References


References


References


References


References


List of frequently used abbreviations, symbols and genes
2PG 2-phosphoglycerate
3PG 3-phosphoglycerate
ATP adenosine triphosphate
BCT1 ATP-dependent bicarbonate uptake system (high affinity, low flux)
bicA gene encoding sodium-dependent bicarbonate uptake system BicA
BicA sodium-dependent bicarbonate uptake system (low affinity, high flux)
CA carbonic anhydrase
CCM CO₂-concentrating mechanism
ccmR gene encoding transcriptional regulator CcmR
ccmR2 gene encoding transcriptional regulator CcmR2
cDNA complementary DNA, synthesized from messenger RNA
Ci inorganic carbon
Chl a chlorophyll a (pigment)
chpY (=cupA) gene encoding CO₂ hydration subunit of CO₂ uptake system NDH-I₃
chpX (=cupB) gene encoding CO₂ hydration subunit of CO₂ uptake system NDH-I₄
cmpA gene encoding bicarbonate-binding subunit of uptake system BCT1
CO₂(aq) carbon dioxide dissolved in water
CO₃²⁻ carbonate
DIC dissolved inorganic carbon
DOC dissolved organic carbon
HCO₃⁻ bicarbonate
gₖCO₂ CO₂ gas influx
gDNA genomic DNA
ftr1-4 genes encoding flavodiiron proteins, involved in oxidative stress protection
I/Iᵢᵣ/Iᵢₑₑᵣ irriadiance / incident irriadiance / irradiance penetrating through vessel
isiA gene encoding iron stress-induced protein
Kₐ₅ half-saturation constant
Kₜ solubility constant of CO₂ gas in water
MC microcystin (hepatotoxin)
mcyB microcystin synthetase gene
NADPH nicotinamide adenine dinucleotide phosphate
NDH-I₃ CO₂ uptake system (high affinity, low flux)
NDH-I₄ CO₂ uptake system (low affinity, high flux)
nhaS1-6 genes encoding sodium/proton antiporters
PAR photosynthetically active radiation, spectral range used for photosynthesis
pCO₂ partial pressure of CO₂
<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>PKS</td>
<td>polyketide synthetase</td>
</tr>
<tr>
<td>ppm</td>
<td>parts per million</td>
</tr>
<tr>
<td>PSI</td>
<td>photosystem I</td>
</tr>
<tr>
<td>PSII</td>
<td>photosystem II</td>
</tr>
<tr>
<td>rbcX</td>
<td>gene encoding RuBisCO chaperone</td>
</tr>
<tr>
<td>ROS</td>
<td>reactive oxygen species, chemically reactive molecules containing oxygen</td>
</tr>
<tr>
<td>RT-qPCR</td>
<td>reverse transcription quantitative polymerase chain reaction</td>
</tr>
<tr>
<td>RuBisCO</td>
<td>ribulose-1,5-bisphosphate carboxylase/oxygenase</td>
</tr>
<tr>
<td>sbtA</td>
<td>gene encoding bicarbonate uptake system SbtA (high affinity, low flux)</td>
</tr>
<tr>
<td>SbtA</td>
<td>sodium-dependent bicarbonate uptake system (high affinity, low flux)</td>
</tr>
<tr>
<td>sbtB</td>
<td>gene found downstream of sbtA, associated with sbtA</td>
</tr>
<tr>
<td>v</td>
<td>gas transfer velocity (piston velocity) across the air-water interface</td>
</tr>
</tbody>
</table>
Summary
Effects of rising CO$_2$ on the harmful cyanobacterium *Microcystis*

Harmful cyanobacteria (‘blue-green algae’) are notorious for causing worldwide ecological and economical problems in eutrophic lakes and reservoirs, where they can produce dense and often toxic blooms. Climate change is foreseen to have large effects on these photosynthetic microorganisms. Yet, while several studies have investigated effects of global warming on harmful cyanobacteria, the implications of rising CO$_2$ have received relatively little attention. Cyanobacteria are often assumed to be favored at low inorganic carbon conditions, because of the presence of an effective CO$_2$-concentrating mechanism (CCM) to fix CO$_2$. But how will they perform at elevated CO$_2$ levels? This thesis investigates the impact of elevated CO$_2$ on various strains of the ubiquitous harmful cyanobacterium *Microcystis aeruginosa*.

