



MATHEMATISCH-NATURWISSENSCHAFTLICHE FAKULTÄT

INSTITUT FÜR BIOCHEMIE UND BIOLOGIE

DISSERTATION

ZUM ERWERB DES AKADEMISCHEN GRADES

doctor rerum naturalium

**Implications of Microcystin Production in
Microcystis aeruginosa PCC 7806**

vorgelegt von

Sven Meißner

geboren am

10.11.1981 in Berlin

Potsdam-Golm, 30.09.2014

This work is licensed under a Creative Commons License:
Attribution – Share Alike 4.0 International
To view a copy of this license visit
<http://creativecommons.org/licenses/by-sa/4.0/>

Published online at the
Institutional Repository of the University of Potsdam:
URN [urn:nbn:de:kobv:517-opus4-75199](http://nbn-resolving.de/urn:nbn:de:kobv:517-opus4-75199)
<http://nbn-resolving.de/urn:nbn:de:kobv:517-opus4-75199>

Erklärung

Hiermit erkläre ich, die vorliegende Arbeit eigenständig verfasst und keine anderen als die angegebenen Hilfsmittel und Quellen benutzt zu haben.

Potsdam-Golm, den 30. September 2014

Contents

Summary	vi
1 General Introduction	1
1.1 Cyanobacteria	1
1.2 Formation of freshwater blooms by cyanobacteria	2
1.3 Photoprotective and antioxidant mechanisms	4
1.4 Carbon concentrating mechanism (CCM)	5
1.5 <i>Microcystis aeruginosa</i>	7
1.6 Toxin production by cyanobacteria	8
1.7 Microcystin and its synthesis	10
1.8 Toxicity mechanism of microcystin-LR	13
1.9 Eco-physiological aspects of microcystin production	13
1.10 Microcystin interaction with proteins	16
1.11 Aim of the study	18
2 On the Significance of Microcystin Conjugate Formation	19
2.1 Abstract	20

2.2	Introduction	21
2.3	Methods	22
2.3.1	Cultivation of cyanobacteria	22
2.3.2	High light experiment	23
2.3.3	Field samples	23
2.3.4	Microcystin extraction	24
2.3.5	Microcystin quantification by LC-MS	24
2.3.6	ELISA	25
2.3.7	Sample preparation for total microcystin quantification	25
2.3.8	SDS-PAGE and Western blot analysis	26
2.3.9	Dot blot analysis	26
2.3.10	Data analysis and evaluation	27
2.3.11	Immuno-fluorescence microscopy (IFM)	27
2.3.12	RubisCO purification and analysis	28
2.4	Results	29
2.4.1	Microcystin quantification in methanol extracts	29
2.4.2	Immunological quantification of total cellular microcystin	30
2.4.3	RbcL is a major target of microcystin interaction	32
2.4.4	Conserved microcystin-protein interaction mechanism	35
2.4.5	Microcystin quantification in field samples	35
2.4.6	Immuno-fluorescence microscopy (IFM)	37
2.5	Discussion	40
2.5.1	Membrane-based quantification of total microcystin	40
2.5.2	Microcystin production is induced by high light	41

2.5.3	Microcystin-protein interaction	41
2.5.4	Biological implications	44
2.5.5	Immuno-fluorescence detection of toxic colonies	47
2.5.6	Open questions	48
3	The Metabolic Adaptation of <i>Microcystis</i> to High Light is Affected by Microcystin and Broadly Different in <i>Synechocystis</i>	49
3.1	Abstract	50
3.2	Introduction	51
3.3	Methods	52
3.3.1	Strains and cultivation	52
3.3.2	High light exposition	52
3.3.3	Glycogen quantification	53
3.3.4	Estimation of cyanophycin content	53
3.3.5	Electron microscopy	54
3.3.6	Sample preparation for GC/MS	55
3.3.7	GC/MS data processing and analysis	56
3.3.8	Statistical analyses and visualization	56
3.4	Results	57
3.4.1	High light, oxygen evolution and medium pH	57
3.4.2	High light induced metabolic differences between strains	58
3.4.3	Central carbon pathway metabolites	62
3.4.4	Amino acids	64
3.4.5	Photorespiration	65
3.4.6	Compatible solutes	68

3.4.7	Quantification of storage compounds	68
3.5	Discussion	73
3.5.1	High light experiment	73
3.5.2	Net photosynthetic activity	74
3.5.3	High light exposition revealed strain specific metabolic differences	76
3.5.4	Central carbon pathway metabolites	77
3.5.5	TCA metabolism	78
3.5.6	Cyanobacterial C4 characteristics	79
3.5.7	Amino acid metabolism	81
3.5.8	Photorespiration	85
3.5.9	Conclusions	87
3.5.10	Limitations and perspectives	89
4	General Discussion & Outlook	93
4.1	Ecological aspects of microcystin production	94
4.2	High light and microcystin	94
4.3	Microcystin and high pH	95
4.4	Sodium depletion phenotype	96
	Bibliography	99
	Appendix	115
	Publications	139
	Deutsche Zusammenfassung	140

Summary

Cyanobacteria produce about 40 percent of the world's primary biomass, but also a variety of often toxic peptides such as microcystin. Mass developments, so called blooms, can pose a real threat to the drinking water supply in many parts of the world. This study aimed at characterizing the biological function of microcystin production in one of the most common bloom-forming cyanobacterium *Microcystis aeruginosa*.

In a first attempt, the effect of elevated light intensity on microcystin production and its binding to cellular proteins was studied. Therefore, conventional microcystin quantification techniques were combined with protein-biochemical methods. RubisCO, the key enzyme for primary carbon fixation was a major microcystin interaction partner. High light exposition strongly stimulated microcystin-protein interactions. Up to 60 percent of the total cellular microcystin was detected bound to proteins, i.e. inaccessible for standard quantification procedures. Underestimation of total microcystin contents when neglecting the protein fraction was also demonstrated in field samples. Finally, an immuno-fluorescence based method was developed to identify microcystin producing cyanobacteria in mixed populations.

The high light induced microcystin interaction with proteins suggested an impact of the secondary metabolite on the primary metabolism of *Microcystis* by e.g. modulating the activity of enzymes. For addressing that question, a comprehensive GC/MS-based study was conducted to compare the accumulation of metabolites in the wild-type of *Microcystis aeruginosa* PCC 7806 and the microcystin deficient $\Delta mcyB$ mutant. From

all 501 detected non-redundant metabolites 85 (17 percent) accumulated significantly different in either of both genotypes upon high light exposition. Accumulation of compatible solutes in the $\Delta mcyB$ mutant suggested a role of microcystin in fine-tuning the metabolic flow to prevent stress related to excess light, high oxygen concentration and carbon limitation.

Co-analysis of the widely used model cyanobacterium *Synechocystis* PCC 6803 revealed profound metabolic differences between species of cyanobacteria. Whereas *Microcystis* channeled more resources towards carbohydrate synthesis, *Synechocystis* invested more in amino acids. These findings were supported by electron microscopy of high light treated cells and the quantification of storage compounds. While *Microcystis* accumulated mainly glycogen to about 8.5 percent of its fresh weight within three hours, *Synechocystis* produced higher amounts of cyanophycin. The results showed that the characterization of species-specific metabolic features should gain more attention with regard to the biotechnological use of cyanobacteria.

1

General Introduction

1.1 Cyanobacteria

Cyanobacteria are Gram-negative eubacteria that owe their name to the presence of bluish pigments. Those accessory pigments are linked to the photosystems required for oxygen-evolving photosynthesis. First cyanobacteria-type organisms could have occurred as early as 3 billion years ago, leading to substantial oxygenation of the earth's atmosphere about 2.4- 2.1 billion years ago (Lyons et al., 2014).

Today's cyanobacteria populate diverse habitats ranging from glaciers to hot thermal springs (Whitton et al., 2012) and as symbionts associated with other organisms such as fungi, heterotrophic bacteria, corals and many more (Usher et al., 2007).

The ultra-structure of cyanobacteria is marked by thick cell walls, more typical for Gram-positive bacteria that ensure a high structural rigidity (Hoiczky and Hansel, 2000). Many cyanobacteria show characteristic intracellular inclusions such as polyphosphate and cyanophycin granules; gas vesicles and carboxysomes (Komarek and Anagnostidis, 1998).

Most relevant for global photosynthetic carbon fixation by cyanobacteria are phytoplankton species. In many fresh- and brackish water environments, some cyanobacteria species are regularly involved in undesired mass developments, so called blooms.

1.2 Formation of freshwater blooms by cyanobacteria



Figure 1.1: Blooms of *Microcystis*, A: Picture of a beach at Lake Templiner See near Potsdam, Germany in August 2009; **B:** Buoyant *Microcystis* colonies in a scoop sample from the surface of river Spree near Friedrichshagen, Germany in August 2009

Nutrient rich fresh water bodies in temperate to tropical climate zones are prone to mass developments of *Microcystis* and some other cyanobacteria species, see Table 1.2. Blooms find their most extreme expression in the formation of floating scums and dense mats.

In eutrophic waters of temperate regions, the composition of the phytoplankton community, usually, follows a distinct seasonal succession, with the establishment of cyanobacterial dominance during summer (Sommer et al., 2012). Abiotic factors related to the formation of blooms include the absence of rain, high temperature and low wind velocity, which support pronounced stratification of the water column into distinct layers (Huisman et al., 2004; Jöhnk et al., 2008; Paerl and Huisman, 2008).

Bloom forming cyanobacteria express gas-filled vesicles, which enables them to float (Thomas and Walsby, 1986; Reynolds et al., 1987). Floating cyanobacteria shade deeper layers and effectively suppress the growth of eukaryotic phytoplankton and macrophytes concurring for light and nutrients (Reynolds et al., 1987; Huisman et al., 2004). Additionally, CO₂ from the atmosphere can directly be assimilated at the surface (Paerl and Ustach, 1982). Increased light absorption by buoyant cyanobacteria further elevates water temperature at the surface and manifests stratification (Paerl and Huisman, 2008). Net oxygen consumption in shaded deeper layers and low mixing within the water column eventually lead to anoxia and mass fish killings (Havens, 2008).

The buoyancy of cyanobacteria is a function of the number and the extent of gas vesicles over the amount of carbohydrate ballast from photosynthesis and turgor pressure (Reynolds et al., 1987). Colony forming *Microcystis* species can vertically migrate within the water column. According to Stoke's law, macroscopic colonies can do this much quicker than smaller ones or single cells. Vertical migration enables *Microcystis* colonies to occupy the most favorable position for e.g. nutrient acquisition in deeper layers, or photosynthesis at the surface.

During cyanobacterial mass developments, the affected habitats are characterized by sharp diurnal changes of oxygen- and inorganic carbon concentrations and the ambient pH (Dunn, 1967; Dokulil and Teubner, 2000). Cells at the water surface are furthermore confronted with high light intensities and damaging UV-radiation. Nonetheless, the formation of floating scum by buoyant colonies is regarded as an elemental part in the life of bloom-forming cyanobacteria (Paerl and Ustach, 1982). To prevent damage and to maintain high photosynthetic activity, effective mechanisms to channel light energy and

to concentrate inorganic carbon are essential.

1.3 Photoprotective and antioxidant mechanisms

Aerobic life is mutually connected with the generation of reactive oxygen species (ROS). Organisms performing oxygenic photosynthesis are in particular exposed to ROS generating conditions, namely high energy flow rates through the photosynthetic electron transport chain and high oxygen concentration. Excess ROS have damaging effects on membranes, proteins and DNA. In that situations, the cells suffer from oxidative stress. Energy-rich UV-radiation also has the potential to damage cellular components directly. However, cyanobacteria evolved a variety of protection mechanisms against oxidative stress and the damaging effects of UV-radiation (Latifi et al., 2009), as summarized in table 1.1.

Table 1.1: Oxidative stress and the defense mechanisms according to (Latifi et al., 2009).

Stressor	Target/ Effect	Defense mechanism
UV-radiation	DNA, proteins, lipids	Sunscreens: mycosporines, MAAs, scytonemin
Excess energy	$^1\text{O}_2$, $\text{O}_2^{\bullet-}$ generation	Energy dissipation: NPQ, Flv1/3, Flv2/4
$^1\text{O}_2$	DNA, proteins, lipids	Antioxidants: α -tocopherol, carotenoids
$\text{O}_2^{\bullet-}$	Lipids, proteins	SOD
H_2O_2	Forms OH^\bullet with Fe^{2+}	Catalases, peroxidases
OH^\bullet	DNA, lipids, proteins	None

The first line of defense comprises small molecules serving as sunscreens to prevent damage by UV-radiation. Mycosporines and mycosporine-like amino acids (MAAs) are small water-soluble molecules, which effectively absorb UV-B radiation (310-365 nm). Scytonemin is a cyanobacteria-specific, lipid soluble pigment deposited at the cell surface. It has an absorption maximum at 370 nm (UV-A) *in vivo* (Latifi et al., 2009).

In the light, ROS evolve at the photosynthetic electron transport chain. The formation of singlet oxygen ($^1\text{O}_2$) occurs at the excited reaction center of photosystem II (PS II),

when the plastoquinone (PQ) pool cannot accept additional electrons. Antioxidants like α -tocopherol and carotenoids can detoxify ($^1\text{O}_2$). The superoxide anion radical $\text{O}_2^{\bullet-}$ is formed by the Mehler reaction at photosystem I (PS I), when electrons are transferred to oxygen instead of ferredoxin. $\text{O}_2^{\bullet-}$ is detoxified by metal containing superoxide dismutase, to form molecular oxygen and hydrogen peroxide (H_2O_2). H_2O_2 is further reduced to water by the action of catalase and peroxidase. Detoxification of H_2O_2 is particularly important, since it can be reduced by Fe^{2+} *via* the Fenton reaction to form the highly reactive hydroxyl radical (OH^\bullet). However, as long as ROS-levels do not exceed a certain threshold, the cells are not suffering oxidative stress.

Energy dissipating mechanisms effectively suppress ROS generation during episodes of over-saturating illumination and carbon limitation. Those include non-photochemical quenching (NPQ) of excitation energy at PS II by the orange carotenoid protein (OCP) sitting at the core of phycobilisomes (Bailey and Grossman, 2008). Excess energy dissipates as heat. Recently, the essential role of flavodiiron proteins in adjustment of the energy flow through the photosystems was described (Helman et al., 2003). The Flv2/Flv4 heterodimer located at the PS II acceptor side serves as photochemical protection mechanism. It allows the control of the PQ-pool redox state and prevents the formation of excess $^1\text{O}_2$ (Bersanini et al., 2014). Additionally, Flv1 and Flv3 proteins sitting at the acceptor side of PS I serve as efficient electron sink, when the amount of the available oxidized ferredoxin is limiting. The electrons are directly transferred to oxygen to form water, and the formation of $\text{O}_2^{\bullet-}$ by the Mehler reaction is effectively circumvented (Allahverdiyeva et al., 2013).

1.4 Carbon concentrating mechanism (CCM)

Planktonic cyanobacteria require the CCM for optimal growth under atmospheric CO_2 concentrations and bicarbonate utilization from the surrounding medium. It serves the purpose to deliver sufficient CO_2 for primary carbon fixation by the enzyme ribulose-1,5-bisphosphate carboxylase/ oxygenase (RubisCO) and to suppress the loss of carbon

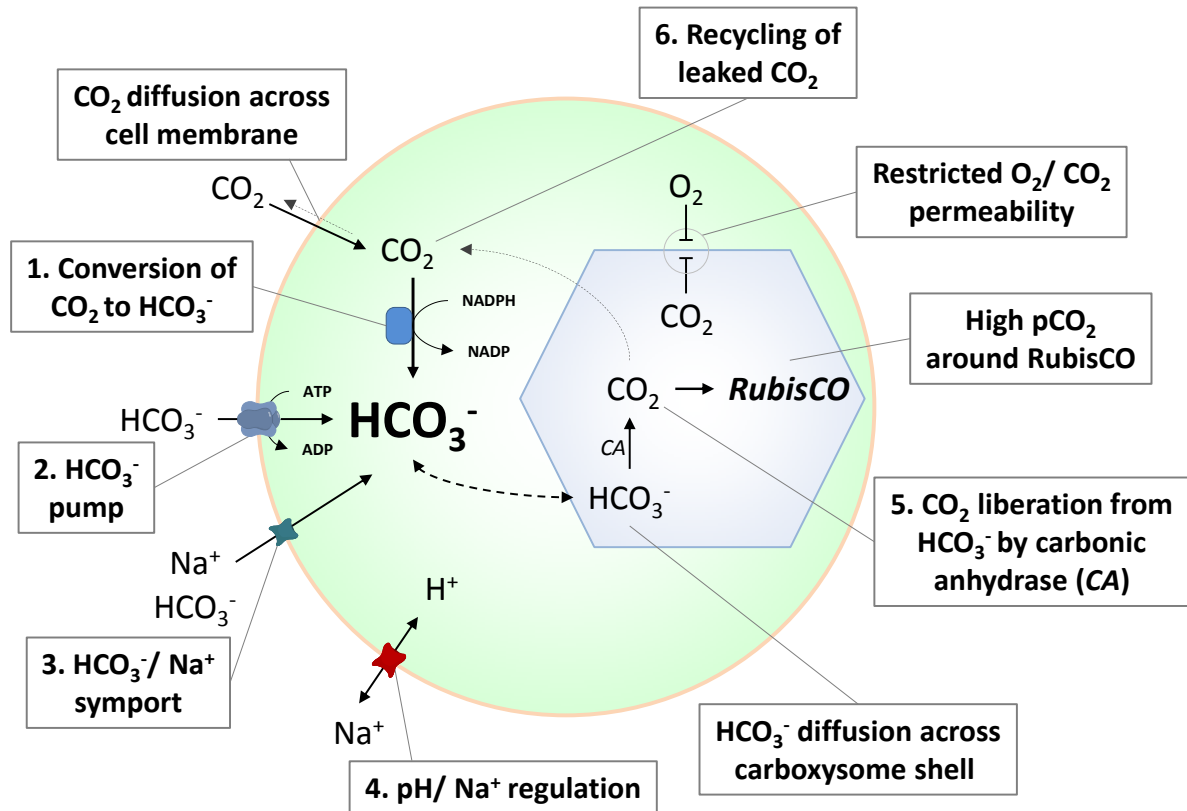


Figure 1.2: Schematic illustration of the β -cyanobacterial carbon concentrating mechanism, broadly adapted from (Price et al., 2008; Price, 2011): The conversion of CO_2 to bicarbonate inside the cell requires energy in the form of NADPH (1). HCO_3^- is actively taken up by ATP-fueled pumps (2), or by $\text{Na}^+/\text{HCO}_3^-$ symport (3). PH homeostasis and sodium ion extrusion is realized by Na^+/H^+ antiport (4). HCO_3^- enters the caboxysome passively, where it is converted to CO_2 by carbonic anhydrase (5). Liberated CO_2 is mostly trapped inside carboxysomes. High CO_2/O_2 ratios inside carboxysomes favor RubisCO carboxylase activity. CO_2 leaking from carboxysomes is recycled by the CCM (6).

due to photorespiration. Accordingly, the CCM is fully active under carbon limitation, whereas it is broadly suppressed to a basal level at high CO_2 availability (Price et al., 2008). Figure 1.2 summarizes the components of the cyanobacterial carbon concentrating mechanism according to (Price et al., 2008; Sandrini et al., 2014). CO_2 either passively entering the cell or produced by cellular respiration is converted to bicarbonate (HCO_3^-) in the cytoplasm by modified plastoquinone oxidoreductase NADPH dehydro-

genase (NDH-1) complexes. In contrast to CO_2 , the charged HCO_3^- molecule hardly diffuses across the cell membrane. Inorganic carbon (C_i) is actively taken up by ATP-fueled, high-affinity bicarbonate transporter BCT1, and by $\text{Na}^+ / \text{HCO}_3^-$ symporters like BicA and SbtA¹ along a sodium-ion electrochemical gradient. Conversion of imported HCO_3^- to CO_2 requires equal amounts of protons, i.e. pH balancing by Na^+ / H^+ antiport (probably by NhaS3). Bicarbonate accumulates in the cytoplasm up to 1.000 times the ambient concentration (Price, 2011).

Carbon fixation by RubisCO takes place inside carboxysomes. Carboxysomes are compartments of capsid-like shape with a proteinaceous shell. In contrast to lipid bilayers, small charged molecules like bicarbonate can passively diffuse through the shell, whereas CO_2 is effectively retained inside. CO_2 liberates from bicarbonate by the action of carbonic anhydrase inside carboxysomes, where it is utilized by RubisCO. CO_2 leaking from carboxysomes or produced by respiration is broadly recycled by the CCM. Oxygen is probably also excluded from the compartment, further suppressing the oxygenase activity of RubisCO (Marcus et al., 1992; Kinney et al., 2011).

1.5 *Microcystis aeruginosa*

The model organism studied in this work was *Microcystis aeruginosa* strain PCC 7806. *Microcystis aeruginosa* is a typical cyanobacterium frequently involved in fresh water blooms. The single spherical cells have a diameter of 2-7 μm and replicate by binary fission. Colonies form from daughter cells, which remain embedded in a common clear mucilage of homogeneous structure. It mostly consists of acetic polysaccharides (Nakagawa et al., 1987) and serves as a matrix to build up colonies of up to 8 mm in size (Komarek and Anagnostidis, 1998). The colonies are of net-like to lobate shape with irregular outlines. *Microcystis* colonies are morphologically diverse and a relation between particular morphotypes and the occurrence of toxic metabolites was reported (Via-Ordorika et al., 2004; Le Ai Nguyen et al., 2012). However, phylogenetic analy-

¹SbtA is not present in every *Microcystis* strain, e.g. PCC 7806 (Sandrini et al., 2014)

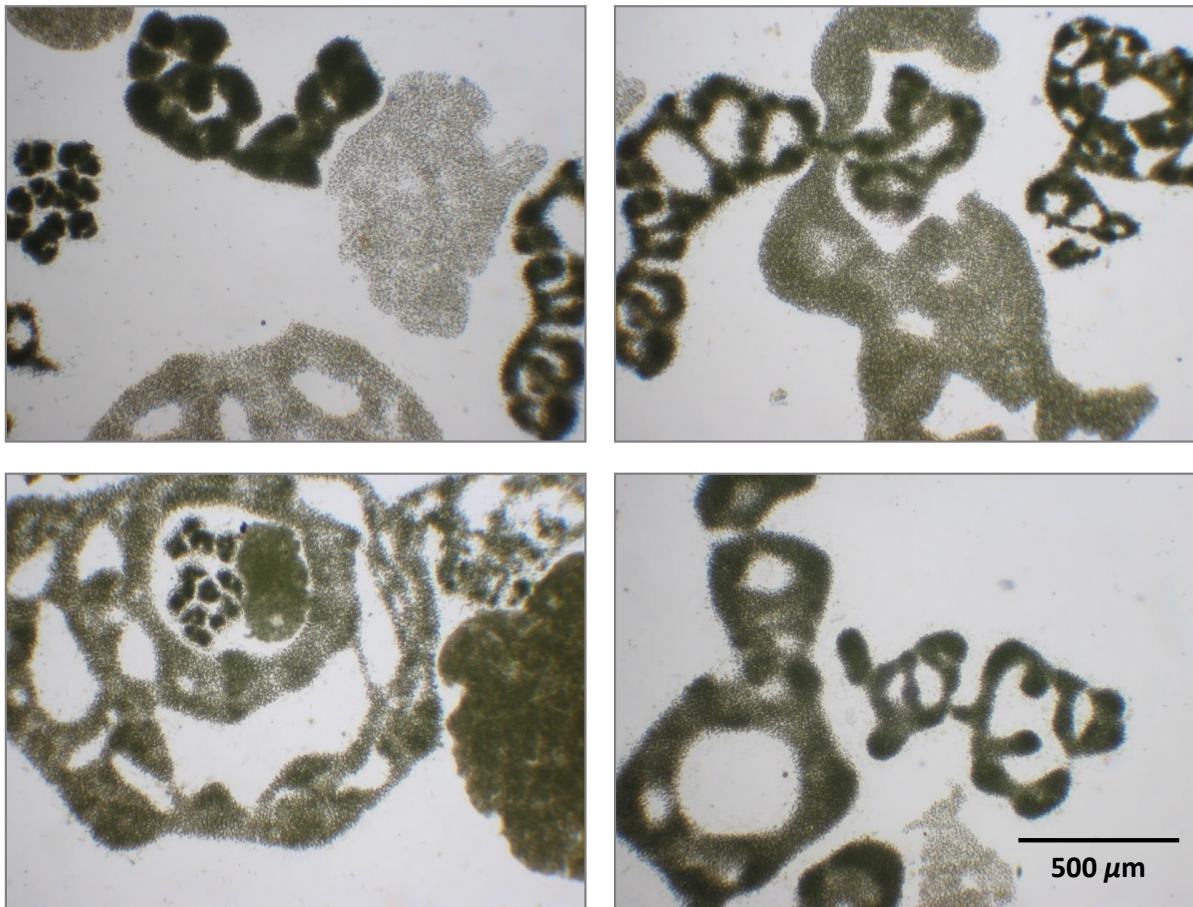


Figure 1.3: Diverse morphology of *Microcystis* colonies in a sample from Lake Wannsee in August, 2013.

sis does not support a clear distinction between different species (Otsuka et al., 2001; Le Ai Nguyen et al., 2012). Moreover, the genomes of *Microcystis aeruginosa* strains are characterized by a common core genome and individual subsets of flexible genes, which indicate a high genetic diversity (Humbert et al., 2013).

1.6 Toxin production by cyanobacteria

Cyanobacterial mass developments have a negative impact on the aesthetic value of most ecosystems. However, many bloom-forming cyanobacteria of fresh- and brackish waters can produce a variety of substances toxic to humans, livestock and wild animals

(Jochimsen et al., 1998; Stewart et al., 2008). The occurrence of toxic cyanobacteria becomes particularly problematic, when reservoirs for drinking water are affected. Table 1.2 lists the most common cyanotoxins found in fresh and brackish water environments and the producers. An early report on fatal intoxication of cattle by cyanotoxins dates back to the 19-th century (Francis, 1878). Especially microcystins are highly problematic cyanotoxins because of their frequent occurrence and high toxicity. Symptoms of oral microcystin consumption include diarrhoea, vomiting and general weakness (DeVries et al., 1993; Briand et al., 2003). Continuous exposition to microcystins could also cause tumor promotion in the liver (Sivonen and Jones, 1999).

Table 1.2: Cyanobacterial toxins and the producing genera involved in harmful fresh- and brackish water algal blooms; Toxicity as lethal dose for 50 % of treated specimens (LD₅₀) in [$\mu\text{g}/\text{kg}$] when intra-peritoneally administered to mice; adapted from (Sivonen and Jones, 1999; Paerl and Otten, 2013).

Compound	Toxicity, LD ₅₀	Producing genera
Cyclic peptides		
Microcystin	Liver, 50-300	<i>Microcystis</i> , <i>Anabaena</i> , <i>Planktothrix</i> , <i>Anabaenopsis</i> , <i>Aphanizomenon</i> , <i>Cylindrospermopsis</i> , <i>Nostoc</i>
Nodularin	Liver, 50-150	<i>Nodularia</i>
Alkaloids		
Anatoxin-a	Nerve synapse, 200	<i>Anabaena</i> , <i>Aphanizomenon</i> , <i>Cylindrospermopsis</i> , <i>Oscillatoria</i> , <i>Planktothrix</i> , <i>Raphidiopsis</i> , <i>Woronichinia</i>
Anatoxin-a(S)	Nerve synapse, 20	<i>Anabaena</i>
Saxitoxin	Nerve axons, 3-10	<i>Anabaena</i> , <i>Aphanizomenon</i> , <i>Cylindrospermopsis</i> , <i>Oscillatoria</i> , <i>Planktothrix</i>
Cylindrospermopsin	Liver, 200	<i>Anabaena</i> , <i>Aphanizomenon</i> , <i>Cylindrospermopsis</i> , <i>Oscillatoria</i> , <i>Raphidiopsis</i>

1.7 Microcystin and its synthesis

Microcystins are cyclic heptapeptides. All microcystins share a common basic structure, see figure 1.4. Positions X and Z are variable L-amino acids and modifications might occur on every amino acid residue. A general feature of all microcystins (and nodularin) is the existence of Adda (3-amino-9-methoxy-2,6,8-trimethyl-10-phenyl-4,6-decadienoic acid).

