba	382712.0 Aa	351101.4 Ab	73750.4 Ba	322707.5 Aab	405843.5 Ab	110152.5 Ba	177649.3 Bbc	1238630.0 Aa
PC 36:3.1	12747.8 Aa	17141.8 Ac	18354.5 Ac	7427.5 Aa	71604.6 Ac	90674.9 Ac	8886.2 Ba	290832.2 Ab	246327.9 Ab	11871.1 Ca	714374.5 Aa	519806.4 Ba
PC 36:5	35581.3 Aa	53479.7 Aa	76277.6 Ab	36152.3 Aa	497941.5 Aa	492896.3 Ab	61098.5 Aa	514515.8 Aa	706339.1 Ab	87362.8 Ba	260830.7 Ba	4592256.4 Aa
PC 36:6	35917.1 Aa	45937.5 Aa	57886.9 Ab	26794.4 Aa	246015.0 Aa	267044.5 Ab	39682.7 Aa	292242.1 Aa	417840.5 Ab	51240.3 Ba	149341.1 Ba	3631978.9 Aa
PC 38:2	36216.5 Aa	43612.1 Ac	49434.1 Ac	19152.4 Ba	54963.1 Abc	71021.4 Ab	31582.6 Ba	74308.9 Aab	83852.0 Aab	35337.8 Ba	86284.5 Aa	95886.2 Aa
PC 38:3	2761.9 Aa	4185.3 Ab	6156.7 Ac	NA	15344.1 Aa	15611.7 Ab	NA	15546.5 Ba	23264.1 Aa	NA	2869.2 Bb	23759.3 Aa
PC 38:3.1	NA	1579.4 Ab	1058.0 Ab	NA	1447.2 Ab	1597.1 Ab	1411.2 Ab	2232.9 Ab	2109.4 Ab	2486.2 Ca	5788.8 Aa	3846.4 Ba
PE 32:1	131215.1 Aa	184828.8 Abc	185159.9 Ac	62074.4 Ba	263011.3 Aab	307970.6 Ab	71836.3 Ca	300670.5 Ba	512768.4 Aa	55849.4 Aa	91851.6 Ac	40064.5 Ad
PE 34:1	286740.6 Aa	379462.2 Aa	386596.6 Aa	132233.1 Bb	328350.1 Aa	378770.2 Aa	168347.2 Cab	305234.3 Ba	435975.0 Aa	144228.7 Ab	161711.0 Ab	132246.4 Ab
PE 34:2	871033.5 Aa	1196325.0 Ac	1225440.4 Ac	419864.2 Ba	1966824.7 Aab	2158304.7 Ab	601480.2 Ba	2350497.8 Aa	2913842.6 Aa	475654.8 Ba	1555236.6 Abc	1687281.1 Abc
PE 34:3	19545.4 Aa	26579.5 Aa	27573.6 Ac	9300.6 Ba	29764.3 ABa	32216.3 Abc	13649.6 Ba	38814.4 Aa	52716.1 Ab	13393.3 Ba	21809.2 Ba	86205.2 Aa
PE 34:4	1869.8 Aa	2444.7 Aa	2560.3 Ac	996.7 Aa	8117.6 Aa	8770.3 Abc	NA	12206.7 ABa	17361.1 Ab	1795.3 Ba	4290.7 Ba	46945.3 Aa
PE 34:5	1066.8 Aa	798.5 Aa	1401.5 Ab	NA	4939.0 Aa	5816.1 Ab	820.0 Ba	13224.9 ABa	19720.2 Ab	NA	3763.2 Ba	61138.2 Aa
PE 34:6	NA	NA	NA	NA	3494.5 Aa	4406.9 Ab	NA	9353.5 Aa	13502.4 Ab	NA	2181.2 Ba	49118.8 Aa
PE 36:1	27913.8 Ba	49499.6 Ab	55398.3 Ac	20114.0 Ca	117607.5 Ba	145657.5 Aa	25769.6 Ba	97179.1 Aa	114324.6 Ab	18806.7 Ba	44072.1 Ab	42635.5 Ac
PE 36:2	1451105.4 Aa	1880464.6 Ab	2160134.5 Ab	710240.0 Ba	3711302.4 Aa	4214377.3 Aa	1076351.4 Ba	3838578.7 Aa	4005914.3 Aa	688853.3 Ba	2055708.1 Ab	2351022.6 Ab
PE 36:3	NA	NA	NA	NA	272180.1 Ba	331042.8 Aa	NA	232494.2 Aa	219152.9 Ab	NA	97228.5 Ab	92494.5 Ac
PE 36:3.1	32156.6 Aa	47593.3 Aa	45856.9 Ab	20916.5 Aa	49687.6 Aa	50647.4 Ab	34768.6 Aa	50818.8 Aa	63733.9 Ab	36449.9 Ba	36795.3 Ba	113584.9 Aa
PE 36:4	124470.7 Ba	158073.1 Aa	141715.8 ABb	51051.5 Bb	84148.6 Ac	113084.3 Ab	55239.1 Cb	117033.1 Bb	187643.9 Aa	47879.2 Ab	68751.8 Ac	40851.4 Ac
PE 36:4.1	59934.0 Aa	86576.0 Aa	84757.1 Ab	31187.3 Aa	79709.7 Aa	85095.0 Ab	57234.0 Aa	86237.9 Aa	113138.6 Ab	49203.5 Ba	67878.0 Ba	229778.3 Aa
PE 36:5	NA	5680.4 Aa	7674.7 Ab	NA	20640.5 Aa	25118.3 Ab	4064.6 Aa	48554.0 Aa	75943.1 Ab	2858.2 Ba	27420.1 Ba	235537.3 Aa
PE 36:6	5184.1 Aa	6595.2 Aa	8471.5 Ab	2729.1 Aa	12516.5 Aa	15576.0 Ab	4640.5 Ba	30053.7 ABa	45005.3 Ab	2950.2 Ba	13159.4 Ba	104568.2 Aa
PE 38:2	6242891.2 Aa	7047089.0 Aa	6907199.4 Aa	2274124.9 Bb	4078555.7 Ab	4835564.0 Ab	2902682.3 Bb	4867679.3 Ab	5859939.0 Aab	2513543.0 Cb	4247767.3 Bb	7132857.2 Aa
PE 38:3	2724.7 Aa	4499.8 Ad	3412.8 Ac	NA	20895.9 Bb	27938.8 Ab	NA	27948.4 Ba	36102.3 Aa	NA	14058.9 Bc	23272.0 Ab
PE 40:1	7589.8 Ba	11061.9 Aa	9970.2 Aa	5309.6 Ba	9250.3 Aa	10401.9 Aa	6554.0 Ba	10447.8 Aa	12134.0 Aa	7109.7 Ba	11911.1 Aa	12173.5 Aa
PE 40:2	86767.3 Aab	119096.7 Ac	123743.5 Ab	53298.3 Bb	134428.2 Ac	158775.4 Ab	98465.1 Bab	217443.0 Ab	252072.9 Aa	134223.7 Ba	287294.0 Aa	265366.9 Aa
PE 40:3	NA	NA	NA	NA	NA	NA	NA	NA	18955.6 Aa	NA	NA	12842.6 Ab

SI Table 11. (continuation) Relative abundance of lipid of *Monoraphidium* sp. BR023 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N	0h 3.5N	0h 7N	10h 0N	10h 3.5N	10h 7N	18h 0N	18h 3.5N	18h 7N	36h 0N	36h 3.5N	36h 7N
PG 32:0	17670.5 Ba	21555.9 Aa	22271.1 Aa	7074.2 Bb	13550.9 Ab	15223.4 Ac	7973.2 Bb	14315.3 Ab	17255.3 Abc	9265.4 Bb	7748.1 Bc	19732.4 Aab
PG 32:1	8070.9 Aa	11917.3 Ab	10094.8 Ac	2829.4 Ba	22116.1 Aa	26715.1 Ac	3351.1 Ca	24776.2 Ba	38775.9 Aa	4377.8 Aa	4223.5 Ab	5682.6 Ac
PG 34:2	184381.7 Aa	240030.8 Abc	224668.6 Ac	71458.7 Bb	305645.6 Aab	349012.5 Ab	94591.7 Cab	343486.2 Ba	470463.6 Aa	73022.0 Cb	183646.5 Bc	361435.4 Ab
PG 34:3	8534.2 Aa	11554.4 Ab	10945.3 Ad	2778.6 Ba	83369.7 Aa	90949.8 Ac	5517.1 Ca	66469.9 Ba	115756.8 Ab	NA Ba	NA Bb	337365.1 Aa
PG 34:4	13002.9 Aa	17705.5 Aab	17288.9 Ac	6719.8 Ba	34254.2 Aab	41264.2 Abc	10699.3 Ba	39489.7 Aa	54252.3 Ab	7698.7 Ba	14623.4 Bb	248660.8 Aa
PG 36:1	39491.8 Ba	63451.9 Ab	65217.8 Ab	20720.1 Cb	78766.1 Bab	98271.1 Aa	31793.9 Cab	91671.7 Ba	109445.6 Aa	27115.7 Cab	62289.4 Ab	42860.2 Bc
PG 36:2	741250.4 Aa	854641.0 Ab	875780.4 Abc	335002.2 Bb	1064538.3 Aab	1199581.9 Aab	459584.7 Bab	1296144.4 Aa	1476250.4 Aa	354989.0 Bb	858240.1 Ab	849915.6 Ac
SQDG 32:0	2539144.4 Aa	2391220.6 Aa	2352230.1 Aa	1264434.9 Ab	1230777.6 Ab	1359238.2 Ac	1296701.9 Ab	1364238.0 Ab	1318269.5 Ac	1348807.1 Bb	1214316.3 Bb	1865231.7 Ab
SQDG 32:1	17551.5 Aa	21418.9 Aa	20815.4 Ab	5294.7 Bb	14011.2 Ab	NA Cc	6824.7 Bb	12583.2 Abc	15608.2 Ab	5690.2 Bb	7141.8 Bc	70516.6 Aa
SQDG 32:2	17158.4 Ba	21341.7 ABa	23031.0 Ab	4769.6 Bb	17940.3 Aa	20477.2 Ab	NA Bb	20556.5 Aa	25598.9 Ab	NA Cb	11255.8 Bb	78123.1 Aa
SQDG 32:3	28468.2 Aa	32884.2 Aa	35430.7 Ab	7235.8 Bb	26174.8 Aab	30582.6 Ab	10183.4 Bb	32441.3 Aa	38177.0 Ab	7949.9 Cb	18360.7 Bb	106814.6 Aa
SQDG 34:0	216113.8 Ba	248959.3 Aa	255674.9 Aa	105276.0 Bb	208118.8 Ab	NA Cb	102222.7 Bb	243842.5 Aa	266379.9 Aa	99985.9 Ab	104485.3 Ac	NA Bb
SQDG 34:1	777089.1 Ba	857427.4 ABa	950796.0 Aa	NA Cb	616580.9 Bb	729103.5 Ab	NA Cb	542894.8 Bb	681504.5 Ab	NA Bb	337883.5 Ac	394033.6 Ac
SQDG 34:2	1258210.1 Aa	1360644.8 Aa	1460863.6 Ab	230783.9 Bb	1182646.9 Aa	1359259.6 Ab	314798.0 Bb	1129577.1 Aa	1321994.1 Ab	242532.9 Cb	626941.8 Bb	2622296.0 Aa
SQDG 34:3	526615.6 Aa	630123.5 Ab	691578.7 Ac	284195.2 Bb	1257292.7 Aa	1419209.7 Ab	473618.6 Bab	1117847.8 Aa	1284151.7 Ab	402144.6 Cab	803870.9 Bb	2690696.1 Aa
SQDG 34:4	14342.9 Ba	17322.4 ABa	21183.6 Abc	2829.5 Bb	16515.4 Aa	18187.5 Ac	3731.7 Bb	19545.1 Aa	24205.6 Ab	1591.3 Cb	6959.2 Bb	43158.2 Aa
SQDG 34:5	9309.4 Aa	11366.7 Aab	13554.5 Ac	1320.6 Bab	13530.3 Aab	16698.7 Abc	1636.6 Bab	17642.4 Aa	23613.7 Ab	NA Bb	6661.4 Bb	53613.3 Aa
SQDG 34:6	6484.9 Aa	7086.0 Aa	9242.9 Ac	1520.4 Ba	12267.5 ABa	13916.8 Abc	1253.0 Ba	18416.4 Aa	25721.8 Ab	NA Ba	5575.8 Ba	78471.3 Aa
TAG 42:0	16191.1 ABb	15312.8 Ba	20697.6 Aa	16764.3 Ab	9371.9 Bb	12765.0 ABb	20950.6 Aab	9386.5 Bb	9719.5 Bb	24015.9 Aa	18386.5 Ba	8148.0 Cb
TAG 42:1	15201.5 Ac	13741.1 Ab	15488.1 Aa	19625.1 Ac	9446.6 Bb	12217.5 Bab	27539.1 Ab	8790.0 Bb	8687.2 Bb	34386.0 Aa	21718.7 Ba	8544.1 Cb
TAG 42:2	2868.9 Ac	2663.3 Ab	2954.7 Aa	3325.9 Ac	1601.0 Bb	2121.2 Ba	6525.1 Ab	1957.3 Bb	1767.6 Ba	9205.5 Aa	4406.2 Ba	1876.4 Ca
TAG 44:0	55651.4 ABbc	48365.9 Ba	67429.6 Aa	43590.5 Ac	30114.6 Bb	38451.4 ABb	61834.5 Ab	28865.0 Bb	29474.3 Bb	82772.0 Aa	51593.1 Ba	29107.6 Cb
TAG 44:1	31080.8 Ac	28492.6 Ab	37659.8 Aa	43641.1 Ac	26844.7 Bb	32831.2 ABa	106431.2 Ab	29592.9 Bb	25534.9 Ba	149687.8 Aa	49441.4 Ba	27315.6 Ca
TAG 44:2	19411.5 Ac	16430.0 Aa	17377.0 Aa	22894.2 Abc	11282.4 Bb	13683.3 Bb	23988.8 Ab	10278.8 Bb	11184.6 Bbc	39523.0 Aa	19274.0 Ba	9862.7 Cc
TAG 46:0	236183.8 ABbc	204126.7 Bab	285094.2 Aa	201126.0 Ac	164135.4 Ab	199127.8 Ab	271919.6 Ab	159741.7 Bb	170111.6 Bb	360621.0 Aa	229444.6 Ba	156315.5 Cb
TAG 46:1	149078.4 Ac	149057.5 Ab	175569.2 Aa	245729.1 Ac	164668.3 Ab	202041.0 Aa	748491.9 Ab	182278.3 Bb	116289.7 Ba	1165697.5 Aa	370353.6 Ba	69345.5 Ca
TAG 46:2	30326.0 Ac	30291.2 Ab	33494.7 Aa	40682.3 Ac	24059.1 Bb	30886.4 ABa	88404.1 Ab	NA Cc	22269.1 Ba	169169.1 Aa	66465.3 Ba	NA Cb
TAG 46:2.1	23773.6 Bc	22035.5 Bb	38460.7 Aa	25809.6 Ac	27056.0 Ab	30982.1 Aab	45970.0 Ab	23383.6 Bb	27020.4 Bab	58787.8 Aa	39965.2 Ba	24357.6 Cb
TAG 46:3	9576.3 Ad	10259.6 Ab	11139.4 Aa	20464.9 Ac	4829.3 Bb	7565.3 Ba	55531.4 Ab	5443.3 Bb	6095.7 Ba	140871.3 Aa	36711.9 Ba	3071.3 Ca

SI Table 11. (continuation) Relative abundance of lipid of *Monoraphidium* sp. BR023 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N		0h 3.5N		0h 7N		10h 0N		10h 3.5N		10h 7N		18h 0N		18h 3.5N		18h 7N		36h 0N		36h 3.5N		36h 7N	
TAG 46:3.1	3236.3	Bc	4405.8	Bab	6086.5	Aa	5824.5	Ab	2615.8	Bc	3296.8	Bb	8977.5	Aa	2941.2	Bbc	2877.2	Bb	NA	Cd	5580.4	Aa	2194.3	Bb
TAG 46:4	2607.6	Ac	1505.2	Ab	2755.6	Aa	3768.2	Ac	1081.6	Bb	1688.5	Bab	9505.9	Ab	1185.3	Bb	1918.2	Ba	23630.4	Aa	7192.4	Ba	NA	Cb
TAG 48:0	1241367.1	Ab	988385.8	Aab	1299294.3	Aa	1312868.1	Ab	748323.5	Bb	908115.4	Bb	1559941.8	Ab	763916.6	Bb	785866.6	Bb	2866354.8	Aa	1180491.3	Ba	672321.8	Cb
TAG 48:1	1186716.7	Ac	986810.6	Ab	1235582.8	Aa	1739235.8	Ac	1057210.3	Ab	1284093.0	Aa	4099633.0	Ab	1063499.2	Bb	820813.1	Ba	7322018.4	Aa	2055695.1	Ba	557848.2	Ca
TAG 48:2	765537.4	Ac	602835.2	Ab	683506.0	Aa	1039434.5	Ac	317636.5	Bb	455073.6	Ba	2561950.0	Ab	323278.2	Bb	310876.4	Ba	5110691.4	Aa	2204865.5	Ba	143238.9	Ca
TAG 48:3	623718.9	Ac	509614.2	Ab	638842.6	Aa	973314.2	Ac	302897.8	Ab	466035.2	Aa	3496855.2	Ab	291509.1	Bb	293449.0	Ba	8311221.9	Aa	3196786.6	Ba	45208.7	Ca
TAG 48:4	122425.9	Ac	96813.6	Ab	114069.1	Aa	266846.0	Ac	50884.7	Bb	81218.1	Ba	718303.3	Ab	39571.4	Bb	45028.3	Ba	1267038.1	Aa	731689.9	Ba	5740.1	Ca
TAG 48:5	61369.6	Ac	52301.0	Ab	66466.6	Aa	154471.8	Ac	37222.9	Ab	59382.9	Aa	577863.4	Ab	29945.6	Bb	32773.6	Ba	1147492.0	Aa	551235.9	Ba	6227.7	Ca
TAG 48:6	19164.8	Ac	15346.9	Ab	21024.9	Aa	59021.0	Ac	14178.4	Ab	23748.3	Aa	312378.1	Ab	11366.6	Bb	13086.6	Ba	677422.1	Aa	380780.1	Ba	3210.3	Ca
TAG 48:7	4145.8	Ac	3694.4	Ab	4838.7	Aa	10574.0	Ac	4528.6	Ab	7667.6	Aa	46620.7	Ab	3343.6	Bb	3624.6	Ba	63965.8	Aa	64873.6	Aa	1273.1	Ba
TAG 48:8	1583.9	Ac	1410.8	Ab	2253.4	Aa	NA	Ac	2619.9	Ab	4390.7	Aa	25752.1	Ab	2150.3	Bb	2590.7	Ba	44677.4	Aa	33620.4	Ba	1601.0	Ca
TAG 48:9	NA	Ac	NA	Ab	NA	Aa	NA	Ac	NA	Ab	795.8	Aa	6465.0	Ab	NA	Bb	NA	Ba	15433.7	Aa	7762.0	Ba	NA	Ca
TAG 50:0	1906605.2	Aab	1485302.3	Aa	2003817.4	Aa	1524535.2	Ab	1344440.6	Aa	1533694.1	Aa	1691225.3	Ab	1339100.7	Aa	1340854.9	Aa	2415313.6	Aa	1483048.7	Ba	1335050.6	Ba
TAG 50:1	16896342.3	Ac	12944730.0	Ab	14906593.9	Aa	29312773.0	Ac	8054319.7	Bb	11077871.2	Ba	57515413.5	Ab	7529455.1	Bb	6829483.1	Ba	105188799.7	Aa	44203863.5	Ba	2776860.4	Ca
TAG 50:2	4195603.0	Ac	3345349.3	Ab	3941622.3	Aa	6460943.9	Ac	2620844.3	Ab	3573912.8	Aa	16973608.7	Ab	2580299.3	Bb	2334733.6	Ba	36737527.4	Aa	13967175.6	Ba	1196668.2	Ca
TAG 50:3	3134061.6	Ac	2385943.8	Ab	2959700.1	Aa	6837116.2	Ac	1642109.3	Bb	2485034.1	Ba	16003231.2	Ab	1139327.5	Bb	1251641.2	Ba	28921610.3	Aa	14961759.4	Ba	160472.5	Ca
TAG 50:4	2382423.9	Ac	1842915.6	Ab	2226128.1	Aa	5511708.5	Ac	977611.4	Bb	1598821.4	ABa	18939887.4	Ab	646230.3	Bb	734473.7	Ba	39459695.8	Aa	16298232.5	Ba	65547.4	Ca
TAG 50:5	1032049.7	Ac	785858.1	Ab	1059566.7	Aa	3201061.5	Ac	400885.8	Bb	671626.7	ABa	11988588.2	Ab	330729.2	Bb	335549.1	Ba	21657677.3	Aa	8462311.0	Ba	49135.7	Ca
TAG 50:6	1895.9	Aa	NA	Ba	NA	Ba	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Aa	NA	Aa	NA	Ab	NA	Aa	NA	Aa
TAG 50:6.1	503956.4	Ac	394323.6	Ab	526871.3	Aa	2236567.3	Ac	224397.9	Ab	374186.7	Aa	12365702.7	Ab	232337.4	Bb	223246.9	Ba	26014107.3	Aa	7013747.2	Ba	46865.5	Ca
TAG 50:7	85652.8	Ac	71709.8	Ab	103307.4	Aa	338819.8	Ac	63034.0	Ab	98513.8	Aa	1597224.4	Ab	44610.9	Bb	51524.3	Ba	2897404.9	Aa	1385797.7	Ba	15167.9	Ca
TAG 50:8	34348.3	Ac	28767.1	Ab	45192.2	Aa	169884.9	Ac	40345.4	Ab	63409.5	Aa	944001.1	Ab	31332.9	Bb	39876.4	Ba	1941959.7	Aa	648574.3	Ba	18275.7	Ca
TAG 50:9	11510.9	Ac	8918.4	Ab	13692.6	Aa	77694.6	Ac	19265.4	Ab	29776.9	Aa	561346.8	Ab	16547.4	Bb	21143.3	Ba	1324415.7	Aa	326326.5	Ba	14230.9	Ca
TAG 52:0	1680212.0	Aa	1333448.8	Aa	1760973.6	Aa	1257012.3	Aa	1244599.4	Aa	1442794.2	Aa	1333460.5	Aa	1180284.0	Aa	1291024.2	Aa	1780744.1	Aa	1236093.9	Aa	1232040.6	Aa
TAG 52:1	7752771.6	Ac	6156442.8	Ab	7930367.8	Aa	11108715.0	Ac	5402514.7	Bb	7201396.1	ABa	22930456.6	Ab	5804238.6	Bb	5531231.0	Ba	46389107.1	Aa	12095141.0	Ba	3661678.4	Ca
TAG 52:2	27927774.3	Ad	21049253.6	Ab	27277934.5	Aa	57312401.9	Ac	18636139.4	Bb	27288574.5	Ba	111481451.5	Ab	15455117.3	Bb	17278103.4	Ba	164276251.3	Aa	90894194.2	Ba	6489171.0	Ca
TAG 52:3	9823653.8	Ac	7341192.3	Ab	9398841.9	Aa	22983090.8	Ac	6060603.9	Bb	8924754.8	Ba	59244688.3	Ab	4602482.3	Bb	4954195.6	Ba	109361793.9	Aa	46640910.4	Ba	1595831.7	Ca
TAG 52:4	4619068.1	Ac	3534704.6	Ab	4648218.4	Aa	13474444.7	Ac	2927308.8	Bb	4364138.7	ABa	43970594.4	Ab	2088431.2	Bb	2326419.0	Ba	87663219.6	Aa	38328708.0	Ba	866964.1	Ca
TAG 52:5	1977478.5	Ac	1468403.3	Ab	2080624.6	Aa	7357131.9	Ac	1192228.6	Bb	1955646.1	Ba	23682289.3	Ab	599276.3	Bb	785713.8	Ba	43842876.1	Aa	18121112.1	Ba	NA	Ca