The following questions are addressed:

1) How variable are the CCMs within the genus *Microcystis*? (Chapter 2)
2) What are the adaptations of *Microcystis* to elevated CO$_2$? (Chapter 3)
3) What are the similarities and differences in CCM gene expression (1) among *Microcystis* strains, and (2) between *Microcystis* and other cyanobacteria? (Chapters 2 and 4)
4) How are the *Microcystis* CCM genes regulated in situ? (Chapter 6)
5) Can genetic variability of the *Microcystis* CCM cause strain-specific differences in growth rate at elevated CO$_2$ concentrations? (Chapters 2 and 4)
6) Does rising CO$_2$ affect the competition between different *Microcystis* strains, and if so, which strains will benefit most? (Chapter 5)
7) What are the effects of rising CO$_2$ on other harmful cyanobacteria? (Chapter 7)
8) Will rising CO$_2$ concentrations stimulate cyanobacterial blooms and make them more toxic? (Chapters 2, 3, 5 and 7)
9) Is potassium ion addition an effective method to combat harmful cyanobacterial blooms? (Chapter 8)

To investigate the first question, 20 *Microcystis* strains from different continents were studied at the gene level. Cyanobacteria often use a combination of CO$_2$ and bicarbonate uptake systems to import inorganic carbon (C$_i$). Genes encoding the two CO$_2$ uptake systems, the ATP-dependent bicarbonate transporter BCT1, the CO$_2$-fixing enzyme RuBisCO and carboxysomes (compartments containing RuBisCO) were detected in all 20 *Microcystis* strains. Eight of the analyzed strains also contain the genes *bicA* and *sbtA*, encoding the sodium-dependent bicarbonate uptake systems BicA and SbtA, respectively. BicA has a low affinity for bicarbonate...
Summary

and high flux rate, whereas SbtA has a high affinity and low flux rate. Affinity refers to the effectiveness of bicarbonate uptake at low bicarbonate concentrations, whereas the flux rate refers to the bicarbonate uptake rate at high bicarbonate concentrations. A unique feature of these *Microcystis* strains is that the genes *bicA* and *sbtA* are present in one operon and are co-transcribed. In contrast to these C₅ uptake generalists, 12 of the 20 analyzed *Microcystis* strains lack either the *bicA* or *sbtA* gene. The results show that *Microcystis* strains have adapted differently to the wide natural variation in CO₂ concentrations.

The second question was answered in chemostat experiments with *Microcystis* PCC 7806. Changes in the transcriptome (expression of all genes in the genome) were monitored from 45 minutes up to 2 weeks after increasing the CO₂ concentration. Surprisingly, elevated CO₂ affected the expression of only a small number of genes. The bicarbonate uptake genes were downregulated at elevated CO₂. Other regulated genes were involved in the stress response of the cells, control of the cellular C/N ratio, and the production of two weakly characterized polyketides. Expression of genes encoding the CO₂ uptake systems, carboxysome, RuBisCO, photosystems, C metabolism and microcystin synthetases did not respond significantly to elevated CO₂.

The third question was answered by exposing batch cultures of six different *Microcystis* strains to elevated CO₂. The high-affinity gene *cmpA* (encoding a subunit of the bicarbonate uptake system BCT1) was downregulated at elevated CO₂ in all strains. Most strains also downregulated *bicA* and *sbtA* at elevated CO₂, but two strains showed constitutive expression of these bicarbonate uptake genes. The high-flux BicA uptake system remained active at high CO₂ levels in all strains containing the *bicA* gene. Interestingly, expression of the high- and low-affinity CO₂ uptake genes of *Microcystis* was not affected by elevated CO₂, which deviates from most other cyanobacterial species that downregulate the high-affinity CO₂ uptake genes. The carboxysome and RuBisCO genes were also constitutively expressed in all *Microcystis* strains. We discovered a new CCM transcriptional regulator gene (*ccmR2*), located upstream of the *bicA*-sbtA operon. Both *ccmR2* and the *bicA*-sbtA operon are so far unique for *Microcystis*.