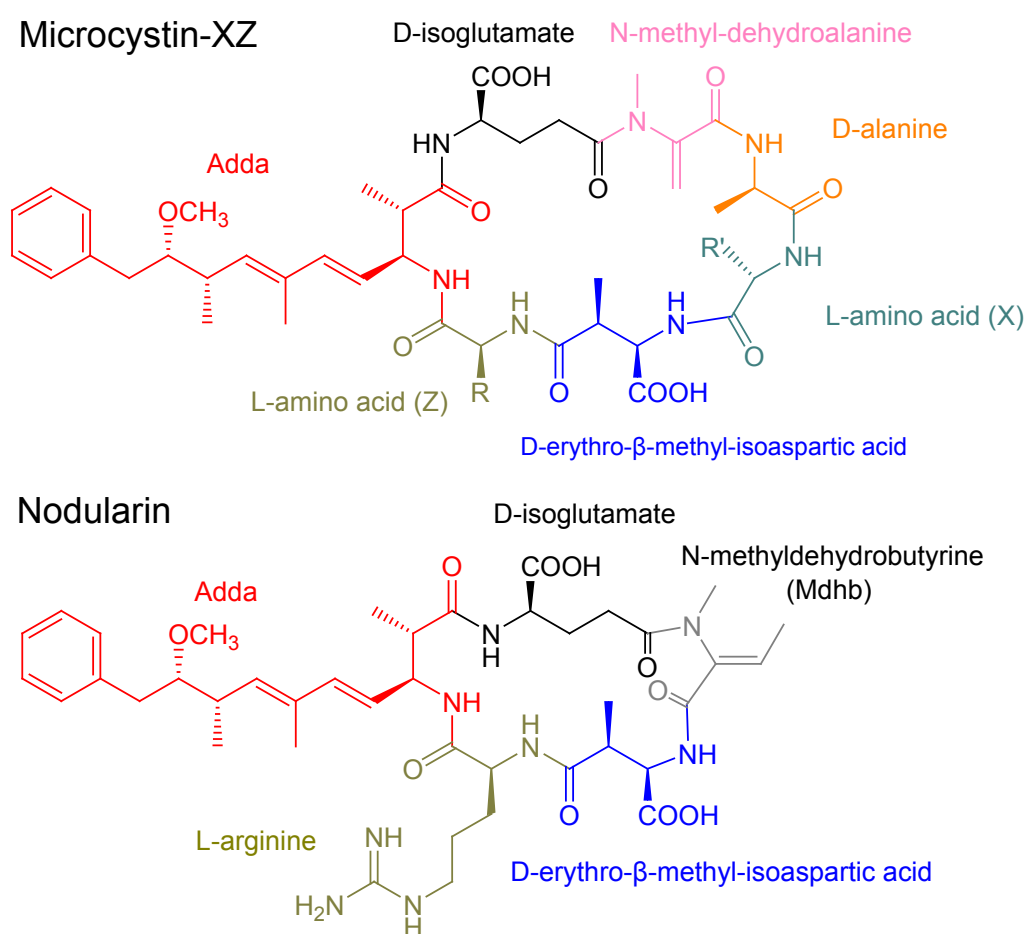


Figure 1.4: Chemical structures of microcystin and nodularin.

A 55 kB gene cluster encodes the machinery required for microcystin biosynthesis (Tillett et al., 2000). It consists of a large multi-enzyme complex including non-ribosomal peptide synthetases (NRPS) for incorporation of non-proteinogenic amino acids, polyketide synthases (PKS), as well as additional modifying enzymes are involved in microcystin synthesis, see figure 1.5. The PKS domains of McyG, D and E synthesize Adda. The PKS modules catalyze the sequential condensation of activated carbonic acids. Modification by the *O*-methyltransferase activity of McyJ and the aminotransferase of McyE completes Adda formation. The other six amino acids are subsequently recognized, activated and incorporated into the peptide chain by the modular NRPS sequence of McyG, A, B, and C. McyI and F are required for D-erythro- β -methyl-aspartic acid formation prior to its incorporation (Dittmann et al., 2013). The thioesterase domain of McyC finally releases the complete heptapeptide.

Nodularins are cyclic pentapeptides produced solely by *Nodularia* species. Their assembly is functionally similar to that of microcystins, except the deletion of two NRPS modules and the activation and incorporation of L-Tyrosine instead of L-Serine, yielding N-methyl-dehydrobutyrate (Mdhb) instead of N-methyl-dehydroalanine (Mdha) (Dittmann et al., 2013).

Many strains of potentially toxic genera had lost the ability to produce microcystins as consequence of point mutations or gene deletion events by insertions of transposable elements into the mcy-gene cluster (Rantala et al., 2004; Christiansen et al., 2006, 2008; Fewer et al., 2011). The co-occurrence of toxic and non-toxic strains raises the question, whether the ability to produce microcystin has an impact on the competitiveness of a strain under certain environmental conditions.

1.8 Toxicity mechanism of microcystin-LR

Microcystin-LR is a frequently occurring and highly toxic microcystin variant (Sivonen and Jones, 1999). The hepatotoxicity of microcystin is owed to the fact that it is selectively imported into liver cells by the multi-specific bile acid transport system (Eriksson et al., 1990a). Its toxicity is based on the ability to inhibit eukaryotic protein phosphatases PP1 and PP2A (Runnegar et al., 1995). The Adda (3-amino-9-methoxy-2,6,8-trimethyl-10-phenyl-4,6-decadienoic acid) moiety of microcystin interacts hydrophobically with the active site of the enzymes. In a second step, microcystin binds covalently *via* the electrophilic alpha-beta unsaturated carbonyl of its methyl-dehydroalanine residue to specific cysteines of the protein phosphatases. Enzyme inhibition leads to hyper-phosphorylation of proteins (Eriksson et al., 1990b), resulting in disorganization of the cytoskeleton microfilaments (Toivola et al., 1994) with necrosis and dissociation of hepatocytes (DeVries et al., 1993; Briand et al., 2003).

1.9 Eco-physiological aspects of microcystin production

Still, the role of microcystin production by cyanobacteria is under debate. Microcystin can account for more than one percent of the dry weight in cyanobacteria samples (Sivonen and Jones, 1999) ; thus, a certain eco-physiological relevance might be anticipated. Since microcystin is a potent inhibitor of eukaryote protein phosphatases, it appears plausible that it primarily serves as a deterrent against grazing zooplankton. However, the microcystin biosynthesis genes are reported to be relatively ancient and that they even pre-date the entire eukaryotic lineage (Rantala et al., 2004). Additionally, grazing on *Microcystis* cells by zooplankton is inhibited regardless of microcystin being present or not (Rohrlack et al., 1999, 2001; Kaebernick et al., 2001). Cyanobacteria in general are of rather poor nutritious value, when compared to e.g. dinoflagellates or diatoms (Muller-Navarra et al., 2004) and are hard to ingest and digest due to mucilaginous envelopments and thick cell walls respectively (Rohrlack et al., 2001). Thus, substantial

decimation of cyanobacteria by filter-feeding zooplankton might not be expected, irrespectively of microcystin production. The assumption that microcystin could primarily function as extracellular allelochemical against eukaryotic algae and macrophytes might also be negated, considering the ancient origin of microcystin synthesis genes.

The currently proposed functions of microcystin production, as well as the environmental factors, which might influence microcystin synthesis, were reviewed recently (Neilan et al., 2013), see figure 1.6. In summary, several studies report effects of culture parameters like phosphorus, nitrogen, trace elements, light, temperature and pH on microcystin production. However, the impact of the changed culture parameters on microcystin synthesis could not be clearly separated from the effects of the parameters on general cell proliferation.

The presence of microcystin outside the cells lead to the assumption that it could serve as info chemical or signal peptide (Schatz et al., 2007). Although McyH shares some homology with ABC-transporters, an active export *via* this route was not demonstrated. However, the addition of external microcystin to *Microcystis* cultures stimulates its production by the cells (Schatz et al., 2007).

The transcription of mcy-genes is initiated at a bidirectional promoter between mcyA and mcyD genes in *Microcystis*. Sequence motifs for the DNA binding proteins Fur (ferric uptake regulator) and NtcA (global nitrogen transcription factor) are located in proximity to the promoter (Ginn et al., 2010). The involvement of NtcA is in particular interesting since it potentially links microcystin synthesis directly with components of energy and carbon metabolism (Alfonso et al., 2001; Vazquez-Bermudez et al., 2002; Tanigawa et al., 2002; Su et al., 2005). Furthermore, the proposed co-induction of microcystin synthesis with iron uptake mechanisms might also point towards a close connection with photosynthesis since flavodiiron proteins are needed for tuning the energy flow through the photosynthetic apparatus (Bersanini et al., 2014; Allahverdiyeva et al., 2013). ROS scavenging enzymes like SOD and catalase also require iron, see 1.1. Analysis of mcy-gene expression was performed to figure out, which specific environmen-

tal stimuli influence the regulation of microcystin synthesis. Accordingly, altered light regimes and iron starvation indeed seem to have an impact on microcystin production (Kaebernick et al., 2000; Sevilla et al., 2008).

Competition experiments with toxic and non-toxic strains furthermore demonstrate that microcystin synthesis becomes advantageous under high light conditions, carbon limitation and elevated temperatures (Jähnichen et al., 2007; Van de Waal et al., 2011; Dziallas and Grossart, 2011).

Proteomic studies comparing the steady-state abundance of proteins in toxic and non-toxic phenotypes came to the conclusion that microcystin production affects the accumulation patterns of enzymes involved in carbon, nitrogen and energy metabolism, as well as in redox control (Zilliges et al., 2011; Alexova et al., 2011; Tonietto et al., 2012). The extracellular glycoprotein MrpC also accumulates differently in microcystin deficient cultures, which might imply a role of microcystin in regulation of colony formation.

The above mentioned studies describe the effects of environmental factors on microcystin production and the differences between toxic and non-toxic strains, without giving any mechanistic explanation for the molecule's exact mode of action. However, electron microscopy of immuno-gold labelled *Microcystis* cells indicate microcystin accumulation around e.g. thylakoids (Young et al., 2005; Gerbersdorf, 2006). This finding already points towards a direct interaction of microcystin with specific components of the cell.

1.10 Microcystin interaction with proteins

Recently, the direct interaction of microcystin with cellular proteins was described (Zilliges, 2007; Zilliges et al., 2011; Ahlert, 2013). The binding partners comprise enzymes involved in carbon and energy metabolism, see figure 1.3. The microcystin-protein interaction was more pronounced under high light conditions and iron limitation, as well as after the addition of hydrogen peroxide (Kehr, 2009; Zilliges et al., 2011). In an attempt to characterize the effect of microcystin binding to proteins, it was shown that the stability of the microcystinylated large RubisCO subunit against proteolysis is higher *in vitro* (Zilliges et al., 2011). A similar effect was recorded for *in vitro* microcystinylated, recombinant phosphoribulokinase (PRK) and the associated CP12 linker protein (Ahlert, 2013).

Table 1.3: Microcystin binding partners that have been identified so far in protein extracts of *Microcystis aeruginosa* PCC 7806 wild-type by Western blot analysis (Zilliges et al., 2011; Ahlert, 2013). n.q., not quantified; n.t., not tested

Protein identity	Category	Differential in WT & $\Delta mcyB$	Microcystin binding <i>in vitro</i>
Small subunit of RubisCO	Photosynthesis	Yes	n.t.
Large subunit of RubisCO	Photosynthesis	Yes	Yes
Phosphoribulokinase	Photosynthesis	Yes	Yes
CP12	Photosynthesis	Yes	Yes
Phycocyanin alpha subunit	Photosynthesis	Yes	n.t.
Phycocyanin beta subunit	Photosynthesis	n.q.	n.t.
Allophycocyanin alpha subunit	Photosynthesis	n.q.	n.t.
Glutathione reductase	Biosynthesis	Yes	n.t.

The currently proposed model of microcystin involvement in cellular processes is summarized in figure 1.6.

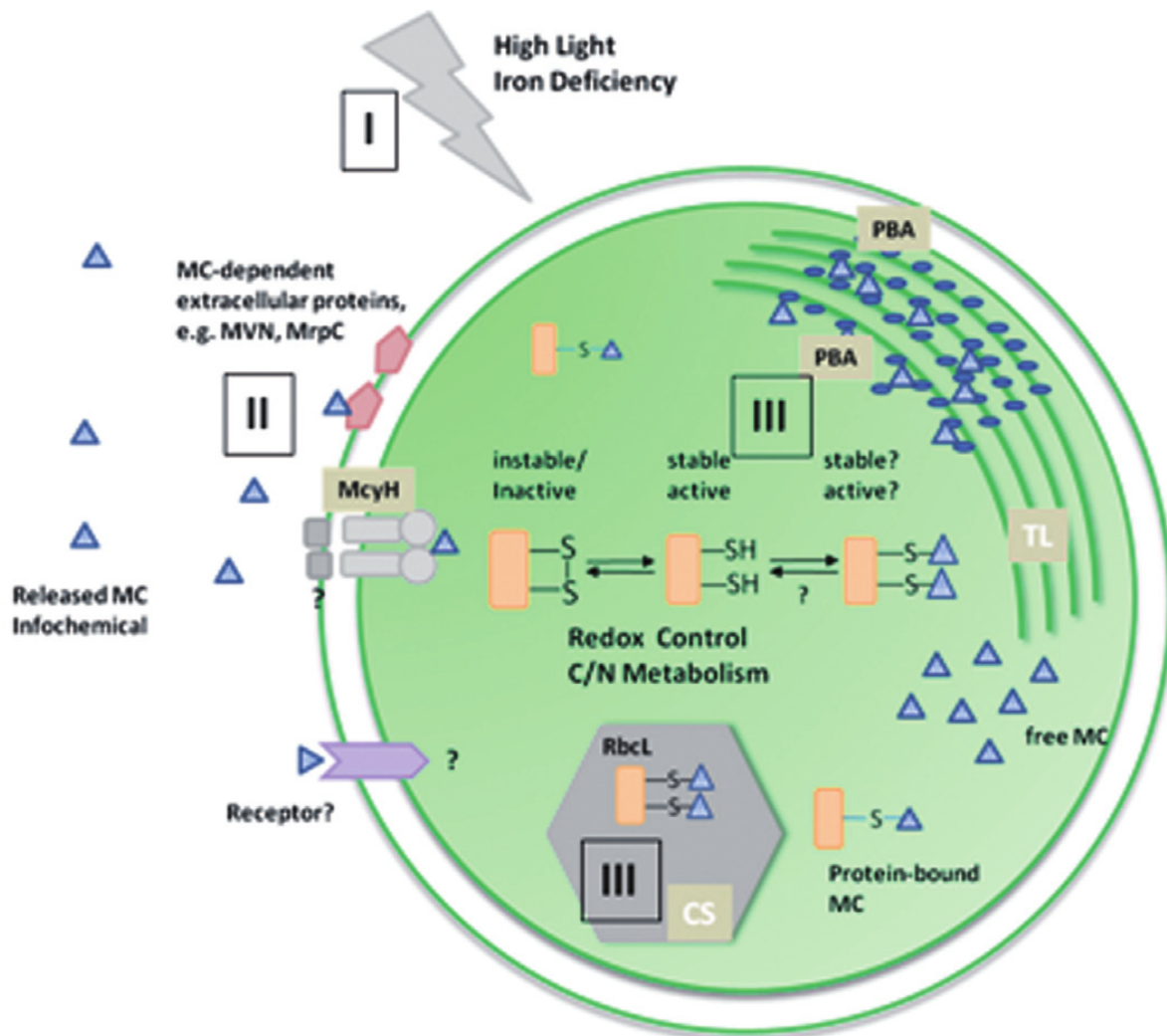


Figure 1.6: Scheme of proposed microcystin functions in *Microcystis aeruginosa*: I) High light and iron limitation stimulate microcystin biosynthesis. II) Some of the microcystin could be exported *via* the ABC transporter McyH. External microcystin, either exported or present due to cell lysis, could act as signal peptide for induction of its own biosynthesis and regulation of extracellular proteins like the glycoprotein MrpC and the lectin MVN, to which it could also bind. III) Parts of intracellular microcystin interact with proteins including phycobilisome antennae proteins (PBA) and the large subunit of Rubisco (RbcL). High light and oxidative stress favour covalent binding to cysteine residues. This binding affects protein stability and could participate in redox regulation of enzyme activity primarily involved in C/N metabolism and redox control. TL, thylakoids; CS, carboxysomes. Figure adopted from (Neilan et al., 2013).

1.11 Aim of the study

According to the currently proposed physiological functions of microcystin, this study aims at further elucidating the involvement of microcystin production in cellular processes of *Microcystis aeruginosa*. Especially its proposed role under putatively stress inducing conditions is addressed. In the first part of this work, the focus is put on high light induced dynamics of microcystin abundances in *Microcystis* cells. The characterization of microcystin-protein interactions is of particular interest.

The second part deals with the impact of high light on cyanobacterial primary metabolism comparing the *Microcystis aeruginosa* 7806 wild-type strain with its microcystin deficient $\Delta mcyB$ mutant and the established model cyanobacterium *Synechocystis* PCC 6803. The consequences of microcystin production on the accumulation of primary metabolites in *Microcystis*, as well as strain-specific differences are of particular interest.

2

On the Significance of Microcystin Conjugate Formation

Most of this chapter's data had recently been published under the title:

”Microcystin production revisited: conjugate formation makes a major contribution”

Sven Meissner¹, Jutta Fastner² and Elke Dittmann¹

¹Department of Microbiology, Institute of Biochemistry and Biology, University of Potsdam, Golm, Germany.

²Federal Environment Agency, Section Drinking Water Treatment and Resource Protection, Berlin, Germany.

Environmental Microbiology, 15(6):1810–1820, 2013

2.1 Abstract

Factors affecting the induction of microcystin production are not well understood. High light stimulates the synthesis of *mcy*-genes and biosynthetic proteins, whereas its effect on the actual cellular microcystin content appears variable. The recent discovery of microcystin- protein conjugate formation *in vivo* opens a new perspective on the dynamics of microcystin production and its primary role in the producing organisms. This study focused on determining the total amounts of cellular microcystin including the non-extractable, i.e. protein bound fraction. A significant part of the total microcystin appeared to be bound to the otherwise inaccessible protein fraction of *Microcystis* and *Planktothrix* strains. High light triggered a very articulated increase of microcystin content in the protein fraction, but, not in extracts analyzed by LC-MS and ELISA. The formation of conjugates contributed to a significant increase of the total microcystin content under high light conditions. Analysis of five different field samples revealed that neglecting the protein fraction leads to underestimation of total microcystin loads. Fi-

nally, the application of immuno-fluorescence microscopy furthermore allowed the identification of toxic colonies in field samples and indicated different grades of microcystin conjugate formation. The effects of protein microcystinylation, as well as its selectivity towards specific residues, are discussed in detail.

2.2 Introduction

In recent decades, the frequency and magnitude of cyanobacterial mass developments have increased in many parts of the world. Toxin production by cyanobacteria like *Microcystis* fuels the concerns of health- and water authorities. Characterization of the factors that affect microcystin production and figuring out its primary biological role might contribute to the establishment of more effective bloom management strategies. To find out more about the kinetics of microcystin production and the physiological role it might play for the producing organisms, it is essential to reliably determine the total microcystin amounts present in the cells. Current microcystin quantification techniques comprise liquid chromatography coupled with diode array detectors (LC-DAD), or more sensitive mass spectrometers (LC-MS) (Sivonen and Jones, 1999). *In vitro* inhibition assays with eukaryotic protein phosphatases are used to quantify microcystins according to their toxic potential (Carmichael and An, 1999; Metcalf et al., 2001). Enzyme-linked immunosorbent assays (ELISA), employing highly specific α -microcystin antibodies are commercially available. Another technique involves oxidative cleavage of the microcystin Adda-moiety to 2-methyl-3-methoxy-4-phenylbutyric acid (MMPB) and its detection by LC-MS or gas chromatography (GC) (Kaya and Sano, 1999). However, the protocols of all the above-mentioned techniques include the microcystin extraction and extensive sample preparation prior to quantification. Consequently, only the free and extractable microcystin fraction is considered for analysis and quantification.

A recent study reports that microcystin binds to proteins of *Microcystis aeruginosa* PCC 7806 *in vivo* and that high light conditions stimulate this effect (Zilliges et al., 2011). Aim of this study thus was to quantitatively assess the impact of changed light

conditions on microcystin-protein interaction and to estimate its significance with regard to the total cellular microcystin pool. To realize this, two immuno-blotting techniques were combined with an established LC-MS method and a commercially available ELISA-kit for microcystin quantification. Low light-adapted cultures of *Microcystis aeruginosa* PCC 7806 and *Microcystis aeruginosa* Nies 843 were exposed to high light, and the microcystin contents were determined in methanol extracts and the methanol-insoluble protein fractions respectively.

Additionally, the phenomenon of microcystin binding to proteins of *Microcystis* was demonstrated to occur also in the natural habitats by analyzing field samples from five different lakes. Finally, immuno-fluorescence microscopy of freshly collected *Microcystis* colonies was employed to differentiate between toxic and non-toxic ecotypes.

2.3 Methods

2.3.1 Cultivation of cyanobacteria

The cyanobacterial strains used in this study were cultured semi-continuously in 1 L Erlenmeyer flasks at 23° C under constant fluorescent light (Philips Master TL-D 58W/865) at a photon flux rate of $8 \mu\text{mol photons} \cdot \text{m}^{-2} \cdot \text{s}^{-1}$. Cell cultures were maintained at optical densities (OD_{750}) between 0.3 and 1.0 by regular dilution with fresh BG-11 medium (Rippka et al., 1979). Three independent biological replicates of the strain *Microcystis aeruginosa* PCC 7806 were included in this study. The microcystin deficient PCC 7806 ΔmcyB mutant strain (Dittmann et al., 1997) served as control. To draw a more general picture, the microcystin producing cyanobacterial strains *Microcystis aeruginosa* Nies 843 and *Planktothrix agardhii* NIVA-CYA 126 were included in this study as well.

2.3.2 High light experiment

For the highlight experiment, 200 mL cyanobacterial cultures were grown to OD_{750} of 0.8-0.9 and exposed to elevated photon flux rates of $250 \mu\text{mol photons} \cdot \text{m}^{-2} \cdot \text{s}^{-1}$. Samples were taken from low light adapted cultures before the onset of highlight exposition (0 h) and after three hours of highlight (3 h). During the highlight experiment, the temperature was monitored, and the pH of the culture medium was recorded (see table 2.1).

Cells from 50 mL culture samples were collected by centrifugation at $6.000 \times g$ and RT for five minutes and washed once with water. The washed sample pellets of about 0.5 mL were inactivated by immediately suspending the cells in 1.5 mL methanol and stored at -20°C until further processing.

Table 2.1: Specifications of the high light experiment samples

Strain	OD_{750}	pH 0 h	pH 3 h HL	$\Delta\text{pH 0 - 3 h HL}$
WT A	0.849	9.47	11.2	1.73
WT B	0.974	9.78	11.09	1.31
WT C	0.876	9.96	11.04	1.08
ΔmcyB	0.698	9.63	10.99	1.36
Nies 843	0.79	9.74	11.03	1.29

2.3.3 Field samples

The field samples were selected from an archive of the Federal Environmental Agency of Germany (Umweltbundesamt, UBA). The samples were taken with a plankton net from five different lakes with cyanobacteria-dominated phytoplankton, see table 2.2. Concentrated samples were lyophilized and stored at -20°C until analysis. For immunofluorescence microscopy (IFM), freshly collected samples from lake Zernsee were used (see 2.3.11).

Table 2.2: Field samples A-E, origin and specifications

Sample	Sampling site	Date	Sample composition
A	Bautzen Reservoir	23.10.1995	<i>Microcystis sp.</i>
B	Wannsee	23.08.1995	<i>Microcystis sp.</i>
C	Müggelsee	29.07.1996	<i>Microcystis sp.</i> ; <i>Anabaena sp.</i>
D	Postweiher	22.08.1995	<i>Microcystis sp.</i>
E	Schwielowsee	01.07.1996	<i>Microcystis sp.</i> ; <i>Anabaena sp.</i>

2.3.4 Microcystin extraction

All cyanobacterial samples were extracted with 75 % methanol as described by Fastner (Fastner et al., 1998). Briefly, the suspended samples were mechanically treated with an ultrasonic probe (Sonopuls UW 3100 MS72, Bandelin, Germany) for one minute, followed by vigorous shaking for 30 minutes on an orbital shaker. The insoluble material was sedimented by centrifugation at 15.000×g for 5 minutes. The procedure was repeated three times. Cleared extracts from each extraction cycle were pooled and kept at -20° C until analysis. The remaining insoluble fractions were suspended in equal volumes of 100 % methanol and stored at -20° C. Nodularin from samples of *Nodularia spumigena* CCY 9414 (kindly provided by Martin Hagemann) was extracted accordingly after the cells had been harvested by vacuum filtration and inactivated in methanol.

2.3.5 Microcystin quantification by LC-MS

Extracted microcystin was quantified by LC-MS analog to (Spoof et al., 2003), employing an API 5500 QTrap mass spectrometer (AB Sciex, USA) equipped with a turbo-ion spray interface, which was connected to an Agilent 2900 series HPLC system (Agilent Technologies, Waldbronn, Germany). Microcystins were separated at 30° C on a Purospher STAR RP-18 end-capped column with dimensions of 30 × 4 mm, packed with 3 μm particles (Merck, Germany). The mobile phase was composed of A: 0.5 % formic acid and B: 0.5 % formic acid in acetonitrile. A mobile phase gradient was run with

25 % B at 0 minutes, to 70 % B at 10 + 1 minutes. 10 μ L of appropriately diluted sample was injected. For the identification and quantification of different microcystin congeners (MCs), standards of [Asp3]-MC-RR; MC-RR; MC-YR; [Asp3]-MC-LR; MC-LR; MC-LW; MC-LF; MC-LA were utilized (Enzo Life Sciences, Germany).

2.3.6 ELISA

The commercial Adda-specific microcystin quantification ELISA was performed according to the manufacturers' protocol (Abraxis LLC, Warminster, PA, USA). Dried cyanobacterial extracts were first dissolved in 100 % methanol and diluted individually with water to concentrations within the recommended range of the assay. The effective methanol concentration of the analyzed samples was \ll 1 %. Photometric data acquisition was acquired with a Varioskan® Flash (Thermo Fisher Scientific Inc. Waltham, MA, USA) plate reader.

2.3.7 Sample preparation for total microcystin quantification

Equal amounts of the pooled extract fraction and the corresponding suspension of insoluble matter were in parallel transferred to fresh tubes each. The extracts were dried in a centrifugal vacuum concentrator and dissolved completely in SDS-PAGE loading buffer (0.5 % SDS; Tris-HCl pH 8.2; 10 % glycerol; 20 mM DTT) by vigorous mixing at RT. Duplicates of a defined microcystin standards were treated equally throughout. The corresponding insoluble material was sedimented by centrifugation, and the methanol was aspirated carefully. Equal volumes of SDS-PAGE loading buffer were added to the air dried pellets. The protein was solubilized by thorough ultrasonication without cooling for three cycles of 30 seconds. All samples were denatured at 85° C for 5 minutes and alkylated with 30 mM iodoacetamide for 10 minutes at RT. Unreacted iodoacetamide was quenched by addition of another 30 mM DTT, and the samples were centrifuged at 13.000 \times g and RT for 10 minutes.