SI Table 11. (continuation) Relative abundance of lipid of *Monoraphidium* sp. BR023 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N		0h 3.5N		0h 7N		10h 0N		10h 3.5N		10h 7N		18h 0N		18h 3.5N		18h 7N		36h 0N		36h 3.5N		36h 7N	
TAG 52:5.1	3036.0	Ab	2510.8	Aa	NA	Aa	NA	Ab	3101.8	Aa	4042.4	Aa	NA	Ab	1425.8	Aa	NA	Aa	135382.8	Aa	22968.2	Ba	NA	Ba
TAG 52:6	937502.5	Ac	732887.1	Ab	1010398.3	Aa	5519830.3	Ac	582392.5	Bb	922726.0	Ba	20155286.3	Ab	300524.4	Bb	403206.4	Ba	37038774.4	Aa	14977956.9	Ba	58071.5	Ca
TAG 52:6.1	NA	Aa	NA	Aa	NA	Aa	NA	Aa	1800.2	Aa	2455.0	Aa	17106.6	Aa	834.3	Aa	NA	Aa	NA	Aa	28976.5	Aa	2568.2	Aa
TAG 52:7	394226.5	Ac	305754.3	Ab	440568.1	Aa	3307141.3	Ac	273968.4	Ab	484951.4	Aa	1863398.1	Ab	165700.7	Bb	213987.9	Ba	37530906.6	Aa	10994292.6	Ba	57216.5	Ca
TAG 52:8	93796.9	Ac	76920.8	Ab	118774.2	Aa	578599.0	Ac	129108.6	Ab	212312.8	Aa	3747984.7	Ab	90427.7	Bb	119240.2	Ba	5897422.7	Aa	2015061.3	Ba	56193.9	Ca
TAG 52:9	23018.9	Ac	19366.1	Ab	31914.7	Aa	220181.0	Ac	56533.7	Ab	91541.5	Aa	1873845.1	Ab	45208.0	Bb	59339.9	Ba	2882543.3	Aa	707004.1	Ba	43110.8	Ca
TAG 54:0	559345.4	ABa	479528.8	Ba	626917.5	Aa	431656.2	Ab	419673.4	Aa	492015.9	Ab	490247.9	Aab	430777.5	Aa	446196.0	Ab	591734.1	Aa	444174.3	Ba	450005.4	Bb
TAG 54:1	2554377.8	Ac	2148596.7	Aa	2812659.7	Aa	2615892.2	Ac	1871236.9	Aa	2316886.5	Aa	3690225.1	Ab	1905503.2	Ba	1997861.6	Ba	7376905.5	Aa	2491490.7	Ba	1719520.6	Ba
TAG 54:2	7685421.1	Ac	6167656.1	Ab	8010122.9	Aab	9337202.7	Ac	6399412.8	Ab	9450557.0	Aa	18247898.9	Ab	6024388.9	Bb	7030580.6	Bab	41170551.5	Aa	13612463.7	Ba	3232132.0	Cb
TAG 54:3	13755443.6	Ad	10288304.3	Ab	14026944.0	Aa	37974608.9	Ac	10974485.6	Bb	16674830.9	Ba	81780290.7	Ab	6766966.7	Bb	8839411.8	Ba	137699455.2	Aa	62519786.3	Ba	3365679.1	Ca
TAG 54:4	6738090.1	Ad	5419855.4	Ab	7168378.8	Aa	21064933.7	Ac	5187259.3	Bb	7605833.9	Ba	55567940.8	Ab	3134646.8	Bb	3824352.7	Ba	99255567.4	Aa	40723085.8	Ba	1858864.9	Ca
TAG 54:5	4136976.0	Ac	3261787.1	Ab	4490053.0	Aa	14405321.5	Ac	3323970.7	Bb	4626480.3	ABa	46677911.4	Ab	2139945.6	Bb	2569499.2	Ba	92987177.3	Aa	40148284.6	Ba	1412770.8	Ca
TAG 54:6	1711580.7	Ac	1355546.2	Ab	1874929.0	Aa	4106121.7	Ac	1232842.8	Ab	1713827.7	Aa	15632307.4	Ab	922517.7	Bb	1087411.6	Ba	29769606.1	Aa	13074367.2	Ba	772660.5	Ca
TAG 54:7	243028.7	Ac	208725.7	Ab	294825.8	Aa	1001063.0	Ac	207053.1	Ab	321778.8	Aa	5488184.3	Ab	129890.7	Bb	178461.6	Ba	12558807.2	Aa	4938362.5	Ba	79028.3	Ca
TAG 54:8	44589.3	Ac	38909.7	Ab	56462.8	Aa	127034.8	Ac	51950.4	Ab	84689.0	Aa	767992.6	Ab	36767.4	Bb	54433.3	Ba	1393423.4	Aa	687961.2	Ba	26266.5	Ca
TAG 54:9	5112.6	Ac	5728.8	Ab	8856.6	Aa	15885.6	Ac	10769.5	Ab	18459.9	Aa	90159.0	Ab	9346.0	Bb	14007.7	Ba	202311.4	Aa	78327.0	Ba	7672.0	Ca
TAG 56:0	53902.4	Bbc	44281.9	Ba	67413.6	Aa	41832.8	Ac	33255.3	Aa	42068.8	Ab	58508.7	Ab	34555.9	Ba	36189.2	Bb	90113.8	Aa	43913.3	Ba	31046.9	Cb
TAG 56:1	140187.2	Ac	124929.3	Ab	166127.4	Aa	270516.9	Ac	97381.9	Bb	133838.5	Ba	603386.5	Ab	99675.6	Bb	102987.8	Ba	1490866.9	Aa	330376.8	Ba	69943.0	Ca
TAG 56:2	470089.0	Ad	408399.7	Ab	532160.4	Aa	1053602.4	Ac	424010.7	Bb	654518.8	ABa	2263472.7	Ab	402071.0	Bb	481158.6	Ba	5004199.7	Aa	1198530.7	Ba	165702.7	Ca
TAG 56:3	1080335.1	Ac	881080.9	Ab	1124672.5	Aab	2592820.7	Ac	1359613.2	Ab	2105827.4	Aa	6185583.1	Ab	870360.1	Bb	1236171.8	Bab	12182940.2	Aa	3187102.2	Ba	169704.0	Cb
TAG 56:4	445574.7	Ac	376769.2	Ab	478531.2	Aab	829479.5	Ac	551284.0	Ab	777019.6	Aa	1899871.8	Ab	350098.4	Bb	447289.8	Bab	2546509.8	Aa	1199403.6	Ba	102221.7	Cb
TAG 56:5	186787.2	Ac	164139.3	Ab	204708.8	Aab	442050.6	Ac	228808.8	Ab	353650.1	Aa	1355773.2	Ab	158210.6	Bb	184220.9	Bab	2594560.3	Aa	1025133.9	Ba	42661.4	Cb
TAG 56:6	39840.6	Ac	40218.9	Ab	44487.0	Aab	84532.7	Ac	53031.5	Ab	88149.3	Aa	312324.6	Ab	38665.4	Bb	41485.0	Bab	486071.6	Aa	271058.7	Ba	11437.7	Cb
TAG 56:7	7887.7	Ac	8950.5	Ab	9865.7	Aa	18765.8	Ac	9205.8	Ab	18048.5	Aa	76189.2	Ab	8296.4	Bb	8686.1	Ba	154873.5	Aa	80699.9	Ba	2623.4	Ca
TAG 58:0	29926.2	Ab	24129.6	Ba	32197.5	Aa	24130.3	Ac	14952.5	Bb	20280.0	Ab	32464.1	Ab	14925.9	Bb	16379.0	Bbc	52511.4	Aa	21141.0	Ba	12651.8	Cc
TAG 58:1	98693.0	Ac	84475.0	Ab	110384.1	Aa	150477.1	Ac	56025.9	Ab	81741.2	Aa	464592.4	Ab	55674.2	Bb	53197.3	Ba	1359891.9	Aa	312298.8	Ba	24391.4	Ca
TAG 58:2	147794.3	Ac	124282.8	Ab	168873.5	Aa	280597.4	Ac	119509.1	Bb	177835.3	ABa	674419.1	Ab	116548.4	Bb	124347.1	Ba	1533567.2	Aa	390706.7	Ba	60629.3	Ca
TAG 58:3	184411.1	Ac	152137.1	Ab	215380.7	Aab	398411.7	Ac	176898.5	Bb	309206.4	ABa	934390.6	Ab	135448.4	Bb	167878.8	Bab	1951669.2	Aa	455769.9	Ba	71324.2	Cb
TAG 58:4	110283.4	Ac	96172.4	Ab	124084.3	Aa	119485.3	Ac	83059.8	Ab	111350.3	Aab	240094.9	Ab	76839.3	Bb	84592.0	Bab	486886.6	Aa	191817.0	Ba	62967.4	Cb

SI Table 11. (continuation) Relative abundance of lipid of *Monoraphidium* sp. BR023 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h 0N		0h 3.5N		0h 7N		10h 0N		10h 3.5N		10h 7N		18h 0N		18h 3.5N		18h 7N		36h 0N		36h 3.5N		36h 7N	
TAG 58:5	22231.9	Ac	18325.4	Ab	22999.9	Aa	30583.7	Ac	13492.3	Ab	17194.9	Aa	107978.9	Ab	13239.6	Bb	12079.6	Ba	213318.7	Aa	75034.0	Ba	NA	Ca
TAG 58:6	14538.4	Ac	12543.8	Ab	16334.3	Aa	25042.4	Ac	9731.1	Ab	14259.6	Aa	167896.9	Ab	10529.6	Bb	10975.5	Ba	360060.7	Aa	80751.2	Ba	8203.1	Ca
TAG 60:0	63303.8	Ac	52027.1	Aa	67770.1	Aa	64320.9	Ac	21444.1	Bb	27863.8	Bb	98957.4	Ab	18576.0	Bb	18645.5	Bb	170768.9	Aa	55650.8	Ba	22176.5	Cb
TAG 60:1	90007.9	Ac	72309.4	Ab	91642.2	Aa	NA	Bd	38731.1	Ab	66179.5	Aab	234941.0	Ab	40984.2	Bb	40038.8	Bbc	651955.0	Aa	144439.2	Ba	NA	Cc
TAG 60:2	120731.3	Ac	101033.1	Ab	133377.4	Aa	162382.4	Ac	89807.5	Ab	144152.6	Aa	532792.2	Ab	88012.7	Bb	89401.0	Ba	1440780.2	Aa	344061.4	Ba	24225.3	Ca
TAG 60:3	64752.3	Ac	55459.4	Ab	72627.3	Aa	83038.2	Ac	51816.1	Ab	81421.7	Aa	260610.6	Ab	49020.4	Bb	49664.7	Bab	645100.3	Aa	175517.4	Ba	20322.3	Cb
TAG 60:4	43927.2	Ac	36501.3	Ab	49044.0	Aa	54900.5	Ac	31603.0	Ab	44669.2	Aa	183063.5	Ab	29873.9	Bb	31434.8	Ba	485217.6	Aa	186751.2	Ba	21279.7	Ca
TAG 60:5	10003.3	Ac	8779.9	Ab	12437.3	Aa	8009.9	Ac	7034.2	Ab	12225.0	Aa	47615.3	Ab	7861.5	Bb	8606.4	Bab	100306.8	Aa	36280.4	Ba	NA	Cb
TAG 60:5.1	17238.5	Ac	15117.7	Ab	17272.4	Aa	11532.1	Ac	NA	Bc	NA	Bb	62684.2	Ab	11038.4	Bbc	7232.0	Bab	129338.1	Aa	37740.8	Ba	NA	Cb
TAG 60:6	12476.7	Ac	10186.9	Ab	12113.5	Aa	7832.0	Ac	4397.7	Ab	7456.3	Aa	95538.9	Ab	9214.6	Bb	6475.8	Ba	204118.1	Aa	43066.1	Ba	2941.8	Ca
FA 16:0	14217717.0	Aa	10736904.7	Ba	10981843.0	Ba	9047770.3	Ab	6090360.4	Ab	7667712.9	Aab	10234216.7	Ab	5233853.3	Bb	5337535.4	Bb	12103500.3	Aab	10144029.6	Aa	5186111.2	Bb
FA 16:1	2484463.0	Aa	2003375.3	Ba	1875501.7	Ba	NA	Ab	NA	Ac	NA	Ab	NA	Ab	NA	Ac	NA	Ab	NA	Bb	1007432.3	Ab	NA	Bb
FA 16:2	8813561.9	Aa	6798519.5	Ba	7257595.8	ABa	2341551.1	Bb	4355749.7	Ab	5502689.4	Aab	3510159.3	Ab	4107097.8	Ab	4068224.8	Ab	3213212.4	Bb	5897426.3	Aab	4324470.3	ABb
FA 16:3	4862159.1	Aa	4003133.2	Aa	3859757.1	Ab	2627964.9	Bb	4411476.6	Aa	5517919.5	Aab	4800589.6	Aa	4282447.7	Aa	4173322.1	Aab	4341264.4	Aab	5471181.1	Aa	5838324.1	Aa
FA 16:4	83989.6	Aa	61294.6	Ba	52923.6	Ba	68103.7	Ab	24132.8	Bb	30285.0	Bb	60012.7	Ab	30949.0	Bb	22667.6	Bb	62849.0	Ab	41068.5	Bb	25613.9	Bb
FA 16:4.1	64087.7	Aa	71551.4	Ac	88648.1	Ac	28276.9	Ca	229698.2	Ba	294466.6	Ab	50026.5	Ba	169424.3	Aab	229274.5	Ab	61563.8	Ba	119325.2	Bbc	495776.5	Aa
FA 18:0	2568615.4	Aa	2397054.3	Aa	2897670.5	Aa	1845119.1	Ab	1481448.5	Ab	1805023.8	Ab	2302321.6	Aab	1204929.6	Bb	1174051.6	Bbc	2585658.9	Aa	1650999.3	Bb	609885.7	Cc
FA 18:1	43265499.7	Aa	37082503.1	Aa	36898622.9	Aa	23422480.3	Ab	25347368.1	Aab	27611035.7	Aab	32685352.5	Aab	18075340.4	Bb	16448817.5	Bbc	37970208.3	Aa	31883356.8	Aa	8856878.1	Bc
FA 18:2	26729953.4	Aa	22136434.0	Aa	24030402.2	Aa	10838193.4	Bb	15490360.8	ABab	19392589.4	Aab	16058450.3	Ab	13419007.4	Ab	13489361.0	Ab	16465761.1	Ab	19347950.8	Aab	16981160.6	Ab
FA 18:3	21988295.5	Aa	18387863.2	Aa	20920774.2	Aab	12791703.3	Bb	20553441.1	Aa	25002083.6	Aab	22874193.8	Aa	18099896.1	Aa	19051952.8	Ab	22352859.3	Aa	24142355.7	Aa	28040903.5	Aa
FA 18:4	1220301.4	Aa	1117761.7	Aa	1206223.4	Aa	523145.3	Bb	1063551.8	Aa	1281335.8	Aa	991991.8	Aa	645473.9	Ab	632452.0	Ab	894561.3	Aab	639311.7	ABb	479218.4	Bb
FA 20:0	111615.0	Ac	127027.7	Aa	125024.9	Aa	123630.6	Abc	97494.7	Bb	116306.1	ABa	140838.6	Ab	86673.1	Bb	103144.2	Ba	178498.5	Aa	126426.4	Ba	75009.9	Cb
FA 20:1	1272475.4	Abc	1264717.6	Aa	1187853.8	Aa	1057908.7	Ac	769641.2	Bb	935866.4	ABa	1440614.1	Ab	530802.0	Bb	578481.6	Bb	1911573.2	Aa	1134460.0	Ba	345573.5	Cb
FA 20:3	27047.7	Aa	26421.4	Aa	29456.8	Ab	11979.2	Bb	29619.5	Aa	36479.2	Aab	21080.9	Aab	25155.6	Aa	26478.3	Ab	20240.8	Cab	34173.4	Ba	44158.4	Aa
FA 22:0	1347365.2	Aa	1213354.7	Ba	1087273.3	Ba	941697.0	Ab	755651.2	Bb	860010.5	Bb	908265.5	Abc	639985.3	Bbc	686390.6	Bbc	831205.0	Ac	476004.2	Bc	806350.5	Bc
FA 22:1	466523.4	Abc	471834.0	Aa	468034.7	Aab	381250.1	Bc	424666.2	ABab	507735.5	Aa	581999.9	Aab	339064.7	Bb	363087.0	Bb	660725.4	Aa	439145.7	Bab	397289.2	Bab
FA 24:1	69257.9	Aa	70643.8	Aa	70008.0	Aa	45986.3	Ab	57026.7	Aab	61922.1	Aa	73941.8	Aa	61537.9	Aab	60907.1	Aa	62882.5	Aab	43461.2	Bb	57129.3	ABa
FA 26:0	131229.2	Ca	124305.5	Ba	139993.9	Aa	55124.9	Cc	72784.1	Bc	88083.9	Ac	74923.3	Cb	94751.1	Bb	93079.9	Ab	62900.2	Cc	72840.5	Bc	89676.3	Ac
FA 28:0	151584.9	Ba	159347.7	Ba	193106.9	Aa	124759.6	Bab	155364.5	Aa	151087.9	ABb	149861.2	Aa	106921.9	Bb	125911.1	ABb	107919.1	Ab	78384.0	Bb	86795.4	ABc

SI Table 11. (continuation) Relative abundance of lipid of *Monoraphidium* sp. BR023 strain grown under three different concentrations of nitrogen (0, 3.5 and 7 mM) in four growth time (0h, 10h, 18h and 36h). Different lowercase letters refer to statistical difference between times within the same nitrogen concentration. Capital letter refer to statistical difference between nitrogen concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h_0N	0h_3.5N	0h_7N	10h_0N	10h_3.5N	10h_7N	18h_0N	18h_3.5N	18h_7N	36h_0N	36h_3.5N	36h_7N
FA 30:0	25528.1 Ba	31117.2 Ba	48121.4 Aa	25857.5 Aa	24583.3 Aab	26990.9 Abc	26998.4 Aa	27376.9 Aa	38036.1 Aab	17600.5 Aa	13995.2 Ab	17416.7 Ac
FA 30:1	75952.5 Aa	80028.8 Ab	78880.8 Ab	86814.5 Ba	135543.0 Aa	134596.1 Aa	103800.5 Aa	116892.1 Aab	138860.8 Aa	63957.2 Aa	38347.4 Ac	50622.4 Ab

SI Table 12. P-values for significant main effects and interactions between the factors (strain, concentration and time) of three freshwater strains (*C. reinhardtii* CC503, *Chlamydomonas* sp. BR020, and *C. vulgaris* BR017) cultured in TAP medium with 5µM rapamycin and control.

	n° cells	µ	Chl a	Chl b	Chl a/b	Carotenoids	Starch
Main effects							
Strain	0.000**	0.000**	0.001**	0.000**	0.000**	0.000**	0.000**
Concentration	0.000**	0.000**	0.002**	0.000**	0.160 ^{NS}	0.008**	0.000**
Time	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**	0.000**
Interaction effects							
Strain x Concentration	0.000**	0.000**	0.692 ^{NS}	0.000**	0.000**	0.076 ^{NS}	0.000**
Strain x Time	0.000**	0.000**	0.031**	0.000**	0.000**	0.000**	0.000**
Concentration x Time	0.000**	0.000**	0.004**	0.000**	0.000**	0.001**	0.000**
Strain x Concentration x Time	0.000**	0.000**	0.238 ^{NS}	0.000**	0.000**	0.286 ^{NS}	0.000**
R²	0.9938	0.9959	0.6087	0.8859	0.8766	0.8274	0.9853

** indicate that effect and interaction are significant at p -value < 0.05;

NS = not significant;

SI Table 13. Relative abundance of primary metabolites of *C. reinhardtii* CC503 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Amino acid	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Alanine	0.000741057	Ab	0.000755865	Ab	0.001052607	Ba	0.001888299	Aa	0.000553517	Ac	0.000638368	Ab
Asparagine	2.52996E-06	Ab	3.66503E-06	Ab	6.31093E-06	Ba	1.05142E-05	Aa	3.87454E-06	Ab	3.77859E-06	Ab
Aspartate	0.000166968	Ab	0.000212635	Ab	0.000351804	Ba	0.000669829	Aa	0.000213945	Ab	0.000243736	Ab
b-Alanine	3.15234E-05	Aa	3.20424E-05	Aa	1.61539E-05	Bb	3.90516E-05	Aa	2.62913E-05	Aa	2.18986E-05	Ab
Butanoic acid, 2-amino-	6.11946E-06	Bc	8.02993E-06	Ac	2.13869E-05	Ba	2.94525E-05	Aa	1.46774E-05	Bb	1.65468E-05	Ab
Citrulline	2.49464E-07	Ab	NA	Ac	1.53433E-06	Ba	3.05085E-06	Aa	1.2477E-06	Aa	1.43107E-06	Ab
Cysteine	2.97408E-08	Ab	3.17626E-08	Ac	8.67687E-08	Ba	1.60597E-07	Aa	8.56038E-08	Aa	7.87654E-08	Ab
Cysteinyl-glycine	3.33889E-07	Ac	3.03455E-07	Ac	1.13688E-06	Aa	1.51687E-06	Aa	7.08522E-07	Ab	8.02123E-07	Ab
Glutamate	0.000542898	Ba	0.000589931	Ab	0.000382694	Bb	0.000713309	Aa	0.000195927	Ac	0.000233998	Ac
Glutamine	1.84984E-05	Ab	2.30039E-05	Ab	0.000214415	Ba	0.000363009	Aa	3.49475E-05	Ab	5.22762E-05	Ab
Glycine	1.74342E-05	Aa	1.85641E-05	Aa	6.45173E-05	Aa	6.09249E-05	Aa	3.47873E-05	Aa	7.05194E-05	Aa
Histidine	1.50895E-05	Aa	1.50395E-05	Ab	4.12972E-05	Ba	0.00011788	Aa	2.47634E-05	Aa	3.81471E-05	Ab
Hydroxyproline	1.63288E-07	Ba	2.12987E-07	Aa	1.35562E-07	Ba	2.32276E-07	Aa	1.12556E-07	Bb	1.08775E-07	Ab
Isoleucine	3.12619E-05	Ab	3.0879E-05	Ac	8.72515E-05	Ba	0.00014346	Aa	7.01511E-05	Aa	7.01906E-05	Ab
Leucine	7.81102E-05	Ab	7.63717E-05	Ac	0.000185341	Ba	0.000312698	Aa	0.000159738	Aa	0.000149504	Ab
Methionine	1.04657E-05	Aa	1.27425E-05	Aa	1.39116E-05	Aa	3.62477E-05	Aa	2.01513E-05	Aa	2.44217E-05	Aa
O-acetyl-serine	2.1476E-05	Aa	2.29752E-05	Aa	1.01626E-05	Bb	1.87863E-05	Ab	5.22955E-06	Ac	6.21116E-06	Ac
Ornithine	2.05519E-05	Ab	2.00369E-05	Ab	0.000110365	Ba	0.000184177	Aa	5.2255E-05	Ab	6.43986E-05	Ab
Phenylalanine	1.20568E-05	Ab	1.2439E-05	Ac	4.3262E-05	Ba	6.57532E-05	Aa	4.61337E-05	Aa	5.20998E-05	Ab
Proline	0.000194185	Aa	0.000255206	Aa	0.000102974	Aa	0.00031157	Aa	0.000111955	Aa	0.000139721	Aa
Pyroglutamic acid	0.000322738	Ac	NA	Bc	0.000964576	Ba	0.00171211	Aa	0.00051468	Ab	0.00057389	Ab
Serine	9.34108E-05	Ab	8.90937E-05	Ab	0.000136853	Ba	0.000256335	Aa	0.000104784	Aab	0.000105201	Ab
Threonine	3.34612E-05	Ac	3.41607E-05	Ac	0.000129353	Ba	0.000215477	Aa	8.33389E-05	Ab	7.48743E-05	Ab
Tryptophan	NA	Bb	1.06657E-05	Ab	2.71379E-05	Ba	4.06807E-05	Aa	2.81196E-05	Ba	3.31822E-05	Aa
Tyrosine	2.46018E-05	Ac	2.44598E-05	Ab	0.000112704	Bb	0.000175602	Aa	0.00015245	Aa	0.000176567	Aa
Valine	0.000101201	Ab	0.00010404	Ab	0.00024732	Ba	0.000436521	Aa	0.000168542	Aab	0.000167857	Ab