The fourth question was answered with an *in situ* study at Lake Kennemermeer (the Netherlands) of a cyanobacterial bloom that contained *Microcystis*. The lake showed large diel fluctuations in bicarbonate, pH and dissolved oxygen as a consequence of the photosynthetic activity of the bloom. Expression of the bicarbonate uptake genes of *Microcystis* was tuned to the diel variation in bicarbonate concentration. In contrast, expression of the CO₂ uptake genes was constitutive, and expression of the RuBisCO and carboxysomal genes was slightly increased during nighttime.
To address the fifth question, a series of laboratory experiments were carried out in batch culture at different CO$_2$ concentrations. The results showed that strains with the high-affinity gene $sbtA$ perform better at low CO$_2$ concentrations, strains with the high-flux gene $bicA$ perform better at high CO$_2$ concentrations, and $bicA$+$sbtA$ strains containing both genes perform well across the entire range of CO$_2$ conditions investigated.

The sixth question was addressed by investigating mixtures with multiple Microcystis strains in laboratory competition experiments and a lake study. The competition experiments and lake study both showed that strains with the high-flux gene $bicA$ have a selective advantage at elevated CO$_2$ levels. These results provide laboratory and field evidence that changes in CO$_2$ availability induce rapid adaptive changes in the genotype composition of harmful cyanobacterial blooms. Hence, future cyanobacterial blooms may have a genetic composition that differs from contemporary blooms.

The seventh question was answered by analyzing recently sequenced genomes of other harmful cyanobacteria, including Anabaena, Aphanizomenon and Planktothrix strains. These cyanobacteria also showed intraspecific variation in the presence of the $bicA$ and $sbtA$ genes, similar to Microcystis, suggesting that they are well adapted to a wide range of CO$_2$ conditions. However, in Anabaena, Aphanizomenon and Planktothrix, $bicA$ and $sbtA$ are not organized in one operon, and in some strains both $bicA$ and $sbtA$ are absent. Presumably, these harmful cyanobacteria display a similar phenotypic variation as Microcystis, with a selective advantage for strains with the high-affinity uptake systems SbtA and/or BCT1 at low CO$_2$ conditions and a selective advantage for strains with the high-flux uptake system BicA at high CO$_2$ conditions.

To address the eighth question, it was shown that there was no direct connection between the presence of the CO$_2$ uptake genes $bicA$ or $sbtA$ and the microcystin synthetase genes. In chemostat experiments with Microcystis PCC 7806, elevated CO$_2$ levels led to a shift from carbon- to light-limited conditions. The strain contained ~2.5 times more unbound microcystins per cell at elevated CO$_2$, indicating that the cells can become more toxic at elevated CO$_2$ levels. Biomass of this strain increased strongly at elevated CO$_2$, suggesting that cyanobacterial blooms will intensify in eutrophic lakes. Furthermore, the dry weight of the cells was reduced twofold, indicating that elevated CO$_2$ can promote buoyancy of the cells, and thus scum layer formation in lakes. Hence, elevated CO$_2$ is foreseen to worsen the problems with Microcystis blooms in eutrophic lakes.

The ninth question was answered by investigating the potassium ion sensitivity of selected laboratory Microcystis strains. Strain PCC 7806, originating from brackish water, was not affected by the increased potassium ion concentration, while the growth of two freshwater Microcystis strains was strongly reduced. The potassium ion sensitivity of the freshwater strains was linked to the absence of specific salt tolerance genes. These results show that the salt
tolerance and potassium sensitivity of Microcystis differ between strains. Hence, on the short run, potassium ion addition might be a successful remediation strategy to combat Microcystis blooms in freshwater lakes, but over time more tolerant Microcystis strains or other cyanobacteria are likely to become dominant.

This thesis contributes to a better understanding of how harmful cyanobacteria respond to climate change. The results show how cyanobacteria subtly adjust their cells at the molecular and physiological level to changes in C₄ availability. Furthermore, the results demonstrate how genetic diversity in the C₄ uptake systems provide cyanobacteria with the potential for rapid microevolutionary adaptation to changes in CO₂ conditions, with a selective advantage for strains with the high-flux bicarbonate uptake gene bicA at elevated CO₂ levels. Hence, one of the key lessons of this work is that future studies of climate change effects should keep in mind the large genetic and physiological variation within species. In total, the results indicate that a further rise of the atmospheric CO₂ concentration is likely to increase the frequency and intensity of cyanobacterial blooms in eutrophic waters, and possibly may also increase their toxicity. The predicted intensification of cyanobacterial blooms should be countered by the reduction of CO₂ emissions and the development of effective methods to combat and prevent harmful cyanobacterial blooms.
Samenvatting
Effecten van stijgend CO₂ op de schadelijke cyanobacterie *Microcystis*