2.3.8 SDS-PAGE and Western blot analysis

Samples were loaded on 12.5 % poly-acrylamide gels. The Laemmli buffer system was employed for electrophoresis, and the runs were stopped before the migration front escaped the gels. Separated proteins and peptides were transferred from the gels onto Amersham® Hybond-C Extra nitrocellulose membrane (GE Healthcare, USA) using a wet blot electrophoresis apparatus (Protean mini; BioRad, USA) with constantly low currents of 9 mA (~ 7 V) overnight. To further support the quantitative binding of proteins and peptides to the membrane and to prevent “blow through”, the transfer buffer contained 20 % methanol (Towbin et al., 1979). After electrophoretic transfer, the membranes were rinsed with water and dried completely. Blocking of the membranes was done with 1 % PVP-40 (Polyvinylpyrrolidone, average molecular weight 40 kDa) dissolved in phosphate buffered saline pH=8 and 0.3 % Tween® 20 (PBS-T). The membranes were washed twice with PBS-T, and the primary antibody was applied at a concentration of 1:10.000. The antibodies were allowed to bind their antigen at 4° C for a minimum three hours. After three washing cycles of at least 10 minutes, the HRP-linked secondary antibodies were applied at the same dilution and incubated at 4° C for at least one hour. Thoroughly washed membranes were reacted with SuperSignal® West Pico substrate (Thermo Fisher Scientific Inc. Waltham, MA, USA) and the chemiluminescence signals were recorded with a ChemiDoc™XRS+ Imager (BioRad, USA). Quantification was carried out using the built in Image Lab™software (BioRad, USA).

2.3.9 Dot blot analysis

The samples for Dot blot were the same as used for Western analysis. Excess dodecyl sulfate was removed from the samples by addition of 50 mM dipotassium phosphate (K_2HPO_4) and incubated at 4° C for two hours (Suzuki and Terada, 1988). Insoluble potassium dodecyl sulfate was removed from the solutions by centrifugation at $10.000\times g$ and RT for one minute.

The samples were appropriately diluted with water and transferred to 96 well plates

(black flat bottom, Greiner). 10 % methanol was added to the samples to support protein binding to nitrocellulose membranes. Immobilization of the sample on the membrane was carried out passively. To that end, pinches of nitrocellulose with a diameter of 6 mm were carefully placed in each well containing 100 μL of sample and equilibrated on an orbital shaker at RT for a minimum of 30 minutes. Subsequent treatment of the membrane pinches inside the wells was identical to that of Western blot analysis.

2.3.10 Data analysis and evaluation

For the estimation of the microcystin content in the samples analyzed by Dot blot, duplicates of a microcystin-LR standard dilution series were run parallel to establish a regression curve for the chemiluminescence signal intensity. In Western blot analysis, a dilution series of a microcystin-LR standard was included in each run. Only values within the linear signal intensity range of the regression curve were considered for microcystin quantification in the samples.

To test whether the high light treatment resulted in significant changes of the detected amounts of microcystin in Dot blot-, Western blot- and ELISA samples, a one-sided paired Student's T-test was performed. Null hypothesis, H_0 : difference of means before and after treatment (3 h - 0 h) = 0; alternative hypothesis H_1 : difference of means (3 h - 0 h) > 0; confidence interval = 95 %; n = 3. Normal distribution of differences between 0 h and 3 h was tested with the Shapiro-Wilk-test.

2.3.11 Immuno-fluorescence microscopy (IFM)

Freshly collected and concentrated field samples were spotted on sample slides and left to dry on air. Subsequent fixation of the immobilized cells was done with -20°C methanol for 20 minutes and acetone for 1 minute. The fixed samples were equilibrated in PBS (phosphate buffered saline, pH 8) for 5 minutes and further permeabilized enzymatically with freshly prepared lysozyme (2 mg/ mL) in PBS-TX (PBS + 0.3 % Triton® X-100) at RT for 5 minutes. The samples were washed thoroughly with PBS-TX and

subsequently blocked with 1 % PVP-40 in PBS-T (PBS + 0.3 % Tween® 20) at 4° C for at least one hour. Antibodies were applied to thoroughly washed samples in PBS-T at concentrations of 1:500 for anti-microcystin antibody and 1:200 for secondary FITC-labeled antibody at 4° C for a minimum of one hour each. Observation and image acquisition was done with an inverted digital fluorescence microscope (AMG EVOS fl, Peqlab, Erlangen, Germany).

2.3.12 RubisCO purification and analysis

Cells from 1 L culture were harvested by centrifugation at 6.000×g for 5 minutes after high light exposition for three hours. The cell pellet was washed once with water and snap frozen in liquid nitrogen. The samples were kept on ice throughout all following extraction steps. First, the cells were opened successively with mild sonication (Sonopuls UW 3100 MS72, Bandelin, Germany) in BEMP buffer (20 mM bicine, 1 mM EDTA, 20 mM MgCl₂, 20 mM NaHCO₃⁻) + 1 mM freshly added DTT until the supernatant remained almost clear after centrifugation for 20 minutes at 20.000×g. The remaining pellet was further sonicated for another five minutes. The proteins of the resulting supernatant were precipitated with 60 % ammonium sulfate after salting out contaminants with 20 % ammonium sulfate. The protein was again dissolved in BEMP and purified by fast protein liquid chromatography (FPLC) using a Superose® 6 gel filtration column with 125 mL bed volume (GE Healthcare, USA), connected to an ÄKTAprime plus™ system (GE Healthcare, USA). Fractions containing RubisCO were concentrated with centrifugal filters (Amicon® Ultra-50K, Millipore, USA). Blue-native PAGE was performed exactly according to the protocol recommended in (Wittig et al., 2006). For Western Blot analysis of RubisCO, see 2.3.8.

2.4 Results

2.4.1 Microcystin quantification in methanol extracts

To characterize the impact of high light illumination on the actual cellular microcystin loads, two standard techniques for microcystin quantification in cyanobacterial extracts were performed in this study, see figure 2.1. The results of LC-MS did not indicate significant high light induced changes of microcystin concentration in PCC 7806. A change of the two microcystin congeners ratio MC-LR to (D-Asp3)-MC-LR was not observed as well.

The values of microcystin quantification obtained by the ELISA were about 60-70 % higher than those of LC-MS in samples of PCC 7806. A significant light dependent increase of 21.6 % was detected by the ELISA, probably indicating the presence of low molecular weight microcystin conjugates, which were not detected by LC-MS.

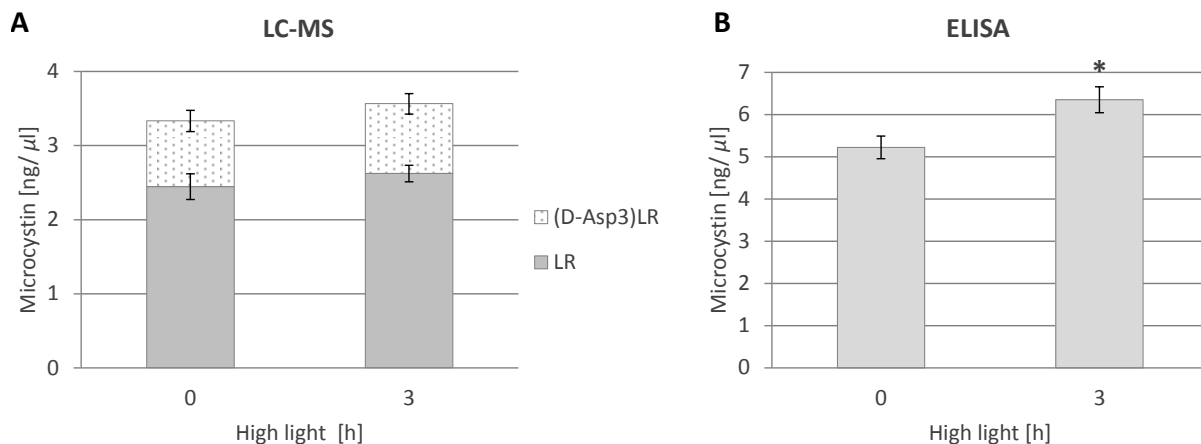


Figure 2.1: Microcystin concentration in methanol extracts of *Microcystis* PCC 7806 wild-type cells from low light adapted cultures before (0 h) and after high light exposition for three hours (3 h). Samples of three independent biological replicates were analyzed by **A**: LC-MS using quantitative standards, and **B**: ELISA commercial kit. Student's *t*-Test on significance resulted in $*p = 0.0244$.

2.4.2 Immunological quantification of total cellular microcystin

Methanol extracts of cyanobacteria samples, commonly used for microcystin quantification, contain mainly low molecular weight substances like chlorophyll and small peptides, whereas the methanol-insoluble fractions consist of high molecular weight proteins after extraction. In order to assess the complete cellular microcystin, both fractions were included for membrane-based immunological quantification. To make use of the obtained fluorescence signals from Western- and Dot blot analysis as a quantitative proxy, a microcystin standard was run simultaneously. Figure 2.2 demonstrates the relation between microcystin concentration and the obtained chemiluminescence signal.

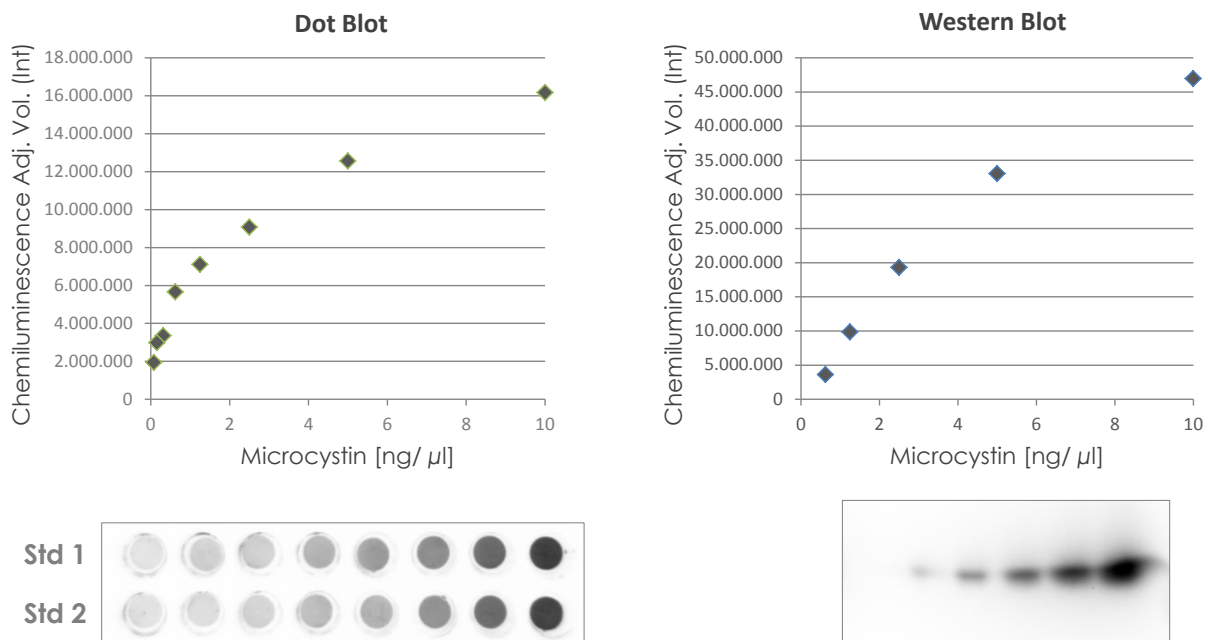


Figure 2.2: Microcystin standard dilution series used to quantify microcystin concentration in biological samples in Western- and Dot blot analysis.

Three independent biological replicates of *Microcystis* PCC 7806 wild were analyzed by membrane-based immunological methods. Figure 2.3 A+B show the results of Western blot analysis. In all three replicates, a high light induced increase of the microcystin-derived signal was detected in the protein fractions ($\sim 55\%$ increase), whereas the signal

intensity remained constant in the extract fractions. The same samples were subjected to Dot blot analysis as visualized in figure 2.3 C+D. Again, the amount of detected microcystin in the extracts remained unchanged after high light exposition for three hours, whereas the increase of the protein-bound microcystin was even more pronounced (~ 3.9 -fold increase). No chemiluminescence signals were detected in the samples of the microcystin deficient $\Delta mcyB$ mutant. However, although the microcystin amounts in the methanol extracts, as determined by Dot blot and Western blot, correlated with those from ELISA and LC-MS, the results should be considered as semi-quantitative due to inherent methodological uncertainties regarding the immobilization of the sample to the membrane.

To draw a more general picture, samples of an identically high light-treated culture of the toxic strain *Microcystis aeruginosa* Nies 843 were processed and analyzed analog to those of the strain PCC 7806. Since no microcystin standards were included, only relative values were obtained for Western- and Dot blot analysis. Figure 2.4 summarizes the results. Analog to the data obtained for PCC 7806, the amount of microcystin in methanol extracts was almost unchanged. The results of LC-MS and the ELISA (A+B) even indicated a slight decrease of extractable microcystin. In marked contrast, the amount of protein-bound microcystin was strongly increased after high light treatment for three hours as became evident by Western blot and Dot blot analysis (2.4 C-F). Initially, 25 % of total cellular microcystin was detected in the methanol-insoluble fraction. After three hours, high light exposition that amount was increased ~ 5 -fold to then ~ 60 % of total cellular microcystin. In total, the microcystin load approximately doubled during that time. Microcystin-protein interaction was more pronounced in Nies 843, which should be further examined in future experiments including more biological replicates.

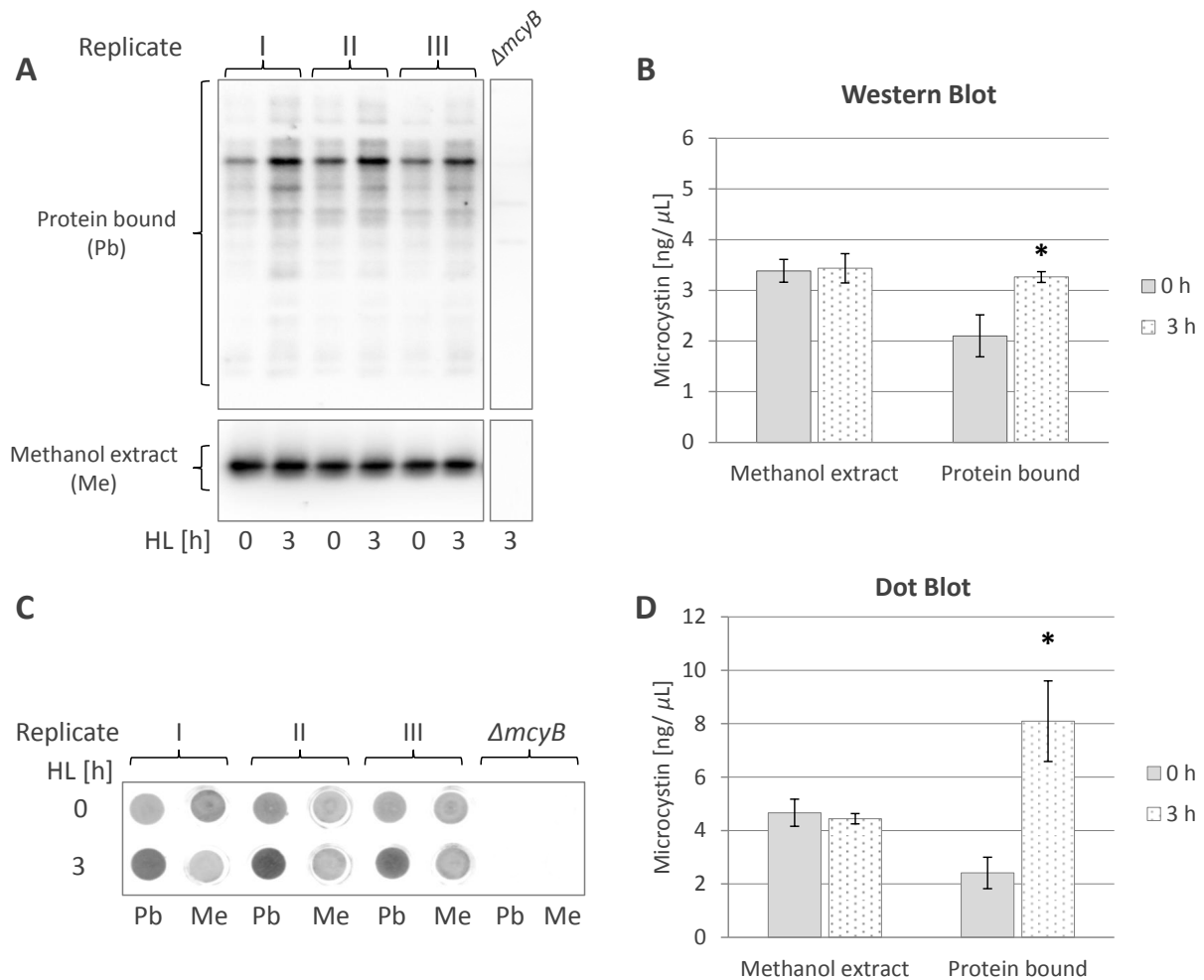


Figure 2.3: Total microcystin quantification by immunological techniques in cells of three independent *Microcystis* PCC 7806 wild-type cultures before (0 h) and after three hours high light exposition (3 h). Samples from a *Microcystis* PCC 7806 $\Delta mcyB$ mutant culture served as control. The determined microcystin quantities were in general agreement with those obtained by LC-MS, see figure 2.2. **A:** Western Blots of methanol insoluble proteins and the corresponding methanol extracts after SDS-PAGE; **C:** Dot Blots of the same samples. **B+D:** Visualization of microcystin quantification data after relation to external microcystin standards, see figure 2.2. * $p = 0.044$ (Western Blot); * $p = 0.0244$ (Dot Blot) according to Student's *t*-Test of significance.

2.4.3 RbcL is a major target of microcystin interaction

As already became visible in the Western Blots of figures 2.3 A and 2.4 C, the major microcystin signal in the methanol-insoluble fractions derived from protein bands

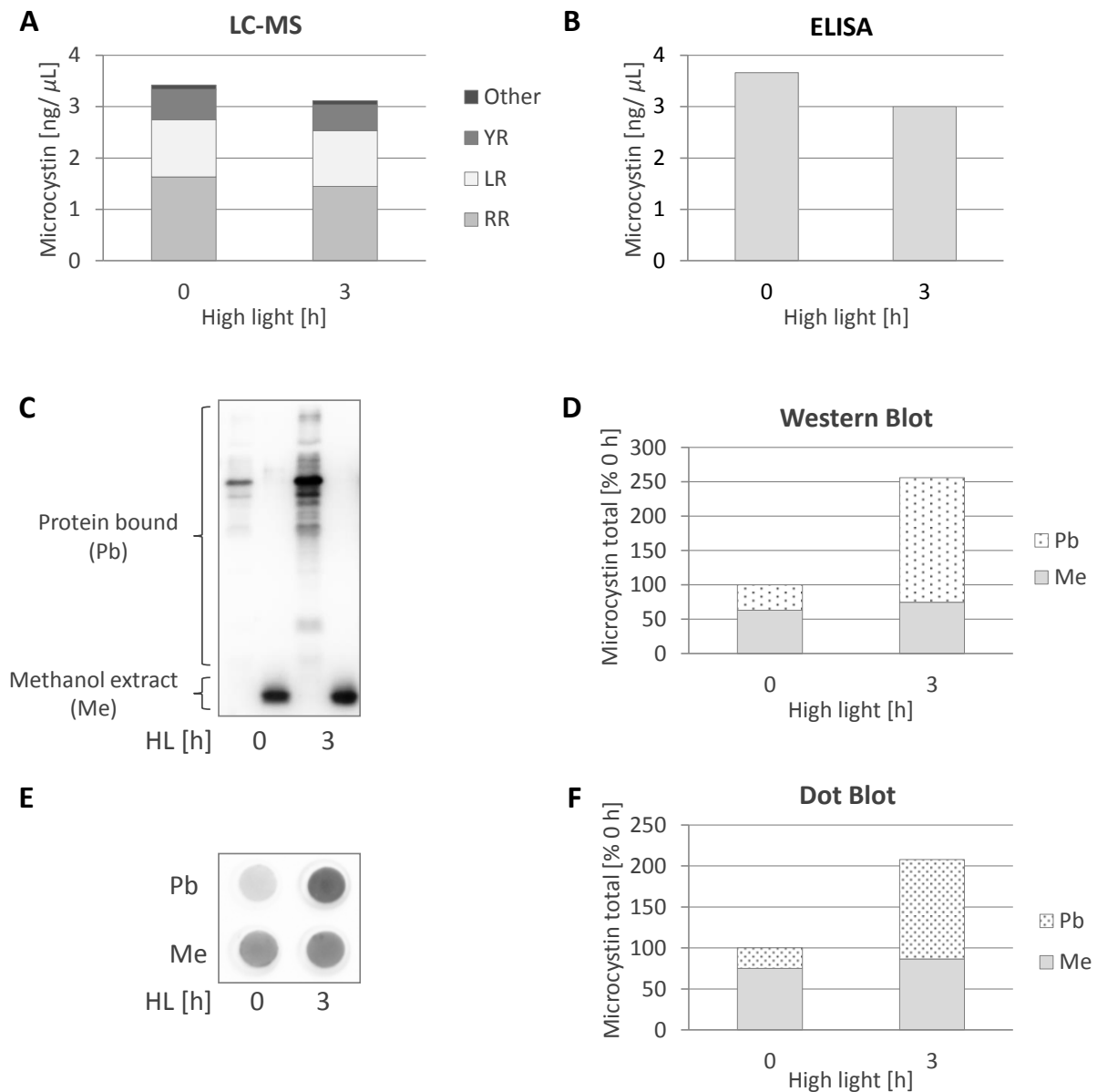


Figure 2.4: Microcystin quantification in samples of *Microcystis aeruginosa* Nies 843 analog to figures 2.1 and 2.3; **A+B**: Microcystin quantification in the methanol extract by LC-MS and ELISA; **C-F**: Immunological determination of the total cellular microcystin content by Western Blot and Dot Blot.

of approximately 50 kDa. Following an attempt to isolate and purify RubisCO from *Microcystis* PCC 7806 wild-type cells after high light exposition revealed that the large subunit of RubisCO was indeed a target for microcystin binding. The extraction procedure implied that the analyzed RubisCO most likely originated from carboxysomes.

Figure 2.5 A illustrates the migration of the 16-mer (L_8S_8) RubisCO enzyme complex in Blue-native PAGE. The same sample was subjected to denaturing SDS-PAGE, followed by Western blot analysis and immunological detection of microcystin, as well as the large RubisCO subunit RbcL (figure 2.5 B). Chemiluminescence signals were detected in both Western blots at the corresponding bands, which confirmed microcystin association with RbcL inside carboxysomes. As became evident from the α -microcystin Western blot, the small RubisCO subunit was not involved in detectable microcystin-protein interactions. The corresponding Coomassie-stained polyacrylamide gel, shown in figure 2.5B, provided a measure of overall RubisCO purity in the analyzed sample.

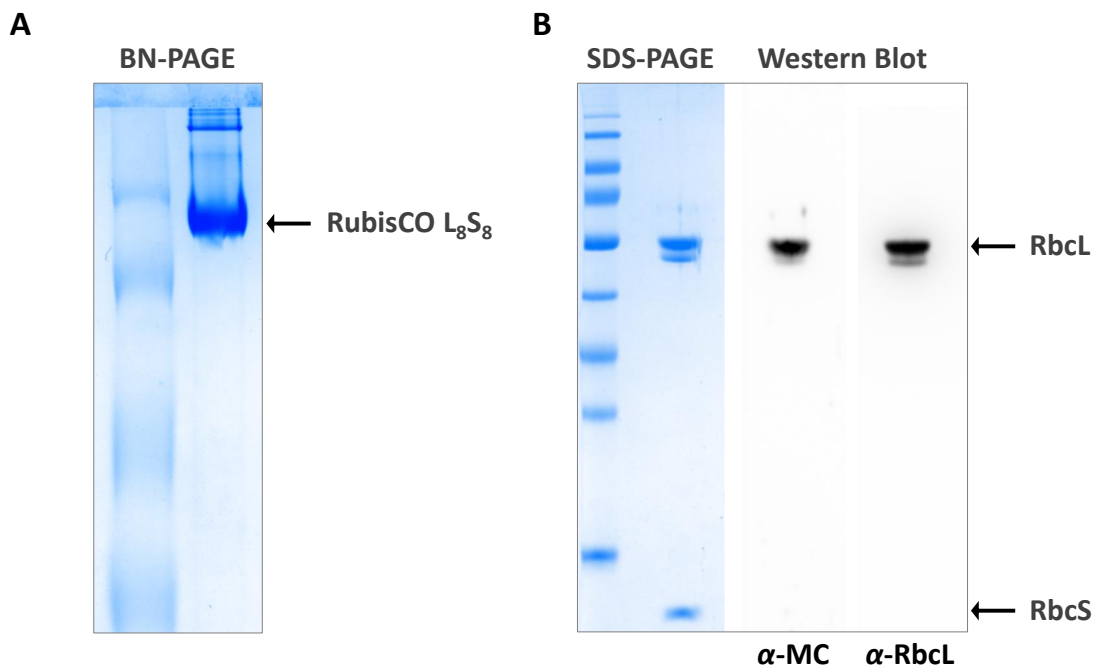


Figure 2.5: Purified RubisCO from high light-treated *Microcystis* PCC 7806 cultures. **A:** Blue-native PAGE of the RubisCO complex consisting of 8 large- and 8 small subunits (L_8S_8) after Coomassie staining. **B:** Denaturing SDS-PAGE of isolated RubisCO; Coomassie-stained gel with protein size marker, as well as RbcL and microcystin detection on the corresponding Western blots. No microcystin signal was detected at RbcS.

2.4.4 Conserved microcystin-protein interaction mechanism

The α , β - unsaturated carbon of the N-methyldehydroalanine moiety of microcystin was shown to bind to thiol groups of cysteines by a Michael type addition mechanism (Runnegar et al., 1995; Zilliges et al., 2011). To clarify whether that mechanism is a unique feature of microcystin and *Microcystis* cells, or if its conserved among other cyanobacteria and even a microcystin related secondary metabolite, protein fractions of *Planktothrix agardhii* NIVA-CYA 126 and *Nodularia spumigena* CCY 9414 were analyzed. Nodularin is a cyclic pentapeptide produced by *Nodularia sp.* It shares many similarities with microcystin like the Adda-moiety, but it contains N-methyldehydrobutyrine instead of N-methyldehydroalanine. Therefore, nodularin theoretically should be able to interact with cysteines *via* Michael addition. The filamentous cyanobacterium *Planktothrix agardhii* NIVA-CYA 126, on the other hand, produces [D-Asp3]-MC-RR and [D-Asp3]-MC-LR, which can also be found in *Microcystis* species.

The proteins of the methanol-insoluble fractions of both strains were separated by SDS-PAGE and electro-blotted to nitrocellulose membranes. The Adda-specific, α -microcystin antibody was used for microcystin and nodularin detection. As illustrated in figure 2.6, both secondary metabolites were present in the insoluble protein fraction after extraction of the cyanobacterial cells. The binding pattern of microcystin in the *P. agardhii* resembled those found in samples of *Microcystis*. The signal of nodularin in the sample of *N. spumigena* was completely different, indicating alternative protein binding partners and probably also a different physiological role of that molecule.

2.4.5 Microcystin quantification in field samples

To test whether conjugate formation of microcystin also occurs in the field and to evaluate the general applicability of the membrane-based microcystin quantification technique, five field samples from different locations were also included in this study, see table 2.2.

LC-MS provided information about the composition of the microcystin pool (figure 2.7

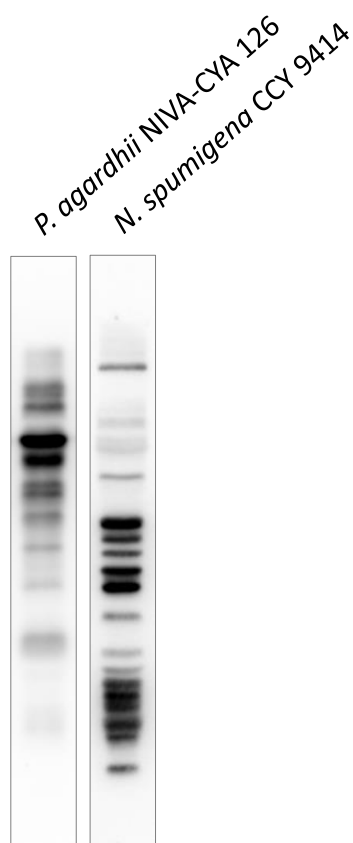


Figure 2.6: Western Blot analysis of methanol-insoluble fractions of *Planktothrix agardhii* NIVA-CYA 126 and *Nodularia spumigena* CCY 9414 cells after methanol extraction. An α -Adda specific microcystin antibody was used.