SI Table 13. (continuation) Relative abundance of primary metabolites of *C. reinhardtii* CC503 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Organic acid	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Ascorbic acid	2.16073E-08	Ab	NA	Ab	1.8137E-06	Aa	3.58932E-06	Aa	2.04487E-06	Aa	2.85334E-06	Aa
Benzoate	5.77268E-06	Aa	8.97847E-06	Aa	3.67198E-06	Aab	5.50973E-06	Aab	1.65194E-06	Ab	2.23128E-06	Ab
Capric acid	1.50914E-07	Ba	2.32344E-07	Aa	1.217E-07	Ba	2.6703E-07	Aa	1.25284E-07	Ba	1.07236E-07	Aa
Citramalate	7.54088E-07	Ab	1.00921E-06	Ab	1.76492E-06	Ba	3.04989E-06	Aa	4.02942E-07	Ab	6.23601E-07	Ab
Citrate	4.74958E-05	Aa	3.91427E-05	Ab	4.49255E-05	Ba	8.17115E-05	Aa	5.53537E-05	Aa	6.52645E-05	Aa
Dehydroascorbate	4.97623E-08	Aa	NA	Ab	NA	Aa	NA	Ab	NA	Ba	4.88017E-07	Aa
Docosanoic acid	-1.04108E-08	Ab	8.87E-09	Ab	8.12303E-08	Aa	1.10652E-07	Aa	1.44778E-07	Aa	1.52289E-07	Aa
Eicosanoic acid methyl ester	2.713E-06	Ba	3.54965E-06	Aa	1.57833E-06	Bb	2.75111E-06	Ab	8.40084E-07	Bc	9.20614E-07	Ac
Fumarate	-1.85532E-06	Bc	NA	Ab	1.07133E-06	Aa	NA	Bb	3.90383E-07	Bb	7.24472E-07	Aa
Galacturonic acid	3.02455E-08	Aa	NA	Aa	1.59854E-07	Aa	7.65773E-08	Aa	7.51238E-08	Aa	9.53884E-08	Aa
Gluconate	6.19734E-07	Ab	6.14438E-07	Ab	2.74505E-06	Aa	3.78094E-06	Aa	3.28626E-06	Aa	3.17553E-06	Aa
Glutaric acid	NA	Ab	NA	Ab	NA	Ab	NA	Ab	9.68973E-07	Aa	9.06244E-07	Aa
Glycerate	1.28407E-06	Ab	7.74268E-07	Ac	3.16007E-06	Ba	4.16026E-06	Aa	1.54389E-06	Ab	2.11151E-06	Ab
Glyceric acid-3-phosphate	4.04299E-06	Ab	2.37279E-06	Ac	1.17311E-05	Aa	1.32341E-05	Aa	4.33042E-06	Ab	6.30442E-06	Ab
Glycolic acid	3.5204E-06	Ab	2.94113E-06	Ab	4.83526E-06	Ba	6.64877E-06	Aa	3.47107E-06	Ab	3.28607E-06	Ab
Hexacosanoic acid methyl ester, n-	6.94187E-07	Aa	6.56747E-07	Aa	3.45612E-07	Ab	5.10962E-07	Ab	2.37404E-07	Ac	2.37691E-07	Ac
Hexadecanoic acid methyl ester, n-	6.9595E-06	Aa	7.54169E-06	Aa	3.40055E-06	Bb	6.59649E-06	Aa	1.89947E-06	Ac	2.05614E-06	Ab
Hexanoic acid, 2-ethyl-	7.18977E-07	Aa	6.81053E-07	Aa	4.19371E-07	Bb	7.11831E-07	Aa	1.86879E-07	Ac	2.16134E-07	Ab
Lactate	1.18948E-05	Ba	1.57375E-05	Aa	1.28819E-05	Ba	1.95555E-05	Aa	6.29269E-06	Bb	7.72497E-06	Ab
Malate	2.57185E-05	Ab	1.97898E-05	Ab	4.09215E-05	Ba	5.55113E-05	Aa	2.58677E-05	Ab	2.76852E-05	Ab
Malonic acid	7.76886E-08	Bc	8.04057E-08	Ac	2.94473E-07	Ba	3.68461E-07	Aa	1.23311E-07	Bb	2.12787E-07	Ab
Nonadecanoic acid methyl ester	2.85495E-08	Aa	2.91996E-08	Aa	1.19476E-08	Bb	2.05978E-08	Ab	6.0222E-09	Bc	1.00799E-08	Ac
Octadecanoic acid	3.76216E-06	Aa	4.53206E-06	Aa	2.76312E-06	Aa	4.73062E-06	Aa	1.3671E-06	Ab	1.53258E-06	Ab
Palmitic acid	2.32406E-05	Ab	2.3743E-05	Ab	5.28728E-05	Aa	7.89529E-05	Aa	2.94674E-05	Ab	3.97193E-05	Ab
Pyruvate	3.3322E-05	Aa	2.81311E-05	Ab	2.34107E-05	Ba	6.18614E-05	Aa	1.61612E-05	Aa	2.02082E-05	Ab
Ribonic acid	5.3245E-08	Ab	4.84009E-08	Ac	1.24858E-07	Ba	1.79805E-07	Aa	7.6503E-08	Ab	1.00709E-07	Ab
Sinapic acid	1.0426E-07	Aa	2.19898E-07	Aa	4.38472E-08	Aa	1.837E-07	Aa	1.58118E-07	Aa	3.23272E-08	Aa
Succinate	1.15252E-05	Ab	1.01796E-05	Ab	2.78142E-05	Ba	4.18524E-05	Aa	1.55235E-05	Ab	1.70808E-05	Ab
Tetracosanoic acid methyl ester	1.69487E-06	Aa	1.6159E-06	Aa	8.24083E-07	Ab	1.27428E-06	Ab	4.7444E-07	Ac	5.27046E-07	Ac

SI Table 13. (continuation) Relative abundance of primary metabolites of *C. reinhardtii* CC503 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Organic acid	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Tetradecanoic acid methyl ester	3.13809E-08	Bb	3.80085E-08	Ab	4.15597E-08	Ba	6.55502E-08	Aa	2.02236E-08	Bb	3.18439E-08	Ab
Threonic acid	3.21615E-06	Ac	3.94434E-06	Ac	7.87618E-06	Ba	1.3115E-05	Aa	5.41505E-06	Ab	5.94493E-06	Ab
2-Oxoglutaric acid	5.02766E-06	Ac	3.96526E-06	Ac	4.98767E-05	Ba	7.96033E-05	Aa	3.66671E-05	Ab	4.45116E-05	Ab
4-hydroxy-benzoic acid	-1.17141E-06	Ab	-1.11703E-06	Ab	-4.5882E-07	Aab	-5.50514E-07	Aab	3.47465E-07	Aa	1.79279E-07	Aa
4-Hydroxycinnamic acid	3.85762E-08	Aa	5.44068E-08	Aa	1.1609E-08	Ab	NA	Ab	NA	Ab	NA	Ab
Sugar	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Altrose	3.69845E-06	Ac	2.91484E-06	Ac	1.74515E-05	Aa	1.58119E-05	Aa	6.04928E-06	Ab	8.17977E-06	Ab
Arabinose	5.52232E-06	Aa	3.92381E-06	Aa	NA	Ab	NA	Ab	NA	Ab	NA	Ab
Fructose	2.79325E-07	Ab	1.95883E-07	Aa	9.08977E-06	Aa	7.67589E-07	Ba	2.54872E-07	Ab	3.48E-07	Aa
Fructose-6-Phosphate	6.25372E-08	Ab	4.14602E-08	Ab	2.59382E-07	Aa	2.00401E-07	Aa	5.84848E-08	Ab	9.81091E-08	Ab
Fucose	4.35137E-06	Aa	3.03677E-06	Aa	NA	Ab	NA	Ab	NA	Ab	NA	Ab
Galactose, 3,6-anhydro-	3.08751E-07	Aa	NA	Ba	NA	Ab	NA	Aa	NA	Ab	NA	Aa
Glucose	NA	Ab	NA	Aa	3.86476E-06	Aa	NA	Ba	NA	Ab	NA	Aa
Glucose-6-Phosphate	6.36146E-06	Ab	3.17553E-06	Ab	3.03723E-05	Aa	2.29238E-05	Aa	6.19411E-06	Ab	1.03583E-05	Ab
Isomaltose	NA	Ab	NA	Aa	1.47805E-08	Aa	NA	Ba	NAN	Ab	NA	Aa
Mannose	1.23418E-06	Aa	1.11197E-06	Ac	NA	Bb	3.83202E-06	Aa	1.50891E-06	Ba	1.87461E-06	Ab
Maltose	1.98547E-07	Aa	2.43468E-06	Aa	1.0821E-06	Aa	1.28142E-06	Aa	4.081E-07	Aa	4.80489E-07	Aa
Melibiose	7.15696E-07	Ab	6.80857E-07	Ab	1.16995E-06	Ba	1.72922E-06	Aa	6.16311E-07	Ab	7.05068E-07	Ab
Raffinose	NA	Ab	NA	Aa	2.03304E-09	Aa	NA	Ba	1.90354E-09	Aa	NA	Ba
Sucrose	1.72199E-07	Ab	1.41549E-07	Aa	5.73769E-06	Aa	1.18097E-07	Ba	7.48147E-08	Ab	6.82539E-07	Aa
Trehalose	7.43306E-06	Ac	9.89392E-06	Ac	5.769E-05	Aa	7.69857E-05	Aa	2.37108E-05	Ab	2.72702E-05	Ab
Xylose	5.52232E-06	Ab	3.92381E-06	Ab	1.03911E-05	Aa	1.15429E-05	Aa	6.33401E-06	Ab	7.51277E-06	Ab
1,6-Anhydro-beta-D-glucose	4.3575E-07	Bb	4.23903E-07	Ab	1.05499E-06	Ba	1.97579E-06	Aa	3.38045E-07	Bb	4.73476E-07	Ab
Arabitol	NA	Ab	NA	Ab	NA	Ab	NA	Ab	6.33188E-06	Aa	7.28698E-06	Aa
Erythritol	NA	Bc	0.00023555	Aa	0.000112852	Ba	0.000193356	Ab	5.49118E-05	Ab	6.90536E-05	Ac
Glycerol	8.10192E-07	Ab	7.84235E-07	Ab	1.40109E-06	Aa	1.67191E-06	Aa	1.33655E-06	Aa	1.53508E-06	Aa
Glycerol 3-P	7.81244E-05	Aab	7.4024E-05	Ab	9.0128E-05	Ba	0.00014376	Aa	5.72E-05	Ab	6.6308E-05	Ab
Mannitol	7.54687E-05	Ab	8.07398E-05	Ab	0.000143469	Ba	0.000254741	Aa	5.62093E-05	Ab	5.70438E-05	Ab

SI Table 13. (continuation) Relative abundance of primary metabolites of *C. reinhardtii* CC503 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Others	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Putrescine	0.000886803	Aa	0.000896921	Aa	0.000444353	Bb	0.000814717	Aa	0.000211891	Ac	0.000186882	Ab
Spermidine	5.52658E-05	Aa	3.67532E-05	Aa	2.12441E-05	Ab	2.98966E-05	Ab	1.3258E-05	Ab	1.70134E-05	Ab
Adenine	2.1516E-05	Aa	1.8166E-05	Ac	2.78758E-05	Ba	4.22594E-05	Aa	2.42036E-05	Aa	2.90363E-05	Ab
Adenosine-5-Monophosphate	3.23885E-08	Aa	2.65329E-08	Aa	NA	Ab	NA	Ab	NA	Ab	NA	Ab
Guanidine	1.09813E-05	Aa	1.28521E-05	Aa	3.62989E-05	Aa	7.54908E-06	Aa	2.82556E-06	Aa	6.1047E-06	Aa
Uracil	2.41139E-05	Ab	2.91132E-05	Ac	6.07426E-05	Ba	9.80172E-05	Aa	4.60741E-05	Aa	4.85151E-05	Ab
4-Aminobutanoate	1.64778E-05	Ab	1.74099E-05	Ac	5.74121E-05	Ba	0.000118077	Aa	5.34703E-05	Aa	4.87387E-05	Ab
Galactinol	NA	Aa	NA	Ab	NA	Ba	6.27147E-07	Aa	NA	Aa	NA	Ab
Isopropyl-beta-D-thiogalactoside	6.89921E-07	Bc	8.30306E-07	Ac	3.45266E-06	Ba	4.79215E-06	Aa	2.34418E-06	Bb	2.541E-06	Ab
Myo-Inositol	9.28223E-06	Ac	9.76764E-06	Ac	5.91547E-05	Ba	9.98736E-05	Aa	2.71936E-05	Ab	2.63811E-05	Ab
Phosphoric acid	0.000129431	Aa	0.00013262	Aa	NA	Ab	NA	Ab	NA	Ab	NA	Ab

SI Table 14. Relative abundance of primary metabolites of *Chlamydomonas* sp. BR020 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Amino acid	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Alanine	0.000246295	Aa	0.000234334	Aa	9.07276E-05	Bb	0.000134983	Ab	NA	Bc	6.33128E-05	Ac
Asparagine	NA	Aa	NA	Ab	1.5724E-07	Ba	2.6267E-06	Aa	7.51047E-08	Aa	4.30303E-07	Ab
Aspartate	2.56611E-05	Aa	2.44641E-05	Ab	2.56673E-05	Ba	5.03328E-05	Aa	1.51881E-05	Bb	2.42023E-05	Ab
b-Alanine	8.36131E-07	Bb	8.07151E-07	Ab	7.15075E-07	Bb	1.86281E-06	Ab	1.8273E-06	Ba	3.30373E-06	Aa
Butanoic acid, 2-amino-	2.21191E-06	Aa	1.63297E-06	Ab	3.0164E-06	Ba	3.95564E-06	Aa	2.60738E-06	Ba	4.69767E-06	Aa
Citrulline	3.95712E-08	Aa	5.34027E-08	Ac	1.27845E-07	Ba	1.15501E-06	Aa	2.01395E-08	Ba	2.61245E-07	Ab
Cysteine	1.74045E-08	Aa	1.40267E-08	Aa	7.17153E-09	Ab	9.8235E-09	Ab	6.43649E-09	Ab	9.76229E-09	Ab
Cysteinyl-glycine	1.67376E-07	Bb	1.65601E-07	Ab	2.38324E-07	Bab	3.67581E-07	Aab	2.932E-07	Ba	5.59834E-07	Aa
Glutamate	9.74416E-05	Aa	9.62866E-05	Aa	3.3717E-05	Bb	4.49974E-05	Ab	1.30186E-05	Bc	2.12031E-05	Ac
Glutamine	1.33331E-07	Aa	1.36034E-07	Ac	1.31993E-07	Ba	4.50035E-06	Aa	6.535E-08	Ba	9.95E-07	Ab

SI Table 14. (continuation) Relative abundance of primary metabolites of *Chlamydomonas* sp. BR020 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Amino acid	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Glycine	2.25832E-06	Aa	2.64137E-06	Aa	4.71681E-06	Aa	9.20016E-06	Aa	2.21143E-06	Aa	1.10995E-05	Aa
Histidine	1.84674E-06	Aa	1.8556E-06	Ac	1.5528E-06	Ba	5.12326E-06	Aa	1.02152E-06	Bb	2.66789E-06	Ab
Hydroxyproline	2.36996E-08	Bb	2.44002E-08	Ab	2.89019E-08	Ba	3.94134E-08	Aa	3.02603E-08	Ba	4.01323E-08	Aa
Isoleucine	9.813E-06	Aa	7.72135E-06	Bc	9.64759E-06	Ba	1.39155E-05	Ab	1.01571E-05	Ba	1.64125E-05	Aa
Leucine	8.24074E-06	Ab	6.81239E-06	Ab	8.77252E-06	Aab	9.90598E-06	Aab	9.95363E-06	Aa	1.1612E-05	Aa
Methionine	2.35003E-06	Aa	2.36498E-06	Ac	2.33875E-06	Ba	3.66611E-06	Ab	2.7722E-06	Ba	4.66942E-06	Aa
O-acetyl-serine	NA	Ac	NA	Ac	8.19872E-07	Ba	1.22147E-06	Aa	3.45613E-07	Bb	5.77605E-07	Ab
Ornithine	2.66213E-05	Aa	2.38553E-05	Aa	1.42089E-05	Bb	1.85785E-05	Ab	3.03066E-06	Bc	8.70972E-06	Ac
Phenylalanine	2.31385E-06	Ab	2.09734E-06	Ab	2.48383E-06	Ab	1.96103E-06	Ab	3.3404E-06	Aa	3.28184E-06	Aa
Proline	0.000115008	Aa	0.000108512	Aa	5.43304E-05	Bb	0.00011777	Aa	2.08132E-05	Bc	5.4423E-05	Ab
Pyroglutamic acid	8.18933E-05	Aa	8.2087E-05	Ab	7.66115E-05	Ba	0.000131303	Aa	3.88864E-05	Bb	6.45299E-05	Ac
Serine	1.01234E-05	Aa	9.83551E-06	Ab	1.09222E-05	Ba	1.89904E-05	Aa	9.54036E-06	Ba	1.59119E-05	Aa
Threonine	5.97028E-06	Aa	5.28611E-06	Ac	7.21496E-06	Ba	1.45648E-05	Aa	5.97579E-06	Ba	1.14016E-05	Ab
Tryptophan	1.60027E-06	Ab	1.48322E-06	Bb	1.84337E-06	Ab	1.31724E-06	Bb	2.04588E-06	Aa	1.91749E-06	Ba
Tyrosine	7.58829E-06	Ab	6.62593E-06	Ab	1.01081E-05	Aa	8.43276E-06	Ab	9.24E-06	Bab	1.27038E-05	Aa
Valine	2.08105E-05	Aa	1.68888E-05	Bb	2.06177E-05	Ba	2.88779E-05	Aa	1.57811E-05	Bb	2.42002E-05	Aa
Organic acid	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Ascorbic acid	2.87075E-07	Ab	1.37281E-07	Ab	6.10596E-07	Ab	7.95115E-07	Ab	1.41027E-06	Aa	1.69581E-06	Aa
Benzoate	7.23882E-07	Aa	7.01512E-07	Aa	3.68273E-07	Ab	3.3329E-07	Ab	1.4446E-07	Ab	3.01151E-07	Ab
Capric acid	1.2873E-08	Ba	1.33751E-08	Aa	1.27994E-08	Ba	1.55214E-08	Aa	1.39424E-08	Ba	2.16271E-08	Aa
Citramalate	4.98925E-08	Bb	6.23961E-08	Ab	6.71628E-08	Ba	1.04416E-07	Aa	3.72665E-08	Bb	5.4643E-08	Ab
Citrate	7.96618E-06	Aa	7.74572E-06	Aa	7.64668E-06	Aa	5.78787E-06	Bb	4.24681E-06	Bb	7.86681E-06	Aa
Dehydroascorbate	1.34733E-06	Ab	1.48802E-06	Ab	2.94412E-06	Ba	4.14201E-06	Aa	3.20027E-06	Ba	4.22292E-06	Aa
Docosanoic acid	3.01679E-09	Ab	1.73812E-09	Ab	1.21579E-08	Aa	1.2176E-08	Aa	7.35833E-09	Aab	7.60667E-09	Aab
Eicosanoic acid methyl ester	3.90365E-07	Aa	3.7049E-07	Aa	1.33029E-07	Ab	1.95565E-07	Ab	5.55123E-08	Ac	1.01977E-07	Ac
Fumarate	NA	Ab	NA	Ab	NA	Ab	NA	Ab	1.42934E-06	Aa	3.21738E-06	Aa
Galacturonic acid	3.25651E-08	Aa	2.4168E-08	Aa	1.2581E-08	Ab	1.50897E-08	Ab	1.00606E-08	Ab	1.27855E-08	Ab
Gluconate	5.63438E-07	Aa	4.49E-07	Aa	3.70673E-07	Aab	4.00729E-07	Aab	2.56323E-07	Ab	2.71473E-07	Ab
Glycerate	1.69103E-07	Ac	1.42861E-07	Ac	3.52679E-07	Ab	2.99015E-07	Ab	4.43036E-07	Aa	5.03019E-07	Aa

SI Table 14. (continuation) Relative abundance of primary metabolites of *Chlamydomonas* sp. BR020 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Organic acid	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Glyceric acid-3-phosphate	7.57055E-07	Aa	7.22208E-07	Aa	7.73247E-07	Aa	8.39075E-07	Aa	7.15894E-07	Aa	6.15435E-07	Aa
Glycolic acid	3.92769E-07	Ab	3.87804E-07	Aa	5.21601E-07	Aa	3.91395E-07	Ba	2.77868E-07	Ab	3.31672E-07	Aa
Hexacosanoic acid methyl ester, n-	8.1146E-08	Aa	9.22869E-08	Aa	3.6356E-08	Ab	4.95886E-08	Ab	1.37138E-08	Ac	1.90806E-08	Ac
Hexadecanoic acid methyl ester, n-	7.48711E-10	Ba	4.475E-09	Aa	1.53521E-09	Aa	9.09831E-10	Ab	3.80531E-10	Aa	NA	Ab
Hexanoic acid, 2-ethyl-	8.62379E-08	Aa	9.31645E-08	Aa	3.45848E-08	Ab	4.58753E-08	Ab	1.45547E-08	Ac	2.29506E-08	Ac
Lactate	3.38973E-06	Aa	3.25081E-06	Aa	2.14363E-06	Ab	2.64079E-06	Ab	1.0618E-06	Ac	1.37479E-06	Ac
Malate	6.28513E-06	Aa	4.35484E-06	Aa	4.62032E-06	Aab	5.34363E-06	Aab	3.64242E-06	Ab	3.87791E-06	Ab
Malonic acid	7.37844E-09	Aa	7.9994E-09	Ab	1.17179E-08	Aa	1.22202E-08	Aab	9.52753E-09	Ba	1.56919E-08	Aa
Nicotinate	NA	Ac	NA	Ac	1.56856E-05	Ba	2.25093E-05	Aa	5.1069E-06	Bb	1.01887E-05	Ab
Nonadecanoic acid methyl ester	3.97496E-09	Aa	3.86506E-09	Aa	1.27937E-09	Ab	1.45169E-09	Ab	4.87216E-10	Ac	7.58459E-10	Ac
Octadecanoic acid	8.57345E-07	Aa	3.63351E-07	Aa	8.57033E-08	Ab	1.68197E-07	Ab	3.79267E-08	Ab	1.18339E-07	Ab
Palmitic acid	1.11258E-05	Aa	6.77778E-06	Aa	3.4639E-06	Ab	4.33795E-06	Ab	1.92647E-06	Ab	2.85753E-06	Ab
Pyruvate	6.64923E-06	Ab	4.68979E-06	Ac	8.28796E-06	Ab	8.18236E-06	Ab	1.60174E-05	Ba	2.45112E-05	Aa
Ribonic acid	1.86863E-08	Ac	1.59376E-08	Ac	2.57329E-08	Ab	3.02602E-08	Ab	3.31584E-08	Aa	3.72715E-08	Aa
Sinapic acid	8.10898E-09	Aa	4.8043E-09	Aa	NA	Ab	NA	Ab	4.55733E-10	Ab	1.69983E-09	Ab
Succinate	1.94161E-06	Ac	1.58299E-06	Ac	4.44701E-06	Aa	4.63663E-06	Aa	2.59862E-06	Ab	3.54556E-06	Ab
Tetracosanoic acid methyl ester	2.04567E-07	Aa	1.83876E-07	Aa	8.26998E-08	Ab	1.03075E-07	Ab	2.95238E-08	Ac	4.71103E-08	Ac
Tetradecanoic acid methyl ester	6.77847E-09	Aa	4.24541E-09	Aa	2.76823E-09	Ab	3.24415E-09	Ab	1.88641E-09	Ab	2.64718E-09	Ab
Threonic acid	1.11041E-06	Aa	1.06749E-06	Aa	1.09886E-06	Aa	1.16106E-06	Aa	5.01271E-07	Ab	5.36881E-07	Ab
2-Oxoglutaric acid	1.15479E-06	Aa	9.01881E-07	Ab	1.65449E-06	Aa	1.34817E-06	Ab	1.50128E-06	Ba	2.31944E-06	Aa
4-hydroxy-benzoic acid	-1.82437E-07	Bb	1.29281E-07	Aa	1.71937E-08	Aa	2.91812E-08	Aab	1.6818E-08	Aa	-6.70379E-09	Ab
4-Hydroxycinnamic acid	3.19501E-09	Aa	2.53542E-09	Aa	5.9636E-10	Ab	6.77986E-10	Ab	4.37846E-10	Ab	2.41063E-09	Ab