Schadelijke cyanobacteriën (‘blauwalgen’) zijn bekende veroorzakers van wereldwijde ecologische en economische problemen in oppervlaktewaterr zijn zoals voedselrijke meren, waar ze dichte en vaak toxische bloeien kunnen vormen. Het is voorzien dat klimaatverandering grote effecten zal hebben op deze fotosynthetische microorganismen. Terwijl verschillende studies de effecten van stijgende temperaturen hebben onderzocht, hebben de mogelijke gevolgen van stijgende CO₂-concentraties tot nog toe weinig aandacht gekregen. Vaak wordt aangenomen dat cyanobacteriën voordeel hebben bij lage CO₂-condities, door de aanwezigheid van een effectief CO₂-concentreermechanisme (CCM) om CO₂ te fixeren. Maar hoe presten ze bij verhoogde CO₂-niveaus? Dit proefschrift onderzoekt de effecten van stijgende CO₂-concentraties op verschillende stammen van de wijdverspreide schadelijke cyanobacterie *Microcystis aeruginosa*.

De volgende vragen worden behandeld:

1) Hoe variabel zijn de CCM’s binnen het genus *Microcystis*? (Hoofdstuk 2)
2) Wat zijn de aanpassingen van *Microcystis* bij verhoogde CO₂-concentraties? (Hoofdstuk 3)
3) Wat zijn de overeenkomsten en verschillen in CCM-genexpressie (1) tussen *Microcystis* stammen onderling, en (2) tussen *Microcystis* en andere cyanobacteriën? (Hoofdstukken 2 en 4)
4) Hoe worden de CCM-genen van *Microcystis* gereguleerd? (Hoofdstuk 6)
5) Kan genetische variatie in de CCM’s leiden tot verschillen in groeisnelheid van *Microcystis* stammen bij verhoogde CO₂-concentraties? (Hoofdstukken 2 en 4)
6) Heeft stijgende CO₂ invloed op de competitie tussen verschillende *Microcystis* stammen, en zo ja, welke stammen hebben het meeste voordeel? (Hoofdstuk 5)
7) Wat zijn de effecten van stijgend CO₂ op andere schadelijke cyanobacteriën? (Hoofdstuk 7)
8) Zullen stijgende CO₂-concentraties bloeien van schadelijke cyanobacteriën stimuleren en hun toxiciteit verhogen? (Hoofdstukken 2, 3, 5 en 7)
9) Is toevoeging van kaliumionen een effectieve methode om schadelijke cyanobacteriën te bestrijden? (Hoofdstuk 8)

Om de eerste vraag te onderzoeken zijn 20 *Microcystis* stammen uit verschillende delen van de wereld op genniveau onderzocht. Cyanobacteriën gebruiken vaak een combinatie van CO₂- en bicarbonaat-opnamesystemen om anorganische koolstof (Cₐ) te importeren in hun cellen. Alle
20 stammen bevatten genen die coderen voor de twee CO₂-opnamesystemen, de ATP-afhankelijke bicarbonaattransporter BCT1, het CO₂-fixatie-enzym RuBisCO en carboxyzomen (compartimenten die RuBisCO bevatten). Acht van de onderzochte stammen hadden ook de genen bicA en sbtA, die coderen voor de natrium-afhankelijke bicarbonaatopnamesystemen BicA en SbtA. BicA heeft een lage affiniteit voor bicarbonaat en een hoge opnamesnelheid, terwijl SbtA een hoge affiniteit heeft en een lage opnamesnelheid. Met affiniteit wordt hier bedoeld de effectiviteit van bicarbonaatopname bij lage bicarbonaatconcentraties, terwijl de opnamesnelheid refereert naar de bicarbonaatopname bij hoge bicarbonaatconcentraties. Een unieke eigenschap van deze Microcystis stammen is dat de genen bicA en sbtA zich bevinden op hetzelfde operon en dus gezamenlijk worden getranscribeerd (co-transcriptie). In tegenstelling tot deze Ci-opnamegeneralisten, misten 12 van de 20 Microcystis stammen het bicA of sbtA gen. De resultaten laten zien dat Microcystis stammen zich op verschillende wijze hebben aangepast aan de natuurlijke variatie in CO₂-concentraties.