A). The arginine containing microcystins MC-LR, RR and YR were the dominating congeners in all field samples. The results of the commercial ELISA (figure 2.7 B), which is based on quantitative detection of the Adda moiety present in all microcystins, suggested a higher microcystin load in 4 out of 5 field samples. Non-standard microcystins, as well as low molecular weight- and methanol-soluble conjugates, probably also contributed to the amounts of microcystin detected by the ELISA kit, but were overlooked by LC-MS. Analysis of methanol extracts and methanol-insoluble fractions of the field samples by Dot blot and Western blot (figure 2.7 C-F) underpinned the above described results obtained from analyzing the lab strain samples, see figures 2.3 and 2.4. A significant amount of microcystin apparently was still present in the methanol-insoluble fraction

after extraction. In Dot blot analysis that portion accounted for 37-53 % of the total cellular microcystin. Relative microcystin quantification by Western blot delivered comparable results, although the amount of protein-bound microcystin appeared higher. The methanol-insoluble fractions contained non-cyanobacterial material, which gave the samples a brownish color. Those impurities probably consisted of exo-polysaccharides, humic substances and the like, which caused a smear on the gels and hindered the separation of proteins to distinct bands. However, the results from Western blot and Dot blot analysis were in line with those obtained from LC-MS and ELISA, but they also indicated that a considerable amount of microcystin was neglected by the standard quantification techniques, which focus on extracts only.

2.4.6 Immuno-fluorescence microscopy (IFM)

The same highly specific α -microcystin antibody that was used in Western Blot and Dot blot analysis was also employed to visualize toxic *Microcystis* colonies by IFM in a freshly collected field sample. Figure 2.8 shows the co-occurrence of toxic and non-toxic colonies in a single sample. Since sample preparation for IFM included extraction with organic solvents (see methods 2.3.11), the detected microcystin was most likely part of the not extractable, i.e. protein-bound fraction. The red auto-fluorescence was due to the presence of phycobiliproteins, since the also red-fluorescing chlorophyll was removed from the samples during sample preparation as well.

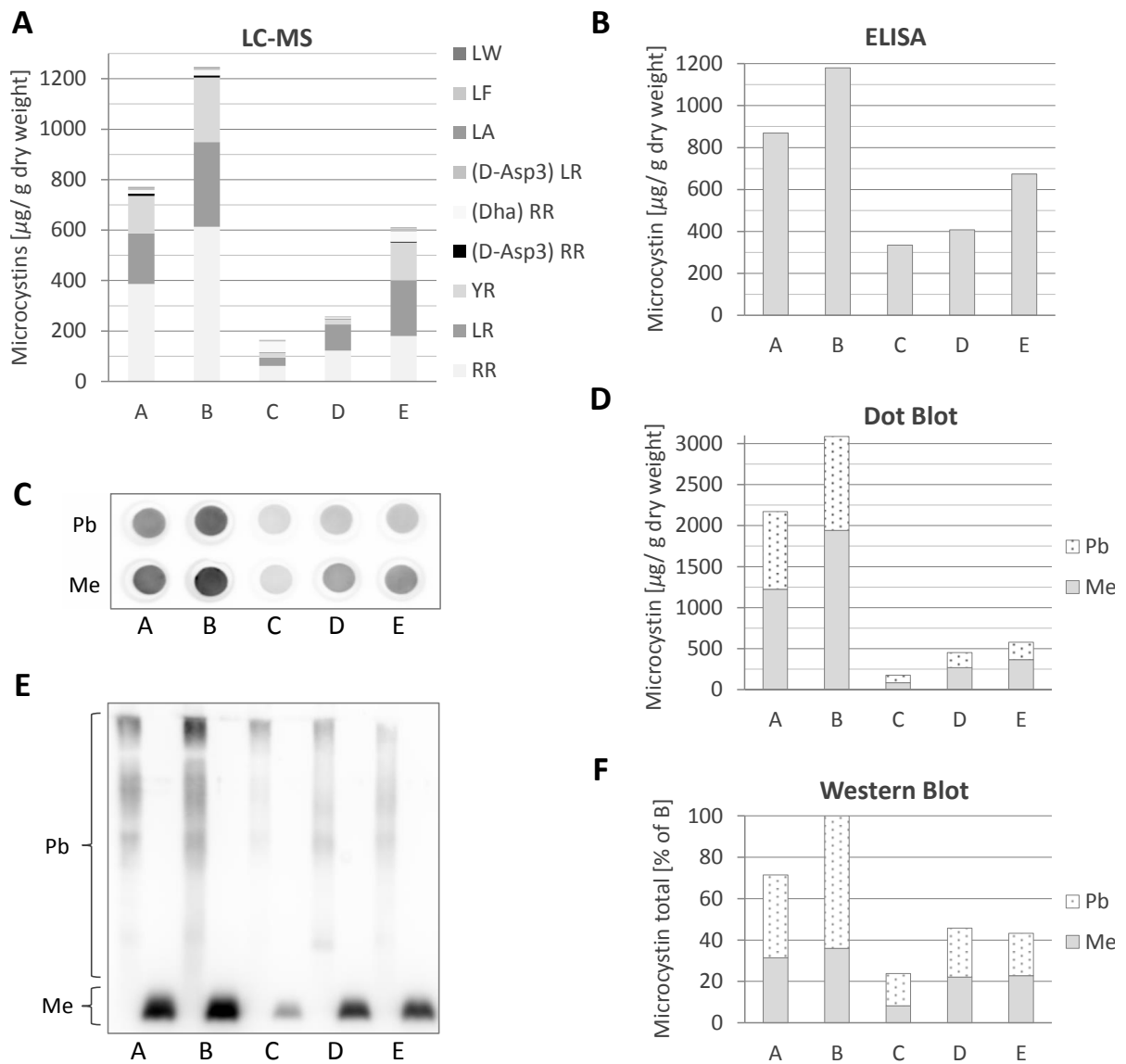


Figure 2.7: Microcystin quantification in field samples **A:** LC-MS of methanol extracts reflected the concentration and the diversity of microcystin congeners. **B:** The ELISA to quantify microcystin in methanol extracts showed higher microcystin loads in 4 out of 5 field samples. **C-F:** Dot blot and Western blot analysis revealed that a significant portion of the total cellular microcystin remained bound to proteins after extraction.

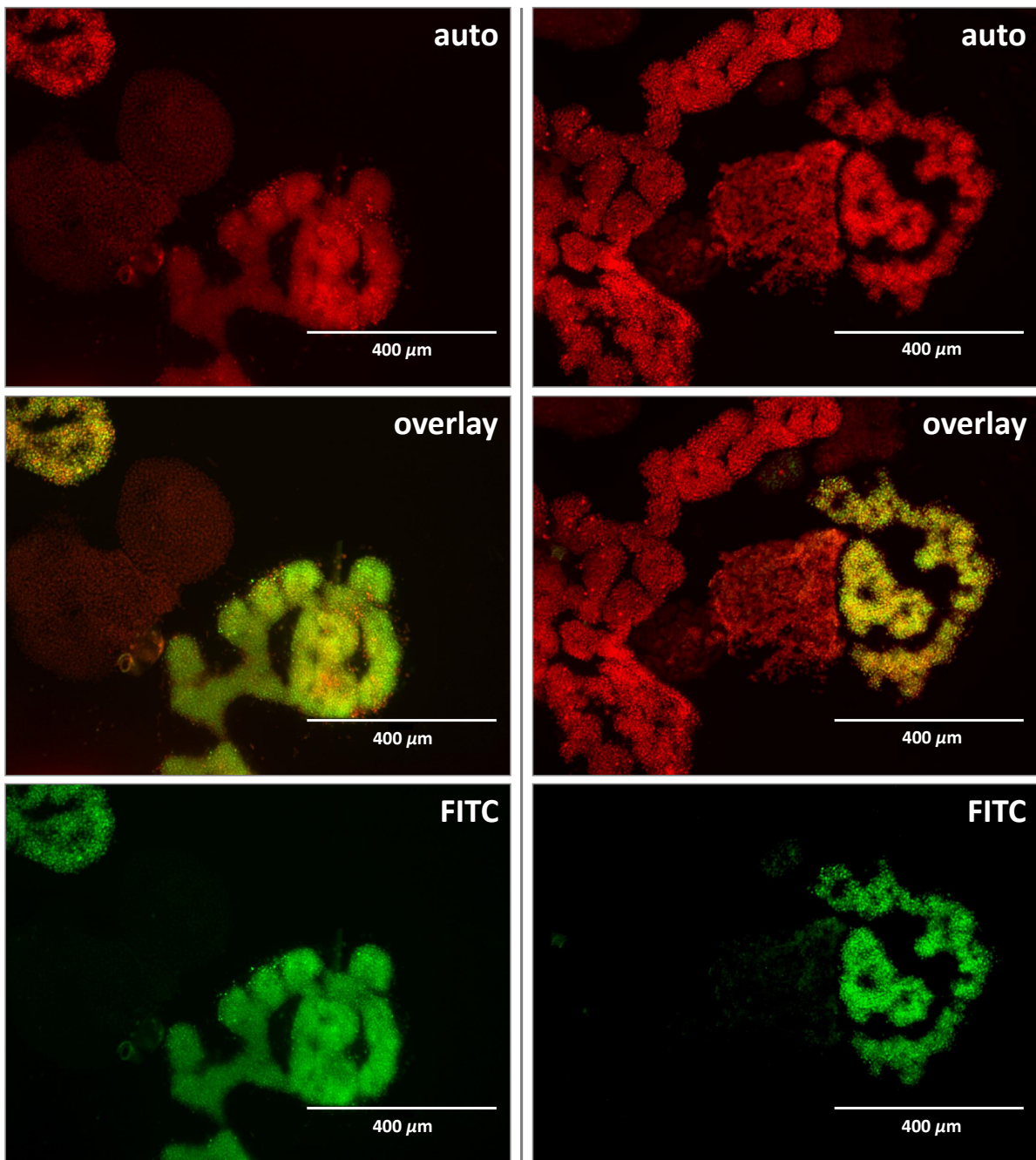


Figure 2.8: Immuno-fluorescence microscopy of field samples. Microcystin-positive colonies can be distinguished from microcystin-negative ones. The upper pictures in each column show the phycobillin-derived autofluorescence of the cyanobacteria. The lower pictures show the FITC-fluorescence signals originating from immunologically labeled microcystin in the samples. The pictures in the middle of each column show the overlays of both fluorescence micrographs.

2.5 Discussion

The dynamics of microcystin production and its interaction with proteins were demonstrated in lab experiments using two toxic *Microcystis* strains. Analysis of purified RubisCO from *Microcystis* cells confirmed that this key enzyme is a major interaction partner for microcystin. Furthermore, Western blot analysis of protein extracts from two other toxic cyanobacterial strains suggested a conserved mode of microcystin interaction with proteins. Field samples of cyanobacteria were also analyzed in this study, to evaluate the applicability of the immuno-blotting techniques for examination of less homogeneous probes and to assess the actual relevance of microcystin-protein interaction in natural cyanobacterial communities. Additionally, immuno-fluorescence microscopy using field samples was employed, to visualize protein-bound microcystin *in situ*.

2.5.1 Membrane-based quantification of total microcystin

None of the applied quantification methods provided a perfect solution for the assessment of the total cellular microcystin loads. The established methods, which focus on microcystin extracts, are highly sensitive and robust, but they do not include the protein-bound fraction. The membrane-based immunological quantification methods described in this study cover the whole cellular microcystin but can only provide a semi-quantitative measure. Nonetheless, the results obtained from Western- and Dot blot analysis of extract samples were in general agreement with those from LC-MS and the commercial ELISA kit.

Protein-blotting methods are intrinsically biased due to binding preferences towards more hydrophobic proteins and peptides and overall limited binding capacities of the membrane. However, the danger of losing especially low molecular weight proteins and peptides during electro-blotting had been overcome by the passive immobilization of the samples in Dot blot approach. A major advantage of the blotting methods was that the proteins were previously denatured, which might support the accessibility of

the antigen for the antibody. Prolonged incubation times and relatively high antibody concentrations might as well supported the detection of protein-bound microcystin in the corresponding samples. Combination of the methods used in this study should have provided a first robust estimate of the indeed biological situation.

2.5.2 Microcystin production is induced by high light

Although the extraction of microcystin was considered as complete, a significant amount of 30-75 % of the total cellular microcystin remained in the methanol-insoluble fraction, depending on the previous treatment. Whereas the amount of extractable microcystin remained almost constant, a clear increase was observed in the protein fraction after high light exposition for three hours. In total, the cellular microcystin load approximately doubled within that time.

Previous studies report high light induced accumulation of *mcy*-gene transcripts (Kaebnick et al., 2000) and *Mcy*-proteins involved in microcystin synthesis (Börner and Dittmann, 2005), whereas the determined microcystin concentrations remain vastly unchanged. Another study reports a positive correlation of microcystin content per cell with light intensity under overall light limiting growth conditions and a negative correlation under excessive illumination (Wiedner et al., 2003). The results obtained in this study might help to explain those somewhat contradictory findings and eventually serve as inspiration for new approaches aiming at deciphering the mystery of microcystin production in cyanobacteria.

2.5.3 Microcystin-protein interaction

The toxicity of microcystin is caused by the inhibition of eukaryotic protein phosphatases. The mode of action involves the specific interaction of the microcystin Adda moiety with a hydrophobic groove of protein phosphatases. This non-covalent interaction is responsible for the immediate toxicity within minutes. Subsequent covalent mi-

crocytin binding to specific cysteine residues *via* Michael-type addition is much slower (Pereira et al., 2013). Chemically, the reaction involves ionization of the cysteine thiol to the reactive thiolate by abstraction of the hydrogen by a molecule of water (base), the transfer of a hydrogen from water to the α, β -unsaturated carbonyl group of N-methyl-dehydroalanine (Mdha) and addition of sulfur to the β -carbon of the Mdha moiety of microcystin.

The formation of microcystin-cysteine conjugates is not restricted to eukaryotic protein phosphatases. *In vitro*, the formation of microcystin with cysteine-containing tripeptide glutathione and the free amino acid cysteine by Michael-type addition is carried out under alkaline conditions (pH \sim 11.5) in a 5 % potassium carbonate solution (Kondo et al., 1992). It is further suggested that for purposes of microcystin detoxification in eukaryotes, the conjugation of microcystin to glutathione *in vivo* is catalyzed by the enzyme glutathione-S-transferase (GST) at physiological pH (Pflugmacher et al., 1998). To answer the question whether conjugate formation of microcystin with cellular proteins in *Microcystis* is catalyzed enzymatically was not within the scope of this study. However, the interaction of microcystin with cysteine residues of cellular proteins was demonstrated *in vitro* (Zilliges et al., 2011). The binding is abolished by previously blocking either the thiols of the proteins with DTNB or the microcystin Mdha reactive moiety with cysteamine.

A change of the intracellular milieu induced by prolonged exposition to high light most likely boosted microcystin interaction with proteins *in vivo*. The electrostatic environment might provide a selectivity mechanism for the microcystinylation of specific cysteine residues textitvia Michael addition. As outlined above, the thiolate rather than the uncharged thiol of cysteine participates in Michael-type addition. The pK_a of a cysteine's sulfhydryl depends on its electrostatic environment, i.e. the net charge character of the neighboring amino acids, see table 2.3.

Negatively charged amino acids (at neutral pH) increase the pK_a of a proximal cysteine-SH and by that lower the deprotonation tendency of cysteine-SH. Conversely, positively

Table 2.3: pK_a of the cysteine thiol in synthetic peptides; adopted from (Lutolf et al., 2001)

Peptide	crr	rcr	cr	cys	rcd	crd	cdr	cd	dcd	cdd
pK_a	8.12	8.22	8.31	8.49	8.50	8.51	8.43	8.57	8.85	8.93

charged amino acids lower the pK_a of a proximal cysteine-SH and support deprotonation to cysteine-S⁻ at already less basic pH (Lutolf et al., 2001).

High light leads to acidification of thylakoid lumen and alkalization of the cytoplasm (Falkner et al., 1976). Prolonged exposition to high light might cause imbalances of intracellular pH homeostasis in cyanobacteria. The alkaline cytoplasm in turn could favor deprotonation of pH-sensitive SH-groups and by that facilitate selective microcystin binding to specific cysteines. Figure 2.9 summarizes possible sites of microcystin-protein interaction *via* Michael addition to cysteines, exemplified by the large RubisCO subunit (RbcL). Data from a previous MALDI-MS approach for identification of microcystin binding partners was included as well.

The question about the fate of the conjugated microcystin remains matter of speculation. The thioether bond between Mdha of microcystin and the cysteine thiol is regarded to be irreversible. Enzymatic activity to cleave off protein-bound microcystin would eventually result in a sudden increase of extractable microcystin quota, which was not observed yet. Degradation of microcystin-protein conjugates by general protein turnover might be the most likely scenario.

In principle, microcystin-glutathione and cysteine conjugates showed much weaker toxicity in mice than purely administered microcystin-LR due to increased metabolism and secretion (Ito et al., 2002). The overall toxicological threat connected with numerous freshwater cyanobacteria is caused by the free and extractable, i.e. reactive microcystin, which is reliably detected by the established quantification techniques. Hence, adaptations of current risk-assessment protocols might not be necessary. For the biological understanding of toxic cyanobacteria, however, future studies should include the protein-bound microcystin fraction, which had been neglected from analysis so far.

1 MVQAKSKGFEQ AGVDYRLTY YTPDYTKDT DLLACFRVTP QPGVPEEAG
 51 AAVAASSTG TWTTVDNL DLDRYKGRG YDIEVPNEQ NQFFCFVAY
 101 LDLFEESVT NILIVGNVFGKALRGLR LEDIRFPVAL IKTFQGPRG
 151 ITVERDKLNK YGRPLLCTI KPKLGLSAN YRAVYECLR GGIDFTKDDE
 201 NINSOPFRW RDRFLFVQA IVKSOAETNE VKGHYLNVA PTCEQMMQA
 251 EFAAEIKTPI IMHDYLTGGFTANTTLKFC RDKGLLIHIIH RAMHAVDRQ
 301 KNHGJHERVL KCLRLSGQ HLHSGTVVK LEGERGITMGFVDMREDYV
 351 EEDRARGIFF TDYASLPGV IVASGGHV WHMPALEIF GDDSCCLQFGC
 401 GTLGPWGNAPGATANVAL EACTIOARNEG RSLAREGNDV IREACRWSPE
 451 LAA/CELWKE IKFEFEAMDT L

D, E: negatively charged; **R, K, H:** positively charged; **hydrophobic** stretch; **MALDI-TOF-MS** covered sequence; **C:** candidate cysteine

Figure 2.9: RbcL primary structure with highlighted: charged amino acids at neutral pH, stretches of hydrophobic amino acids probably buried inside the enzyme complex, sequence fragments covered in a previous study (MALDI-MS by S. Mikkat, University of Rostock), cysteine residues possibly interacting with microcystin. Note that the previous MALDI-MS approach covered 51 % of the RbcL sequence, including 5 out of 12 cysteines, but none of the proposed candidate cysteines.

2.5.4 Biological implications

The results from the experiments performed in the laboratory indicated that microcystin interaction with proteins was triggered by a shift from low- to high light illumination in two different toxic *Microcystis* strains. At their habitats, cyanobacteria are exposed to fluctuating environmental conditions. Especially extreme high light intensities at the water surface might pose a challenge to the organism. Thus, a major aim of this study was to test whether microcystin conjugate formation can also be observed in the field. Although it could not be figured out to what environmental conditions the field samples were exposed before they were collected, the detection of a significant amount of total cellular microcystin in the insoluble protein fraction underlined the relevance of the phe-

nomenon as such for toxic cyanobacteria at their natural habitat.

As previously reported and confirmed in this study, the large RubisCO subunit (RbcL) is a major target for microcystinylation (Zilliges et al., 2011; Meissner et al., 2013). The effects resulting from microcystin-protein interactions are not well understood yet. An experiment focusing on the stability of RbcL in cell extracts of *Microcystis* show that the microcystinylated form is more resistant against proteolysis by the serine protease subtilisin (Zilliges et al., 2011). The same effect was also observed for phosphoribulokinase (PRK), another enzyme participating in carbon fixation *via* the CBB (Christine Ahlert, Master thesis). Microcystinylated, recombinant PRK of *Microcystis* PCC 7806 was less susceptible towards degradation by subtilisin than the non-microcystinylated control *in vitro*.

Studies on RubisCO from the green algae *Chlamydomonas reinhardtii* report that the enzyme's turnover rate is increased under oxidizing conditions (Marin-Navarro and Moreno, 2003). Oxidation of the protein thiols leads to the formation of disulphide bridges between specific cysteine residues, which in turn induced a conformational change of the whole protein. As a consequence, an otherwise hidden loop of RbcL becomes accessible for proteolysis by subtilisin. Following cleavage at that specific site, the RubisCO L₈S₈ holoenzyme complex disassembles, and the subunits are degraded completely.

Another study on *Synechocystis* PCC 6803 RubisCO reports dissociation of the hexameric enzyme complex into single subunits upon oxidation and disulfide formation between conserved cysteines, but without the additional action of a protease (Marcus et al., 2003). However, in both studies the dissociation of the holoenzyme was prevented by alkylation of the cysteine thiols prior to oxidation. Thus, it might be speculated that microcystinylation of specific cysteine residues might stabilize a stable structure of the RubisCO L₈S₈ complex under oxidizing conditions. Interestingly, a decline of enzyme activity upon microcystinylation was neither observed for RubisCO (carboxylase activity) in cell extracts nor for recombinant PRK *in vitro* (Christine Ahlert, Master thesis). Alkylation of the accessible cysteines with iodoacetate leads to a decrease of RubisCO activity in *Synechocystis* PCC 6803 (Marcus et al., 2003).

Another aspect of protein microcystinylation during high light might be the protection of essential cysteine residues against random carbonylation by various reactive substances. For instance, lipid peroxidation occurs under oxidative stress conditions and induces the accumulation of e.g. 4-hydroxynonenal (HNE) as degradation product (Madian and Regnier, 2010). HNE is an α, β -unsaturated hydroxyalkenal with the potential to form protein adducts *via* Michael addition to the amino acids cysteine \gg histidine $>$ lysine, with possibly adverse effects on enzyme activity (Doorn and Petersen, 2002; Dalle-Donne et al., 2006). HNE modifications are considered as a general marker for oxidative stress and can be detected in cyanobacteria (Allahverdiyeva et al., 2013), see 2.10.

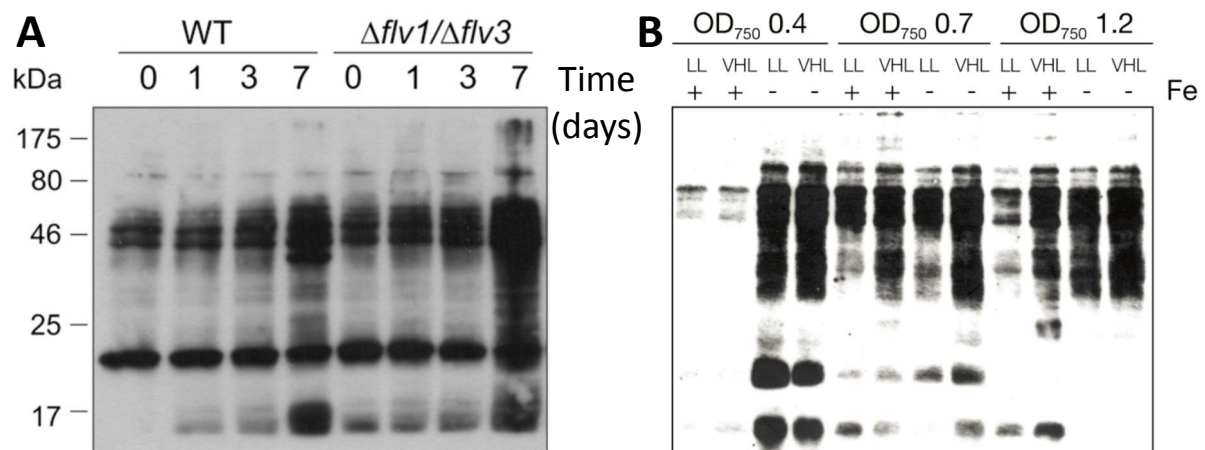


Figure 2.10: Carbonylation vs. microcystinylation of cyanobacterial proteins *in vivo*. **A:** OxyBlot™ (Millipore, USA) of cell extracts from *Synechocystis* WT and a flavodiiron protein 1/3 ($\Delta flv1/\Delta flv3$) double-mutant after exposure to fluctuating light conditions for the indicated time (days). The blot shows protein-HNE adducts as general indicator for oxidative stress, figure from the supplement of (Allahverdiyeva et al., 2013). **B:** Anti-microcystin Western blot of *Microcystis* PCC 7806 WT cell extracts from culture samples taken at different optical densities. High light (VHL = $500 \mu\text{mol photons} \cdot \text{m}^{-2} \cdot \text{s}^{-1}$) and iron limitation (-Fe) strongly induced microcystin-protein interaction, figure from (Kehr, 2009). The optical resemblance between A and B might indicate similar binding characteristics to proteins of microcystin and HNE.

Adduction of microcystin and HNE to proteins share the same mechanism. A physiolog-

ical role of microcystin to prevent random alkylation of critical cysteines during episodes of oxidative stress appears likely.

Microcystin binding to proteins was also observed for the genus *Planktothrix*. Nodularin, which might be considered as a minimalistic type of microcystin, was found to bind to proteins of the producing organism *Nodularia* as well. Microcystinylated proteins was also detected in field samples, which further underlined the general relevance of the phenomenon. Thus, the specific binding of microcystin to proteins might be an ancient type of post-translational modification to stabilize enzymes to keep the metabolic machinery intact under critical environmental conditions.

2.5.5 Immuno-fluorescence detection of toxic colonies

The application of immuno-fluorescence based methods to detect toxic phenotypes could provide a valuable tool to characterize the composition of the cyanobacterial community. In this study, the microcystin specific fluorescence signals allowed the differentiation between toxic and non-toxic colonies in a field sample. Sample preparation for IFM includes the extraction of microcystin during fixation and membrane permeabilization with methanol and acetone. Thus, the detected FITC signals most probably were derived from the not extractable-, protein-bound microcystin fraction. The differing fluorescence intensities between individual colonies furthermore suggested non-uniform relevance of microcystin interaction with proteins and could also indicate differences between the observed specimens concerning their recent environmental past.

Many non-microcystin producing phenotypes harbor *mcy*-genes and the genome copy number of potentially toxic genotypes can differ between single strains and even during different growth phases (Kurmayer and Kutzenberger, 2003). Hence, immuno-fluorescence methods could be used for evaluation and complementation of RT-PCR based approaches for assessing potential threats connected with cyanobacterial toxins in the field and might help to elucidate a possible ecological role of microcystin-protein interaction.

2.5.6 Open questions

Still there are many open questions concerning microcystin-protein interactions. In future studies, the exact microcystin binding residues of cellular proteins have to be determined, which would allow closer characterization of the microcystinylation mechanism and its possible effects. So far, mass spectrometric attempts (MALDI-MS) failed to tackle that issue successfully. The use of enriched protein- or peptide fractions as well as alternative ionization strategies such as, e.g. electron spray ionization (ESI), might be the key to identify microcystinylated fragments. Finally, further fragmentation of the peptides and analysis of the fragments by MS/MS might supply unambiguous evidence for the mode and specificity of microcystin-protein interaction.

The questions about microcystin involvement on regulating enzyme activities and its impact on the general metabolism of *Microcystis aeruginosa* are addressed in the following chapter.

3

The Metabolic Adaptation of *Microcystis* to
High Light is Affected by Microcystin and
Broadly Different in *Synechocystis*

Most of this chapter's data had recently been published under the title:

”Metabolomic analysis indicates a pivotal role of the hepatotoxin microcystin in high light adaptation of *Microcystis*”

Sven Meissner¹, Dirk Steinhauser² and Elke Dittmann¹

¹Department of Microbiology, Institute of Biochemistry and Biology, University of Potsdam, Golm, Germany.