SI Table 14. (continuation) Relative abundance of primary metabolites of *Chlamydomonas* sp. BR020 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Sugar	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Altrose	4.27695E-07	Aa	3.56446E-07	Aa	4.22012E-07	Aa	4.13957E-07	Aa	1.8019E-07	Ab	2.8223E-07	Ab
Fructose	5.62248E-08	Aa	4.60573E-08	Aa	4.35943E-08	Aa	7.04147E-08	Aa	3.3785E-08	Aa	3.61255E-08	Aa
Fructose-6-Phosphate	3.72283E-08	Aa	4.85037E-08	Aa	4.2742E-08	Aa	4.37231E-08	Aa	1.96393E-08	Ab	2.57208E-08	Ab
Fucose	3.93182E-07	Aa	3.33681E-07	Ab	3.72135E-07	Ba	6.86453E-07	Aa	3.17515E-07	Ba	5.80338E-07	Aa
Galactose, 3,6-anhydro-	NA	Aa	NA	Ac	3.93824E-08	Ba	9.68212E-07	Aa	4.22232E-08	Ba	1.76593E-07	Ab
Glucose	NA	Aa	NA	Ab	NA	Ba	5.61373E-07	Aa	NA	Aa	NA	Ab
Glucose-6-Phosphate	3.11984E-06	Ab	3.87125E-06	Ab	4.68763E-06	Aa	5.0011E-06	Aa	2.0033E-06	Ac	2.65041E-06	Ac
Isomaltose	NA	Ab	NA	Aa	NA	Ab	NA	Aa	3.3432E-09	Aa	NA	Ba
Mannose	1.22714E-07	Aa	1.3372E-07	Aa	1.37332E-07	Aa	1.61298E-07	Aa	1.17687E-07	Aa	1.19242E-07	Aa
Maltose	2.8108E-08	Ba	3.69485E-08	Aa	3.07128E-08	Ba	3.41219E-08	Aa	NA	Bb	2.32564E-08	Ab
Melibiose	4.78329E-08	Ab	5.14463E-08	Ab	7.61172E-08	Aa	7.58228E-08	Aa	NA	Ac	NA	Ac
Raffinose	1.07097E-09	Aa	NA	Ba	NA	Ab	4.52936E-10	Aa	3.94305E-10	Aab	3.7818E-10	Aa
Sucrose	2.15021E-06	Aa	2.00171E-06	Aa	6.53461E-07	Bb	9.85857E-07	Ab	2.66932E-07	Ac	NA	Bc
Trehalose	1.82468E-07	Ac	2.19018E-07	Ac	9.857E-07	Aa	1.29028E-06	Aa	4.8974E-07	Ab	3.9597E-07	Ab
Xylose	1.3777E-06	Aa	1.6047E-06	Aa	7.64558E-07	Ab	NA	Bb	NA	Ac	NA	Ab
1,6-Anhydro-beta-D-glucose	7.27594E-08	Aa	6.15342E-08	Ab	6.68076E-08	Ba	1.05984E-07	Aa	1.09E-07	Aa	8.86E-08	Aab
Arabitol	NA	Ab	NA	Ab	7.08158E-07	Aa	9.59933E-07	Aa	6.78933E-07	Ba	1.27962E-06	Aa
Erythritol	3.06038E-05	Aa	2.67946E-05	Ba	8.96333E-06	Bb	1.24759E-05	Ab	3.66436E-06	Bc	6.26266E-06	Ac
Glycerol	3.49367E-07	Aa	2.92669E-07	Ba	2.59499E-07	Ab	2.84192E-07	Aa	1.69722E-07	Ac	1.97039E-07	Ab
Glycerol 3-P	2.05627E-05	Aa	1.79128E-05	Ba	9.32275E-06	Bb	1.259E-05	Ab	4.19109E-06	Bc	6.67083E-06	Ac
Mannitol	1.81542E-07	Ab	1.36972E-07	Ab	2.86528E-07	Aa	4.61905E-07	Aa	3.48493E-07	Aa	3.9112E-07	Aa
Others	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Putrescine	1.37366E-05	Aa	1.22231E-05	Aa	6.60017E-06	Bb	1.2571E-05	Aa	3.03562E-06	Bb	7.25253E-06	Ab
Spermidine	1.68908E-05	Aa	1.4134E-05	Aa	4.64733E-06	Ab	4.78855E-06	Ab	1.6661E-06	Ab	3.39491E-06	Ab
Adenine	2.53247E-06	Ba	2.78568E-06	Aa	1.79745E-06	Bb	2.08919E-06	Ab	1.75698E-06	Bab	2.97539E-06	Aab
Adenosine-5-Monophosphate	1.13779E-08	Aa	NA	Ba	NA	Ab	NA	Aa	NA	Ab	NA	Aa
Guanidine	3.29671E-06	Aa	1.57243E-06	Aa	4.47788E-07	Aa	1.7189E-06	Aa	7.12291E-07	Aa	6.69291E-06	Aa
Uracil	3.80566E-06	Aa	2.83091E-06	Bab	2.76841E-06	Ab	3.12968E-06	Aa	1.43149E-06	Bc	2.30873E-06	Ab
4-Aminobutanoate	1.9124E-06	Aa	1.75031E-06	Ab	2.73413E-06	Ba	5.12937E-06	Aa	2.02047E-06	Ba	4.86825E-06	Aa

SI Table 14. (continuation) Relative abundance of primary metabolites of *Chlamydomonas* sp. BR020 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Others	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Isopropyl-beta-D-thiogalactoside	NA	Ab	NA	Ac	4.11166E-07	Aa	3.81693E-07	Ab	4.32391E-07	Ba	5.59514E-07	Aa
Myo-Inositol	1.29254E-06	Ab	1.39692E-06	Ab	2.6649E-06	Aa	2.22016E-06	Aa	1.95566E-06	Aa	2.24098E-06	Aa
Phosphoric acid	1.78206E-05	Aa	1.75532E-05	Aa	NA	Ab	NA	Ab	NA	Ab	NA	Ab

SI Table 15. Relative abundance of primary metabolites of *Chlorella vulgaris* BR017 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Amino acid	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Alanine	0.000309687	Aa	0.00033118	Aa	9.22756E-05	Ab	NA	Bb	NA	Ac	NA	Ab
Asparagine	NA	Ab	NA	Aa	NA	Ab	NA	Aa	3.7484E-08	Aa	NA	Ba
Aspartate	6.49463E-05	Aa	6.93182E-05	Ab	3.63988E-05	Bb	0.000100314	Aa	NA	Bc	2.25273E-05	Ac
b-Alanine	1.933E-06	Aa	1.77693E-06	Ab	2.95691E-06	Ba	7.97662E-06	Aa	3.47137E-06	Aa	5.67878E-06	Aa
Butanoic acid, 2-amino-	4.88998E-06	Aa	5.20099E-06	Ab	4.92191E-06	Ba	1.33295E-05	Aa	6.09202E-06	Aa	5.30458E-06	Ab
Citrulline	1.57766E-07	Aa	1.53721E-07	Ab	1.83054E-07	Ba	2.36865E-06	Aa	NA	Aa	9.61995E-08	Ab
Cysteine	2.73787E-08	Ba	3.68985E-08	Aa	9.49971E-09	Bb	2.0493E-08	Ab	1.38478E-08	Ab	1.28287E-08	Ac
Cysteinyl-glycine	1.85049E-07	Aa	2.1376E-07	Ab	1.68742E-07	Ba	5.05745E-07	Aa	2.11177E-07	Aa	2.30935E-07	Ab
Glutamate	0.000133153	Aa	0.000129875	Aa	3.13936E-05	Bb	8.45646E-05	Ab	1.29011E-05	Ac	1.92124E-05	Ac
Glutamine	4.36109E-07	Aa	4.86261E-07	Ab	2.92068E-07	Bab	2.48876E-06	Aa	6.69059E-08	Ab	2.30018E-07	Ab
Glycine	6.98454E-06	Aa	1.09928E-05	Aa	1.02714E-05	Aa	4.92601E-05	Aa	6.53912E-06	Aa	7.60675E-06	Aa
Histidine	4.29389E-06	Aa	4.74924E-06	Ab	3.20792E-06	Ba	1.20314E-05	Aa	2.51519E-06	Aa	2.65889E-06	Ab
Hydroxyproline	5.99372E-08	Ba	7.69925E-08	Ab	5.70328E-08	Bab	1.25754E-07	Aa	4.17651E-08	Ab	4.83455E-08	Ac
Isoleucine	2.18311E-05	Aa	2.3105E-05	Ab	1.5903E-05	Bb	4.20441E-05	Aa	1.3906E-05	Bb	1.92942E-05	Ab
Leucine	2.05944E-05	Aa	2.22422E-05	Ab	1.5215E-05	Bb	2.97849E-05	Aa	1.40966E-05	Ab	1.43092E-05	Ac
Methionine	6.94925E-06	Aa	7.37125E-06	Ab	5.62503E-06	Bab	1.31582E-05	Aa	4.37863E-06	Ab	4.02841E-06	Ac
O-acetyl-serine	NA	Ba	2.59788E-06	Aa	8.34099E-07	Ba	2.33029E-06	Aa	3.61408E-07	Aa	5.41738E-07	Ab
Ornithine	5.19978E-05	Aa	6.46139E-05	Aa	2.32966E-05	Bb	6.9817E-05	Aa	2.0151E-06	Ac	4.07599E-06	Ab

SI Table 15. (continuation) Relative abundance of primary metabolites of *Chlorella vulgaris* BR017 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Amino acid	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Phenylalanine	5.19467E-06	Aa	5.83463E-06	Ab	4.82574E-06	Ba	8.64584E-06	Aa	5.90019E-06	Aa	4.46952E-06	Bc
Proline	0.000138051	Aa	0.000153782	Ab	6.15234E-05	Bb	0.000242314	Aa	1.73815E-05	Ac	3.88427E-05	Ac
Pyroglutamic acid	0.000191757	Aa	0.000213088	Ab	9.3421E-05	Bb	0.000251752	Aa	3.85486E-05	Ac	5.77801E-05	Ac
Serine	3.50846E-05	Ba	4.30843E-05	Ab	1.83153E-05	Bb	5.50441E-05	Aa	1.19811E-05	Ab	1.80295E-05	Ac
Threonine	1.70696E-05	Ba	1.97981E-05	Ab	1.17861E-05	Bb	3.58517E-05	Aa	8.09308E-06	Bc	1.19475E-05	Ac
Tryptophan	3.27922E-06	Ba	4.46471E-06	Aa	3.90776E-06	Ba	5.2594E-06	Aa	3.91869E-06	Aa	2.83772E-06	Bb
Tyrosine	1.65234E-05	Ab	1.99974E-05	Ab	2.78484E-05	Ba	3.72267E-05	Aa	1.2759E-05	Ab	1.49955E-05	Ac
Valine	4.77258E-05	Aa	4.7392E-05	Ab	3.25321E-05	Bb	8.70613E-05	Aa	1.79913E-05	Ac	2.49538E-05	Ac
Organic acid	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Ascorbic acid	2.63339E-07	Ab	1.95304E-07	Ab	8.92962E-07	Ab	1.55086E-06	Ab	1.75408E-06	Aa	3.37612E-06	Aa
Benzoate	8.12027E-07	Ba	1.07103E-06	Aa	4.1478E-07	Bb	7.24E-07	Ab	1.96667E-07	Bc	1.88995E-07	Ac
Capric acid	NA	Bb	1.79554E-08	Ab	1.85981E-08	Ba	3.75816E-08	Aa	7.59777E-09	Ab	7.98083E-09	Ac
Citramalate	5.78772E-08	Ba	9.40286E-08	Ab	8.96136E-08	Ba	2.50579E-07	Aa	NA	Ab	NA	Ac
Citrate	7.00233E-06	Aa	7.59741E-06	Ab	8.29975E-06	Ba	2.12247E-05	Aa	6.00364E-06	Aa	7.32957E-06	Ab
Docosanoic acid	7.64595E-09	Bab	8.62017E-09	Aab	8.45314E-09	Ba	1.64246E-08	Aa	2.4586E-09	Bb	5.3739E-09	Ab
Eicosanoic acid methyl ester	4.8875E-07	Aa	4.33521E-07	Aa	1.456E-07	Bb	4.01E-07	Aa	6.09602E-08	Ab	1.02329E-07	Ab
Fumarate	NA	Ab	NA	Ab	NA	Ab	NA	Ab	1.28033E-06	Aa	1.50016E-06	Aa
Galacturonic acid	2.14003E-08	Aa	1.09032E-08	Bb	1.62527E-08	Bab	2.76286E-08	Aa	6.22009E-09	Ab	1.18871E-08	Ab
Gluconate	4.36142E-07	Aa	3.93808E-07	Aab	3.27058E-07	Ba	4.76253E-07	Aa	1.87845E-07	Bb	3.05849E-07	Ab
Glutaric acid	NA	Ab	NA	Ab	NA	Ab	NA	Ab	1.43828E-07	Ba	1.75524E-07	Aa
Glycerate	2.1702E-07	Bb	3.62982E-07	Ab	3.97388E-07	Ba	8.80551E-07	Aa	3.3312E-07	Aab	2.97127E-07	Ab
Glyceric acid-3-phosphate	9.68E-07	Ba	1.70815E-06	Aa	5.06747E-07	Ba	1.47E-06	Aa	4.28917E-07	Aa	1.71567E-07	Ab
Glycolic acid	5.92298E-07	Ba	8.07126E-07	Aa	5.90042E-07	Ba	8.10736E-07	Aa	3.82419E-07	Ab	3.00479E-07	Ab
Hexacosanoic acid methyl ester, n-	1.34332E-07	Aa	1.21046E-07	Aa	4.0884E-08	Ab	7.13371E-08	Ab	1.32515E-08	Ac	2.08799E-08	Ac
Hexadecanoic acid methyl ester, n-	NA	Bb	4.24974E-09	Aa	9.62895E-10	Aa	-8.14088E-10	Bc	3.55495E-10	Aab	3.12633E-10	Ab
Hexanoic acid, 2-ethyl-	1.20853E-07	Aa	1.30677E-07	Aa	3.61755E-08	Bb	9.10449E-08	Ab	1.42149E-08	Ac	1.87261E-08	Ac
Lactate	4.95637E-06	Aa	5.38107E-06	Ab	2.17439E-06	Bb	6.75666E-06	Aa	8.66344E-07	Ac	6.92473E-07	Ac
Malate	1.04585E-05	Ba	1.09996E-05	Aa	5.1505E-06	Bb	9.9693E-06	Ab	3.89288E-06	Bc	5.28318E-06	Ac
Malonic acid	4.0808E-08	Ba	6.04498E-08	Ab	3.57721E-08	Ba	8.14386E-08	Aa	6.11231E-09	Ab	9.81221E-09	Ac

SI Table 15. (continuation) Relative abundance of primary metabolites of *Chlorella vulgaris* BR017 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Organic acid	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Nonadecanoic acid methyl ester	4.567E-09	Aa	4.1059E-09	Aa	9.5557E-10	Bb	3.04204E-09	Ab	NA	Ab	5.40349E-10	Ac
Octadecanoic acid	8.20233E-07	Aa	6.32127E-07	Aa	2.93355E-07	Bb	8.64E-07	Aa	6.16869E-08	Ab	8.95444E-08	Ab
Palmitic acid	6.78687E-06	Ba	9.7005E-06	Aa	5.81159E-06	Ba	1.14534E-05	Aa	1.73014E-06	Bb	1.65218E-06	Ab
Pyruvate	9.24459E-06	Ab	1.39417E-05	Ab	2.14174E-05	Ba	4.33273E-05	Aa	2.12913E-05	Aa	1.97494E-05	Ab
Ribonic acid	2.42238E-08	Ab	2.69701E-08	Ac	2.87286E-08	Bb	5.70829E-08	Aa	4.5557E-08	Aa	4.37941E-08	Ab
Sinapic acid	1.13195E-08	Aa	5.04393E-09	Aa	6.42325E-09	Aa	2.78475E-08	Aa	4.53369E-09	Aa	3.57142E-09	Aa
Succinate	4.3276E-06	Aab	5.16616E-06	Ab	6.30077E-06	Ba	1.50923E-05	Aa	3.31794E-06	Ab	3.73712E-06	Ab
Tetracosanoic acid methyl ester	2.9726E-07	Aa	2.7756E-07	Aa	7.87604E-08	Bb	1.83488E-07	Ab	2.95864E-08	Ab	5.04017E-08	Ac
Tetradecanoic acid methyl ester	4.60495E-09	Aa	5.10391E-09	Ab	3.56596E-09	Ba	9.36909E-09	Aa	1.74475E-09	Aa	2.83669E-09	Ab
Threonic acid	1.43964E-06	Ba	1.79243E-06	Aa	8.84816E-07	Bb	2.06712E-06	Aa	4.30892E-07	Ac	5.10946E-07	Ab
2-Oxoglutaric acid	2.50065E-06	Aa	3.22144E-06	Aa	2.51249E-06	Aa	4.10803E-06	Aa	8.97909E-07	Ab	5.91972E-07	Ab
4-hydroxy-benzoic acid	-2.01039E-07	Ab	-1.3203E-07	Ab	2.58095E-08	Aa	-5.94373E-08	Aa	2.35537E-08	Aa	1.24905E-08	Aa
4-Hydroxycinnamic acid	6.34224E-07	Aa	3.44136E-09	Aa	NA	Aa	4.10022E-09	Aa	NA	Aa	NA	Aa
Sugar	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Altrose	1.11845E-06	Aa	6.78676E-07	Aa	4.23147E-07	Aa	1.32085E-06	Aa	5.26069E-08	Ab	7.08154E-08	Ab
Fructose	1.63917E-07	Aa	2.32984E-06	Aa	1.09929E-07	Aa	1.5928E-06	Aa	2.054E-08	Aa	1.71569E-08	Aa
Fructose-6-Phosphate	5.48019E-08	Aa	7.13968E-08	Ab	5.04585E-08	Ba	1.57824E-07	Aa	2.78993E-09	Aa	3.44674E-09	Ac
Fucose	4.33798E-07	Ba	5.97539E-07	Ab	NA	Bc	1.62371E-06	Aa	2.46798E-07	Ab	3.08055E-07	Ac
Galactose, 3,6-anhydro-	NA	Aa	NA	Ab	NA	Ba	5.89532E-07	Aa	NA	Aa	NA	Ab
Glucose	NA	Aa	NA	Ab	NA	Ba	6.52468E-07	Aa	NA	Aa	NA	Ab
Glucose-6-Phosphate	5.02361E-06	Aa	8.5488E-06	Ab	4.44697E-06	Bab	1.49712E-05	Aa	3.15049E-07	Ab	3.83281E-07	Ac
Mannose	2.69712E-07	Aa	2.12288E-06	Aa	3.0248E-07	Aa	1.93849E-06	Aa	7.26277E-08	Aa	1.06581E-07	Aa
Maltose	5.72525E-08	Bb	1.13608E-07	Ab	1.09933E-07	Ba	1.84868E-07	Aa	NA	Bc	NA	Ac
Melibiose	1.60621E-07	Aa	1.6474E-07	Aa	9.9948E-08	Bb	1.64256E-07	Aa	5.26581E-08	Ac	6.87417E-08	Ab
Raffinose	NA	Ba	1.3615E-09	Aa	NA	Aa	NA	Ab	2.9385E-10	Aa	2.27157E-10	Ab
Sucrose	3.14537E-06	Aa	2.60005E-06	Ba	NA	Bb	1.88853E-06	Ab	2.60611E-07	Ab	4.40413E-07	Ac
Trehalose	4.99671E-06	Ab	6.98695E-06	Ab	8.83469E-06	Ba	1.6438E-05	Aa	1.22406E-07	Ac	1.60892E-07	Ac
Xylose	1.34516E-06	Aa	1.50471E-06	Aa	NA	Ab	NA	Ab	NA	Ab	NA	Ab
1,6-Anhydro-beta-D-glucose	1.79287E-07	Aa	1.63756E-07	Ab	1.82932E-07	Ba	5.95141E-07	Aa	6.33323E-08	Aa	5.35103E-08	Ab

SI Table 15. (continuation) Relative abundance of primary metabolites of *Chlorella vulgaris* BR017 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Sugar	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Arabitol	NA	Ab	NA	Ab	1.3065E-06	Ba	3.081E-06	Aa	3.79979E-07	Ab	3.77418E-07	Ab
Erythritol	3.87312E-05	Aa	3.49911E-05	Ba	9.01801E-06	Bb	2.44804E-05	Ab	3.84981E-06	Ac	5.45673E-06	Ac
Glycerol	4.38974E-07	Aa	5.10274E-07	Aa	2.47818E-07	Bb	5.18624E-07	Aa	1.24221E-07	Ac	1.46753E-07	Ab
Glycerol 3-P	2.77834E-05	Aa	2.73157E-05	Aa	9.95499E-06	Bb	2.50757E-05	Aa	4.07541E-06	Ac	6.22728E-06	Ab
Mannitol	4.68086E-07	Aa	3.2155E-06	Aa	1.14694E-06	Aa	4.27033E-06	Aa	1.17751E-07	Aa	2.11245E-07	Aa
Others	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
Putrescine	1.56056E-05	Ba	2.34738E-05	Aa	NA	Ab	NA	b	2.11068E-06	Ab	4.15839E-06	Ab
Spermidine	1.0822E-05	Ba	1.66562E-05	Aa	4.84477E-06	Bb	7.72447E-06	Ab	1.36719E-06	Bc	1.15896E-06	Ac
Adenine	3.7775E-06	Ba	4.99199E-06	Ab	3.32E-06	Ba	6.78372E-06	Aa	1.76566E-06	Ab	2.188E-06	Ac
Guanidine	9.99804E-07	Aa	9.349E-06	Aa	1.01488E-06	Aa	1.04536E-05	Aa	8.17507E-07	Aa	4.79864E-07	Aa
Uracil	3.08936E-06	Aa	2.90288E-06	Ab	3.40562E-06	Ba	6.48899E-06	Aa	1.75506E-06	Ab	2.30336E-06	Ab
4-Aminobutanoate	7.15635E-06	Aa	6.34141E-06	Ab	6.59812E-06	Ba	1.712E-05	Aa	3.06179E-06	Ba	7.3134E-06	Ab
Galactinol	NA	Ab	NA	Ab	2.03213E-07	Ba	4.26472E-07	Aa	NA	Ab	NA	Ab
Isopropyl-beta-D-thiogalactoside	3.53017E-07	Aab	4.32069E-07	Ab	5.1476E-07	Ba	9.36596E-07	Aa	2.91045E-07	Ab	3.86775E-07	Ab
Myo-Inositol	1.14623E-06	Aa	1.13469E-06	Ac	1.9659E-06	Ba	7.02265E-06	Aa	1.92778E-06	Aa	2.3569E-06	Ab
Phosphoric acid	2.1735E-05	Aa	2.16649E-05	Aa	5.4106E-06	Ab	NA	Bb	NA	Ac	NA	Ab