De tweede vraag is beantwoord met behulp van chemostaatexperimenten met Microcystis PCC 7806. Veranderingen in het transcriptoom (expressie van alle genen in het genoom) van deze stam werden bekeken van 45 minuten tot 2 weken na het verhogen van de CO₂-concentratie. De verhoogde CO₂-concentratie had slechts effect op de expressie van een verrassend klein aantal genen. De bicarbonaatopnamegenen waren omlaag gereguleerd bij verhoogde CO₂. Andere gereguleerde genen waren betrokken bij de stress respons van cellen, controle van de cellulaire C/N ratio en de productie van twee nader te karakteriseren polyketides. De verhoogde CO₂-concentratie leidde niet tot significante veranderingen in genexpressie van de CO₂-opnamesystemen, het carboxysoom, RuBisCO, de fotosystemen, het C metabolisme en de microcystine synthetases.

De vierde vraag is beantwoord met een veldstudie in het Kennemermeer (Nederland) van een cyanobacteriële bloei met *Microcystis*. Het meer vertoonde grote dagelijkse schommelingen in bicarbonaat, pH en opgelost zuurstof als een gevolg van de fotosynthese-activiteit van de bloei. Expressie van de bicarbonaatopnamegenen van *Microcystis* was afgestemd op de dagelijkse variatie in de bicarbonaatconcentratie. Expressie van de CO₂-opnamegenen vertoonde echter geen dagelijkse variatie en expressie van de RuBisCO- en carboxysoomgenen was iets verhoogd tijdens de nacht.

Om de vijfde vraag te onderzoeken zijn een serie van laboratoriumexperimenten uitgevoerd in batch-culturen bij verschillende CO₂-concentraties. De resultaten laten zien dat stammen met het hoge-affiniteit-gen *sbtA* beter presteren bij lage Cᵣ-concentraties, stammen met het hogesnelheids-gen *bicA* beter presteren bij hoge Cᵣ-concentraties, terwijl stammen die beschikken over beide genen goed presteren over het hele bereik van onderzochte Cᵣ-condities.

De zesde vraag is onderzocht door mengsels van verschillende *Microcystis* stammen te bestuderen in laboratorium competitie-experimenten en in een veldstudie van een cyanobacteriële bloei in een eutroof meer. De competitie-experimenten en de veldstudie laten beide zien dat stammen met het hogesnelheids-gen *bicA* een selectief voordeel hebben bij verhoogde Cᵣ-concentraties. De resultaten leveren zowel experimenteel als observationeel bewijs dat veranderingen in de Cᵣ beschikbaarheid leiden tot snelle adaptieve veranderingen in de genotypesamenstelling van schadelijke cyanobacteriën. Dit suggereert dat cyanobacteriële bloeien in de toekomst waarschijnlijk een genetische samenstelling zullen hebben die verschilt van de huidige bloeien.


De achtste vraag is beantwoord door aan te tonen dat er geen direct verband is tussen de aanwezigheid van de Cᵣ-opnamegenen *bicA* of *sbtA* en de microcystine-synthetase-genen. In chemostaatexperimenten met *Microcystis* PCC 7806 leidde verhoogde CO₂-concentraties tot een verschuiving van koolstof-gelimiteerde naar licht-gelimiteerde condities. De stam bevatte ~2.5 keer meer ongebonden microcystine per cel bij verhoogde CO₂-concentraties, wat
aangeeft dat de cellen toxischer kunnen worden bij stijging van het CO₂-niveau. De biomassa van de stam was sterk toegenomen bij verhoogde CO₂-concentraties, wat suggereert dat cyanobacteriële bloeien in eutrofe meren intenser worden. Daarnaast was het drooggewicht van de cellen gehalveerd, wat doet vermoeden dat verhoogde CO₂-concentraties het drijfvermogen van cellen kan bevorderen en daarmee de vorming van drijflagen in meren kan stimuleren. Deze resultaten geven aan dat stijgende CO₂-concentraties de problemen met Microcystis in eutrofe meren waarschijnlijk zullen verergeren.

De negende vraag is beantwoord door onderzoek naar de kaliumgevoeligheid van geselecteerde Microcystis stammen. Stam PCC 7806, die oorspronkelijk is geïsoleerd uit brak water, werd niet beïnvloed door verhoogde kalium concentraties, terwijl de groei van twee zoetwater Microcystis stammen sterk gereduceerd werd. De kaliumgevoeligheid van de zoetwater stammen lijkt samen te hangen met de afwezigheid van specifieke genen betrokken bij zoutwatertolerantie. Dit laat zien dat Microcystis stammen verschillen in hun zoutwatertolerantie en kaliumgevoeligheid. Het gevolg is dat kaliumtoevoeging op korte termijn een succesvolle beheersmethode kan zijn om Microcystis bloeien in zoet water te bestrijden, maar dat op de langere termijn waarschijnlijk minder kaliumgevoelige Microcystis stammen of andere tolerante cyanobacteriën de dominantie zullen overnemen.