²Max Planck Institute of Molecular Plant Physiology, Potsdam-Golm, Germany

Environmental Microbiology, 2014

3.1 Abstract

Recent studies suggest beneficial effects of microcystin production under high light intensities and inorganic carbon limitation. In this study, the metabolic response to elevated light conditions was studied in the microcystin producing cyanobacterium *Microcystis aeruginosa* PCC 7806, its microcystin deficient $\Delta mcyB$ mutant strain and the widely used model cyanobacterium *Synechocystis* PCC 6803. A comprehensive GC/MS-based metabolomics study was conducted and combined with quantification of storage compounds and estimation of net photosynthetic activity. The obtained dataset revealed differences between *Microcystis* wild-type and the $\Delta mcyB$ mutant strain concerning photorespiration and the accumulation of general stress related metabolites. Huge differences between *Microcystis* and *Synechocystis* in terms of resource utilization and storage under high light conditions became evident as well. This study provides new insights into the metabolic diversity of cyanobacteria, the specific lifestyle of bloom-forming *Microcystis* and the role of microcystin.

3.2 Introduction

Microcystis is one of the major species frequently involved in freshwater cyanobacterial blooms often culminating in the formation of floating scums. Survival and proliferation in such habitats implies the existence of efficient adaptations to resist sharp physico-chemical gradients and strong diurnal shifts of inorganic carbon availability and oxygen concentration due to photosynthetic activity at daytime and respiration in the night. Especially the resistance to very high light conditions at the water surface might pose a major threat. Several studies report advantageous effects of microcystin production under carbon limitation (Jähnichen et al., 2007) and prolonged exposition to high light (Kardinaal et al., 2007; Van de Waal et al., 2011; Zilliges et al., 2011). Microcystin was also found to have an impact on the transcriptome and the proteome of the producing organism (Zilliges et al., 2011; Tonietto et al., 2012). Another feature of microcystin is its ability to bind directly to proteins *in vivo* and by that modulate the stability of enzyme complexes (Zilliges et al., 2011) and possibly also their functionality. Thus, involvement of microcystin in regulating the activity of enzymes of the primary metabolism in *Microcystis* might be anticipated but remains elusive yet.

To tackle that question, the impact of a light intensity change from low to high on the metabolism of cyanobacteria was examined. The metabolic dynamics of the toxic *Microcystis* strain PCC 7806 wild-type were compared with those of the microcystin deficient mutant PCC 7806 $\Delta mcyB$. For means of interspecies comparison and to put the gained information into context with already published metabolomic studies, a widely used model cyanobacterium *Synechocystis* PCC 6803 was also included in this study. The measurement of glycogen and cyanophycin accumulation in the cells, as well as parameters such as oxygen evolution and pH in the medium, were included to characterize net photosynthetic activity of the different genotypes. The GC/MS metabolomic approach followed in this study provided snapshots of the metabolic constitution of the low light adapted cells before and after exposition to elevated light intensity for one hour and three hours respectively.

3.3 Methods

3.3.1 Strains and cultivation

Each of the strains *Microcystis aeruginosa* PCC 7806, $\Delta mcyB$ (Dittmann et al., 1997) and *Synechocystis* PCC 6803 were cultured in 5 independent biological replicates. Semi-continuous cultures of about 100 mL were grown in 0.5 L Erlenmeyer flasks and maintained at optical densities (OD_{750}) between 0.3 and 0.9 by regular dilution with fresh BG-11 medium (Rippka et al., 1979). The strains were cultured at 25° C without external aeration or permanent shaking under constant fluorescent light (Philips Master TL-D 58W/ 865) with a photon flux rate of $15 \mu\text{mol photons} \cdot \text{m}^{-2} \cdot \text{s}^{-1}$.

The biovolume was calculated by multiplying the cell number present at a certain OD_{750} with the strain-specific average cell volume. Cell numbers were determined by counting cells in a Thoma chamber (0.0025 mm² grids, 0.01 mm depth) with the help of a digital microscope (AMG EVOS fl, Peqlab, Erlangen, Germany) and ImageJ analysis software (Rasband WS. ImageJ, U.S. National Institutes of Health, Bethesda, Maryland, USA). Cell diameters were determined with the above-mentioned microscope as well. Cell volumes were calculated assuming a spherical shape of the cells.

Table 3.1: Biovolume: Cell diameter, cell number at $OD_{750} = 1$ and corresponding biovolumes for *M. aeruginosa* PCC 7806 and *Synechocystis* PCC 6803

Strain	Diameter [μm]	Cells $\cdot \text{mL}^{-1} \cdot \text{OD}^{-1}$	Biovolume [$\mu\text{L} \cdot \text{mL}^{-1} \cdot \text{OD}^{-1}$]
PCC 7806	3.39	$6.69 \cdot 10^7$	1.36
PCC 6803	2.35	$2.04 \cdot 10^8$	1.39

3.3.2 High light exposition

A shift from light limitation to carbon limitation, with all accompanying secondary effects, was intended to trigger physiological reactions and adaptations, which might also

be relevant in the field during cyanobacterial mass developments. Intentionally, buffering substances, as well as supplementation with excess inorganic carbon were excluded from the growth medium.

For the experiments, the cultures were grown to optical densities of 0.7 ($0.96 \pm 0.06 \mu\text{L}$ cells/ 1 mL culture). The light intensity was elevated from 15 to 250 $\mu\text{mol photons} \cdot \text{m}^{-2} \cdot \text{s}^{-1}$. Photon flux rate was measured with a LI-250A light meter and a spherical sensor (LI-COR® Biosciences, USA). Oxygen concentration and pH of the cultures were determined with a PCE-PHD 1 probe (PCE Deutschland GmbH, Meschede, Germany). The temperature remained constant at 25° C during the time of exposition.

3.3.3 Glycogen quantification

For glycogen quantification, samples were taken from three independent cultures of each strain. Cells from 1 mL culture were collected by centrifugation at each time point and immediately fixed in ethanol. The ethanol was discarded by pelleting the samples in a centrifuge and careful aspiration of the liquid. All samples were dried completely on air. The glycogen of each sample was hydrolyzed to glucose in 100 μL 3.5 % sulfuric acid for 40 minutes at 100° C. For colorimetric determination of the glucose content, 1 mL of 6 % (v/v) *o*-toluidine in acetic acid was added to each hydrolysate and incubated for another 7 minutes at 100° C. Subsequently the samples were cooled on ice for 5 minutes and centrifuged briefly at room temperature. The reaction product had an absorption maximum at 635 nm, which was measured with a bench top photometer (Applied Science) under a fume hood. A calibration curve was established for quantification in parallel with the help of identically processed glycogen standards.

3.3.4 Estimation of cyanophycin content

Three independent replicates of each low light adapted strain were sampled after 0, 1, 2 and 3 hours of high light exposition. Cyanophycin was extracted according to the protocol of (Simon and Weathers, 1976). Cells from 10 mL culture were washed once

with water and stored -20° C until further processing on the same day. The cells were re-suspended in water containing 0.5 % Triton X-100 and extracted by shaking at 4° C overnight. *Synechocystis* samples required further mechanical treatment on a cell mill (Retsch, Germany) for 15 minutes. The samples were centrifuged at 20.000×g and 4° C for 30 minutes. The pellets were washed with water three times. Cyanophycin was dissolved in 0.1 M HCl at RT on a shaker for 1 hour. The samples were cleared by centrifugation, and the obtained extracts were analyzed by SDS-PAGE. For the estimation of the cyanophycin content the Coomassie stain intensity of the diffuse band between 25 and 35 kDa was quantified using Image Lab™ software (BioRad, USA).

3.3.5 Electron microscopy

To prevent artifacts due to collapse of gas vesicles during centrifugation, the cells from 2 mL culture were collected by fast vacuum filtration (Krall et al., 2009). Immediately after collection, the cells were suspended in 100 µL 100 mM sodium cacodylate buffer pH 7.0 containing 2.5 % glutaraldehyde and 2 % formaldehyde for fixation at RT for 1h and at 4° C overnight. Subsequently, the cells were embedded in 1.5 % low melting agarose (Sieve GP, Biozym, Oldendorf, Germany) and immediately spread on microscopy sample slides. After solidification of the agarose, cubes of less than 1 mm³ were cut, transferred into fresh 1.5 mL tubes and washed 3 times for 10 minutes in 100 mM sodium cacodylate buffer. The samples were post-fixed at RT for 90 minutes with 2 % OsO₄ in 100 mM sodium cacodylate buffer and subsequently washed in water. Dehydration was done in a graded ethanol series and acetone. The specimens were embedded in Agar low viscosity resin (Agar Scientific Elektron Technology UK Ltd, Stansted, United Kingdom). Ultra-thin sections were stained with uranyl acetate, as well as lead citrate. Imaging was carried out on a Philips CM100 transmission electron microscope operating at 100 kV. Electron microscopy was conducted in cooperation with Prof. Dr. Otto Baumann, Potsdam University, Golm, Germany.

3.3.6 Sample preparation for GC/MS

Cells from cyanobacterial cultures at optical densities of 0.7 were harvested by fast vacuum filtration under the corresponding light conditions of the experiment (Krall et al., 2009). Durapore® PVDF hydrophilic filters with a diameter of 25 mm and a pore size of 0.45 μm (Millipore, USA) were used. After aspiration of the medium, the filters with adhering cells were rapidly transferred to fresh 1.5 mL microcentrifuge tubes and frozen in liquid nitrogen immediately. The samples were stored at -80°C until metabolite extraction. In total, samples of five independent biological replicates of each of the three genotypes, taken at 3 different time points were analyzed. The analytical background was assessed with the help of five extraction blanks i.e. filters without adhering cells that were identically processed as follows.

Metabolite extraction was done by a one-step extraction procedure as described in (Huege et al., 2011). In short, 1 mL of $\leq -15^{\circ}\text{C}$ cold 90 % (v/v) methanol extraction solution supplemented with 0.8 $\mu\text{g}/\text{mL}$ U- ^{13}C -sorbitol ¹ was added to the frozen samples, followed by immediate vortexing for 1 minute. Subsequently, the samples were further extracted in an ice-cooled bath-type sonicator 2 times for 5 minutes, as well as vigorous shaking by an orbital shaker for another 90 minutes at 4°C . The filters were removed carefully from the tubes and the extracts centrifuged at $10.000\times g$ and 4°C for 5 minutes. From the extracts, a fraction of 900 μL was transferred to fresh 1.5 mL tubes and subsequently dried in a vacuum concentrator at RT in the dark. The samples were stored at -20°C for a maximum of one week until analysis.

Extracellular metabolites were also analyzed. To that end, the spent medium of 2 mL culture samples was cleared from cells by centrifugation at $10.000\times g$ and 4°C for 5 minutes. 1.5 mL of the medium was transferred to fresh tubes and centrifuged as above to exclude any cell transfer. Finally, 750 μL of the cleared supernatant was again transferred to fresh tubes and dried in a vacuum concentrator as described above.

Metabolite analysis was carried out according to an established protocol for the quan-

¹U- ^{13}C -sorbitol served as internal analytical standard for assessment of extraction variability

tification of metabolites from cyanobacterial extracts including various classes of small molecules such as sugars, sugar alcohols, organic acids, amino acids and nucleosides, as well as various lipophilic substances (Krall et al., 2009; Huege et al., 2011).

Metabolite derivatization and GC-EI-TOF-MS analysis with m/z acquisition of 85–750 were performed as described (Huege et al., 2011). A mixture of fatty acid methyl esters (FAMES) was included during derivatization and used as internal marker system to adjust the retention index (RI) for chromatographic retention time variation (Krall et al., 2009).

3.3.7 GC/MS data processing and analysis

GC/MS data was processed and analyzed by Dr. Dirk Steinhauser (Max-Planck-Institute, Golm, Germany). Non-targeted alignment of chromatograms was followed by curating of the aligned peaks to obtain a targeted peak library of low redundancy for ultimate peak extraction and quantification. The obtained dataset comprised 45 sample profiles with 501 peaks and a total of 2082 (9.23 %) missing values. The compounds were identified by using reference compound libraries of commercially available standards (Kopka et al., 2005; Krall et al., 2009; Huege et al., 2011).

3.3.8 Statistical analyses and visualization

Data analysis was performed by D. Dirk Steinhauser (Max-Planck-Institute, Golm, Germany) according to (Sokal and Rohlf, 1995) and (Legendre and Legendre, 1998) using R 3.0.2 (R Development Core Team, 2013). Hierarchical cluster analysis (HCA) with average linkage clustering was used to draw cluster trees. The number of supported clusters was estimated using gap statistic (Tibshirani et al., 2001). Factors for two-way ANOVA were genotype, treatment (as time) and genotype-treatment interaction. Mean differences were estimated with Tukey's HSD method, and the p -values were corrected by Benjamini–Yekutieli correction (Benjamini and Yekutieli, 2001).

3.4 Results

3.4.1 High light, oxygen evolution and medium pH

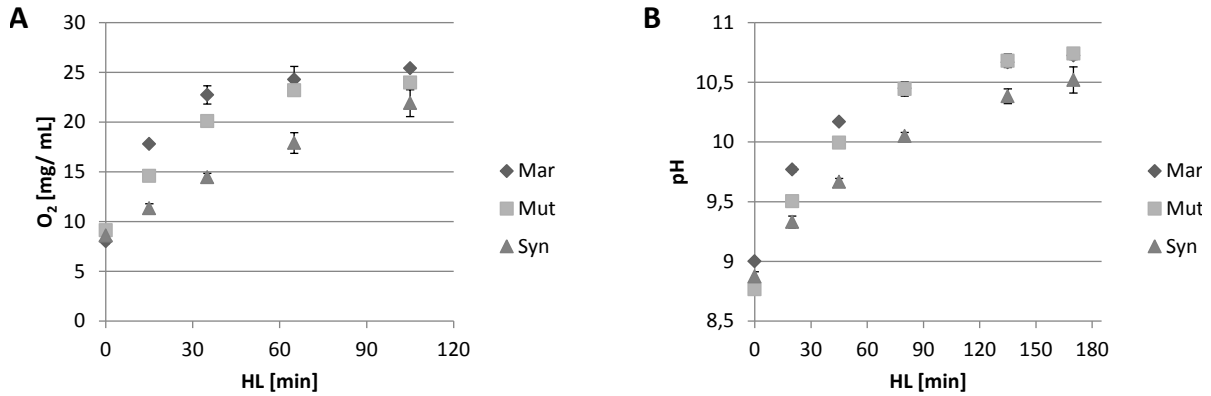


Figure 3.1: Net photosynthesis of three independent cultures of each cyanobacterial strain under high light **A**: Oxygen evolution; **B**: pH dynamics in the culture medium after the onset of high light illumination. Whiskers indicate the standard deviation from the means in each diagram.

Oxygen evolution served as a direct proxy of net photosynthetic activity during the first half of the experiment. Initially, the oxygen concentration of light limited cultures was in equilibrium with the atmosphere, which indicated that the light intensity was close to the photosynthetic compensation point. High light illumination led to oxygen over-saturation of the culture medium. The steepest increase was observed in wild-type *Microcystis* cultures. Oxygen evolution in the *Microcystis* $\Delta mcyB$ mutant cultures was significantly lower than in the cultures of the wild-type during the first 15 minutes of the experiment and was even more lagging behind in the cultures of *Synechocystis*. For p -values of significance test, see table 3.3. Since oxygen escaped steadily from the cultures into the atmosphere, only the first three values could serve as a measure for net photosynthesis. However, the pH as an indirect measure for the CO₂ uptake from the medium by cyanobacterial cells might also roughly reflect net photosynthesis. Indeed, the increase of pH behaved proportionally to oxygen evolution in all three strains. *Microcystis* wild-type cultures again showed the significantly steepest increase during the first

45 minutes of the high light treatment followed by $\Delta mcyB$ mutant- and *Synechocystis* cultures.

3.4.2 High light induced metabolic differences between strains

The above described differences already suggested strain-specific metabolic traits. The heat map of figure 3.2 shows those 193 metabolites, which were present in all cyanobacterial strains and which accumulated significantly different in at least one of the tested-, low light adapted genotypes after exposition of the respective cultures to high light for one hour [T1], or for three hours [T3]. The biggest cluster comprised those metabolites, which accumulated in a similar fashion in all three genotypes (cluster A, n=68), indicating a conserved response to high light illumination. Among the identified metabolites were mainly amino acids, as well as compounds of the CBB and the TCA. However, for many other metabolites, species specific changes were detected. Metabolites, which accumulated specifically in *Synechocystis*, but were vastly unchanged in *Microcystis* comprised metabolites of the clusters B (specific decrease, n=8) and F (specific increase, n=46). Cluster F includes the amino acids glycine, arginine, proline, glutamine and norleucine, which did not accumulate significantly different in *Microcystis* cultures under high light.

Several metabolites accumulated specifically in both *Microcystis aeruginosa* genotypes, as visualized in cluster D (specific increase, n=32) and G (specific decrease, n=2). Most remarkably, high light illumination led to specific accumulation of a number of metabolites only in *Microcystis* wild-type cells (cluster C, n=34), but neither in the *Microcystis* $\Delta mcyB$ mutant genotype, nor in *Synechocystis* cells. Although the metabolites of this cluster, except 1,3-dihydroxyacetone, could not be classified yet, a substantial impact of microcystin production on the metabolism of *Microcystis* might be anticipated.

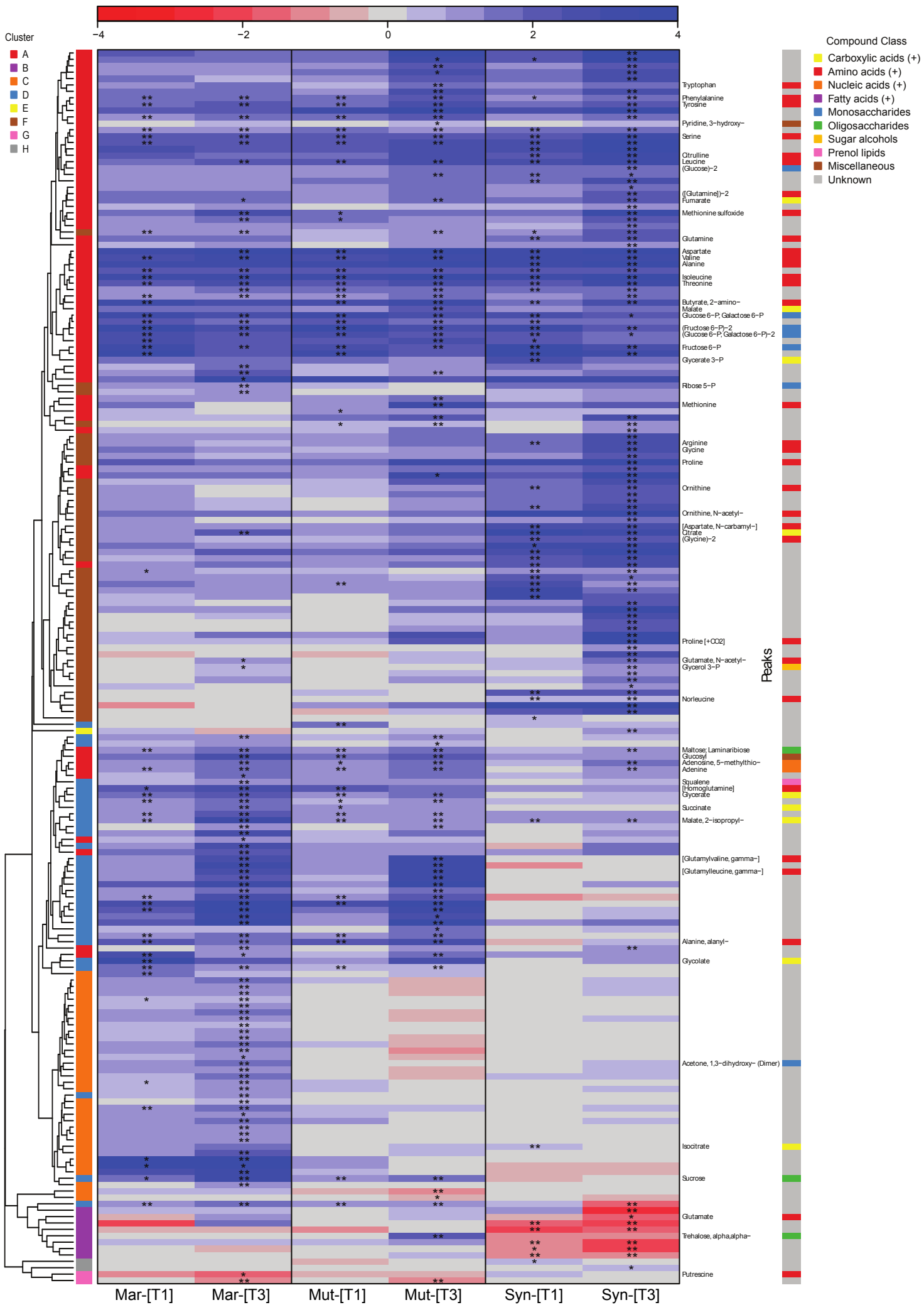


Figure 3.2: Cluster tree and heat map visualization of the 193 peaks with a significant light dependent change in at least one genotype. The color coded scale above the heat map represents a measure for log₂-fold changes of means after high exposition of low light adapted cells after 1 hour [T1] and after 3 hours [T3]. The genotypes are denoted as Mar: *Microcystis* PCC 7806 wild-type; Mut *Microcystis* 7806 $\Delta mcyB$ mutant; Syn: *Synechocystis* PCC 6803. Significant changes as determined by Tukey's HSD method are marked with asterisks: * $p \leq 0.05$ and ** $p \leq 0.01$. Names of identified metabolites are right beside the heat map. Substance classes are color encoded by the neighbouring bar at the right side. Clusters of the color coded hierarchical cluster tree on the left separates metabolite groups with specific accumulation patterns. Cluster A summarizes substances with a similar light dependent accumulation pattern across all genotypes. Clusters F and B indicate *Synechocystis* PCC 6803 specific responses not present in either of both *Microcystis* PCC 7806 genotypes. Cluster D denotes responses conserved in both *Microcystis* PCC 7806 genotypes but not in *Synechocystis* PCC 6803. Cluster C indicates responses unique for only the *Microcystis* wild-type but not for any of the other genotypes.

Mar vs. Mut

To better figure out the impact of microcystin production on the metabolome of *Microcystis*, data of *Synechocystis* was excluded from the analysis. In total, 85 out of the 501 metabolites (17 %) accumulated significantly different in *Microcystis* wild-type (Mar) and the $\Delta mcyB$ mutant strain (Mut) upon high light illumination, as illustrated in the sub-heatmap and cluster tree shown in figure 3.3. Most of the differences between the two genotypes became apparent after three hours of high light exposition.

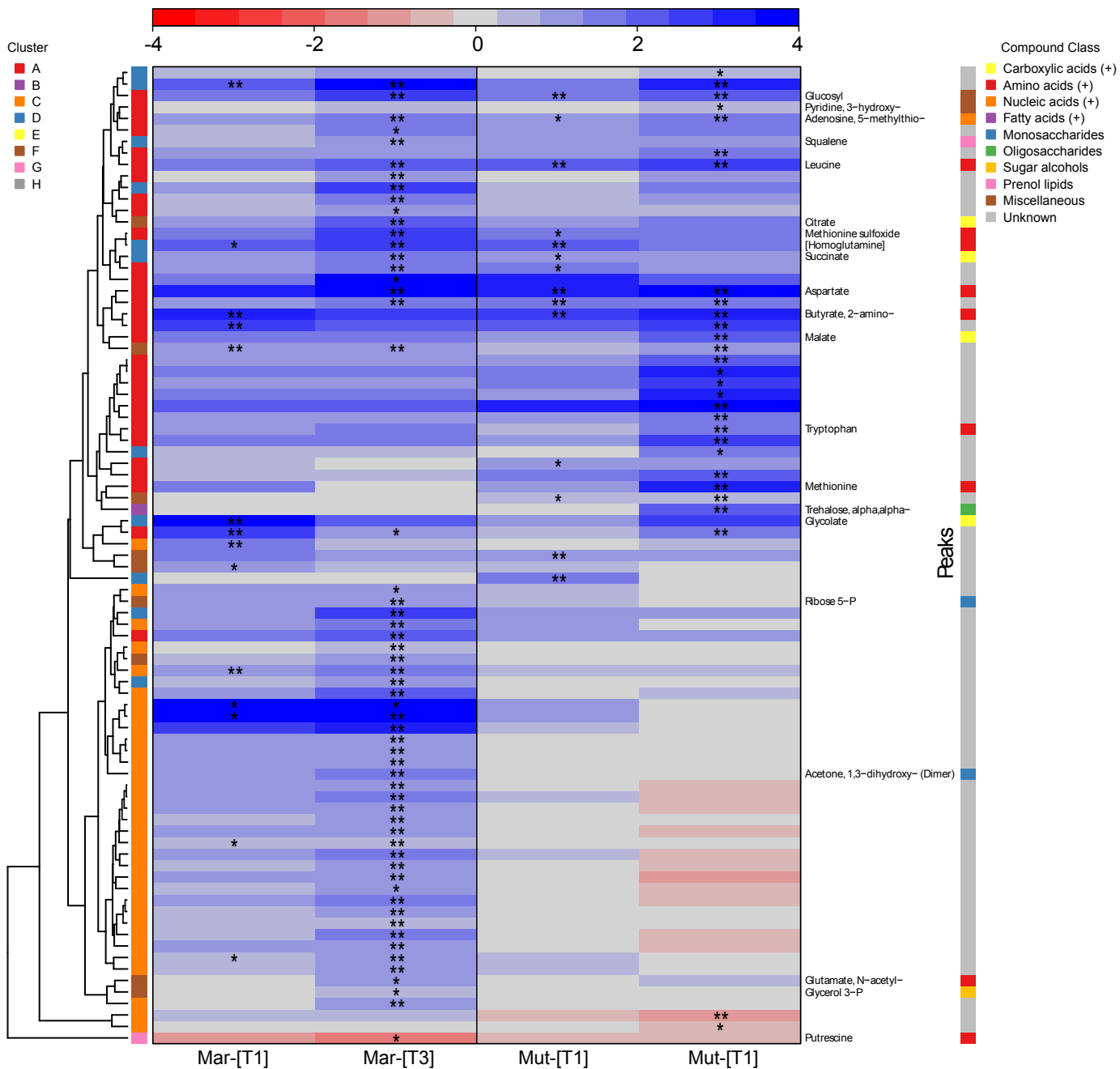


Figure 3.3: Cluster tree and heat map visualization of 85 peaks showing significant high light induced differences between *Microcystis aeruginosa* PCC 7806 wild-type (Mar) and the microcystin deficient $\Delta mcyB$ mutant strain (Mut) after one hour [T1] and after three hours [T3]. The scale of log₂-fold changes to initially low light adapted cells is placed above the heat map. Asterisks denote significant changes according to Tukey's HSD with $*p \leq 0.05$ and $**p \leq 0.01$. At the right side are the metabolite names of annotated peaks and the bar gives the chemical class as explained in the top-right legend. Metabolites were separated into groups according to their accumulation pattern and visualized on the as color coded hierarchical cluster tree on the left.

3.4.3 Central carbon pathway metabolites

Intermediates, especially those of the Calvin-Benson-Bassham cycle (CBB), are denoted by rather small pool sizes and fast turnover rates. Accordingly, the following bar diagrams represent steady state levels of metabolite concentrations under the applied conditions at the sampling time points. They do not reflect fluxes of e.g. carbon through specific metabolic routes, but rather indicate metabolite accumulation due to rate-limiting reactions (bottlenecks), overall up- or downshift of the utilization loads of certain pathways, as well as accumulation of stable intermediates for purposes of e.g. cell homeostasis, or storage.

The concentration of the CBB pathway intermediates was overall strongly increased 3-4-fold the initial values in all three strains after one hour of high light exposition. Interestingly, the levels of ribulose-5-phosphate (R5P) in *Synechocystis* were constantly about 3-4 times lower than those in the *Microcystis* strains. After three hours of illumination, the concentration of most CCB intermediates had dropped again to 2-3 times the initial levels. Glucose-6-phosphate (G6P), which links the CBB and glycogen synthesis, showed essentially similar temporal dynamics. A clear difference between *Microcystis* and *Synechocystis* was found in phosphoenolpyruvate (PEP) and pyruvate levels. Whereas *Microcystis* showed decreasing PEP concentrations after one hour of high light, the PEP and pyruvate levels in *Synechocystis* rose. The overall dynamics of PEP and pyruvate in *Synechocystis* were comparable to those of CBB intermediates and G6P, which might indicate channeling of assimilated carbon from the CBB towards the TCA. Indeed, citrate and isocitrate showed similar temporal dynamics. In contrast, PEP concentrations declined and pyruvate remained constant in *Microcystis* after one hour of high light.