SI Table 16. Relative abundance of lipids of *C. reinhardtii* CC503 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
DGDG 32:0	116629.7213	Bc	204649.0991	Ac	308916.5594	Bb	495289.9671	Ab	637651.9658	Ba	795010.3593	Aa
DGDG 32:1	46410.75159	Bc	80618.59898	Ac	216505.5559	Bb	324040.4776	Ab	394992.4327	Ba	513690.8027	Aa
DGDG 32:2	15866.12385	Ab	27643.01974	Ab	30695.54513	Ab	48107.99968	Ab	78434.39973	Aa	90361.28872	Aa
DGDG 32:3	81986.46535	Bb	152010.5606	Ab	134939.6409	Bb	229927.8687	Ab	363576.1989	Ba	441848.1642	Aa
DGDG 32:3.1	262562.7226	Bc	470430.1241	Ac	1066107.576	Bb	1703973.312	Ab	2179838.988	Ba	2788907.664	Aa
DGDG 34:0	44897.72905	Bb	77781.8091	Ab	214885.4998	Ba	303079.6908	Aa	287626.5332	Ba	354297.3683	Aa
DGDG 34:1	3190589.803	Bc	5593287.724	Ac	11844746.98	Bb	17749551.58	Ab	17013906.02	Ba	21700766.96	Aa
DGDG 34:2	3153791.206	Bb	5766949.575	Ab	14572637.89	Ba	22053328.1	Aa	19062806.43	Ba	24286314.86	Aa
DGDG 34:3	6078840.99	Bc	10997334.76	Ac	31795848.61	Bb	55637536.46	Ab	48461704.35	Ba	65476761.16	Aa
DGDG 34:4	1319303.203	Bc	2632236.029	Ac	6632756.924	Bb	9393201.35	Ab	8875395.122	Ba	11640032.56	Aa
DGDG 34:5	2274571.497	Ab	4169689.409	Ac	10107290.3	Ba	15042885.51	Ab	NA	Bb	22117770.65	Aa
DGDG 34:6	8789206.064	Bc	15313637.25	Ac	29318557.35	Bb	45953074.03	Ab	50161996.26	Ba	73213807.04	Aa
DGDG 36:2	13176.39143	Ba	24326.97777	Ab	NA	Bb	68016.06742	Aa	NA	Ab	NA	Ac
DGDG 36:5	65575.23385	Ac	118616.4271	Ac	288423.0864	Ab	268551.2256	Ab	444924.0309	Aa	456139.5811	Aa
DGDG 36:6	853419.6205	Ab	1558012.123	Ab	1774816.842	Ab	2025317.185	Ab	3151580.355	Aa	3104878.782	Aa
MGDG 34:1	NA	Bb	NA	Ab	449131.8036	Ba	831965.1498	Aa	750963.5324	Ba	985153.454	Aa
MGDG 34:3	42945.88039	Bb	82146.84049	Ab	445404.3382	Ba	821694.4417	Aa	551343.1027	Ba	714087.3847	Aa
MGDG 34:4	87852.78298	Aa	153888.9425	Ab	NA	Ba	1228938.583	Aa	NA	Ba	1090985.509	Aa
MGDG 34:4.1	16808.70138	Bb	34131.46666	Ab	29726.84552	Bab	75758.3589	Aab	65511.66708	Ba	63675.01308	Aa
MGDG 34:5	464627.9552	Ba	931613.9335	Aa	NA	Ab	NA	Ab	581975.0324	Ba	1170895.925	Aa
MGDG 34:6	412425.3256	Bb	760916.0633	Ab	1293286.893	Ba	2442457.479	Aa	1841964.678	Ba	2529602.557	Aa
MGDG 34:7	1348151.823	Bb	2478085.103	Ab	2035893.978	Bab	4389142.06	Aab	3527109.614	Ba	4708344.579	Aa
MGDG 34:7.1	1000371.353	Bb	1760160.854	Ab	1285369.642	Bab	2528462.165	Aab	1996585.524	Ba	2756547.752	Aa
MGDG 36:5.1	37115.52296	Bb	58262.62438	Ab	44546.69028	Bab	84441.13913	Aab	69104.47595	Ba	95177.01865	Aa
MGDG 36:6	87636.90696	Aab	175968.9172	Aab	97912.93513	Ab	121127.5767	Ab	248482.1303	Aa	186108.3855	Aa
SQDG 32:0	4193324.453	Bb	7885060.093	Ac	7845175.643	Ba	13272660.16	Ab	NA	Bc	16522096.33	Aa
SQDG 32:1	139389.6591	Ab	227160.2472	Aa	179367.3697	Ab	240662.6639	Aa	355649.4537	Aa	NA	Bb
SQDG 32:2	26910.22833	Bb	53667.14863	Aa	NA	Ac	NA	Ab	45614.97465	Aa	54838.36825	Aa
SQDG 32:3	32230.98025	Ab	NA	Bb	46773.89003	Aa	50834.1836	Aa	NA	Ac	NA	Ab

SI Table 16. (continuation) Relative abundance of lipids of *C. reinhardtii* CC503 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
SQDG 34:1	NA	Ab	NA	Ab	1651133.804	Ba	2402725.469	Aa	NA	Ab	NA	Ab
SQDG 34:2	295077.1093	Ab	574343.5906	Ab	2613813.321	Aa	3662149.712	Aa	2858107.19	Aa	3060136.632	Aa
SQDG 34:3	3424754.785	Bc	6222441.976	Ac	6484369.57	Bb	9624875.386	Ab	11373250.34	Ba	11717507.12	Aa
SQDG 34:4	40530.81287	Ab	81846.20915	Ab	75224.48647	Ab	90086.28094	Ab	130625.1889	Aa	128980.5617	Aa
SQDG 34:4.1	9247.308606	Ab	18019.67455	Ab	13453.11756	Ab	18633.55797	Ab	33604.96664	Aa	32952.00715	Aa
SQDG 34:6	89477.11182	Ab	168711.6213	Ab	170094.7012	Ab	176630.8258	Ab	270099.0356	Aa	255515.5446	Aa
DAG 34:2	38107.24515	Ac	74090.4557	Ab	737333.7723	Ab	1216126.545	Aa	1448083.486	Aa	NA	Bb
DAG 34:3	222175.5041	Ac	478733.814	Ac	1313191.662	Ab	1924845.829	Ab	3036738.334	Aa	3127221.693	Aa
DAG 34:4	11284.20406	Ab	NA	Ab	84513.66509	Ab	NA	Bb	181745.1353	Aa	240568.8433	Aa
DAG 34:5	18170.30627	Ac	35786.73607	Ac	74068.32883	Ab	124490.5344	Ab	188780.3844	Aa	242381.026	Aa
DAG 34:6	70087.56111	Ab	147612.1719	Ab	98947.08093	Ab	158671.9139	Ab	345716.8815	Aa	337969.8262	Aa
DAG 36:1	2283.286688	Ab	4548.702188	Ab	30492.70359	Aa	NA	Bb	33174.14408	Ba	58291.02974	Aa
DAG 36:3	4830.669509	Ab	9262.997053	Ab	151704.6252	Aa	208114.2283	Aa	161416.8583	Aa	207469.1668	Aa
DAG 36:4	NA	Bb	NA	Ab	266253.8485	Ba	442995.2919	Aa	304791.2821	Ba	436839.1095	Aa
DAG 36:5	9915.951989	Ab	21225.80126	Ab	226197.8569	Aa	296901.5172	Aa	267201.1088	Aa	327346.3928	Aa
DAG 36:6	19235.13712	Ac	42146.88405	Ac	143054.5264	Ab	199731.2207	Ab	288047.1231	Aa	337990.7869	Aa
LysoPC 16:0	4543.713525	Ab	17652.01094	Ac	97134.74961	Ba	223325.631	Aa	119733.4725	Aa	133761.9836	Ab
LysoPC 16:0.1	7751.617028	Ab	13820.52303	Ab	33967.62487	Ab	49266.37378	Ab	117804.822	Aa	126987.076	Aa
LysoPC 18:1	57971.79437	Ab	114692.9386	Ab	211420.2087	Ab	318002.9247	Ab	874098.3817	Aa	1150442.963	Aa
LysoPC 18:1.1	803017.2668	Ab	2169530.216	Ab	2144526.86	Ab	4400787.712	Ab	8450019.061	Aa	10704580.46	Aa
LysoPC 18:2	16212.67077	Ac	31975.02826	Ac	177113.8243	Ab	291569.9306	Ab	578595.6056	Aa	498706.6462	Aa
LysoPC 18:2.1	14977.84701	Ab	27551.69837	Ab	126707.7606	Aa	118557.8691	Aa	79693.90431	Aa	117410.5484	Aa
LysoPC 18:3	2373.546423	Ac	4496.46395	Ac	26490.09646	Ab	37640.81389	Ab	63625.56477	Aa	57801.58796	Aa
LysoPC 18:3.1	3980.533971	Ab	8256.57771	Ab	41398.04853	Aa	34841.97812	Aa	25415.57088	Aa	33436.89265	Aa
PC 32:3	13961.99097	Aa	19229.18697	Aa	27286.77613	Aa	35822.4009	Aa	NA	Ba	45382.11422	Aa
PC 34:2	NA	Ab	NA	Ab	1095658.351	Aa	1280767.096	Aa	NA	Ab	NA	Ab
PC 34:3	78616.48399	Ab	171683.8973	Ab	464228.3996	Aa	526474.0196	Aa	176561.8662	Ab	241940.7915	Ab
PC 34:5	10106.56085	Aa	13041.42234	Aa	23857.92243	Aa	28320.22941	Aa	NA	Ba	35462.45731	Aa
PC 34:6	26518.65071	Ab	41658.66989	Ab	87210.96482	Aab	115128.2072	Aab	117391.9384	Aa	184674.9282	Aa

SI Table 16. (continuation) Relative abundance of lipids of *C. reinhardtii* CC503 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
PC 36:1	308465.3196	Bb	635889.0777	Ab	387110.0789	Bb	515607.2529	Ab	1617344.213	Ba	2104829.644	Aa
PC 36:2	11914276.96	Bb	21547792.27	Ab	14699407.95	Bb	22289157.63	Ab	61795264.93	Ba	81143758.86	Aa
PC 36:3	69151.73611	Ab	129840.5968	Ab	319275.5876	Ab	410951.1794	Ab	927117.2529	Aa	1434142.248	Aa
PC 36:3.1	2498631.886	Ab	4487725.793	Ab	3126206.602	Ab	5226486.724	Ab	15945326.31	Aa	20782215.5	Aa
PC 36:5	312966.7301	Ab	668258.269	Ab	2507133.794	Aa	3019133.599	Aa	1266871.213	Ab	1785546.078	Ab
PC 36:6	69136.90323	Ab	140027.9781	Ab	367328.5083	Aa	423214.2442	Aa	255437.0812	Aa	311160.1262	Aa
PC 38:2	39931.0282	Bb	69931.71921	Ab	33118.06747	Bb	48881.56875	Ab	110216.4699	Ba	161424.336	Aa
PC 38:3	2221.762645	Ab	4521.458636	Ab	25445.12161	Aa	30061.31017	Aa	14334.34833	Aa	20511.25924	Aa
PC 38:3.1	15046.31577	Bb	28513.53729	Ab	18841.11935	Bb	31640.86504	Ab	76566.61732	Ba	96489.24764	Aa
PE 32:1	36265.32419	Bb	78227.3439	Ab	381024.3581	Ba	550225.5146	Aa	316856.5905	Ba	446103.1427	Aa
PE 34:2	794464.9136	Bb	1465706.827	Ab	3943852.835	Ba	5705283.107	Aa	4263839.393	Ba	5842135.384	Aa
PE 34:3	31562.79944	Ab	57764.14609	Ab	266466.5392	Aa	350020.5288	Aa	343224.0035	Aa	426200.745	Aa
PE 34:4	9199.471529	Ab	16770.57023	Ab	37073.46067	Ba	47979.72993	Aa	26443.06141	Aa	NA	Bc
PE 34:5	6266.747826	Ab	11392.29967	Ab	19692.94786	Aa	21711.56871	Aa	15065.65401	Aa	18858.93153	Aa
PE 34:6	2715.247575	Ab	4055.98632	Ab	6884.336865	Ab	6305.862464	Ab	10657.04499	Aa	14080.69236	Aa
PE 36:2	6151354.354	Bb	10865828.66	Ab	8082372.746	Bb	11924238.98	Ab	13486357.64	Ba	18616005.29	Aa
PE 36:3	1359945.931	Bb	2401179.828	Ab	2641940.064	Ba	4324848.861	Aa	3369137.692	Ba	4583695.417	Aa
PE 36:4	83901.10036	Bb	167812.9142	Ab	334584.5211	Ba	471898.3638	Aa	165161.7833	Bb	242097.737	Ab
PE 36:5	38632.37095	Bb	84602.17599	Ab	104245.5903	Ba	127063.1743	Aa	58849.78332	Bb	76557.29852	Ab
PE 36:6	10530.42612	Ac	21175.91546	Ac	60373.78783	Ab	72765.99256	Ab	85647.82822	Aa	114294.3149	Aa
PE 38:2	1149694.31	Bb	2071422.042	Ab	1435269.104	Bb	2147144.466	Ab	5079314.698	Ba	6368339.006	Aa
PE 38:3	278134.4976	Bb	517805.4209	Ab	450577.249	Bb	785658.095	Ab	1062380.561	Ba	1395844.959	Aa
PE 40:2	277479.2555	Bb	510704.8517	Ab	299097.7968	Bb	464414.0715	Ab	1579538.406	Ba	2281960.326	Aa
PE 40:3	5869.212202	Ab	9498.67403	Ab	13603.69606	Ab	NA	Ab	61715.41462	Aa	77012.01214	Aa
PG 34:2	93736.8566	Bc	180905.8371	Ac	309373.1289	Bb	410532.4403	Ab	415081.9349	Ba	568437.4063	Aa
PG 34:3	19701.48057	Bb	43974.48813	Ab	77149.76687	Ba	104255.3461	Aa	67401.76803	Ba	93211.44995	Aa
PG 34:4	1098574.617	Ab	NA	Bc	1568600.059	Ab	2070856.449	Ab	2710991.812	Aa	3090725.997	Aa
PG 36:2	919380.5704	Bb	1866913	Ab	1381201.88	Bb	1874703.657	Ab	2807927.923	Ba	3448445.443	Aa
PG 36:3	30098.53693	Ac	NA	Ac	56493.56862	Ab	63220.19642	Ab	143575.0095	Aa	152151.8597	Aa

SI Table 16. (continuation) Relative abundance of lipids of *C. reinhardtii* CC503 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
TAG 42:0	9908.984945	Bb	24249.55578	Ab	26959.15432	Ba	48363.58674	Aa	25875.6782	Ba	38142.37712	Aa
TAG 42:1	3690.784371	Ab	NA	Ac	53624.22457	Ba	126166.1697	Aa	41065.07438	Aa	58887.70144	Ab
TAG 44:0	36543.24304	Ab	86052.58001	Ac	249542.2294	Ba	622528.1718	Aa	211368.6038	Ba	339354.3588	Ab
TAG 44:1	18424.63968	Ab	41155.11179	Ab	283736.9014	Ba	860055.0514	Aa	102767.7594	Ab	155852.7766	Ab
TAG 46:0	69015.88361	Bb	154929.7366	Ab	314551.6579	Ba	634243.3514	Aa	466793.8062	Ba	702773.3498	Aa
TAG 46:1	95931.91946	Ab	227654.5615	Ac	5680889.699	Ba	17050581.23	Aa	3303225.111	Ba	6158192.344	Ab
TAG 46:2	25711.85333	Ab	54098.08088	Ac	3551520.947	Ba	10457346.39	Aa	1720633.264	Aab	3290000.008	Ab
TAG 46:2.1	13081.17956	Ac	29140.3847	Ac	112295.6081	Ba	339305.1518	Aa	41228.67315	Bb	89677.64495	Ab
TAG 48:0	125747.6195	Ab	277445.4699	Ab	2969639.332	Ba	6790457.457	Aa	4605247.06	Ba	7652768.475	Aa
TAG 48:1	203360.0682	Ab	478097.4541	Ac	7167008.627	Ba	18101789.97	Aa	6203581.673	Ba	11106734	Ab
TAG 48:2	39809.32386	Ab	80474.42081	Ab	4102967.057	Ba	10032257.05	Aa	4553204.323	Ba	8005787.927	Aa
TAG 48:4.1	4336.440579	Ab	8338.352425	Ac	556708.5287	Ba	1349654.742	Aa	454571.4286	Ba	784007.4245	Ab
TAG 48:5	633.8263475	Aa	882.9098179	Aa	NA	Ab	NA	Ab	NA	Ab	NA	Ab
TAG 50:0	76818.1254	Ab	152680.8506	Ab	623556.29	Ba	1221946.003	Aa	626663.6339	Ba	983314.6248	Aa
TAG 50:1	677092.4257	Ab	1551239.106	Ab	52249888.45	Ba	123333101.9	Aa	69181386.06	Ba	123675286.6	Aa
TAG 50:2	348201.7887	Ab	727082.9119	Ab	46337500.32	Ba	110790018.6	Aa	59438443.74	Ba	109638999.3	Aa
TAG 50:3	546467.1826	Ab	916858.9656	Ab	36784808	Ba	93102878.42	Aa	61633924.68	Ba	98318947.63	Aa
TAG 50:4	104702.6461	Ab	202841.0041	Ab	12702072.13	Bab	30589121.32	Aa	21065514.37	Ba	39217710.7	Aa
TAG 50:5	39103.46935	Ab	73095.38357	Ab	5496202.169	Bab	15064702.16	Aa	10096283.05	Ba	19082911.68	Aa
TAG 50:6	61273.45343	Bc	101376.4112	Ac	3003869.376	Bb	8172133.354	Ab	6764473.381	Ba	12046455.12	Aa
TAG 50:7	1823.997914	Bc	1640.524603	Ac	205780.9769	Bb	550463.5243	Ab	442261.6631	Ba	783699.6753	Aa
TAG 50:8	1269.178153	Bb	2559.953693	Ab	157300.3878	Ba	415202.9541	Aa	318740.5925	Ba	549547.148	Aa
TAG 50:9	2550.43235	Bc	4654.714356	Ac	125186.3451	Bb	283642.063	Ab	368453.6896	Ba	533999.0441	Aa
TAG 52:0	56724.80021	Bb	112966.5279	Ab	160979.3879	Ba	309764.8847	Aa	153583.4459	Ba	239548.2574	Aa
TAG 52:1	321637.3892	Ac	736002.7265	Ac	16781569.62	Ba	38990400.06	Aa	9401527.372	Bb	16752708.98	Ab
TAG 52:2	703213.5109	Ab	1484814.909	Ac	55629960.74	Ba	131378797.3	Aa	43771131.16	Ba	80424623.9	Ab
TAG 52:3	316324.1614	Ab	655339.7993	Ac	52301518.75	Ba	112855740.3	Aa	44483606.85	Ba	83827541.44	Ab
TAG 52:3.1	23038.52062	Ab	45562.8967	Ab	3183192.205	Ba	7945932.377	Aa	3909739.916	Ba	6948958.751	Aa
TAG 52:4	357749.3066	Ab	730954.1849	Ab	52107009.81	Ba	122381929	Aa	58411914.26	Ba	106312840.8	Aa

SI Table 16. (continuation) Relative abundance of lipids of *C. reinhardtii* CC503 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
TAG 52:4.1	141460.569	Ab	265835.3505	Ab	20120228.4	Ba	43755836.78	Aa	33166213.18	Ba	53147918.41	Aa
TAG 52:5	110701.9146	Ab	228750.0317	Ab	25702577.93	Ba	63709541.81	Aa	32194909.34	Ba	59273611.2	Aa
TAG 52:5.1	153054.5436	Bb	305083.2887	Ab	22456809.63	Ba	47792451.29	Aa	34948443.25	Ba	61240353.55	Aa
TAG 52:6	147562.4771	Ab	270018.6803	Ab	13421434.46	Bab	36629426.93	Aa	24663761.41	Aa	34398006.9	Aa
TAG 52:6.1	219608.8307	Bc	411470.3933	Ac	18095705.64	Bb	38923904.2	Ab	33022012.02	Ba	53329267.82	Aa
TAG 52:7	21183.50722	Ab	40898.31084	Ab	2910890.988	Bab	7614762.362	Aa	4449933.86	Ba	7895891.285	Aa
TAG 52:8	9829.602835	Ab	18804.9894	Ab	1052678.264	Bab	2905686.189	Aa	1740872.28	Ba	3133935.767	Aa
TAG 52:9	15950.16675	Bc	29556.74755	Ac	380209.7972	Bb	943571.3247	Ab	927893.2366	Ba	1373565.848	Aa
TAG 54:0	20621.86453	Bb	38053.97303	Ab	55827.71848	Ba	96310.3047	Aa	56993.51108	Ba	74741.49886	Aa
TAG 54:1	89510.69138	Ab	171737.7075	Ac	2368518.641	Ba	4224434.754	Aa	871618.5681	Ab	1475993.533	Ab
TAG 54:2	217303.8865	Ac	422430.532	Ac	11461890.08	Ba	21333729.18	Aa	5634760.317	Bb	11056445.77	Ab
TAG 54:3	373636.9251	Ab	697301.3555	Ac	17877705.98	Ba	30845204.96	Aa	6961807.223	Bb	13668550.09	Ab
TAG 54:4	230920.534	Ab	457845.5934	Ac	21024068.08	Ba	34736726.57	Aa	8442512.113	Bb	16053051.84	Ab
TAG 54:5	120314.7533	Ac	247807.419	Ac	20984191.18	Ba	32537247.76	Aa	7601130.193	Ab	11576596.19	Ab
TAG 54:6	61988.00293	Bc	139305.4079	Ac	13072443.51	Ba	20022098.78	Aa	5562172.535	Bb	9261266.27	Ab
TAG 54:7	33587.92276	Bc	82633.91618	Ac	7710577.041	Ba	12918764.45	Aa	4902926.894	Bb	7201516.096	Ab
TAG 54:8	9326.819325	Bb	22761.44721	Ab	2443231.582	Ba	4488597.953	Aa	2062165.962	Ba	2946025.016	Aa
TAG 54:9	8119.436773	Bb	18678.48015	Ab	754438.2055	Ba	1560709.638	Aa	1139205.666	Ba	1389020.352	Aa
TAG 56:0	13787.60875	Bb	25872.42233	Ab	37885.36006	Ba	64766.25722	Aa	37195.42461	Ba	50190.99485	Aa
TAG 56:1	13274.36843	Ab	24865.36745	Ac	422282.2287	Ba	683173.319	Aa	137886.6054	Bb	256229.9028	Ab
TAG 56:2	27834.30287	Ab	55435.99038	Ac	996563.3315	Ba	1636357.615	Aa	355842.2505	Bb	721416.0984	Ab
TAG 56:3	15425.1847	Ab	30837.61362	Ab	1469465.418	Aa	1712918.913	Aa	460673.6149	Ab	NA	Ab
TAG 56:4	14836.30826	Ab	28217.86927	Ab	1793399.774	Aa	1725476.727	Aa	460161.8451	Ab	853470.6748	Ab
TAG 56:5	8552.761815	Ab	16131.48562	Ab	2461012.861	Aa	2177066.576	Aa	716595.216	Ab	1004826.704	Ab
TAG 56:5.1	NA	Ab	NA	Ab	253215.6343	Ba	527249.6268	Aa	264096.5576	Ba	512781.8779	Aa
TAG 56:6	4751.814365	Ab	9970.788236	Ab	1986132.76	Aa	1638795.124	Aa	540345.9088	Ab	886056.7987	Ab
TAG 56:7	4748.218354	Ac	8227.345663	Ac	1044159.378	Aa	1073147.934	Aa	389410.5127	Ab	571229.9262	Ab
TAG 58:0	6552.792256	Bb	12078.64433	Ab	24015.20078	Ba	44962.88776	Aa	27788.9543	Ba	42526.40345	Aa
TAG 58:1	12814.12316	Ab	23611.77909	Ac	424131.8732	Ba	739190.1095	Aa	157135.7519	Ab	265688.7932	Ab