Dit proefschrift draagt bij aan een beter begrip van hoe schadelijke cyanobacteriën reageren op klimaatverandering. De resultaten laten zien hoe cyanobacteriën hun cel op moleculair en fysiologisch niveau op subtiele wijze kunnen aanpassen aan de C₄ beschikbaarheid. Ook laten de resultaten zien dat de genetische diversiteit in C₄-opnamesystemen van cyanobacteriën kan leiden tot een snelle micro-evolutie, waarbij de genotype samenstelling van de bloei zich aanpast aan veranderingen in de CO₂-concentratie. Hierbij hebben stammen met het hogeneltigheds-bicarbonaatopnamegena bicA een selectief voordeel bij hoge C₄-concentraties. Een van de belangrijkste lessen van dit werk is daarom dat toekomstige studies naar de effecten van klimaatsverandering attent moeten zijn op de genetische en fysiologische variatie binnen soorten. Alles samenvattend geven de resultaten aan dat verdere stijging van de CO₂-concentratie waarschijnlijk zal leiden tot een toenemen van de frequentie en intensiteit van cyanobacteriële bloeien in eutrofe wateren, en mogelijk ook de toxiciteit van deze bloeien zal verhogen. De voorspelde toename van cyanobacteriële bloeien zou kunnen worden beperkt door reductie van de CO₂-uitstoot en door de verdere ontwikkeling van effectieve methoden om schadelijke cyanobacteriën te bestrijden.
After several years of hard work it is finally done! Time went by very fast and so much changed since I started working here at the Science Park of Amsterdam in February 2011. I really enjoyed being part of the Aquatic Microbiology (AMB) group and I learned a lot. Yet, I could not have done the work presented in my thesis without the help of several other people. Also many people made my stay at the University of Amsterdam more pleasant, or supported me outside working hours.

First I would like to thank Jef. As my promoter, supervisor of the TOP project and group leader, you guided my research into the right direction and I really learned a lot from you. With my molecular background, ecology was a relatively new aspect for me, and I thank you for introducing me to this field. I also admire your aim for perfection, and your enthusiasm for and dedication to the research of this thesis.

Of course I also want to thank Hans. As my co-promoter and daily supervisor, we had a lot of meetings and discussions. I thank you for introducing me to the worlds of cyanobacteria and photosynthesis. I really like that you granted me a lot of freedom during the last years. Your biochemistry background was very useful for the fine-tuning of experiments and for bright interpretations of results, and your large network of people also proved to be very useful. You really were a source of inspiration during the project.

Next, I would like to thank Jolanda. In the beginning of the project I learned a lot from you about Microcystis and inorganic carbon chemistry. Although we were both involved in the TOP project, theoretical modeling and molecular work in the lab did not always overlap. However, during several occasions exchanging knowledge proved to be very useful.

I am also grateful to Pieter and Bas. Without you, the labs would turn into chaos. I know that sometimes I asked for seemingly impossibly things, but in the end everything turned out fine. I really enjoyed the fieldwork in 2013 with you and other colleagues, especially the adventures with the lab boat (and in early stages the Intertoys boat).

I also want to thank Amanda. We started with our PhD at about the same time at the AMB group. Although we worked on very different projects, parts of our research sometimes overlapped and we could help each other out. Your presence in the ‘PhD room’ and in the canteen was really enjoyable. The after-work activities together with other people from the group were also really fun. I will definitely miss you and the Thanksgiving dinners on your house boat!
Next I would like to thank my former master students, Serena, Robert and Dennis. I thank Serena for all the hard work and many analyses during the chemostat experiment with Microcystis PCC 7806. Thanks to your accuracy and positive spirit, the experiment really was a success. I thank Robert for all the efforts during the fieldwork in 2013. We set out with good and bad weather, and we sometimes encountered lakes without blooms, and other times lakes with a stinky Microcystis scum layer, dead fish and occasionally even a dead rabbit. Especially the 24-hour experiment was hard work with hardly any sleep, but in the end it was also quite fun and the results turned out to be really nice. I thank Dennis for maintaining and analyzing numerous Microcystis cultures and generating a ton of data. Your organizational skills and persistence really made this part of the research a success. I wish you all success in your future lives.