The most surprising discovery of the metabolic study was that *Microcystis* samples only contained almost undetectable amounts of isocitrate under the conditions of the experiment. The almost undetectable levels of isocitrate might imply that *Microcystis* synthesizes 2-oxoglutarate (2-OG) in an alternative manner, at least during illumina-

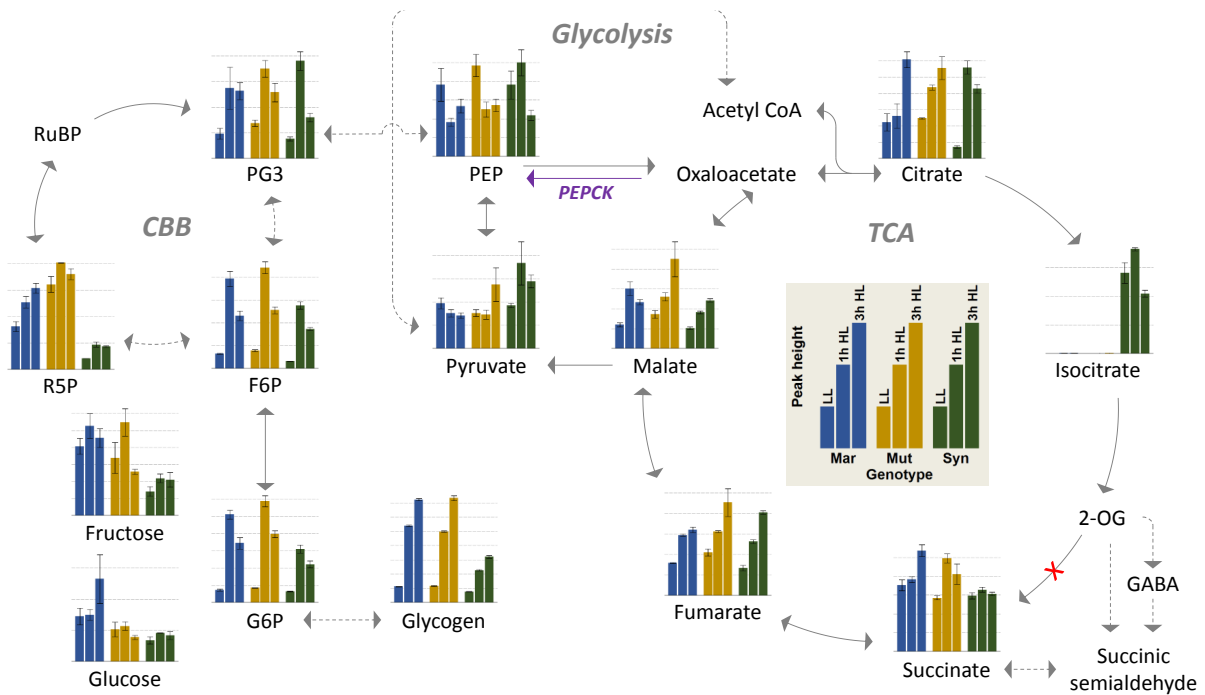


Figure 3.4: Impact of high light on the central carbon metabolism; The scheme comprises bar-plots of the measured metabolites involved in the Calvin-Benson-Besham cycle (CBB), glycolysis, and tri-carbonic acid metabolism (TCA), as well as tightly connected compounds. The proposed shunts to close the TCA-cycle *via* succinic semialdehyde are also included. The *Microcystis* specific enzyme PEPcarboxykinase is highlighted in purple. RuBP, ribulose-1,5-bisphosphate; PG3, 3-phosphoglycerate; PEP, phosphoeno/pyruvate; 2-OG, 2-oxoglutarate; a diagram explaining the bar-plots can be found inside the TCA.

tion. Alternatively, it might be inferred that isocitrate turnover is extremely fast and the pool size is very low, or that its synthesis is down-regulated to very low levels in *Microcystis*, but not in *Synechocystis* under the conditions of the experiment.

The overall dynamics of C-4 intermediates in all three strains and citrate in *Microcystis*, differed from those of the CBB in that their levels increased during the whole three hours of high light exposition. Only in 7806 WT, the malate levels behaved like CBB intermediates and might point towards the involvement of microcystin in carbon shuffling between malate and CBB during prolonged high light illumination.

3.4.4 Amino acids

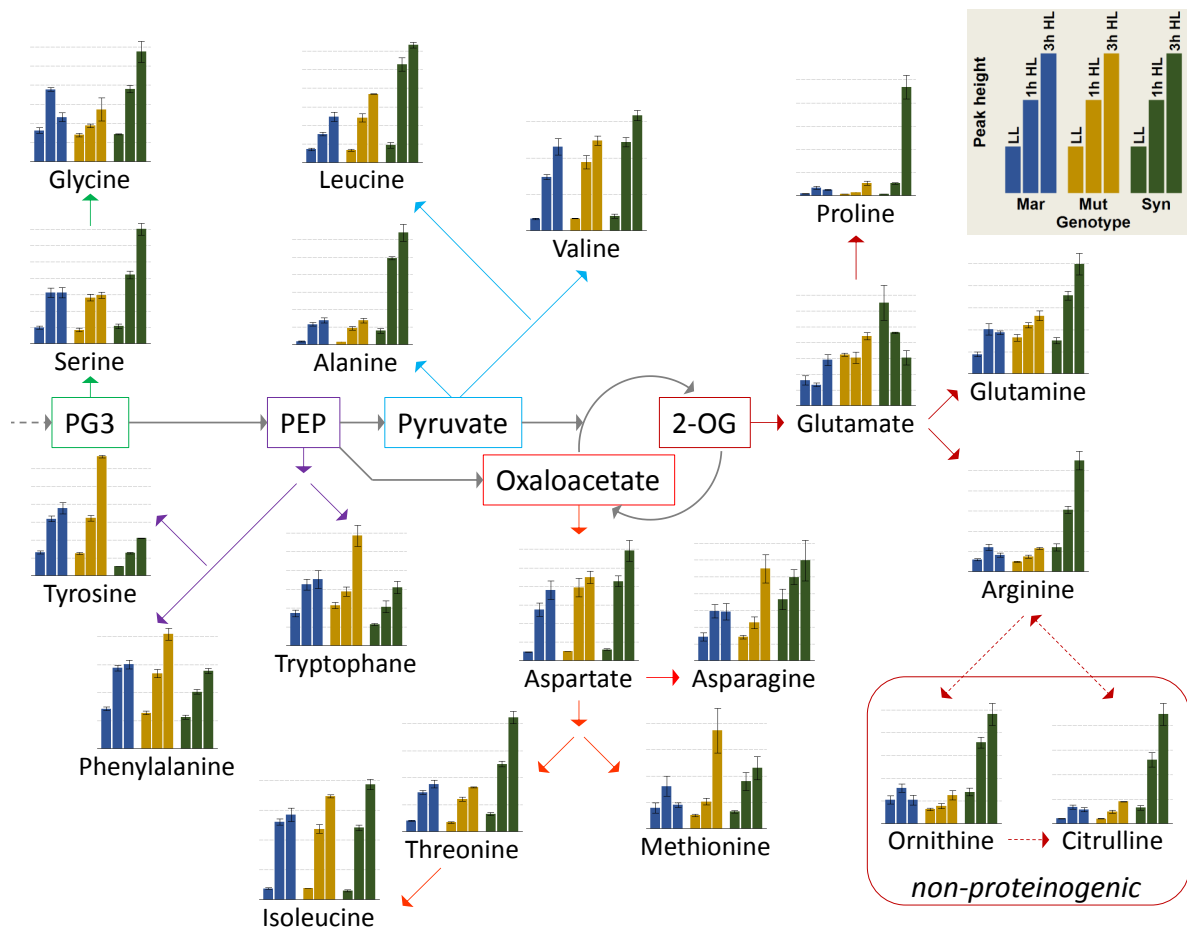


Figure 3.5: Amino acid accumulation during high light exposition and their proposed metabolic origins. The description of the bar-plots can be found at the upper right corner. PG3, 3-phosphoglycerate; PEP, phosphoenolpyruvate; 2-OG, 2-oxoglutarate

During high light exposition, the accumulation of most amino acids was increased in all strains, as visualized in figure 3.5. However, some substantial and species-specific differences became apparent with regard to groups of amino acids deriving from distinct precursor metabolites. Serine and glycine levels were stronger increased in *Synechocystis*, probably indicating a higher utilization rate of 3-phosphoglycerate. Though, both amino acids could also originate from photorespiration, which will be presented later in section 3.6. Levels of amino acids synthesized from PEP were in general more increased in *Microcystis* cultures, especially in those of the microcystin deficient $\Delta mcyB$

mutant. The accumulation of pyruvate derived alanine and leucine, but not valine was more pronounced in *Synechocystis* cultures. Amino acids of the aspartate family showed strong increases, which might indicate a connection to active β -carboxylation of PEP by PEPcarboxylase utilizing bicarbonate to form the precursor metabolite oxaloacetate. The strongest species-specific differences were observed for 2-oxoglutarate derived amino acids. Whereas the levels of those amino acids were almost unaffected in both *Microcystis* genotypes, a pronounced increase became evident in the samples of *Synechocystis*. Only the glutamate concentration declined from initially high levels. It seems likely that the synthesis of glutamate could not keep pace with its further rate of utilization into related amino acids, as well as in photorespiration 3.6.

The almost constant levels of 2-oxoglutarate related amino acids found in *Microcystis* cells are probably connected with the above reported absence of isocitrate, (see 3.4) and might further indicate rather low involvement of an oxidative TCA metabolism during illumination. In sharp contrast, *Synechocystis* appeared to channel lots of assimilates from the CBB towards the TCA for synthesis 2-OG and the derived amino acids.

3.4.5 Photorespiration

Photorespiration is a result of the RubisCO-oxygenase activity, which is favored under conditions of low carbon-to-oxygen ratios during illumination. The immediate products of RuBP oxygenation are one molecule of PG3 and one molecule of 2-Phosphoglycolate (2PG). 2PG is a potent inhibitor of the glycolytic enzymes triosephosphate isomerase and phosphofructokinase in plants (Anderson, 1971; Kelly and Latzko, 1976) and thus needs to be metabolised quickly. Cyanobacteria possess highly effective carbon concentrating mechanisms, which are supposed to effectively restrict 2PG formation to basal levels under standard conditions (see 1.2).

In this study the first measured photorespiratory intermediate was glycolate, see figure 3.6. In *Microcystis* wild-type cells, an 8-fold increase of glycolate was detected after one

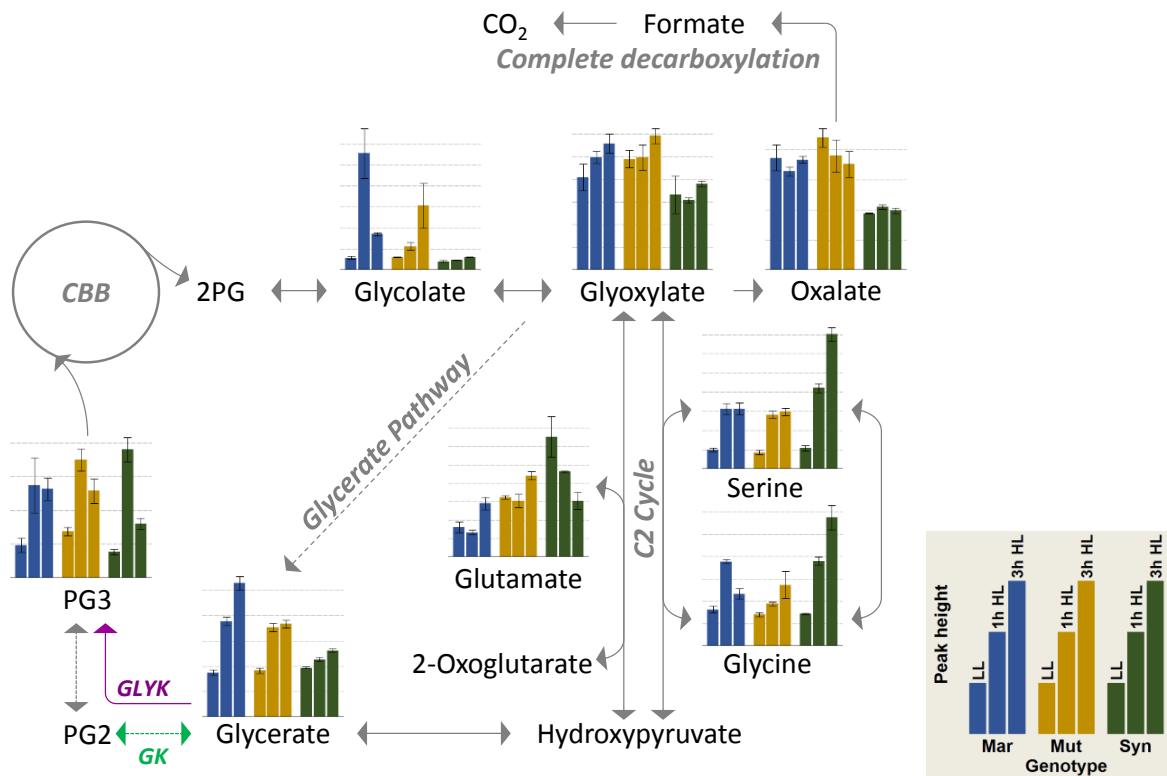


Figure 3.6: Photorespiration: Routes of the RuBP-oxygenation product 2-phosphoglycolate (2PG) metabolism and associated metabolites. The description of the bar-plots is displayed at the lower right corner.

hour of high light exposition. Interestingly, the amount of glycolate had declined again to values of about 3-fold the initial concentration after three hours of high light. In the $\Delta mcyB$ mutant, the glycolate concentration was only moderately increased after one hour, but steadily continued to rise to 4-fold the initial value after three hours of high light exposition.

From all of the other measured metabolites, only glycerate could serve as an additional indicator for high light-induced photorespiratory activity in *Microcystis*. Here, the values steadily increased in *Microcystis* wild-type 2.5-fold and 2-fold in the $\Delta mcyB$ mutant. It might be worth noting that the *Microcystis* genome encodes for a plant-type D3-glycerate kinase (GLYK), which directly catalyzes the phosphorylation of glycerate to 3-phosphoglycerate (PG3). In *Synechocystis* on the other hand, the conversion of glycerate to PG3 requires the concerted action of a class I glycerate kinase (GK) and a

phosphoglycerate mutase. The presence of GLYK could indicate a higher relevance of PG3 regeneration *via* the glycerate pathway in *Microcystis*.

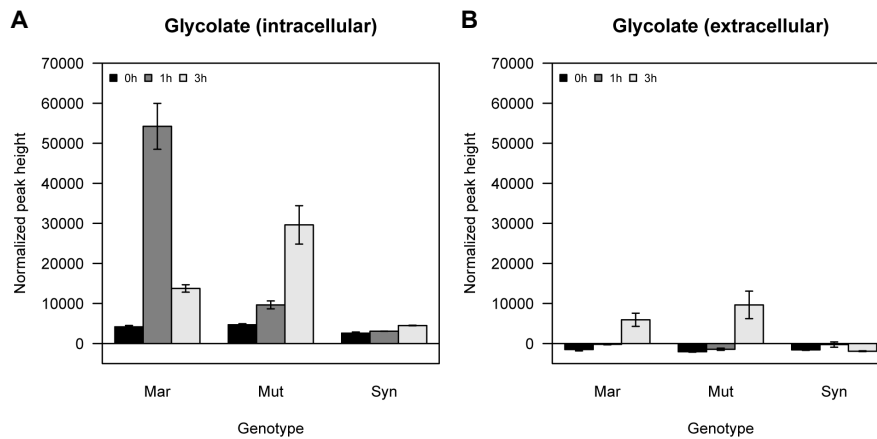


Figure 3.7: Glycolate accumulation inside the cells, A and in the culture medium, B of *Microcystis* wild-type (Mar), $\Delta mcyB$ mutant (Mut) and *Synechocystis* (Syn) cultures during high light exposition.

Interestingly, some of the produced glycolate was also found in the medium of *Microcystis* cultures after three hours of high light, which indicated secretion of at least parts of the photorespiratory intermediate, see figure 3.7. However, the relatively high intracellular amounts in *Microcystis* wild-type after one hour and the comparably low extracellular amounts occurring only after three hours of high light indicated metabolism of most of the produced glycolate by the cells.

Synechocystis cells showed only indirect signs of photorespiration during the entire time of high light exposition. Although not unequivocally assignable to photorespiratory metabolism, the decline of glutamate levels, as well as the increase of serine and glycine concentrations could eventually hint towards active glyoxylate processing to hydroxypyruvate *via* the plant like C2 oxidative photosynthetic carbon cycle. However, the measured intracellular glycolate levels remained at a constantly low level, and none of it was found excreted into the medium, see figure 3.7. Either the photorespiratory machin-

ery of *Synechocystis* was running so extremely efficient that no glycolate and glyoxylate built up or the oxygenation of RuBP was efficiently suppressed under the applied high light conditions in *Synechocystis*.

3.4.6 Compatible solutes

Compatible solutes are protective substances that have stabilizing effects on cell components and are reported to be synthesized in response to general stress (Klähn and Hagemann, 2011). The *Microcystis* mutant strain accumulated highest levels of the compatible solutes sucrose and trehalose, see figure 3.8. Prolonged high light exposition further increased their concentrations. The loss of microcystin synthesis eventually caused metabolic imbalances, which in turn led to elevated stress levels in the *Microcystis* mutant under the experimental conditions.

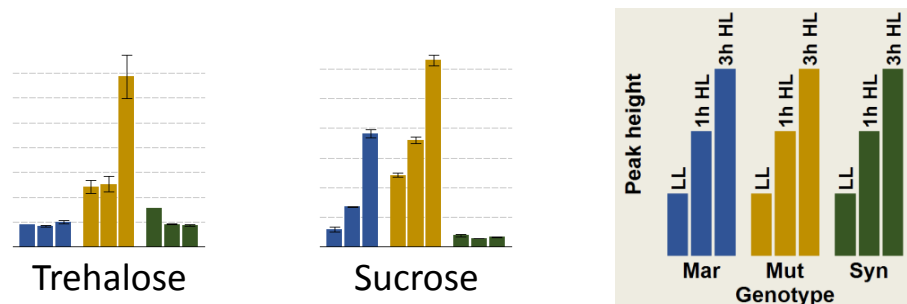


Figure 3.8: Compatible solutes -Accumulation of sucrose and trehalose might indicated a general stress response, most pronounced in *Microcystis* mutant cells. The description of the bar-plots is displayed at the right.

3.4.7 Quantification of storage compounds

Since metabolite fluxes could not be determined, it is indispensable to quantify the end products of photosynthesis to estimate the main metabolic routes indirectly. The electron micrographs of figure 3.9 show representative cells of the three cyanobacteria

strains before and after three hours of high light exposition. *Microcystis* cells were densely packed with coarse glycogen granules (Gg), which occupied almost all available space in the cytoplasm and between thylakoids. Though to a lower extent, *Synechocystis* also showed accumulation of glycogen granules, which were fine and did not cover the whole cytoplasmic space. The inclusions only visible in *Synechocystis* high light samples probably represent cyanophycin granules (Cp), for comparison see (Li et al., 2001). Interestingly, cells of the PCC 7806 $\Delta mcyB$ mutant appeared to possess higher numbers of gas vesicles than the wild-type (not systematically determined).

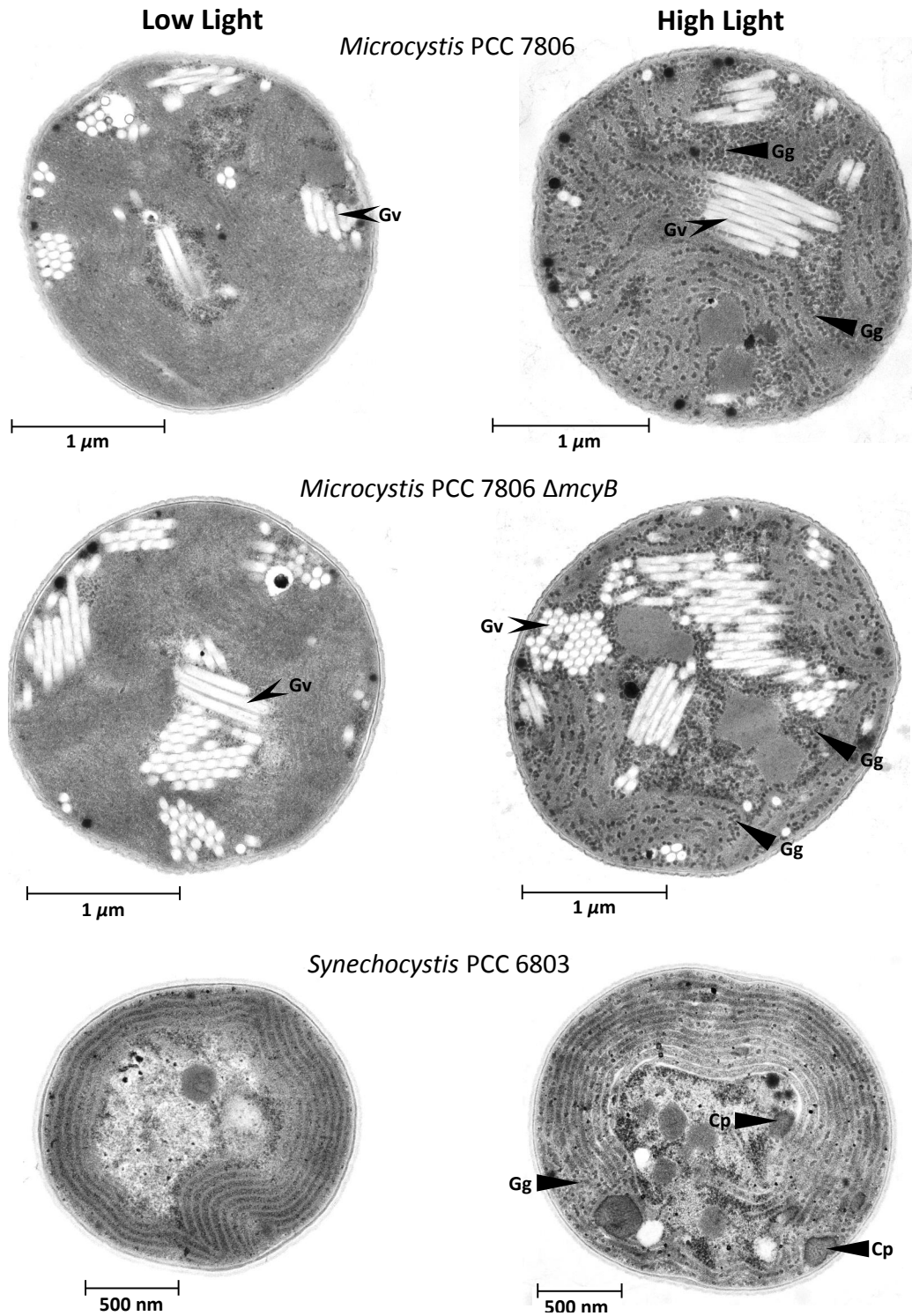


Figure 3.9: Electron microscopy of cells before (left) and after high light exposition for three hours (right); Gg, Glycogen granules; Gv, Gas vesicles; Cp, Cyanophycin; pictures were taken by Prof. Dr. Otto Baumann, Potsdam University.

Glycogen is supposed to be the main storage compound of reduced carbon in cyanobacteria. Thus, it was used as a relative measure to estimate the overall net photosynthetic activity of the cyanobacterial strains *via* the Calvin-Benson-Bassham cycle under the conditions of the experiment.

Figure 3.10 shows that the glycogen levels in all three strains were low in the beginning. Over the whole time of the experiment, glycogen levels increased in all strains, which indicates no absolute inorganic carbon depletion even after three hours of high light exposition. Both *Microcystis* strains showed about two times higher total glycogen accumulation per biovolume than *Synechocystis*. Although not tested significant (see table 3.5), the *Microcystis* wild-type accumulated slightly more glycogen than the microcystin deficient mutant during the first 90 minutes, which in turn accumulated more glycogen during the second half of the experiment. Interestingly, all three strains accumulated glycogen with a higher rate during the first 90 minutes and continued at a lower rate for the following 90 minutes. Note that glycogen accounted for about 8.5 % of the fresh weight in *Microcystis* and for about 4 % in *Synechocystis* at the end of the experiment.

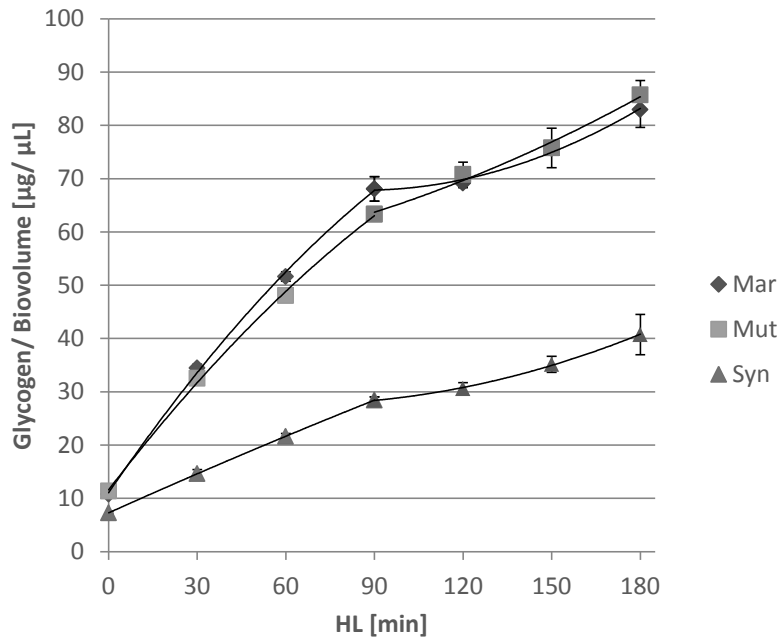


Figure 3.10: Glycogen accumulation per biovolume in cells of the cyanobacterial strains during high light exposition for three hours.

Cyanophycin, a polypeptide consisting of the two amino acids arginine and aspartate, is another typical storage compound of cyanobacteria. Granules of that copolymer became visible in electron micrographs of high light treated *Synechocystis* cells, but not in those of *Microcystis*, see 3.9. Relative determination of cyanophycin accumulation during high light exposition indeed revealed strain-specific differences. *Synechocystis* strongly accumulated cyanophycin, whereas both *Microcystis* genotypes did not, see figure 3.11 and supplement figure 3.14. In *Synechocystis* cyanophycin accumulated in a sigmoid fashion with the strongest increase between two and three hours under high light, which coincides with the decline of glycogen accumulation. In contrast, the cyanophycin content in both *Microcystis* genotypes declined during the first hour of the experiment and increased again to approximately the initial values within the following two hours. Please note that the bar diagram in figure 3.11 represents only relative cyanophycin concentrations. Considering the original Coomassie-stained gel of *Synechocystis* shown in figure 3.11 B) it became apparent that the low light adapted cells initially lacked almost any cyanophycin.