SI Table 16. (continuation) Relative abundance of lipids of *C. reinhardtii* CC503 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
TAG 58:2	22009.06122	Ab	44233.72692	Ab	590777.18	Ba	950934.0382	Aa	NA	Bb	185923.5623	Ab
TAG 58:3.1	10147.32527	Ab	20878.83849	Ab	716246.2591	Aa	718614.6004	Aa	121230.5339	Ab	190386.1037	Ab
TAG 58:5	605.4304678	Ab	957.0264156	Ab	NA	Ab	NA	Ab	22448.97895	Ba	42332.73892	Aa
TAG 58:6	843.6633655	Ab	1446.655774	Ac	54828.89968	Ba	90295.63816	Aa	65265.27648	Aa	60274.31572	Ab
TAG 60:0	1697.616024	Bb	3426.036411	Ab	4498.951044	Ba	8757.368185	Aa	5810.278533	Ba	8230.862471	Aa
TAG 60:1	8873.460961	Ab	16530.25957	Ab	299744.8445	Ba	668532.5873	Aa	294840.98	Ba	563898.4195	Aa
TAG 60:2	13346.91325	Ab	27130.35577	Aa	397890.9531	Aa	NA	Ba	NA	Ab	NA	Aa
TAG 60:4	8717.891168	Ab	20535.97817	Ab	287437.4828	Ba	452526.2446	Aa	41130.87562	Ab	74754.5981	Ab
TAG 60:5	3867.320422	Ba	8482.778344	Aa	NA	Ab	NA	Ab	NA	Ab	NA	Ab
TAG 60:5.1	680.928666	Ab	NA	Ab	NA	Ab	NA	Ab	33745.89466	Ba	64462.24524	Aa
TAG 60:6	62320.17137	Ab	112552.6137	Ab	521262.0413	Ab	905001.5399	Ab	1972834.101	Aa	2650841.9	Aa
FA 16:0	400625.8585	Ab	755495.5616	Ab	2272363.155	Ab	3604707.353	Ab	9019936.882	Aa	9385814.504	Aa
FA 16:2	14242.95921	Ab	25279.44978	Ab	62573.81431	Ab	76756.78255	Ab	299417.3611	Aa	312623.7337	Aa
FA 16:3	14047.29493	Ab	22946.24655	Ab	117583.9712	Ab	141559.1052	Ab	576469.1025	Aa	592468.9203	Aa
FA 18:0	415253.1757	Ac	828547.8485	Ac	1344401.636	Ab	2336619.543	Ab	3299828.602	Aa	3826420.131	Aa
FA 18:1	NA	Ac	NA	Ac	10400995.12	Ab	17754146.76	Ab	28187525.13	Aa	34801451.13	Aa
FA 18:2	477853.087	Ac	881461.2602	Ac	7584363.125	Ab	11777934.54	Ab	17291082.66	Aa	19353362.97	Aa
FA 18:3	8490642.948	Ab	15102461.2	Ab	31080965.09	Ab	50087753.54	Ab	86993451.3	Aa	86923010.7	Aa
FA 20:0	9327.772871	Bb	19002.62966	Ab	32548.00855	Ba	59857.32941	Aa	53383.71355	Ba	58880.90041	Aa
FA 20:1	25048.61341	Ac	42381.59119	Ac	152323.0385	Ab	205697.6365	Ab	315229.2428	Aa	315960.7923	Aa
FA 20:3	9812.992612	Ac	17915.03472	Ac	32130.54046	Ab	50345.15101	Ab	81692.16692	Aa	82451.71993	Aa
FA 22:0	5261.321787	Bc	9840.617702	Ac	31341.92357	Bb	43135.10229	Ab	45548.21629	Ba	55376.93857	Aa
FA 22:1	2179.134596	Ac	3882.855405	Ac	5988.301788	Ab	10880.06318	Ab	12104.28696	Aa	14740.08863	Aa
FA 24:0	13527.28666	Bc	23447.39667	Ac	66482.62622	Bb	113872.3065	Ab	132875.1132	Ba	167926.9384	Aa
FA 24:1	800.5878357	Ab	1310.714868	Ab	3059.56916	Aa	4129.3648	Aa	4895.995559	Aa	3747.50665	Aa
FA 26:0	15460.6199	Ab	27530.48131	Ab	149792.1848	Ab	268187.2213	Ab	674178.3773	Aa	835611.6644	Aa
FA 28:0	3080.343168	Ab	6068.314153	Ab	10255.53384	Ab	20190.10814	Ab	52506.31878	Aa	56862.86634	Aa
FA 30:0	1247.89056	Ac	2011.768685	Ac	2283.587886	Ab	4717.446497	Ab	6294.399519	Aa	7288.269737	Aa

SI Table 17. Relative abundance of lipids of *Chlamydomonas* sp. BR020 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
DGDG 32:0	46028.55655	Ab	66039.00307	Aa	44511.25764	Ab	52203.88655	Aa	200999.5898	Aa	72100.95902	Ba
DGDG 32:1	13670.42597	Ab	19798.45036	Aa	14956.81401	Ab	24924.11817	Aa	79118.80526	Aa	36240.06954	Ba
DGDG 32:2	37919.70683	Ab	56016.14001	Aa	65399.3837	Ab	55614.23995	Aa	301638.4371	Aa	79512.5058	Ba
DGDG 32:3	183631.1578	Ab	264093.1695	Aa	309118.0724	Ab	323416.3307	Aa	1167609.88	Aa	552849.7776	Ba
DGDG 32:3.1	78119.41938	Ab	109122.7356	Ab	111603.8803	Bb	205240.7619	Ab	584598.6903	Aa	333439.7523	Ba
DGDG 34:0	21824.78391	Ab	31692.67218	Aa	18189.96562	Ab	17706.1369	Aa	99317.91604	Aa	34891.67024	Ba
DGDG 34:1	1570285.43	Ab	2390968.762	Aa	1573781.737	Ab	2090834.074	Aa	6781000.187	Aa	2811627.571	Ba
DGDG 34:2	2847339.309	Ab	4254362.847	Aa	2437538.541	Ab	2820113.66	Aa	8522342.308	Aa	2954488.345	Ba
DGDG 34:3	2689765.644	Ab	3952048.339	Aa	2733399.159	Ab	4262172.283	Aa	9735922.32	Aa	5167660.178	Ba
DGDG 34:4	2230608.377	Ab	3246144.096	Aa	2496623.985	Ab	2278876.904	Aa	11218965.38	Aa	2717815.766	Ba
DGDG 34:5	7395039.096	Ab	10150453.31	Aa	8558394.057	Ab	10568330.75	Aa	38673302	Aa	13122302.1	Ba
DGDG 34:6	18382217.75	Ab	26029207.54	Ab	27282378.82	Ab	40543972.44	Aab	126484572.9	Aa	62764920.6	Ba
DGDG 36:2	10225.32727	Ba	18306.90858	Aa	NA	Ab	NA	Ab	NA	Ab	NA	Ab
DGDG 36:4	144608.7499	Ab	210116.0281	Aa	199153.9118	Ab	287042.9791	Aa	646227.8719	Aa	343603.6242	Ba
DGDG 36:5	511090.1514	Ab	742933.0646	Ab	675030.9695	Bb	1110556.613	Aab	2166668.957	Aa	1437968.979	Ba
DGDG 36:6	1340840.988	Ab	1940185.742	Ab	1580603.004	Ab	2786691.786	Ab	6594847.964	Aa	5298811.72	Aa
MGDG 34:1	89529.74876	Ab	128103.3249	Ab	144156.7069	Ab	200969.1348	Ab	875838.4996	Aa	524577.8602	Ba
MGDG 34:2	NA	Ac	NA	Ac	153331.5324	Ab	141419.355	Ab	700317.4251	Aa	365246.6088	Ba
MGDG 34:3	473715.8731	Ab	720830.3989	Aa	459653.8832	Ab	757893.8824	Aa	1814017.683	Aa	1033420.558	Ba
MGDG 34:4	1073634.625	Ab	1538037.087	Aa	812235.7945	Ab	1276045.062	Aa	2410565.604	Aa	1429418.27	Ba
MGDG 34:4.1	5529.839754	Bb	13193.06424	Aa	NA	Ab	NA	Ab	22306.07859	Aa	NA	Bb
MGDG 34:5	11169.78676	Ab	14627.84866	Ab	18674.07742	Ab	31517.88234	Ab	142776.4951	Aa	63703.75871	Ba
MGDG 34:6	1563105.412	Ab	2222283.18	Aa	1156589.583	Ab	1876880.311	Aa	2952377.349	Aa	2108643.092	Aa
MGDG 34:7	301248.7743	Ab	343075.8049	Ab	384117.9595	Ab	422024.1484	Ab	2175195.229	Aa	1500540.844	Aa
MGDG 36:5	223356.736	Ab	273533.7256	Ab	148535.3658	Ab	374760.6226	Ab	486473.1115	Aa	395054.6653	Aa
MGDG 36:5.1	46679.45423	Aa	NA	Bb	29904.49818	Ba	47109.75352	Aa	NA	Bb	60295.99091	Aa
MGDG 36:6	322498.725	Bb	465703.2653	Ab	278095.3963	Bb	589652.4152	Ab	844721.467	Ba	871561.8956	Aa

SI Table 17. (continuation) Relative abundance of lipids of *Chlamydomonas* sp. BR020 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
SQDG 32:0	1375540.086	Ab	2147591.419	Aa	1671934.186	Ab	2237803.794	Aa	6688967.318	Aa	3494054.054	Ba
SQDG 32:1	21953.99463	Aa	33214.58439	Aa	25023.16736	Aa	26995.41225	Aa	NA	Ab	NA	Ab
SQDG 32:2	52129.00585	Ab	66416.66596	Ab	86295.52591	Ab	92098.40078	Aab	471969.7077	Aa	170298.436	Ba
SQDG 32:3	139690.4536	Ab	203838.6936	Ab	262882.6101	Ab	358058.5484	Ab	1494310.013	Aa	822826.5452	Ba
SQDG 34:1	546911.1191	Ab	867013.647	Aa	735254.0031	Ab	803471.3983	Aa	2403302.954	Aa	1124241.447	Ba
SQDG 34:2	2977566.397	Ab	4437582.645	Aa	3095418.019	Ab	2411963.887	Aa	11672951.21	Aa	3524202.991	Ba
SQDG 34:3	3306887.081	Ab	5495838.449	Aa	3870336.123	Ab	5671947.03	Aa	16060869.24	Aa	8453820.614	Ba
SQDG 34:4	23541.28396	Ab	30645.47775	Aa	21535.95546	Ab	19704.61829	Aa	98482.50406	Aa	42499.18628	Ba
SQDG 34:4.1	NA	Ab	NA	Ac	NA	Bb	16535.87086	Ab	55601.59196	Aa	36335.10255	Ba
SQDG 34:6	141427.3372	Aa	NA	Bb	NA	Ab	NA	Ab	NA	Bb	833885.7764	Aa
DAG 34:1	46787.94959	Ac	45537.7434	Ac	83193.43621	Ab	180696.3415	Ab	220747.8678	Aa	204519.3289	Aa
DAG 34:2	83931.33748	Ab	93727.69659	Ab	95247.29349	Ab	138984.7377	Aab	441860.2143	Aa	214695.674	Ba
DAG 34:3	55504.00387	Ab	64770.45932	Ab	67955.69508	Ab	124266.1206	Aab	328435.0654	Aa	182590.0106	Ba
DAG 34:4	59552.84673	Ab	58887.44263	Aa	94247.12846	Ab	117855.4806	Aa	487728.4102	Aa	128450.8724	Ba
DAG 34:5	261826.8195	Ab	243823.564	Aa	357197.184	Ab	473833.4781	Aa	1672063.911	Aa	525262.8083	Ba
DAG 34:6	771112.3987	Ab	689994.134	Ab	1176279.508	Ab	1973720.668	Aab	5702205.747	Aa	2543753.316	Ba
DAG 36:1	995.721439	Ab	NA	Bb	1434.996118	Bb	2948.160957	Aa	3603.634772	Aa	3935.24296	Aa
DAG 36:3	43634.11303	Ab	46421.30138	Ab	65225.66415	Ab	157461.4808	Ab	288723.2382	Aa	268091.5034	Aa
DAG 36:4	NA	Ab	62921.14593	Ab	74195.15394	Ab	211945.1796	Ab	443833.123	Aa	437320.7332	Aa
DAG 36:5	152874.665	Ab	168907.0394	Ab	212098.8282	Ab	454175.3817	Aab	1126908.133	Aa	670415.3545	Ba
DAG 36:6	113569.2261	Ab	125954.9152	Ab	174278.7481	Bb	393540.712	Aa	919565.3409	Aa	620315.7479	Ba
LysoPC 16:0	51261.87453	Ab	72192.91179	Aa	348563.1913	Ab	136300.7621	Aa	3312390.834	Aa	489681.4161	Ba
LysoPC 16:0.1	9813.006747	Ab	13260.56906	Ab	17771.67083	Ab	21278.59845	Ab	113912.9751	Aa	56929.46415	Ba
LysoPC 16:2	9283.004921	Ab	20421.00564	Aa	12761.51832	Ab	6137.065561	Aa	119149.7151	Aa	22929.17924	Ba
LysoPC 16:3	74287.43121	Ab	133253.7226	Ab	84640.93294	Ab	98051.80121	Ab	596239.5614	Aa	266500.0217	Ba
LysoPC 18:1	195004.744	Ab	307650.0118	Ab	244521.3893	Ab	233724.8238	Ab	2145349.444	Aa	811354.0596	Ba
LysoPC 18:1.1	1516421.599	Ab	2154330.573	Ab	1809466.721	Ab	2520286.048	Ab	7947829.035	Aa	5388794.539	Ba
LysoPC 18:2	66309.25042	Ab	105694.9764	Aa	213823.566	Ab	93446.09096	Aa	2009741.686	Aa	323180.6252	Ba
LysoPC 18:2.1	173287.8787	Ab	297010.5749	Ab	200474.1448	Ab	233196.872	Ab	935565.7933	Aa	551719.8682	Ba

SI Table 17. (continuation) Relative abundance of lipids of *Chlamydomonas* sp. BR020 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
LysoPC 18:3	87361.93507	Ab	123684.5259	Aa	551727.7131	Ab	194835.4547	Aa	4895722.456	Aa	968976.6506	Ba
LysoPC 18:3.1	167904.2636	Ab	284288.9615	Ab	157247.9973	Ab	201735.2513	Ab	723656.0436	Aa	450622.8635	Ba
PC 32:0	NA	Ab	NA	Ab	NA	Bb	6392.153173	Aab	25602.03432	Aa	12429.24502	Ba
PC 32:1	19245.55687	Ab	27234.95921	Ab	32909.49757	Ab	50596.46322	Ab	276220.481	Aa	159081.7083	Ba
PC 32:1.1	55290.39102	Ab	75627.06688	Ab	94945.59301	Ab	90266.90802	Aab	640458.1527	Aa	196695.2118	Ba
PC 32:2	1184360.731	Ab	1595925.107	Aa	2091792.192	Ab	1946017.225	Aa	14255257.74	Aa	3484659.001	Ba
PC 32:3	4280607.041	Ab	5610758.648	Ab	7093565.356	Ab	8278671.497	Ab	42493692.54	Aa	18156387.8	Ba
PC 32:4	54213.98039	Ab	80855.52512	Ab	149047.4037	Ab	90310.82947	Ab	1671571.536	Aa	343142.3219	Ba
PC 34:2	2610926.95	Ab	3590923.423	Ab	4402206.539	Ab	6299965.74	Aab	21114113.86	Aa	9820887.314	Ba
PC 34:3	2163910.301	Ab	2936050.14	Ab	3405796.506	Ab	4980844.644	Ab	23387722.48	Aa	10449467.87	Ba
PC 34:4	1094964.048	Ab	1561405.615	Ab	2119151.519	Ab	2186325.443	Aab	20553324.69	Aa	5525836.807	Ba
PC 34:5	2618799.409	Ab	3479741.714	Ab	5205591.77	Ab	6135611.185	Aab	51993568.15	Aa	16477653.06	Ba
PC 34:6	3582068.87	Ab	4998718.013	Ab	11003734.86	Ab	14209277.06	Ab	102682770.5	Aa	42770198.57	Ba
PC 36:1	153870.1249	Ab	198653.8945	Ab	271224.147	Ab	396491.5601	Aab	2019320.077	Aa	937095.4856	Ba
PC 36:2	5375584.263	Ab	6723550.439	Ab	8331483.397	Ab	13565126.02	Ab	63545892.07	Aa	38841648.15	Ba
PC 36:3	505797.7096	Ab	703342.6418	Ab	796342.5623	Ab	1256540.486	Ab	4070107.539	Aa	2287481.917	Ba
PC 36:3.1	471228.6031	Ab	601347.7762	Ab	937648.3172	Ab	1456487.627	Ab	9030539.605	Aa	5159650.122	Ba
PC 36:5	7435728.521	Ab	10365147.48	Ab	10777753.09	Ab	15168817.88	Ab	53857238.36	Aa	27027823.14	Ba
PC 36:6	7175748.603	Ab	9784371.757	Ab	10298722.83	Ab	15494633.58	Ab	57979052.14	Aa	32506057.28	Ba
PC 38:2	13117.4768	Ab	17955.94315	Ab	19498.58679	Ab	30512.77543	Ab	148133.3743	Aa	97214.92393	Aa
PC 38:3	27701.50839	Ab	35794.05185	Ab	42451.8539	Ab	42505.91266	Ab	198829.8344	Aa	102108.5745	Ba
PC 38:3.1	3287.102094	Ab	3307.217491	Ab	4563.131325	Ab	7446.779544	Ab	40915.46158	Aa	19470.13914	Ba

SI Table 17. (continuation) Relative abundance of lipids of *Chlamydomonas* sp. BR020 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
PE 32:1	18958.91666	Ac	31537.37436	Ab	171505.0762	Ab	272280.5076	Aa	539314.3349	Aa	303695.3983	Ba
PE 34:2	NA	Ac	NA	Ab	1823331.442	Ab	2790461.817	Aa	6600761.538	Aa	3440096.189	Ba
PE 34:3	440537.5538	Ab	697330.8294	Aa	368886.193	Bb	667941.4808	Aab	887565.7789	Aa	379184.0088	Bb
PE 34:4	200700.1124	Ab	299068.38	Aa	166862.1242	Ab	250968.408	Aa	619261.621	Aa	218435.3518	Ba
PE 34:5	449587.79	Ab	691969.779	Aa	432990.296	Ab	614598.0748	Aa	1670383.171	Aa	553414.9048	Ba
PE 34:6	383922.2046	Ab	590538.6441	Ab	556731.1125	Ab	841926.4009	Aab	2986903.107	Aa	1321853.183	Ba
PE 36:2	4214077.187	Ab	6383316.193	Aa	4585614.518	Bb	7861246.315	Aa	7724433.364	Aa	5007949.864	Ba
PE 36:3	551196.879	Ab	800882.0178	Ab	738073.0154	Bab	1218079.558	Aa	1015770.582	Aa	532504.6274	Bb
PE 36:4	768220.3334	Ab	1159559.486	Aa	553647.044	Bb	1002028.138	Aab	1626496.595	Aa	630066.9879	Bb
PE 36:5	1637513.126	Ab	2582526.741	Aa	1846574.789	Ab	2861770.824	Aa	5523778.743	Aa	2442817.076	Ba
PE 36:6	870438.1919	Ab	1281086.736	Aa	1136998.113	Ab	1859483.42	Aa	4005385.435	Aa	1840800.883	Ba
PE 38:2	585405.9439	Ab	727042.0526	Ab	835153.7531	Ab	1428127.157	Ab	2725983.863	Aa	1903812.31	Aa
PE 38:3	79977.15885	Ab	98243.15212	Aa	110143.8644	Ab	185987.8711	Aa	312185.7949	Aa	174410.3032	Ba
PE 40:2	57073.65399	Ab	75552.37699	Ab	86304.05559	Ab	136667.6532	Ab	794295.7052	Aa	548536.9735	Aa
PE 40:3	37475.15962	Ab	54520.98362	Ab	48142.74461	Ab	62799.04458	Ab	225383.1796	Aa	110846.6308	Ba
PE 40:4	49085.43419	Ab	68754.63423	Ab	71263.23576	Ab	94623.83427	Ab	409085.7012	Aa	184943.7895	Ba
PG 34:2	639229.9857	Ab	1052456.733	Aa	727333.8388	Ab	725028.7502	Aa	2329765.694	Aa	892416.5384	Ba
PG 34:3	746187.5627	Ab	1143757.854	Aa	821998.8773	Ab	897635.6741	Aa	3003793.576	Aa	1303208.814	Ba
PG 34:4	579213.4912	Ab	916168.1176	Ab	932400.4528	Ab	1036807.41	Aab	4090421.407	Aa	1935258.939	Ba
PG 36:2	1172612.949	Ab	1688877.273	Aa	1435129.866	Ab	NA	Bb	3493395.61	Aa	2368120.134	Ba
PG 36:3	32466.95011	Ab	48110.99146	Ab	53840.84778	Ab	NA	Bc	107501.2979	Aa	109193.9006	Aa
TAG 42:0	9379.464433	Ab	13222.8044	Aa	7697.855283	Bb	19234.76628	Aa	21907.39758	Aa	16644.53212	Aa
TAG 42:1	7320.874838	Aa	11312.99661	Ab	16888.44774	Ba	74088.68352	Aa	15180.07846	Aa	NA	Ab
TAG 42:2	1257.851124	Ab	1522.247359	Aa	NA	Ac	NA	Ab	4460.05462	Aa	NA	Bb
TAG 44:0	36522.68646	Aa	50130.04783	Aa	20713.05267	Ba	51916.00085	Aa	41384.60722	Aa	32536.63925	Aa
TAG 44:1	22534.95057	Ab	34432.30466	Ab	83125.44173	Ba	267984.0093	Aa	44192.92173	Aab	36498.45678	Ab
TAG 46:0	59731.09835	Ab	84144.26414	Aa	45808.84143	Bb	95257.56584	Aa	103045.8158	Aa	82665.15648	Aa
TAG 46:1	441326.6265	Aa	638455.8052	Ab	606308.5779	Ba	2389885.842	Aa	145954.851	Aa	191738.45	Ab
TAG 46:2	163229.4939	Aa	238644.9463	Ab	129343.4448	Ba	351160.8443	Aa	110037.5228	Aa	76633.99473	Ac