I want to thank Merijn and Jason for the pleasant collaborations during the last years. I would also like to thank the other (former) members of the AMB group, Gerard, Petra, Maayke, Pascale, Corrien, Michael, Elisa, Quan-Xing, Fleur, Anouk, Verena, Joost, Suzanne, Dina, Ruben, Tom V, Tom B, Veerle, Emily, Lex, Muhe, Catarina, Anne-Catherine, Charlotte, Cherel, Tim B, Tim P, Erik, Estelle, Qian, and students that did an internship in the group, for support during the project and the pleasant time during and after work hours. The AMB group has really changed and expanded a lot since I started. I really enjoyed the visits to the Polder and Brouwerij ‘t IJ, other ‘borrels’, the soccer/volleyball during summer days after work, and the stories or discussions during lunch time. I am sure I will see several of you around in the future.

I would like to thank the Netherlands Organisation for Scientific Research (NWO) for funding this project. I would like to thank Leo Hoitinga for assistance with the analysis of the numerous DIC samples. I want to express my gratitude to Gertjan Bon of the UvA glass workshop for constructing several essential glass components for the experiments, including the large 1m columns for the NaOH and silica pellets, the chemostat vessels, and the glass O$_2$ optode vessels. It really takes great skill to create these glass items.

I would like to thank my previous classmates of Life Science & Technology, Geert, Martijn, Bas, Régis, Ruben and the mathematician Floris, for the amusing “Halve Liter Woensdag” gatherings, which kept me going. I would like to thank the people of the Slagwerkgroep de Vliegende Hollander Terneuzen for the fun times on Friday evenings in the early phase of my PhD. I would like to thank my housemates for making my stay in Leiden more pleasant. I would like to thank my family, Menno, Mieke, Nydia, Emanuel, as well as my grandparents, for their support. Finally, I would like to thank Deborah for support during the last phase of my PhD and making my life more meaningful.
Curriculum Vitae
Giovanni Sandrini was born on the 16th of June 1986, in Terneuzen, the Netherlands. After completing secondary school at the Zeldenrust-Steelant College in Terneuzen in 2004, he completed the bachelor and master program of Life Science & Technology organized by a collaboration between Leiden University and Delft University of Technology. During his bachelor internship he worked on the isolation and genetic analysis of novel streptomycetes from soil samples, in the Microbial Development group of prof. dr. Gilles van Wezel at Leiden University. During his masters he did his industrial internship at the Netherlands Organisation for Applied Scientific Research (TNO) in Delft, in the group of dr. Harald J. Ruijssenaars, where he used genetic engineering on the solvent tolerant soil bacterium *Pseudomonas putida* S12 to allow it to grow on lignocellulose hydrolysate. He did his master research internship at the nidrovirus group of prof. dr. Eric J. Snijder, at the Leiden University Medical Center (LUMC), under supervision of dr. Clara C. Poshuma and dr. Sjoerd van den Worm, where he investigated the presence of an RNA proofreading mechanism in coronaviruses. He graduated in 2010, with the major Functional Genomics. Early 2011, he started his PhD in the group of Aquatic Microbiology of prof. dr. Jef Huisman at the University of Amsterdam, under supervision of dr. Hans C.P. Matthijs. The work of his PhD is described in this thesis and resulted in several publications. He also presented the results of this thesis at national and international conferences.
Curriculum Vitae

Publications


Sandrini G, Ji X, Verspagen JMH, Tann RP, Slot PC, Luimstra VM, Schuurmans JM, Matthijs HCP, Huisman J. Rapid microevolutionary adaptation of harmful cyanobacteria to changes in CO₂ availability. (submitted manuscript)

Sandrini G, Tann RP, Schuurmans JM, Van Beusekom SAM, Matthijs HCP, Huisman J. Diel variation of gene expression of the CO₂-concentrating mechanism during a harmful cyanobacterial bloom. (submitted manuscript)


Attended conferences

ESF-EMBO symposium on Molecular Bioenergetics of Cyanobacteria: From Cells to Community. Sant Feliu de Guixols, Spain, April 2011.


9th European Workshop on the Molecular Biology of Cyanobacteria. Texel, the Netherlands, September 2014.

15th International Symposium on Phototrophic Prokaryotes. Tübingen, Germany, August 2015.