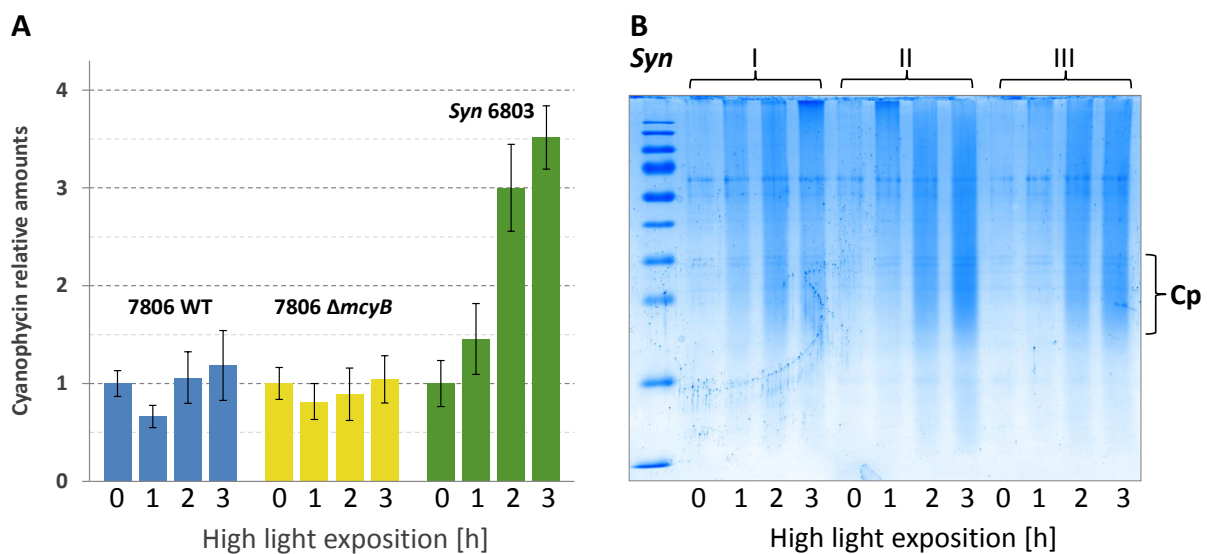


Figure 3.11: Cyanophycin: A, Relative accumulation upon high light illumination. Error bars indicate the standard deviation from the mean of three replicates each. **B**, Coomassie-stained gel of *Synechocystis* extracts from three replicates (I-III); Cp, cyanophycin smear area used for relative quantification. For gels of *Microcystis* extracts, see 3.14.

3.5 Discussion

This study aimed at characterizing the cyanobacterial metabolism under changing light conditions. For the first time, the *Microcystis aeruginosa* PCC 7806 wild-type and its $\Delta mcyB$ mutant strain was included in a metabolomics analysis and compared with the established model cyanobacterium *Synechocystis* PCC 6803. Valuable information about the role of microcystin in *Microcystis*, as well as conserved and strain-specific metabolic features was gained. The experimental set-up was chosen with the intention to simulate conditions as they might also be encountered at the natural habitat of *Microcystis*. A shift from low to high light directly increased photosynthesis rates of the cells and lead to marked changes of dependent secondary parameters, such as culture pH, oxygen concentration and inorganic carbon availability, which most likely had an impact on cyanobacterial adaptation processes during the experiment. The dynamics of those parameters might have been restricted by e.g. including pH buffering substances in the medium, blow out the produced oxygen by external aeration and by the supplementation of the cultures with additional sodium bicarbonate or CO₂ as source for inorganic carbon. However, all this artificial and never complete manipulations were intentionally excluded for the price of not knowing which exact parameter triggered what effect, but for the benefit of obtaining a more general and probably more representative picture of cyanobacterial adaptations as they might also be expected to take place in the field.

3.5.1 High light experiment

As intended, the onset of high light illumination triggered a marked increase of dissolved oxygen and the pH in the culture medium of all strains. *Microcystis* and *Synechocystis* showed distinct differences in photosynthetic activity and accumulation patterns of central carbon pathway intermediates, amino acids and storage compounds. Also, photorespiration seems to be of higher relevance in *Microcystis* under the conditions of the

experiment. A clear impact of microcystin on the metabolism of *Microcystis* to high light conditions, and its accompanying secondary effects might be inferred from the collected data.

3.5.2 Net photosynthetic activity

In this experiment oxygen evolution and glycogen accumulation served as a direct measure for net photosynthetic activity. Low initial glycogen contents, as well as oxygen concentrations in equilibrium with the atmosphere, indicated light limitation under the standard culture conditions before elevating the light intensity. During high light exposition the pH values correlated proportional with oxygen evolution and therefore could serve as an additional proxy for net photosynthesis; i.e. CO₂ or proton uptake, for the complete duration of the experiment.

Net photosynthesis was clearly lower in cultures of *Synechocystis*, which was reflected by comparably low glycogen content of the cells and moderate oxygen evolution. The capacity of the *Microcystis* strains to produce glycogen was significantly higher, which might indicate specific capabilities due to the original life style of the species.

In the field, *Microcystis* species regularly participate in cyanobacterial mass developments. Under those conditions, it might be of fundamental importance for the cells to harbor machinery that utilizes inorganic carbon as fast as possible and to store it in a reduced form as glycogen. *Microcystis* species synthesize gas-filled vesicles and usually form macroscopic colonies. The interplay with the assimilate ballast lets them actively migrate between different layers of the water column (Reynolds et al., 1987). In theory, low ballast of reduced carbon and lowered turgor would let colonies quickly rise to the water surface for utilization of light energy and inorganic carbon. Floating colonies could acquire CO₂ directly at the water-atmosphere interface. Conversely, high ballast of reduced carbon and increased turgor would let them sink to deeper layers, where the availability of inorganic nutrients is higher. Note that the glycogen content accounted for about 8.5 % of the fresh weight in *Microcystis* after three hours exposition to high

light. The elevated levels of compatible solutes, especially in the *Microcystis* $\Delta mcyB$ mutant, might also suggest an adaptation to increase the turgor for reversal of buoyancy (Reynolds et al., 1987).

In contrast, *Synechocystis* has a different lifestyle in that this species does not participate in the formation of cyanobacterial mass developments. The cells do not possess gas vesicles, and the formation of buoyant colonies was not reported yet. The original habitat of *Synechocystis* therefore might have favored a different strategy when sudden changes of light intensities are encountered by the organism.

In general, all three tested genotypes accumulated glycogen throughout the experiment, indicating neither severe photoinhibition nor net carbon loss due to photorespiration during the three hours of high light illumination. Interestingly, all strains showed a pronounced simultaneous decline of the glycogen accumulation rate after 90 minutes, which might indicate a general adaptation to the light conditions of the experiment. Depletion of C_i and limitation of glycogen accumulation to the rate of CO_2 diffusing into the medium might explain that phenomenon. This conclusion is in line with the only moderate pH increase between 90 and 180 minutes of high light exposition.

An important aspect of *Microcystis* species is their ability to produce various secondary metabolites with often yet unknown functions. In the case of microcystin, as one of the most intensely studied cyanobacterial secondary metabolites, a significant role in physiological adaptation becomes more and more evident, which is also reflected by the differences observed in this study between the two *Microcystis* strains PCC 7806 wild-type and its microcystin deficient $\Delta mcyB$ mutant. Oxygen evolution was significantly lower in the $\Delta mcyB$ mutant during the first minutes after the shift from low- to high light, see table 3.3. Also, the steeper pH increase in the medium and faster glycogen accumulation point towards a specific function in inorganic carbon acquisition during adaptation to increased light intensities.

In previous studies it was shown that microcystin can bind to proteins (Zilliges et al., 2011), see also chapter 2 of this work. It binds covalently to thiol groups of cysteines

and by that lowers the susceptibility of proteins towards proteolytic digest. Especially the change of light conditions from low to high supports the interaction of microcystin with cellular proteins, with the large subunit of the carbon fixing enzyme RubisCO as one of the major targets.

The question about whether or not microcystin production has an impact on enzyme activities was the motivation for conducting the metabolomics approach discussed in the following.

3.5.3 High light exposition revealed strain specific metabolic differences

The heat map 3.2 provided a representative estimate of the differential metabolite accumulation in the three strains used in this study after transfer of the cultures to high light. From a total of 501 peaks detected in each of the 45 chromatograms, 193 showed significant light-induced changes in at least one of the three strains. About one-third (n=68) of the 193 variable peaks represented substances, which accumulated in all three strains simultaneously, indicating a conserved cyanobacterial reaction triggered by a shift from low- to high light. The remaining two-thirds (125) of accumulated non-uniformly in the three strains. About 28 % of the 193 light dependent metabolites were specifically changed only in *Synechocystis*, 18 % in both *Microcystis* strains, but not in *Synechocystis* and another 18 % were only changed in the microcystin producing *Microcystis* wild-type. Despite not knowing the exact identity of many of the detected compounds it might be concluded that:

1. High light changed the metabolic constitution of all strains
2. The metabolomic changes were species specific
3. Microcystin production influenced the metabolism of *Microcystis*

3.5.4 Central carbon pathway metabolites

High light exposition triggered a sharp increase of most measured CBB intermediates in all tested strains after one hour. This finding appears plausible, since it was assumed that the cultures were grown under light limiting conditions just above the light compensation point, which was also reflected by low initial oxygen concentrations and low glycogen contents. However, the onset of high light illumination presumably triggered the activation of key CBB enzymes and the accumulation of CBB intermediates. During the first minutes of high light illumination, the so-called induction period, most of the existing triose phosphates and newly assimilated carbon are used to build up intermediates for acceleration of the CBB. After one hour of high light exposition, the amount of the measured CBB intermediates might reflect the maximum capacity of the cycle in the tested genotypes. The observed decrease of CBB intermediates after three hours of high light might be explained by general down-regulation of the cycle due to the limitation by inorganic carbon. However, still, the concentrations of CBB intermediates in the cells were about 2-3 times higher at that time as they were in light-limited cultures.

The general accumulation pattern of CBB intermediates was not observed for ribose-5-phosphate (R5P), which additionally accumulated about three times higher in *Microcystis* cultures. However, R5P is also strongly involved in the synthesis of nucleotides, co-enzymes and proteins. For that reason, the observed concentrations of R5P could not exclusively be linked to its role as CBB intermediate but indicated strong strain-specific differences not explainable yet.

Metabolites involved in glycolysis showed non-uniform accumulation patterns. PEP levels declined from comparably high initial concentrations in both *Microcystis* genotypes but were elevated in *Synechocystis* after one hour of high light exposition. At the end of the experiment, the PEP levels were highly similar in all three strains. Pronounced channeling of assimilates from the CBB towards TCA might be assumed for *Synechocystis*, since the accumulation pattern of PEP resembled that of CBB intermediates, as well as those of citrate and isocitrate. The glycolytic formation of pyruvate yielding addi-

tional ATP, as well as channeling of assimilates towards citrate, is probably suppressed in *Microcystis* in the light. The different accumulation patterns of 2-oxoglutarate derived amino acids in both species further supported this assumption, see 3.5.7.

3.5.5 TCA metabolism

The very low levels of detected isocitrate in both *Microcystis* strains was highly unexpected and had never been reported for cyanobacteria before. Both species harbor the same set of respective genes. Hence, a *Microcystis*-specific regulation of isocitrate synthesis and/ or metabolism might be inferred. In general, cyanobacteria do not perform TCA metabolism in the appearance of the classical TCA-cycle, as present in e.g. aerobic heterotrophs since the enzyme complex of 2-oxoglutarate dehydrogenase is absent. Huge efforts have been undertaken to find enzyme candidates in cyanobacteria to bridge the missing step of the cycle. Recently, 2-oxoglutarate dehydrogenase and succinic semi-aldehyde dehydrogenase were finally figured out as most promising candidates (Zhang and Bryant, 2011). An alternative route from 2-oxoglutarate over γ -aminobutyric acid (GABA) and succinic semialdehyde to succinate was described. To what extent a closed TCA cycle is required for photoautotrophic growth remains to be clarified in the future. However, the relatively low levels of isocitrate in *Microcystis* might even challenge the assumption that 2-OG is produced *via* decarboxylation of isocitrate by the enzyme isocitrate dehydrogenase, although present. It might be proposed that the oxidative reactions of the TCA, which yield additional ATP and NADH, were mostly down-regulated during illumination. Nonetheless, even under light limiting conditions [T0] almost no detectable isocitrate was present in *Microcystis* cells, which might indeed indicate a strain-specific peculiarity.

Alternatively, the pool size of isocitrate could have been smaller in *Microcystis*. The conversion of citrate to 2-oxoglutarate *via cis*-aconitate and isocitrate by aconitase and isocitrate dehydrogenase were possibly carried out in a very condensed way. For exam-

ple, the formation of a functional complex including both enzymes could also explain the very little amounts of detectable isocitrate that were present in *Microcystis* cells.

If citrate was indeed not further metabolized to isocitrate in *Microcystis*, it appears almost certain that the TCA-cycle metabolites malate, fumarate and succinate originated mainly from β -carboxylation of PEP to form oxaloacetate by the action of PEPcarboxylase. From an energetic perspective, it generally appears favorable also for *Synechocystis* to employ these parts of the TCA mainly in a reductive fashion, to regenerate ADP and NADP for maintaining high photosynthetic activity. Additionally, carbon fixation by PEPcarboxylase utilizes bicarbonate with high affinity and is not bothered with (undesirable) competing reactivity like RubisCO at low $\text{CO}_2 : \text{O}_2$ ratios.

PEPcarboxylase is an essential enzyme in cyanobacteria (Luinenburg and Coleman, 1990). Significant amounts of inorganic carbon are primarily fixed by PEP carboxylation (Young et al., 2011). The observed accumulation of oxaloacetate-derived metabolites and amino acids could suggest that the action of PEPcarboxylase becomes even more relevant in situations of high photosynthetic activity marked by high oxygen concentrations and CO_2 deprivation.

3.5.6 Cyanobacterial C4 characteristics

The above discussed primary carbon fixation *via* PEP carboxylation is a common feature among certain vascular land plants employing the C4- or crassulacean acid metabolism (CAM) to concentrate CO_2 around RubisCO. It might be speculated that cyanobacteria also employ at least parts of that type of carbon concentrating mechanism. Flux analysis experiments in *Synechocystis* PCC 6803 already showed a substantial flow of carbon from malate towards pyruvate (Yang et al., 2002; Young et al., 2011), characteristic for C4-type plants. Mutants of *Synechocystis* PCC 6803 with knocked out malic enzyme were also shown to grow much slower than the wild-type under constant illumination (Bricker et al., 2004).

Besides the very effective utilization of bicarbonate by PEPcase, a positive side effect

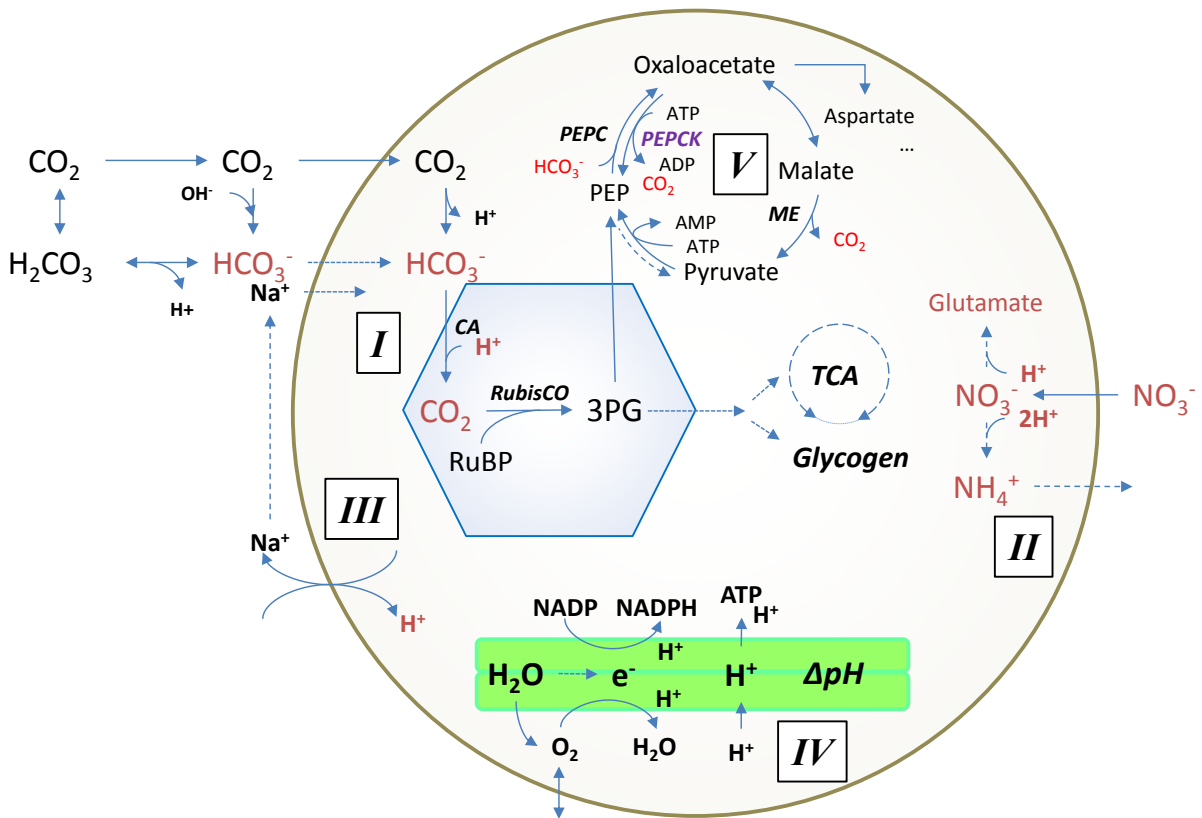


Figure 3.12: Scheme of selected metabolic features affecting the intracellular pH during photosynthesis: **[I]** denotes the assimilation of bicarbonate from the surrounding medium, which requires equimolar amounts of protons, i.e. pH_{in} balancing. **[II]** illustrates nitrate import and reduction. Assimilation of nitrate *via* ammonium into glutamate requires one balancing proton, excretion of ammonium two. **[III]** shows proton import from the medium in exchange with sodium ions. **[IV]** illustrates the pH-neutral light energy metabolism and redox control by oxygen reduction to water. **[V]** highlights the direct bicarbonate assimilation route *via* PEP-carboxylation and the synthesis of organic acids for pH_{in} balancing. Metabolic cycling *via* malate and pyruvate for means of dissipation of excess energy might be inferred as well (Young et al., 2011; Nogales et al., 2012). Direct pyruvate synthesis from PEP is broadly suppressed in the light (You et al., 2014).

of that C4-type carbon concentration would be the temporal accumulation of organic acids, which might positively contribute to maintaining cellular pH homeostasis during episodes of high light illumination, see 3.12. Since bicarbonate is one of the main inorganic carbon sources for autotrophic cyanobacterial growth, the need for effective

pH regulation appears inevitable. Nitrate reduction to ammonium and its utilization in amino acid synthesis also requires equimolar amounts of protons, see equation 3.1. Balancing of the cytoplasmic pH is probably achieved by the concerted action of proton import from the medium *via* e.g. Na^+ / H^+ antiporters (Miller et al., 1984; Billini et al., 2008) and probably also by the synthesis and accumulation of molecules with a high pH buffering capacity such as organic acids like malate, fumarate and also citrate, as was observed in this study.

A discriminating feature between the cyanobacterial species is the presence of the enzyme PEPcarboxykinase (PEPCK) in the genome of *Microcystis* PCC 7806. This enzyme directly catalyzes the reaction from oxaloacetate back to PEP with the help of only one molecule ATP, releasing CO_2 and ADP. Compared to the regeneration of PEP from malate by the action of malic enzyme NADP^+ and pyruvate-phosphate dikinase, which *in summa* requires 2 ATP ($\text{AMP} + \text{PP}_i$ is released), the action of PEPCK theoretically saves 50 % of the energy.

Carbon fixation for e.g. carbohydrate synthesis mutually depends on RuBP carboxylation by RubisCO. Thus, the presence of PEPCK could indicate a higher relevance of temporal C4-metabolites accumulation in bloom-forming *Microcystis*. The efficient conversion of e.g. malate to PEP and CO_2 *via* oxaloacetate might be advantageous in supporting RuBP carboxylation after a change from CO_2 limiting conditions and excess light to moderate illumination. Interestingly, PEPCK is also encoded in the genomes of confirmed alkalophils and cyanobacteria living in dense mats, where bicarbonate can be assumed to be the major source of inorganic carbon.

3.5.7 Amino acid metabolism

The onset of high light illumination triggered a pronounced accumulation of most amino acids in all tested strains. The experimental set-up did not allow statements about the exact origin of the measured amino acids. Hence, it can not be distinguished, whether

Table 3.2: PEPCK distribution among cyanobacterial species; selection of *Microcystis* PCC 7806 homologues according to BLASTp (<http://blast.ncbi.nlm.nih.gov/Blast>)

Strain	Habitat	Accession
<i>Coleofasciculus</i> sp. PCC 7420	microbial mats	WP_006104302
<i>Geitlerinema</i> sp. PCC 7407	mats on different substrates	YP_007108527
<i>Cyanothece</i> sp. PCC 7822	rice fields	YP_003890568
<i>Pleurocapsa</i> sp. PCC 7327	alkaline lakes	YP_007083253
<i>Oscillatoria acuminata</i> PCC 6304	mats on different substrates	YP_007088744
<i>Arthrospira platensis</i> Nies-39	alkalophilic, (sub)tropical	YP_005068380

the observed accumulation of amino acids was due to proteolytic degradation of proteins or *de novo* synthesis. However, the apparent accumulation of cyanophycin granules in *Synechocystis* rather point towards net amino acid and peptide synthesis (Kolodny et al., 2006).

Of the primarily 3-phosphoglycerate derived amino acids serine and glycine, a stronger high light induced increase was observed in *Synechocystis* cells. Though, both amino acids could also be products of the C2 photorespiratory cycle, which might have a higher relevance in *Synechocystis*. Amino acids originating from PEP accumulated most in cells of the *Microcystis* $\Delta mcyB$ mutant, which might imply a regulatory role of microcystin in certain biosynthesis steps of those amino acids. Pyruvate-derived amino acids, especially alanine and leucine accumulated stronger in *Synechocystis*.

Taking into account the proposed flow of carbon from PEP carboxylation to oxaloacetate via malate and the malic enzyme back to pyruvate (Young et al., 2011), it appeared plausible that the associated amino acids accumulated due to this type of carbon cycling in *Synechocystis*. *Microcystis* on the other hand employs the enzyme PEPCK and therefore might accumulate higher amounts of PEP derived amino acids originating from oxaloacetate.

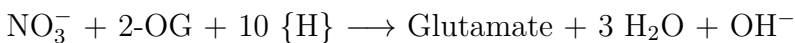
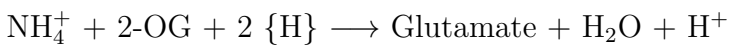
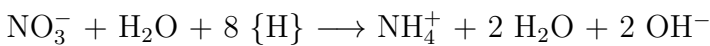
Amino acids of the aspartate family increasingly accumulated in all three strains during high light exposition, probably underlining the importance of PEP carboxylation in cyanobacteria. PEPC activity is regarded to be essential in cyanobacteria (Luinenburg

and Coleman, 1990). For methionine, the strongest increase was observed in the $\Delta mcyB$ *Microcystis* mutant, which again suggests an active role of microcystin in regulating amino acid metabolism.

Much stronger accumulation was observed for 2-oxoglutarate derived amino acids in *Synechocystis*. Especially the levels of proline and arginine, as well as the arginine-associated and non-proteinogenic amino acids ornithine and citrulline were significantly more abundant in *Synechocystis*. As already discussed above (see also 3.5.6), the data might suggest that *Microcystis* probably did not fuel TCA metabolism *via* PEP towards isocitrate and 2-oxoglutarate, at least not during illumination.

Aspects of nitrate reduction

Nitrate is the main nitrogen source in the culture medium used in this experiment. Its reduction to ammonium requires huge amounts of energy and probably take part in balancing the flow of reducing power derived from the photosystems. For eukaryotic algae, the reduction of nitrate to ammonium and even its excretion was described under carbon limitation (Azuara and Aparicio, 1983). Excretion of ammonium was also reported for filamentous, nitrogen-fixing cyanobacteria, which constitutively produce heterocysts (Ploug et al., 2011). The observation that *Synechocystis* resists relatively high ammonium concentrations in the growth medium, which are otherwise toxic for eukaryotic photoautotrophs may underlines the importance of nitrate reduction under certain conditions (Dai et al., 2014).



(3.1)

The pronounced accumulation of amino acids especially in *Synechocystis* and, though to a lesser extent also in *Microcystis*, point towards high relevance of nitrate reduction in cyanobacteria under the conditions of the experiment. Nitrate reduction and subsequent assimilation involve equimolar proton uptake (Kohl and Nicklisch, 1988). Thus, the pH increase in the culture medium might in part be attributed to nitrate reduction, see equation 3.1 (adopted from (Kohl and Nicklisch, 1988)) and figure 3.13 and 3.12.

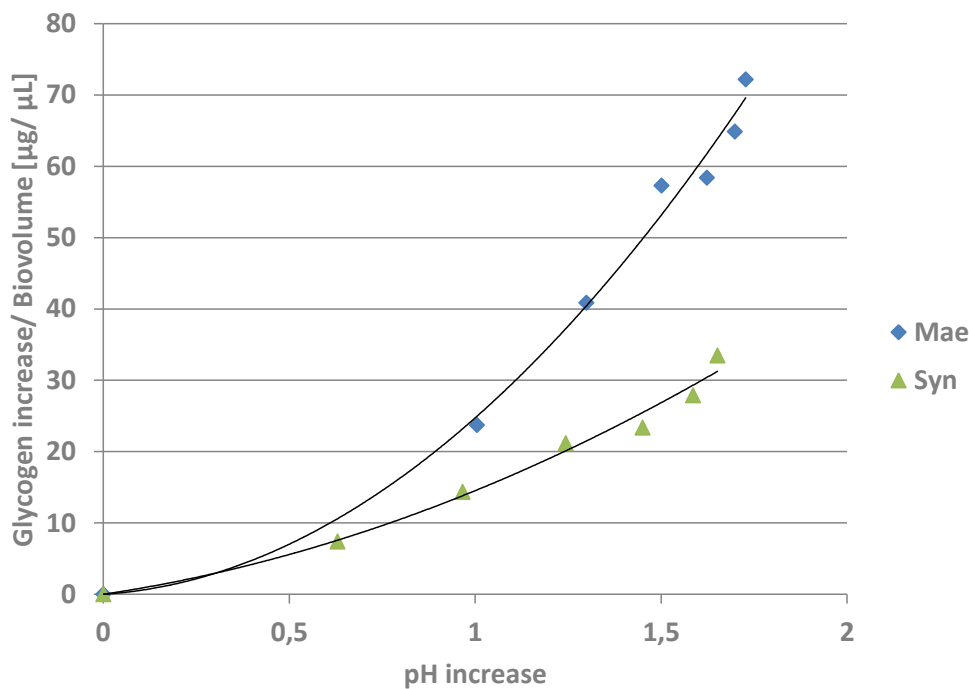


Figure 3.13: Glycogen accumulation over pH increase: The amount of glycogen in *Synechocystis* (Syn) increased only about 50 % of that in *Microcystis* (Mae), whereas the pH increase was almost similar. Less C_i was transformed to glycogen, but higher rates of nitrate assimilation and cyanophycin synthesis probably drove the pH increase in *Synechocystis* to equally high values.

During high light exposition, *Microcystis* and *Synechocystis* showed almost similar pH increases in the medium, whereas the contents of glycogen and cyanophycin differed substantially between both species. *Microcystis* obviously utilized mainly inorganic carbon for glycogen synthesis that drove the increase of the medium pH. Of course, cyanophycin accumulation also requires C_i assimilation. However, substantially higher rates of ni-

trate reduction must be assumed for *Synechocystis*, which contributed to the elevation of the pH in the medium accordingly.

3.5.8 Photorespiration

Under normal conditions, cyanobacteria employ an array of mechanisms to channel excess light energy reaching the cells towards manifold directions, e.g. non-photochemical quenching (NPQ) (Bailey and Grossman, 2008) and photoreduction of oxygen to water (Hackenberg et al., 2009; Allahverdiyeva et al., 2011), as well as metabolic cycling (Young et al., 2011; Nogales et al., 2012) and nitrate reduction, to prevent damage and to maintain favorable intracellular conditions for the production of biomass. In that context, photorespiration must not be thought of as primarily faulty and wasteful metabolic burden, since it is an integral part of the energy channeling network in oxygenic photosynthesis (Tolbert, 1997) and eventually contributes to optimal biosynthesis efficiency of e.g. serine and glycine (Knoop et al., 2010).