SI Table 17. (continuation) Relative abundance of lipids of *Chlamydomonas* sp. BR020 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
TAG 46:2.1	NA	Ab	NA	Ac	NA	Bb	109873.451	Aa	41973.00209	Aa	33004.48949	Ab
TAG 46:4	NA	Aa	NA	Ab	8451.928093	Ba	45926.63156	Aa	NA	Aa	NA	Ab
TAG 48:0	192118.4512	Ba	277788.4676	Aa	122541.8235	Ba	293163.8398	Aa	196148.9883	Ba	223878.6187	Aa
TAG 48:1	386820.4123	Ab	587233.5049	Ab	1578246.162	Ba	4735263.649	Aa	470394.7972	Ab	693634.4958	Ab
TAG 48:2	561840.9091	Aa	821458.6061	Ab	870257.6349	Ba	3947540.629	Aa	549169.7142	Aa	1220722.409	Ab
TAG 48:3	918937.8422	Aa	1272132.241	Ab	558204.8408	Ba	4974080.111	Aa	1017951.213	Ba	2628124.188	Ab
TAG 48:4	62009.2549	Aa	78733.20128	Ac	64724.32868	Ba	715554.7177	Aa	199355.4942	Ba	446430.5286	Ab
TAG 48:4.1	68372.24106	Ba	99028.24905	Aa	43701.53968	Aa	NA	Bb	NA	Ab	NA	Ab
TAG 48:5	70538.70794	Aa	89646.11973	Ac	49651.71753	Ba	561108.5724	Aa	177154.1244	Aa	305251.4281	Ab
TAG 48:6	41747.81961	Aa	52049.33925	Ab	33412.90229	Ba	398428.2478	Aa	134834.0154	Ba	277866.5265	Aa
TAG 48:7	5002.892684	Ab	5411.20381	Ab	3759.686614	Bb	31898.10077	Aa	31195.82244	Aa	29795.66393	Aa
TAG 48:8	6201.738854	Ab	6280.434508	Ab	4061.609538	Bb	30477.6193	Aa	32082.54316	Aa	28002.29558	Aa
TAG 48:9	3741.944805	Ab	2912.875522	Ab	2445.565096	Bb	21698.71644	Aa	23682.18709	Aa	27310.28214	Aa
TAG 50:0	100664.161	Aab	144457.448	Aa	79714.12632	Bb	179949.5312	Aa	149260.179	Aa	131633.1017	Aa
TAG 50:1	7834039.444	Aa	10820726.95	Ac	8873938.21	Ba	42316856.39	Aa	8372953.839	Ba	22179423.15	Ab
TAG 50:2	4648315.355	Aa	6208832.742	Ab	4728611.534	Ba	17790976.13	Aa	4943224.194	Aa	8140923.681	Ab
TAG 50:3	1194062.8	Aa	1702215.848	Ac	1187252.223	Ba	9500029.064	Aa	2247126.89	Ba	5392554.534	Ab
TAG 50:4	1136143.889	Aa	1587352.459	Ac	1077027.124	Ba	13208978.63	Aa	2500517.363	Ba	8406888.901	Ab
TAG 50:5	784048.6376	Aa	1041970.564	Ac	577855.2365	Ba	6722208.344	Aa	1866234.995	Ba	3615050.905	Ab
TAG 50:6	730368.1461	Aa	996411.5381	Ac	544325.9576	Ba	7585504.36	Aa	1716281.912	Ba	4800528.106	Ab
TAG 50:7	64983.53681	Ab	80836.45293	Ab	62446.96556	Bb	676392.8132	Aa	339321.9669	Aa	493166.7734	Aa
TAG 50:8	78165.93635	Ab	89648.00126	Ab	79038.88643	Bb	468932.5051	Aa	392374.9969	Aa	365117.3908	Aa
TAG 50:9	81231.63681	Ab	85545.62573	Ab	85165.27621	Bb	444895.7493	Aa	373755.8513	Aa	467789.6706	Aa
TAG 52:0	72627.31885	Ab	102566.2924	Aa	58549.36192	Bb	123073.4833	Aa	136678.0895	Aa	111161.6165	Aa
TAG 52:1	1414789.377	Aa	2037473.117	Ab	2852858.075	Ba	11528126.15	Aa	1133806.592	Ba	3372990.54	Ab
TAG 52:2	7937682.594	Aa	11339626.65	Ac	16022316.53	Ba	68522389.21	Aa	14515437.05	Ba	44409669.45	Ab
TAG 52:3	4658695.511	Aa	6544621.064	Ac	6289924.89	Ba	36033735.96	Aa	10186230.49	Ba	23032928.27	Ab
TAG 52:4	4032681.324	Aa	5698481.205	Ac	3988583.325	Ba	39105411.67	Aa	8372129.016	Ba	25872166.29	Ab
TAG 52:4.1	8477.936595	Ba	12850.90115	Aa	NA	Ba	46201.21698	Aa	16657.85962	Ba	45959.32055	Aa

SI Table 17. (continuation) Relative abundance of lipids of *Chlamydomonas* sp. BR020 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
TAG 52:5	1742351.5	Aa	2546036.645	Ac	1433453.356	Ba	10536952.23	Aa	3976072.552	Aa	6581460.382	Ab
TAG 52:5.1	9294.28745	Aa	13180.44327	Ab	15968.13006	Ba	120846.134	Aa	9990.88134	Ba	57525.46162	Ab
TAG 52:6	NA	Aa	NA	Ac	489025.8157	Ba	7166093.651	Aa	1782085.492	Ba	4577168.655	Ab
TAG 52:6.1	5263.48224	Ab	6447.849645	Ab	5010.808138	Bb	20466.63413	Aa	19501.87607	Aa	16478.88634	Aa
TAG 52:7	517628.2271	Aa	668843.9277	Ab	487086.3454	Ba	6915215.551	Aa	1816229.177	Ba	4793453.73	Aa
TAG 52:8	377057.6607	Ab	489940.6063	Ab	631174.0649	Bb	1995342.458	Aa	2542044.706	Aa	1624933.926	Ba
TAG 52:9	521224.0549	Ab	697906.1421	Ab	1183756.408	Ab	2303414.34	Aa	4157337.101	Aa	2821701.036	Ba
TAG 54:0	31363.58301	Ab	45142.59268	Aa	25754.22888	Bb	45619.03408	Aa	61725.56393	Aa	47193.66955	Aa
TAG 54:1	136922.7985	Aa	200616.502	Ac	113391.6277	Ba	690536.8281	Aa	180330.998	Ba	425179.7057	Ab
TAG 54:2	1036128.555	Aa	1546341.856	Ac	1324690.906	Ba	6743819.416	Aa	1174424.86	Ba	3748320.261	Ab
TAG 54:3	2470681.278	Aa	3663054.437	Ab	3670802.955	Ba	28418203.81	Aa	5931074.205	Ba	23233226.9	Aa
TAG 54:4	1368501.817	Aa	2081745.988	Ab	1965658.2	Ba	20953057.48	Aa	3745316.822	Ba	14530607.52	Aa
TAG 54:5	1405584.094	Aa	2090160.939	Ab	2271061.43	Ba	28602807.57	Aa	5090000.719	Ba	21453458.19	Aa
TAG 54:6	586189.6748	Aa	853955.1873	Ac	898802.4836	Ba	11141334.2	Aa	2789504.151	Ba	7533053.981	Ab
TAG 54:7	325928.3162	Aa	494501.581	Ab	484487.5047	Ba	6813926.926	Aa	1995608.827	Ba	5054643.131	Aa
TAG 54:8	174105.7104	Ab	280771.1069	Ab	262214.7182	Bb	1558428.68	Aa	1269122.418	Aa	1376576.977	Aa
TAG 54:9	72867.35962	Ab	115313.2816	Ab	123186.9837	Bb	431692.6744	Aa	605573.6376	Aa	500500.4693	Aa
TAG 56:0	23421.93712	Ab	33986.11605	Aa	17821.45379	Bb	31360.31673	Aa	46922.5938	Aa	35824.39231	Aa
TAG 56:1	21421.94038	Aa	29872.95552	Ac	18933.65479	Ba	132422.5944	Aa	35352.71611	Ba	90955.89156	Ab
TAG 56:2	71933.70446	Aa	106601.1322	Ac	89689.64445	Ba	557646.2559	Aa	103973.643	Ba	310441.8279	Ab
TAG 56:3	159406.8721	Aa	238235.2762	Ab	263678.2771	Ba	1718073.803	Aa	284647.4967	Ba	1228828.018	Aa
TAG 56:4	111637.5579	Aa	168519.399	Ac	154826.4491	Ba	930851.2552	Aa	228678.8911	Ba	597808.9525	Ab
TAG 56:5	70143.87344	Aa	100877.0589	Ab	129256.8633	Ba	1129424.298	Aa	186987.3289	Ba	795521.6476	Aa
TAG 56:6	32658.73292	Aa	46179.08045	Ab	49947.72217	Ba	348968.6615	Aa	112074.9219	Ba	240749.1567	Aa
TAG 56:7	11029.53797	Aa	15463.77485	Ab	14984.02725	Ba	161196.0815	Aa	41230.3841	Ba	118592.6178	Aa
TAG 58:0	10036.39657	Ab	13942.33037	Aa	7385.483166	Bb	13786.44842	Aa	19673.96151	Aa	14662.69958	Aa
TAG 58:1	20657.70723	Aa	31128.67477	Ab	17399.9397	Ba	112770.4629	Aa	35065.72582	Ba	85100.38522	Aa
TAG 58:2	24047.62577	Aa	34498.28555	Ac	48194.43287	Ba	214590.6999	Aa	42226.57942	Ba	110353.1847	Ab
TAG 58:3	NA	Ab	NA	Ac	104697.1174	Ba	237693.6556	Aa	32687.09776	Ab	53697.94408	Ab

SI Table 17. (continuation) Relative abundance of lipids of *Chlamydomonas* sp. BR020 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
TAG 58:3.1	19943.3692	Ab	29467.20817	Ab	NA	Ac	NA	Ac	47993.94303	Aa	82704.3185	Aa
TAG 58:4	NA	Ab	NA	Aa	35732.62674	Aa	NA	Ba	34161.39289	Aa	NA	Ba
TAG 58:5	4003.143866	Aa	5605.441295	Ab	4823.243193	Ba	26993.89555	Aa	10565.8578	Ba	19232.33129	Aa
TAG 58:6	4970.048375	Aa	7078.831028	Ab	4502.740881	Ba	41402.54281	Aa	9696.501197	Ba	33282.29897	Aa
TAG 60:0	2689.854833	Ab	3924.586622	Aa	1984.40789	Ab	3468.421044	Aa	5288.805662	Aa	3587.224404	Aa
TAG 60:1	15915.28496	Aa	20703.23921	Ab	10675.62888	Ba	65920.27028	Aa	25056.97478	Ba	61594.81937	Aa
TAG 60:2	21637.74459	Aa	32050.27559	Ac	26157.60009	Ba	143989.9516	Aa	37555.83666	Ba	99950.63958	Ab
TAG 60:3	12585.35233	Ab	19180.24353	Ac	78982.24467	Ba	225202.2998	Aa	47426.56116	Aab	84589.42133	Ab
TAG 60:4	7448.499139	Aa	10704.8994	Ac	32664.65309	Ba	102795.1571	Aa	29566.74757	Ba	63786.57914	Ab
TAG 60:5	7269.402822	Aa	12076.09249	Ab	7889.988301	Ba	31249.90894	Aa	12394.65483	Aa	21156.09161	Aab
TAG 60:5.1	NA	Ab	NA	Ab	NA	Bb	17397.49062	Aa	13389.5604	Aa	19422.51284	Aa
TAG 60:6	2817.551198	Aa	4775.553491	Ab	3321.509933	Ba	28064.25731	Aa	9055.186995	Ba	28068.63183	Aa
FA 16:0	517360.9737	Ab	683305.4251	Ab	713342.5496	Ab	847982.8126	Ab	3083215.588	Aa	1996201.831	Ba
FA 16:2	162114.642	Ab	192469.2774	Ab	541036.6135	Ab	492493.9907	Ab	6601405.97	Aa	1623896.924	Ba
FA 16:3	332464.9559	Ab	380280.1386	Ab	1136403.449	Ab	1595229.791	Ab	11796995.95	Aa	4122491.277	Ba
FA 18:0	834515.6569	Ab	1090206.71	Aa	777583.4235	Ab	1173654.352	Aa	2377843.699	Aa	1720923.248	Ba
FA 18:1	8682238.352	Ab	10189635.06	Ab	10462149.13	Ab	12736701.36	Ab	43596604.08	Aa	31111381.98	Ba
FA 18:2	1081733.815	Ab	1506563.629	Ab	4000585.783	Ab	3225223.414	Ab	36537470.49	Aa	11428654.05	Ba
FA 18:3	3278094.403	Ab	4421514.632	Ab	10934367.39	Ab	13687227.1	Ab	94035324.39	Aa	48822965.06	Ba
FA 20:0	13338.9385	Ab	17781.40864	Ab	13022.24283	Ab	19536.70101	Ab	35165.02693	Aa	30414.45325	Aa
FA 20:1	30267.83017	Ab	39739.03131	Ab	37986.18918	Ab	46487.72758	Ab	164237.5835	Aa	115758.9296	Ba
FA 20:3	4647.337901	Ab	7079.766025	Ab	7744.966517	Ab	8242.893189	Ab	40814.8256	Aa	27947.5139	Ba
FA 22:0	13828.03452	Ab	19754.84663	Ab	11056.77059	Ab	17125.98056	Ab	31946.83797	Aa	26737.2832	Aa
FA 22:1	2076.577502	Ab	4749.441448	Aa	3711.168276	Ab	5045.541157	Aa	17514.76372	Aa	8416.018607	Ba
FA 24:0	26212.45394	Ab	39071.85878	Ab	30745.07031	Ab	38524.17898	Ab	124773.884	Aa	72978.71939	Ba
FA 24:1	909.7376008	Ab	1248.596309	Ab	1091.600741	Ab	1798.641432	Ab	7280.754553	Aa	3134.543053	Ba
FA 26:0	14216.36294	Ab	19558.03386	Aab	13489.39316	Ab	16707.63149	Ab	47819.61768	Aa	29505.1145	Ba
FA 28:0	4513.992976	Ab	6282.080303	Aa	3661.011042	Ab	5899.005031	Aa	12966.58692	Aa	8031.855683	Ba
FA 30:0	1705.360776	Bb	2779.051945	Aa	1397.888273	Ab	1942.589788	Aa	3610.68023	Aa	2464.626775	Ba

SI Table 18. Relative abundance of lipids of *Chlorella vulgaris* BR017 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
DGDG 32:0	33309.10611	Ab	45284.82892	Aa	50204.09006	Ab	36432.69552	Aa	123553.1942	Aa	43006.02036	Ba
DGDG 32:1	12154.68903	Ab	12503.86105	Aa	17528.75478	Ab	13116.04543	Aa	67362.71609	Aa	29868.85001	Ba
DGDG 32:2	25601.91407	Ab	35464.38054	Aa	51369.06973	Ab	21117.95417	Ba	161483.4241	Aa	52522.5256	Ba
DGDG 32:3	104791.2864	Ab	143415.3686	Ab	194556.6029	Ab	93292.43833	Ab	655496.2166	Aa	396598.8779	Ba
DGDG 32:3.1	65147.00701	Ab	91346.55698	Ab	100431.0129	Ab	143197.5123	Aab	254328.9482	Aa	189965.3177	Ba
DGDG 34:0	22088.24472	Ab	29185.17256	Aa	48044.64619	Aab	43853.8264	Aa	59448.29572	Aa	24716.00253	Ba
DGDG 34:1	1299846.951	Ab	1764856.025	Aa	1831224.027	Ab	1114974.534	Aa	4414748.019	Aa	1924015.456	Ba
DGDG 34:2	2614666.733	Ab	3431920.167	Aa	3208806.857	Aab	1739809.565	Bb	3971473.257	Aa	1775419.643	Bb
DGDG 34:3	2038362.67	Ab	2691220.952	Aa	2765472.507	Ab	2536780.225	Aa	4025995.817	Aa	2567957.689	Ba
DGDG 34:4	2982707.838	Ab	3708207.213	Aa	3260211.018	Ab	985546.6479	Bb	6735222.52	Aa	3504814.464	Ba
DGDG 34:5	7746123.234	Ab	9273897.041	Ab	11363592.47	Ab	7796035.599	Bb	20980682.34	Aa	13287931.54	Ba
DGDG 34:6	18253577.02	Ac	22191165.58	Ac	33973026.84	Ab	29037165.81	Ab	64355877.78	Aa	53728774.58	Aa
DGDG 36:2	17941.61444	Aa	NA	Ba	NA	Ab	NA	Aa	NA	Ab	NA	Aa
DGDG 36:4	193806.3095	Aa	247571.4947	Aa	210173.3783	Aa	91363.4206	Bb	287061.3081	Aa	200733.554	Ba
DGDG 36:5	526220.1862	Ab	661652.3284	Aa	608078.3102	Ab	310374.5259	Bb	1017515.601	Aa	803511.4043	Aa
DGDG 36:6	1111488.267	Ab	1404638.622	Ab	1243149.962	Ab	1073754.638	Ab	3071697.015	Aa	2115045.687	Ba
MGDG 34:1	44156.07938	Ac	62329.35944	Aa	321889.192	Ab	247345.9303	Aa	857736.7023	Aa	251910.9105	Ba
MGDG 34:2	NA	Ac	85433.4654	Aa	288551.9695	Ab	182831.3847	Aa	525111.1134	Aa	158720.457	Ba
MGDG 34:3	313752.2314	Ab	NA	Ab	660461.91	Ab	537393.7229	Aa	1211318.22	Aa	NA	Bb
MGDG 34:4	972744.3681	Ab	987563.1311	Ab	1002991.914	Ab	881200.7584	Ab	1648603.153	Aa	1212247.524	Aa
MGDG 34:4.1	NA	Bb	13082.71811	Aa	12184.92598	Aa	NA	Bb	15509.01487	Aa	NA	Bb
MGDG 34:5	8795.255502	Ab	13319.07044	Ab	15461.91066	Bb	41515.11268	Aa	45917.74116	Aa	38724.75835	Aa
MGDG 34:6	1448766.537	Ba	1368046.46	Aa	1309513.34	Ba	1946191.319	Aa	1639773.873	Ba	2295818.732	Aa
MGDG 34:7	240895.6753	Ab	375514.9857	Ab	566219.7608	Ab	628693.9014	Ab	1094646.369	Aa	1496602.558	Aa
MGDG 36:5	237479.9147	Aab	241438.2233	Aab	181658.8354	Ab	146091.9575	Ab	355533.9574	Aa	370107.0742	Aa
MGDG 36:5.1	41999.89973	Ab	36962.65021	Ab	30389.49834	Ab	46151.4366	Ab	55063.22402	Aa	59774.51355	Aa
MGDG 36:6	237203.7688	Ab	262707.9442	Ab	237613.4435	Ab	221443.0126	Ab	518284.7172	Aa	563193.093	Aa

SI Table 18. (continuation) Relative abundance of lipids of *Chlorella vulgaris* BR017 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
SQDG 32:0	1361316.709	Ab	1776788.29	Ab	1433648.696	Ab	1660571.281	Ab	3764112.653	Aa	2915133.574	Ba
SQDG 32:1	17003.25752	Ba	24992.62366	Aa	NA	Ab	NA	Ab	NA	Ab	NA	Ab
SQDG 32:2	53458.93338	Ab	63345.78765	Bb	64842.0887	Ab	30337.78122	Bb	251018.1252	Aa	180243.5561	Ba
SQDG 32:3	125342.5337	Ab	151725.4138	Ab	181010.0781	Ab	123281.2718	Ab	848757.4976	Aa	833556.2286	Aa
SQDG 34:1	361769.2736	Ab	517987.484	Ab	555084.8924	Ab	285741.104	Ab	2115133.325	Aa	1226458.39	Ba
SQDG 34:2	2961766.596	Bb	3758764.437	Aa	2586728.87	Ab	1340785.504	Bb	6548582.385	Aa	3052573.916	Ba
SQDG 34:3	2842834.494	Ab	3522019.913	Ab	3186215.979	Ab	3597846.107	Ab	7405279.758	Aa	6751976.92	Aa
SQDG 34:4	28380.94599	Ab	28133.99062	Ab	28054.81769	Ab	13167.43306	Ab	121415.1443	Aa	63996.92835	Ba
SQDG 34:4.1	NA	Ab	NA	Ac	NA	Bb	8626.005834	Ab	20963.37911	Ba	35494.76328	Aa
SQDG 34:6	144039.7013	Ac	155677.5327	Ab	380919.0816	Ab	141473.9641	Bb	1635116.151	Aa	894158.2063	Ba
DAG 34:1	111119.7426	Ab	139690.9118	Ab	537432.3719	Ba	946157.8792	Aa	176529.2226	Ab	120563.2051	Ab
DAG 34:2	91225.69971	Ac	104545.6134	Aab	228800.2337	Ab	NA	Bb	358045.8947	Aa	118857.414	Ba
DAG 34:3	66149.75776	Ab	70374.13213	Aa	135315.8858	Ab	137708.2457	Aa	301799.4941	Aa	127018.9756	Ba
DAG 34:4	102866.5905	Ab	86453.84054	Aa	162855.0015	Ab	96505.20575	Aa	280896.8634	Aa	104108.887	Ba
DAG 34:5	395016.3278	Ab	304884.8756	Bb	432990.0152	Ab	297744.8391	Bb	915379.8429	Aa	503258.5041	Ba
DAG 34:6	920143.6262	Ab	692249.5621	Ab	1198605.517	Ab	1112938.114	Ab	2518472.081	Aa	1999995.009	Aa
DAG 36:1	2690.264144	Ab	2538.91261	Ab	7336.920769	Aa	8994.690166	Aa	2414.93752	Ab	2554.086173	Ab
DAG 36:3	62199.93611	Ab	83668.99568	Ab	191764.8741	Aa	242612.8912	Aa	246649.657	Aab	136829.5267	Aab
DAG 36:4	89332.68735	Ab	86889.15071	Ab	211179.7477	Bab	409986.4165	Aa	385691.55	Aa	229543.6567	Aab
DAG 36:5	252737.3455	Ab	224445.9355	Aa	346956.642	Ab	335873.8561	Aa	916711.4093	Aa	473829.7869	Ba
DAG 36:6	175229.4648	Ab	158006.8165	Ab	229499.4148	Ab	264525.8783	Ab	689547.5919	Aa	498917.2795	Aa
LysoPC 16:0	133594.1283	Ab	256129.6271	Ab	834777.5154	Aa	275931.2213	Bb	883156.8232	Ba	1737610.345	Aa
LysoPC 16:0.1	8420.661345	Ac	10238.56996	Ac	30160.77478	Ab	30488.50709	Ab	46237.88081	Aa	62490.15188	Aa
LysoPC 16:2	6743.75469	Ab	9877.466566	Ab	16230.62167	Ab	4319.701879	Bb	45943.7055	Aa	30351.12926	Ba
LysoPC 16:3	39452.40043	Ab	84570.80147	Ab	68971.37724	Ab	58304.5693	Ab	458182.9707	Aa	203227.3324	Ba
LysoPC 18:1	189620.6315	Ab	249361.8806	Ab	458596.8754	Ab	517520.1084	Ab	1122671.906	Ba	1846572.963	Aa
LysoPC 18:1.1	1607032.188	Bc	2605206.4	Ac	4055758.825	Bb	5376131.622	Ab	6502064.963	Ba	8533274.748	Aa
LysoPC 18:2	101019.055	Ab	118436.2503	Ab	425115.9688	Aa	107957.293	Bb	643302.9248	Aa	983158.1266	Ba
LysoPC 18:2.1	96597.50269	Bb	207016.5101	Ab	137930.9804	Ab	111048.9198	Ab	565420.1767	Aa	341812.9985	Ba

SI Table 18. (continuation) Relative abundance of lipids of *Chlorella vulgaris* BR017 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
LysoPC 18:3	167798.2967	Ab	200319.3986	Ab	1004637.755	Aa	254421.3248	Bb	1696224.304	Ba	3004443.794	Aa
LysoPC 18:3.1	74303.53976	Bb	163202.6807	Ab	93828.28916	Ab	90891.61756	Ab	471708.9935	Aa	266284.2871	Ba
PC 32:0	3754.566816	Ac	3488.30926	Ab	11411.27839	Ab	11762.36303	Aa	17649.36891	Aa	9424.136096	Ba
PC 32:1	28071.78213	Ab	38621.23817	Ab	60353.56966	Ab	58262.6072	Ab	223040.2117	Aa	143985.4304	Ba
PC 32:1.1	79044.92068	Ab	101649.8617	Aa	137997.0969	Ab	72715.3537	Aa	803727.5804	Aa	252399.7403	Ba
PC 32:2	1566730.962	Ab	1902727.785	Ab	3274915.57	Ab	1890454.691	Ab	9560587.74	Aa	3860671.843	Ba
PC 32:3	5289808.234	Ab	6554729.087	Bb	9741159.009	Ab	6938921.041	Bb	29909430.6	Aa	21379165.67	Ba
PC 32:4	79528.24241	Ab	116992.2204	Aa	222912.7749	Ab	59471.08021	Ba	1719317.542	Aa	NA	Ba
PC 34:2	3773537.996	Ab	4699665.999	Aa	6939444.294	Ab	4989540.715	Aa	12364600.94	Aa	6690936.03	Ba
PC 34:3	3154472.372	Ab	3786624.657	Aa	5571650.739	Ab	3932337.966	Aa	18545848.67	Aa	8201748.513	Ba
PC 34:4	1707384.075	Ab	2429806.483	Aab	3514350.287	Ab	1499777.606	Ab	20949919.3	Aa	6499383.686	Ba
PC 34:5	3735738.036	Ab	5048162.733	Ab	11008939.54	Ab	5049021.097	Ab	51533347.77	Aa	19163126.23	Ba
PC 34:6	5318404.051	Ac	6576824.027	Ab	21346226.2	Ab	13778139.22	Ab	94168987.92	Aa	50034293.23	Ba
PC 36:1	334239.0635	Ac	301711.8486	Ac	950825.819	Ab	1119994.005	Ab	2221043.252	Aa	1641908.34	Ba
PC 36:2	11663273.81	Ac	10308228.59	Ac	26703059.82	Ab	33310442.3	Ab	68759969.9	Aa	62578214.83	Aa
PC 36:3	847185.1576	Ab	1034691.813	Ab	1840313.55	Ab	1242265.734	Ab	3442016.271	Aa	2493907.669	Aa
PC 36:3.1	1388887.54	Ac	1323732.308	Ac	4998794.472	Ab	6596384.284	Ab	12830863.62	Aa	12439600.43	Aa
PC 36:5	8725357.154	Ab	11498649.84	Ab	15119362.77	Ab	10601094.12	Ab	43507314.99	Aa	25975426.53	Ba
PC 36:6	7798832.361	Ab	9767869.139	Ab	13815661.71	Ab	11638356.25	Ab	52996373.36	Aa	32980692.38	Ba
PC 38:2	46233.65512	Bc	38872.99742	Ac	93317.6843	Bb	145262.9031	Ab	177620.1022	Ba	249028.0291	Aa
PC 38:3	41537.36888	Ab	52625.98071	Aa	79633.52575	Ab	42438.87152	Aa	176893.0027	Aa	74527.76812	Ba
PC 38:3.1	7122.41998	Ac	6328.410038	Ac	22655.20531	Ab	27312.98851	Ab	43492.99989	Aa	40014.43945	Aa
PE 32:1	280983.3257	Ac	211236.826	Ac	995847.5512	Aa	1283753.679	Aa	559022.3103	Ab	515580.6384	Ab
PE 34:2	2488583.169	Ac	2265353.336	Ac	6945358.291	Aa	7639176.264	Aa	5734673.966	Ab	4590589.783	Ab
PE 34:3	447543.6599	Aab	556002.951	Aa	326218.3832	Ab	258411.0851	Ab	604723.3494	Aa	345999.3579	Bab
PE 34:4	241000.9375	Ab	262579.751	Aa	188135.0874	Ab	131192.5614	Ab	438791.3524	Aa	201295.2276	Bab
PE 34:5	557892.5914	Ab	642296.7946	Aa	581959.6359	Ab	374662.3997	Aa	1074261.597	Aa	478177.5361	Ba
PE 34:6	464611.2851	Ab	558064.0046	Ab	903620.2412	Ab	676256.7749	Aab	2397533.683	Aa	1150930.36	Ba
PE 36:2	4257288.461	Ab	3665722.781	Ab	5390140.834	Aa	7192369.333	Aa	5152539.171	Aab	4971550.216	Aab

SI Table 18. (continuation) Relative abundance of lipids of *Chlorella vulgaris* BR017 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
PE 36:3	415527.9384	Ac	375545.2127	Ac	1315736.445	Aa	1690980.281	Aa	987482.1962	Ab	717353.0685	Ab
PE 36:4	753791.1136	Ab	855323.5955	Aa	494534.4531	Ab	339279.7905	Ab	1172266.426	Aa	491553.0843	Bab
PE 36:5	1920080.032	Ab	2387108.825	Aa	1706954.903	Ab	1233212.314	Ab	3388615.67	Aa	1689862.775	Bab
PE 36:6	1007134.199	Ab	1300553.432	Aa	1169351.706	Ab	917403.2733	Aa	2442735.036	Aa	1420027.859	Ba
PE 38:2	964852.6333	Ab	822889.1468	Ab	2789930.338	Aa	3249087.677	Aa	2364860.443	Aa	2254307.191	Aa
PE 38:3	121412.2445	Ac	113098.6785	Ac	701690.8904	Aa	844603.3194	Aa	419966.821	Ab	332802.1958	Ab
PE 40:2	138299.8051	Ac	122552.0388	Ac	410229.4898	Ab	511398.2351	Ab	1399503.301	Aa	1297017.279	Aa
PE 40:3	48419.41081	Ab	59231.93972	Ab	78971.72226	Ab	50859.79731	Ab	318296.2759	Aa	195454.8233	Ba
PE 40:4	67255.35631	Ab	82414.3091	Aab	84993.25585	Ab	55920.57448	Ab	303728.8207	Aa	134730.1683	Ba
PG 34:2	633949.5062	Ab	769646.1404	Aa	958955.9103	Ab	633220.8548	Ba	1534818.695	Aa	688756.8866	Ba
PG 34:3	635606.2275	Ab	811335.6008	Aa	955245.5415	Ab	734590.3636	Aa	2275450.06	Aa	1143726.571	Ba
PG 34:4	435519.4557	Ab	554175.8219	Ab	534894.1072	Ab	331564.6913	Ab	2360067.259	Aa	1280353.138	Ba
PG 36:2	1514881.415	Ac	1455172.346	Ac	2555835.099	Aa	3196051.645	Aa	2075652.401	Ab	2417559.207	Ab
PG 36:3	36139.74044	Ab	34141.87011	Ab	138091.1516	Aa	162583.1472	Aa	130444.9023	Aa	140152.4836	Aa
TAG 42:0	21595.69319	Aa	31879.11466	Ab	27148.75967	Ba	49777.66495	Aa	16637.94066	Aa	15547.72027	Ac
TAG 42:1	31644.7949	Aa	32984.97337	Ab	115503.1328	Ba	400434.032	Aa	11083.16155	Aa	14568.13475	Ab
TAG 42:2	3253.104966	Ab	3528.729995	Ab	14341.27288	Ba	36242.4051	Aa	NA	Ab	NA	Ab
TAG 44:0	62181.6741	Aab	77624.18433	Ab	79764.32378	Ba	153784.9256	Aa	27337.4787	Ab	32454.03025	Ac
TAG 44:1	212694.0226	Aab	244415.3449	Ab	1036454.555	Ba	3128823.094	Aa	24287.34112	Ab	29762.68258	Ab
TAG 44:2	21195.96474	Ab	23910.41327	Ab	112136.4796	Ba	278134.5379	Aa	NA	Ab	NA	Ab
TAG 46:0	164070.7213	Aab	191180.6859	Ab	257205.6338	Ba	452768.1557	Aa	71142.14711	Ab	72865.69328	Ab
TAG 46:1	1811882.945	Aab	2069300.328	Ab	7464796.406	Ba	22746471.75	Aa	49278.97359	Ab	76275.87395	Ab
TAG 46:2	197593.7316	Ab	203800.2115	Ab	1238399.103	Ba	2759826.449	Aa	NA	Ab	NA	Ab
TAG 46:2.1	117163.7113	Aab	116744.6398	Ab	584323.2925	Ba	1848616.215	Aa	28029.51708	Ab	39316.23383	Ab
TAG 46:3	17555.31777	Ab	17088.22227	Aa	126657.6877	Aa	NA	Bb	NA	Ac	NA	Ab
TAG 46:4	6484.468649	Ab	NA	Bc	22642.52372	Ba	33814.47739	Aa	4154.045413	Ab	6399.860326	Ab
TAG 48:0	398720.7137	Bb	471256.8734	Ab	592589.4198	Ba	886408.2937	Aa	180987.7996	Bc	205483.8247	Ac

SI Table 18. (continuation) Relative abundance of lipids of *Chlorella vulgaris* BR017 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
TAG 48:1	7662756.941	Aab	8475639.407	Ab	24899790.1	Ba	64963204.55	Aa	265360.1614	Ab	377587.4195	Ab
TAG 48:2	1201770.421	Ab	1369360.719	Ab	8965938.003	Ba	19155165.77	Aa	329055.7485	Ab	523581.2888	Ab
TAG 48:3	607892.5686	Aa	758404.031	Ab	1632364.107	Ba	6425684.369	Aa	702622.8094	Aa	1081553.463	Ab
TAG 48:4	87016.00099	Ab	104307.4114	Ab	337689.6748	Ba	950870.964	Aa	182223.7339	Aab	215163.1443	Ab
TAG 48:5	82067.26799	Aa	96926.86479	Ab	235589.999	Ba	761789.3992	Aa	163657.7039	Aa	134902.6724	Ab
TAG 48:6	51197.54493	Aa	59984.47103	Ab	134955.9501	Ba	608208.2583	Aa	141544.0405	Aa	111790.1763	Ab
TAG 48:7	10559.22124	Ab	12448.62293	Ab	23669.40383	Aab	37795.82194	Aa	37752.1962	Aa	20564.82013	Bab
TAG 48:8	11472.59473	Ab	14824.23366	Ab	21766.39606	Ab	40034.61034	Aa	53233.80344	Aa	25112.69926	Bab
TAG 48:9	6601.451362	Ab	7465.152072	Ab	13660.87345	Aab	30811.18255	Aab	40003.52917	Aa	31929.81213	Aa
TAG 50:0	331918.6449	Aa	373352.807	Ab	370357.8282	Ba	625285.395	Aa	125755.7146	Ab	141979.224	Ac
TAG 50:1	23590536.44	Aab	27238841.39	Ab	52024844.28	Ba	118474665.5	Aa	6726429.452	Ab	12318277.17	Ab
TAG 50:2	9410207.158	Ab	10415759.13	Ab	43666975.72	Ba	89839075.89	Aa	2874945.43	Ab	3924783.126	Ab
TAG 50:3	1665297.813	Ab	2052945.923	Ab	9322235.23	Ba	14905734.1	Aa	1907378.648	Ab	2753577.483	Ab
TAG 50:4	1351740.759	Aa	1685696.592	Ab	4316464.477	Ba	15989625.76	Aa	2122878.06	Aa	3355432.148	Ab
TAG 50:5	846226.967	Aa	1077026.626	Ab	2742447.528	Ba	8445745.359	Aa	1497523.524	Aa	1347282.398	Ab
TAG 50:6	666032.3695	Aa	795430.2767	Ab	2298638.595	Ba	9426528.011	Aa	1414683.676	Aa	1311744.419	Ab
TAG 50:7	144295.2765	Aa	159233.9615	Ab	377428.0315	Ba	886707.3192	Aa	470547.7564	Aa	228954.0835	Ab
TAG 50:8	172954.1405	Ab	182396.2916	Ab	329917.5417	Bab	652352.7914	Aa	591407.841	Aa	216082.549	Bb
TAG 50:9	165771.4016	Ab	153287.9196	Ab	275582.5136	Bb	630954.4137	Aa	726195.4371	Aa	298772.3792	Bb
TAG 52:0	193567.775	Aa	216179.1774	Ab	211326.5309	Ba	346835.2839	Aa	133724.2799	Aa	124875.1245	Ab
TAG 52:1	16107202.3	Aab	17070322.29	Ab	24301799.93	Ba	69496472.57	Aa	796237.8383	Ab	2189931.57	Ab
TAG 52:2	29144762.14	Ab	32858908.59	Ab	92654779.13	Ba	172473039.2	Aa	11418996.28	Ab	22884121.7	Ab
TAG 52:3	8993630.915	Ab	10859205.7	Ab	45286803.97	Ba	84829707.69	Aa	6555672.634	Ab	10852732.74	Ab
TAG 52:4	3463618.63	Ab	4450938.305	Ab	11527890.27	Ba	38784233.58	Aa	5681257.521	Aab	8623543.815	Ab
TAG 52:4.1	8787.801512	Ab	9130.665493	Aa	NA	Ac	NA	Ab	14050.99779	Aa	2859.360648	Ba
TAG 52:5	1586335.665	Ab	2014741.56	Ab	3666098.64	Ba	11894180.54	Aa	2443961.8	Aab	2129627.563	Ab
TAG 52:5.1	2869.547419	Ab	2532.237557	Ab	28261.12153	Ba	165414.3653	Aa	4316.035156	Ab	7294.71143	Ab
TAG 52:6	862398.7402	Aa	976516.7978	Ab	2631604.293	Ba	8394464.879	Aa	1477141.794	Aa	1554562.234	Ab
TAG 52:6.1	NA	Ab	NA	Ab	14943.62958	Ba	33526.32712	Aa	3768.548697	Ab	3447.180594	Ab

SI Table 18. (continuation) Relative abundance of lipids of *Chlorella vulgaris* BR017 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
TAG 52:7	985728.5223	Aa	839005.9022	Ab	2191625.686	Ba	7615206.544	Aa	1479760.599	Aa	1388987.18	Ab
TAG 52:8	625927.2209	Aa	674827.2727	Ab	1103810.214	Ba	1894599.71	Aa	1270059.1	Aa	779609.5776	Ab
TAG 52:9	638648.328	Ab	655785.7285	Ab	1023650.756	Bab	1930174.244	Aa	1413524.28	Aa	1163127.223	Ab
TAG 54:0	38846.53682	Aa	38509.64321	Aa	42794.46636	Aa	63877.23155	Aa	41534.06785	Aa	47990.46506	Aa
TAG 54:1	408613.0947	Aab	465504.8111	Ab	716147.8036	Ba	2745864.032	Aa	117181.4075	Ab	307552.1498	Ab
TAG 54:2	2190878.1	Ab	2492003.973	Ab	6651213.206	Ba	17192522.17	Aa	718241.2353	Ab	2224887.471	Ab
TAG 54:3	3737489.253	Ab	4965491.18	Ab	15059765.52	Ba	28847203.63	Aa	5019713.789	Ab	11096866.18	Ab
TAG 54:4	1814136.12	Aa	2387363.944	Ab	5851904.795	Ba	20410101.59	Aa	2575904.906	Aa	5704830.752	Ab
TAG 54:5	1897796.172	Aa	2654090.937	Ab	6700669.295	Ba	26169799.53	Aa	3369940.642	Aa	6713521.278	Ab
TAG 54:6	831852.7546	Aa	1182246.112	Ab	2846101.459	Ba	10199612.06	Aa	1633400.23	Aa	2178833.44	Ab
TAG 54:7	537862.675	Aa	708875.76	Ab	1466395.393	Ba	5669977.261	Aa	1215631.37	Aa	1258839.056	Ab
TAG 54:8	330115.2055	Aa	439479.4958	Ab	656397.0513	Ba	1579997.816	Aa	781027.0052	Aa	546276.8898	Ab
TAG 54:9	127802.2641	Ab	149665.9945	Ab	188767.444	Bab	493973.6804	Aa	339272.7859	Aa	281019.8166	Ab
TAG 56:0	26298.44151	Aa	25050.65914	Aa	24428.10577	Aa	38868.54893	Aa	32158.39498	Aa	35055.42173	Aa
TAG 56:1	47149.21924	Ab	49683.52855	Ab	114288.7693	Ba	401918.4259	Aa	20807.25726	Ab	66512.31791	Ab
TAG 56:2	224761.7775	Ab	272621.9163	Ab	803629.8886	Ba	2508327.008	Aa	65416.74104	Ab	208493.7098	Ab
TAG 56:3	312061.3007	Ab	401662.2301	Ab	1120325.514	Ba	2270033.101	Aa	156339.63	Ab	459258.1181	Ab
TAG 56:4	160326.6187	Ab	207667.4936	Ab	446855.9911	Ba	914169.4313	Aa	105252.1285	Ab	244905.2005	Ab
TAG 56:5	108576.5636	Aab	148339.7053	Ab	346310.1726	Ba	1017390.619	Aa	72685.37198	Ab	187425.4863	Ab
TAG 56:6	45547.33872	Ab	64299.90692	Ab	140764.6706	Ba	303615.0814	Aa	46709.88577	Ab	61844.36997	Ab
TAG 56:7	15597.21965	Aa	21862.29805	Ab	46557.4873	Ba	112851.1954	Aa	19060.53325	Aa	16802.30976	Ab
TAG 58:0	10994.18474	Ba	10649.85618	Aa	10605.56921	Ba	18930.39333	Aa	12465.87391	Ba	15491.65295	Aa
TAG 58:1	36017.50803	Ab	40013.49531	Ab	86655.71778	Ba	297101.0869	Aa	27605.04985	Ab	53894.48404	Ab
TAG 58:2	165027.4401	Aab	181852.8229	Ab	704254.7922	Ba	2163923.378	Aa	26640.03818	Ab	72403.97886	Ab
TAG 58:3	167131.3543	Ab	172916.7268	Ab	1616447.333	Ba	2935472.978	Aa	24821.5379	Ab	NA	Ab
TAG 58:3.1	NA	Ab	NA	Ab	NA	Ab	NA	Ab	26083.73197	Ba	46356.17288	Aa
TAG 58:4	49064.54179	Ab	52609.11374	Ab	706344.9161	Aa	848499.7555	Aa	15784.19404	Ab	NA	Ab
TAG 58:5	8203.044892	Ab	7901.901281	Ab	37931.24261	Ba	86759.73992	Aa	16468.79306	Ab	10784.84462	Ab
TAG 58:6	7271.02021	Ab	7399.943124	Ab	31991.59275	Ba	151385.9244	Aa	15509.71516	Aab	13516.54181	Ab

SI Table 18. (continuation) Relative abundance of lipids of *Chlorella vulgaris* BR017 strain grown under two different concentrations of rapamycin (0 and 5µM) in three growth time (0h, 24h and 48h). Different lowercase letters refer to statistical difference between times within the same rapamycin concentration. Capital letter refer to statistical difference between rapamycin concentrations in same time according to the Tukey test (P<0.05). Metabolite not detected is represented by NA.

Lipids	0h Control		0h 5µM rap		24h Control		24h 5µM rap		48h Control		48h 5µM rap	
TAG 60:0	3330.683312	Ab	2977.713601	Ab	5184.397348	Aa	5653.50148	Aa	3778.846639	Ab	4163.663576	Ab
TAG 60:1	19947.18621	Aa	23671.95997	Ab	50463.24144	Ba	154992.5795	Aa	20643.7941	Aa	40415.927	Ab
TAG 60:2	114187.8934	Aab	120639.2216	Ab	369173.1151	Ba	1135974.149	Aa	28194.79448	Ab	55621.15197	Ab
TAG 60:3	190849.8425	Ab	195319.8607	Ab	1297111.755	Ba	2941965.759	Aa	20069.96202	Ab	38258.53663	Ab
TAG 60:4	36454.18473	Ab	38436.57778	Ab	527080.0347	Aa	639294.0529	Aa	18607.37505	Ab	33591.28148	Ab
TAG 60:5	11676.84518	Ab	10987.53967	Ab	45048.38002	Ba	98279.21341	Aa	14853.12003	Ab	12892.25433	Ab
TAG 60:5.1	NA	Ab	NA	Ab	48514.91327	Ba	82386.51959	Aa	8580.216096	Ab	10907.00335	Ab
TAG 60:6	5986.21273	Ab	6672.742706	Ab	28058.7234	Ba	119396.5767	Aa	7366.238962	Ab	10876.12013	Ab
FA 16:0	454081.2202	Ab	642118.2684	Ab	1715127.862	Aa	2027802.714	Aa	2140396.696	Aa	1969654.046	Aa
FA 16:2	183024.0389	Ab	305270.9019	Ab	1216850.357	Ab	540204.7293	Ab	4388283.475	Aa	3238523.234	Aa
FA 16:3	275258.5359	Ab	436366.478	Ab	1923019.779	Ab	1620464.938	Ab	7812081.73	Aa	8332121.959	Aa
FA 18:0	637931.8324	Ab	835939.8527	Ab	1062208.81	Aa	1435338.58	Aa	1228945.948	Aa	1187920.22	Aa
FA 18:1	7973349.919	Ab	7899639.853	Ab	14700649.44	Aa	17340705.82	Aa	15696210.79	Aa	22279585.07	Aa
FA 18:2	1103098.138	Ab	1425306.569	Ab	7045891.283	Ab	3314767.514	Ab	21508729.08	Aa	17577943	Aa
FA 18:3	2362277.834	Ab	3124973.318	Ab	13349592.42	Ab	12458972.05	Ab	58449784.82	Aa	51330080.68	Aa
FA 20:0	14739.43295	Ab	15166.58268	Ab	35610.04782	Aa	45360.8524	Aa	24336.68025	Ab	23589.53837	Ab
FA 20:1	58378.36248	Ab	64910.9495	Ab	138263.0142	Aa	130567.4682	Aa	129573.0121	Aa	139453.0499	Aa
FA 20:3	5074.066827	Ac	5817.989642	Bc	11555.28716	Ab	7918.748455	Bb	22311.31331	Aa	16549.5463	Ba
FA 22:0	15641.61745	Ab	13939.01901	Ab	27342.64237	Aa	34411.09943	Aa	34084.32934	Aa	32833.73564	Aa
FA 22:1	3467.311938	Ab	4993.739918	Ab	14873.6684	Aa	12392.90113	Aa	9203.788421	Aa	10782.95852	Aa
FA 24:0	29508.15352	Ac	30763.46656	Ac	58864.84196	Ab	65897.09503	Ab	107109.6215	Aa	101843.0909	Aa
FA 24:1	2235.880002	Ab	2144.34259	Ab	10643.61547	Aa	11539.21584	Aa	4768.667917	Ab	2553.632589	Ab
FA 26:0	16118.30468	Ab	17302.97521	Ab	32323.0326	Aa	34948.52729	Aa	52085.91837	Aa	35287.00144	Aa
FA 28:0	4368.651476	Ab	5383.220836	Aa	5804.393811	Ab	6165.132789	Aa	10914.14594	Aa	7343.55538	Ba
FA 30:0	1815.495838	Ab	1848.003546	Ab	1769.797667	Aab	2300.517903	Aab	2899.340885	Aa	2646.255584	Aa