Photorespiration in the strict sense, i.e. net oxygen consumption and mobilization of stored carbon for oxidation, was not observed in any of the tested strains, see 3.10. In a broader sense, photorespiration was observed as changed accumulation patterns of metabolites involved in the regeneration of 3-phosphoglycerate from 2-phosphoglycolate. Of all detected and identified metabolites, which were directly assignable to photorespiration, only glycolate showed a significant intracellular increase in *Microcystis* PCC 7806 WT after one hour highlight and after three hours in the $\Delta mcyB$ mutant. Also, excretion of glycolate was observed in both *Microcystis* strains after three hours but not in *Synechocystis*. The intracellular glycolate levels of *Synechocystis* remained constant during the experiment as well, indicating that either photorespiration was running highly efficient, or that detectable photorespiration possibly did not occur at all in that strain under the applied light conditions.

The discrepancy between the dynamics of intracellular glycolate levels and the directly following photorespiratory intermediate glyoxylate in *Microcystis* might be explained by

fundamentally different concentrations of both metabolites under low light conditions. The initially higher concentration of glyoxylate could also indicate metabolic origins different from glycolate. During highlight, the additional glyoxylate produced from glycolate as a direct product of RuBP oxygenation eventually contributed only relatively little to the overall bigger glyoxylate pool. (Knoop et al., 2010) suggested that in cyanobacteria glyoxylate could serve as sole precursor for glycine, serine and cysteine synthesis instead of 3-phosphoglycerate. Thus, a certain level of photorespiration was probably also realized under low light to fuel glyoxylate production. The relatively strong increase of glycolate in *Microcystis* wild-type after one hour could point towards an imbalance of the photorespiratory metabolism directly after elevation of the light intensity, which was overcome after three hours. In cells of the *Microcystis* mutant glycolate levels were not as much increased as in the wild-type after one hour, but after three hours. It would be interesting to see, what happens if the cells were further exposed to high light.

Although not unequivocally attributable to photorespiration, the levels of glycerate in *Microcystis* might indicate regeneration of PG3 *via* the glycerate pathway, especially in the microcystin producing *Microcystis* wild-type. The involvement of the C2 photorespiratory cycle in *Microcystis* might be suggested as well since the accumulation pattern of glycine generally reflected that of glycolate. The presence of a plant-like D3-glycerate kinase could underline an overall higher relevance of PG3 regeneration in *Microcystis* than in *Synechocystis*.

Despite the fact that no significant increase of glycolate levels were detected in *Synechocystis*, the accumulation of serine and glycine could eventually hint towards active photorespiration *via* the C2 cycle. Interestingly, the levels of both amino acids showed the same accumulation pattern in *Synechocystis* as e.g. glutamine and arginine, whose production also involved glutamate. Taken together, it appears likely that the glyoxylate mutually produced by oxygenation of RuBP during photosynthesis indeed served as alternative precursor for glycine and serine synthesis in the tested cyanobacterial strains as proposed by (Knoop et al., 2010).

Glycolate excretion

After three hours both *Microcystis* genotypes had excreted glycolate into the medium, which indicated that parts of the RuBP oxygenation product was not regenerated to PG3 by the cells. Glycolate excretion could eventually be attributed to the specific lifestyle of *Microcystis*. In general, autotrophic phytoplankton benefits from a rich heterotrophic bacterial community for means of re-mineralization of organic matter (Kühl et al., 1996; Kirkwood et al., 2006). Heterotrophs growing on macroscopic colonies in turn are better protected against grazing by zooplankton and benefit from cyanobacterial exudates as source of reduced carbon. Thus, for colony-forming *Microcystis* exudation of e.g. glycolate does not imply complete loss of carbon. High water temperature and low concentrations of N and P limits bacterial growth efficiency (Del Giorgio and Cole, 1998). Under bloom conditions, most of the nutrients (N, P) are fixed as biomass, which means that most of the exudate reduced carbon cannot be utilized by heterotrophs for biomass formation and is again mainly lost by respiration CO₂. The formation of colonies by cyanobacteria could eventually establish a spatially restricted closed bacterial loop so that carbon once acquired effectively remains therein (Tchernov et al., 2003). Accordingly, non-colony forming species like *Synechocystis* would restrict DOC exudation and total loss of carbon.

3.5.9 Conclusions

GC/MS analysis revealed a number of metabolites whose accumulation was affected by microcystin production. Interestingly, many of the respective differences between the *Microcystis* strains were unique for the wild-type, which made the microcystin deficient mutant appear more similar to the control strain *Synechocystis*. Unfortunately, most of those metabolites were unknowns, which limited the number of conclusions that could be drawn from the dataset. However, among the differentially accumulating metabolites in the two *Microcystis* genotypes were several amino acids, the compatible solutes su-

crose and trehalose as well as glycogen and glycolate. The differences in glycolate and glycogen accumulation during the first hour of the experiment might indicate an overall higher initial activity of RubisCO in the microcystin producing wild-type in both directions. During the following two hours of the experiment glycolate accumulated stronger in the microcystin deficient mutant cultures and the glycogen contents of both *Microcystis* genotypes were leveled out as well. It was previously shown that microcystin binds mainly to RubisCO especially during prolonged high light exposition and by that stabilizes the enzyme (Zilliges et al., 2011). It might be speculated that microcystinylation has an activity-modulating effect on RubisCO in both directions and by that eventually plays a role in fine-tuning of the carbon metabolism in *Microcystis* under changing conditions. Together with the elevated levels of stress related compatible solutes in the microcystin deficient *Microcystis* mutant these findings support the hypothesis that microcystin is indeed involved in the regulation of the primary metabolism and by that could contribute to the reported competitive advantage of microcystin producing *Microcystis* genotypes under high light (Zilliges et al., 2011) and carbon limitation (Jähnichen et al., 2007; Van de Waal et al., 2011).

Biotechnological aspects

The data obtained throughout this study support the notion that cyanobacterial species differ substantially in utilizing assimilates. Including *Synechocystis* in this study revealed strain specific metabolic responses to the same experimental conditions. High light exposition of low light adapted cells triggered strain-specific responses, which was reflected by the non-uniform accumulation pattern of many key metabolites. The differences between the two species became most obvious in the very low levels of isocitrate in *Microcystis* cells and the varied accumulation of 2-OG derived amino acids. Furthermore, photorespiration seems of lower relevance in *Synechocystis* under the applied conditions. Remarkably, neither the described capability of *Microcystis* to accumulate glycogen to about 8.5 % the fresh weight, nor the feature of *Synechocystis* to strongly accumulate cyanophycin within only three hours of elevated light exposition had been re-

ported before and would probably not have been observed under constant lab conditions. Although sharing essentially the same primary-metabolic features, different cyanobacteria species obviously follow distinct strategies to accumulate and store assimilates. Hence, metabolomic screening of available strains at changing growth conditions could accelerate the development of strategies for the profitable use of cyanobacteria as source of renewable energy or for the production of base products of the chemical industry.

3.5.10 Limitations and perspectives

Metabolomics is one of the currently most exciting scientific fields, which will contribute strongly to the understanding of the living world. Compared to other widely used -omics approaches, metabolomics is probably the most direct way to examine the effects of environmental stimuli on an organism. Transcriptomics, for example, cannot give least evidence for the amount of gene products due to e.g. posttranscriptional modification events, whereas proteomics cannot provide information about e.g. actual enzyme activities. Metabolomics, on the other hand, directly displays the impact of environmental stimuli on an organism's constitution and can provide straight information about the adaptation of an organism. However, stable metabolite quantities do not imply an unchanged utilization ballast of the respective pathway. For example, increased flux velocities through a metabolic route yielding in accumulation of storage metabolites or finally growth are not necessarily represented.

Prerequisites for valid and reproducible metabolome analysis are optimized sampling procedures, robust extraction protocols as well as sensitive and versatile metabolite identification and quantification facilities. Not less important are thorough data processing and profound statistical analysis.

One of the major shortcomings of this metabolomic study was the inability to determine the absolute amounts of metabolites, as well as metabolic fluxes. Thus, some of the conclusions drawn from the existing dataset concerning, e.g. the extent of PEP-

carboxylation and C4-characteristics of cyanobacteria are rather speculative and require additional evidence. The most fundamental limitation of the metabolomics approach followed in this study laid in the incomplete metabolite library, which covered only 104 out of 501 detected metabolites. Consequently, the extension of metabolite libraries is most urgently needed. The application of structure elucidating nuclear magnetic resonance (NMR) in metabolomic analysis of cyanobacteria could further help to figure out, which metabolites are present.

Bioinformatics of the post-genomic era can give valuable information on possible metabolic routes to be expected in an organism. Today, many of the proposed cyanobacterial metabolic pathways are hypothetical, and even the existence of basic routes lack experimental evidence. The combination of metabolic flux analysis with untargeted transcriptomics and robust biochemical characterization of candidate enzymes might help to close the yet persisting gaps of the cyanobacterial metabolic network in the near future. For example, to solve the isocitrate conundrum of *Microcystis*, enzyme assays in cell extracts aiming at the conversion steps from citrate to 2-oxoglutarate might yield a convincing explanation. The general TCA metabolism might also be examined by pulse-chase analysis with C¹³-labeled/ unlabeled substrates.

Additionally, this metabolomics study focused on the effects of high light treatment on low light adapted cells. Additionally, metabolites not present in each of the strains were not considered for analysis. Thus, the existing dataset should be further examined to figure out general strain-specific differences apart from those induced by treatment with high light.

The glycogen concentration served as a measure for net photosynthesis and suggested overall higher rates for *Microcystis*, which was in line with the observed oxygen evolution. However, glycogen was not the only storage compound in *Synechocystis*. Nitrate reduction to ammonium also triggers pH increase 3.5.7, but not oxygen evolution. It thus was concluded that *Synechocystis* channeled more energy towards amino acid, protein

as well as cyanophycin synthesis, whereas *Microcystis* produced more carbohydrates. To get a general estimate about how effective light energy and nutrients are channeled under the experimental conditions, all of the known storage compounds including poly- β -hydroxyalkanoate might be quantified as well. Alternatively, the dynamics of the cell's elemental composition could be analyzed and compared. Calorimetry and determination of the C, O, H, N, S, P, (Fe) content in cyanobacteria cells might yield valuable information about their general assimilation and adaptation strategies.

Finally, the effect of microcystinylation on the activity of selected enzymes such as RubisCO should be analyzed *in vitro*. The activity of enzymes in $\Delta mcyB$ mutant extracts could be measure with and without previous microcystinylation. The combination with a targeted GC/MS- or LC/MS-based analysis would eventually even allow the determination of the RubisCO oxygenase activity.

Appendix

Tables of estimated p -values using the Tukey's HSD test for differences of means comparing *Microcystis aeruginosa* PCC 7806 (Mar) with the $\Delta mcyB$ mutant (Mut) or with *Synechocystis* PCC 6803 (Syn) at the corresponding time points, p -value ≤ 0.05 in bold

Table 3.3: Oxygen evolution upon high light exposition

t_{min}	0	15	35	65	105
Mar vs. Mut	0.98499	0.02679	0.12952	0.98884	0.89269
Mar vs. Syn	0.99999	$6.18 \cdot 10^{-7}$	$2.79 \cdot 10^{-9}$	$8.48 \cdot 10^{-7}$	0.01065

Table 3.4: pH dynamics upon high light exposition:

t_{min}	0	20	45	80	135	175
Mar vs. Mut	0.00049	$4.81 \cdot 10^{-5}$	0.02015	1	1	1
Mar vs. Syn	0.27769	$4.82 \cdot 10^{-10}$	$1.13 \cdot 10^{-11}$	$5.89 \cdot 10^{-9}$	$1.51 \cdot 10^{-5}$	0.00369

Table 3.5: Glycogen accumulation upon high light exposition

t_{min}	0	30	60	90	120	150	180
Mar vs. Mut	1	0.999	0.797	0.319	1	1	0.999
Mar vs. Syn	0.919	$1.25 \cdot 10^{-11}$	$1.06 \cdot 10^{-12}$	$1.06 \cdot 10^{-12}$	$1.06 \cdot 10^{-12}$	$1.06 \cdot 10^{-12}$	$1.06 \cdot 10^{-12}$

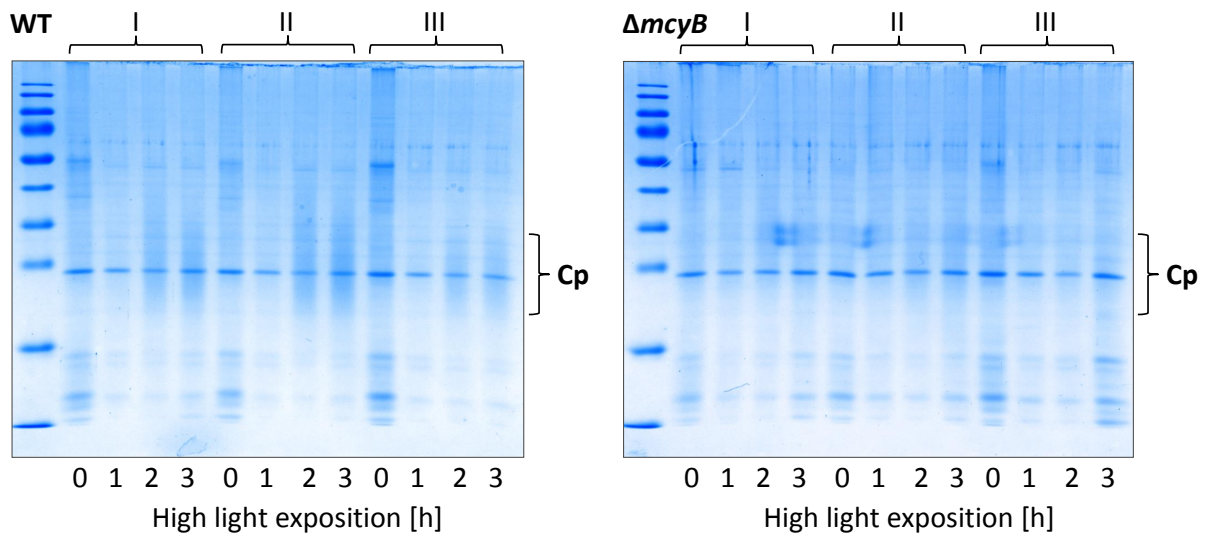


Figure 3.14: Cyanophycin accumulation in three replicates (I-III) of both *Microcystis* genotypes upon high light illumination; Coomassie-stained gels used for relative quantification, see figure 3.11.

4

General Discussion & Outlook

The two previous chapters treated two aspects of microcystin production in *Microcystis* under changing light conditions separately that are mutually connected with each other. Hence, the intention of this final chapter is to provide a synthesis of the drawn conclusions and to give a brief outlook on current- and future studies focusing on the relation between microcystin and pH.

4.1 Ecological aspects of microcystin production

The ancestor of all today's potentially toxic cyanobacteria had the ability to produce microcystin (Rantala et al., 2004). It might be speculated that microcystin synthesis once had been a mutual prerequisite for those cyanobacteria under the ancient environmental conditions. The co-occurrence of toxic and non-toxic strains today might be the consequence of a lowered selection pressure that once favored microcystin producing phenotypes. Thus, the question arises, whether microcystin production is still relevant, at least temporarily or whether it is completely dispensable and just a relic.

However, considering the high overall cost of microcystin synthesis and the maintenance of the genes involved most probably imply a still significant biological role. The co-occurrence of toxic and non-toxic strains might also imply a certain threshold for a trade-off between the cost of microcystin production and its beneficial effects today. It might be argued that microcystin production enables the corresponding phenotypes to occupy sub-niches within chemotypically heterogeneous *Microcystis* communities.

4.2 High light and microcystin

Microcystin production is probably induced by changes of the energy and nutrient status of the cell (Kaebernick et al., 2000; Straub et al., 2011; Humbert et al., 2013). This finding is in line with the observation that the global transcription regulator NtcA binds to the microcystin promoter in *Microcystis* PCC 7806 (Ginn et al., 2010). NtcA is supposed to orchestrate nitrogen uptake and its incorporation into carbon skeletons according to the energy and nutrient status of the cell. Corresponding genes putatively regulated by NtcA furthermore comprise components of the carbon concentrating mechanism (CCM), RubisCO, proteins of photosystem II and I, as well as NADH dehydrogenases, thioredoxin and iron stress-induced protein (Su et al., 2005). Iron also plays a pivotal role in adjusting the cellular redox balance (Helman et al., 2003; Allahverdiyeva et al., 2013).

Association of the transcription factor Fur (ferric uptake regulator) with the promoter region of mcy-genes (Sevilla et al., 2008) furthermore suggests a relation of microcystin to factors connected with high photosynthetic activity such as the cytoplasmic pH.

The results of the metabolomics study point towards the same direction. High light induced the significantly different metabolite accumulation patterns in toxic and nontoxic *Microcystis* PCC 7806.

4.3 Microcystin and high pH

Energization of the photosynthetic apparatus in the light establishes a chemiosmotic pH gradient across the thylakoid membrane, leading to marked alkalinization of the cytoplasm. During illumination the cytoplasmic pH is around 8, which is reflected by the maximum activities of RubisCO and cyanophycin synthetase at around pH 8.2. The cytoplasmic pH could eventually be much higher, when the external medium pH exceeds values greater than 10. Cyanobacteria assimilate significant amounts of the anionic compounds nitrate and bicarbonate during photosynthesis, which implies the existence of effective mechanisms to maintain intracellular pH homeostasis. Otherwise, the cells must have evolved adaptations to tolerate high intracellular pH, at least temporarily.

In the lab, the shift of cultures from low to high light-induced microcystin production and its interaction with proteins. Results of a first experiment using the pH indicator and vital stain Neutral red indeed suggested a pronounced increase of intracellular pH under prolonged high light exposition in *Microcystis*, see figure 4.1. The mechanism of microcystin covalent binding to proteins *in vivo* probably depends on the cytoplasmic pH, see 2.3 and role of microcystin in stabilizing proteins against proteolysis had been demonstrated earlier (Zilliges et al., 2011). However, effects of protein microcystinylation such as protection against e.g. random carbonylation or against damage caused by non-physiologically high pH as well as enzyme-activity modulating properties might be anticipated but need further examination.

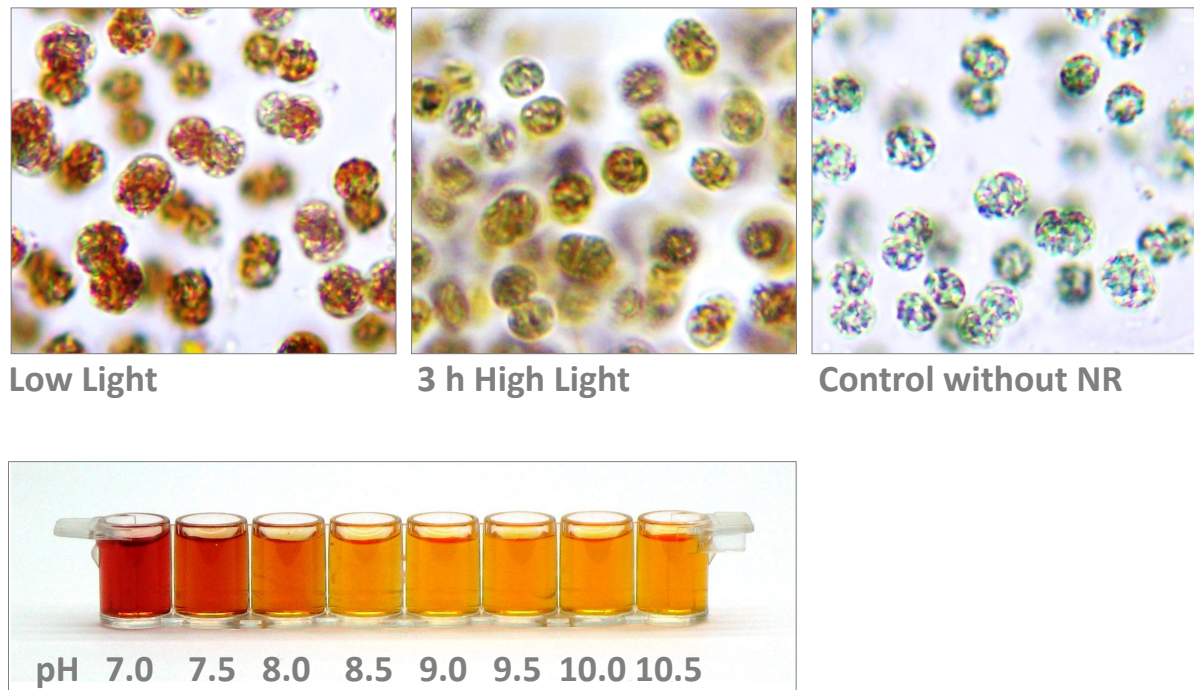


Figure 4.1: Intracellular pH: A *Microcystis* culture was exposed to high light conditions for 3 hours, mixed 1:20 with a 1 % Neutral red BG 11 solution and incubated for 10 minutes before observation. Cells from a low light adapted culture were treated equally. Unstained cells served as control. Under low light conditions the intracellular pH appears to be around 7 or lower. The yellow colour of Neutral red indicates elevated cytoplasmic pH above ≥ 8.5 after high light exposition. Figure from (Meissner et al., 2014).

4.4 Sodium depletion phenotype

The strain-specific differences in terms of medium pH increase and glycogen accumulation presented in figure 3.13 were the initial motivation to grow *Synechocystis* PCC 6803, the microcystin producing strain *Microcystis aeruginosa* PCC 7806 and the deficient $\Delta mcyB$ mutant in sodium depleted BG-11 medium under standard low light conditions. Sodium is needed for bicarbonate uptake, which requires $\text{HCO}_3^- / \text{Na}^+$ symport (Kaplan et al., 1984) and pH balancing that involves Na^+ / H^+ antiporters. Both components are encoded in a single gene cluster suggesting their concerted action (San-

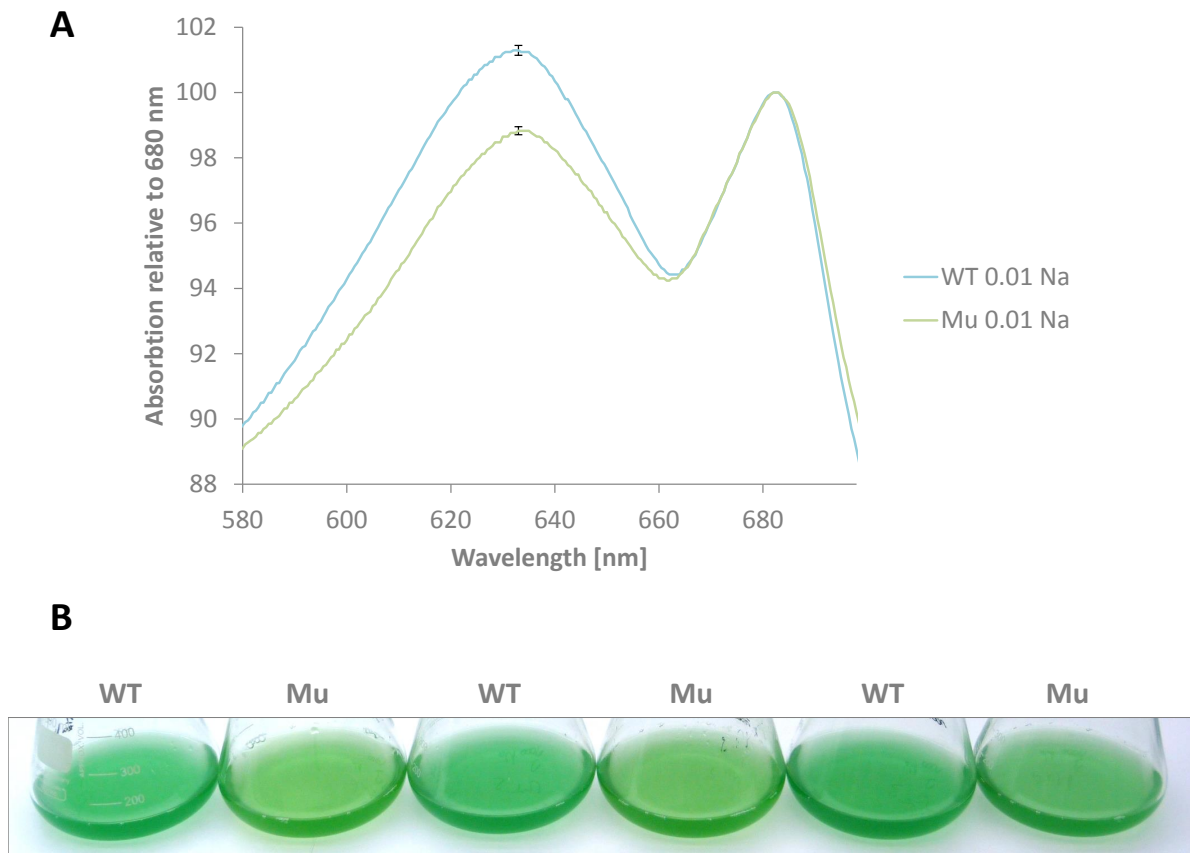


Figure 4.2: Impact of sodium depletion, A: illustrates the absorption spectra of *Microcystis* PCC 7806 wild-type (WT) and the microcystin deficient $\Delta mcyB$ mutant (Mu) grown at 1 % of the usual sodium concentration. **B:** is a photograph of the respective cultures.

drini et al., 2014).

Sodium deprivation repeatedly induced pronounced phenotypic differences between the *Microcystis* wild-type and the $\Delta mcyB$ mutant, see figure 4.2. The ratio between PS-II accessory phycobiliproteins (632 nm) and chlorophyll a (680 nm) was reduced in the $\Delta mcyB$ mutant but not in the wild-type. Two out of three *Synechocystis* culture replicates obviously did not survive the low sodium content in the medium and could not be analyzed further.

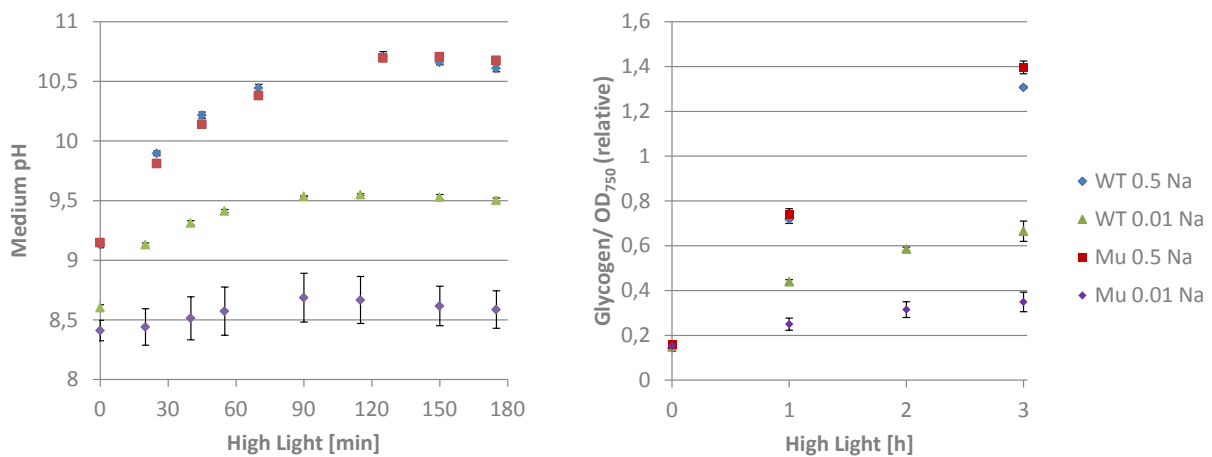


Figure 4.3: High light and sodium depletion: The $\Delta mcyB$ mutant (Mu) showed less photosynthetic activity at 1 % of the usual sodium concentration as reflected by lower pH increase in the medium and less glycogen accumulation when compared to the wild-type (WT). 50 % sodium concentration had no detectable impact on either strain.

High light exposition of the sodium depleted cultures indicated a higher photosynthetic activity in the wild-type, as became visible by higher amounts of stored glycogen and the increase of the medium pH, see figure 4.3.

In which way microcystin was involved in phenotype induction remains the matter of future research. However, elevated microcystin production and higher growth rates of the *Microcystis* PCC 7806 wild-type compared to the deficient $\Delta mcyB$ mutant under sodium depletion were already reported (Jähnichen et al., 2007). Whether the microcystin dependent sodium depletion phenotype is primarily caused by C_i limitation due to impairment of $\text{Na}^+/\text{HCO}_3^-$ symport (Jähnichen et al., 2007) or Na^+/H^+ antiport for maintaining pH homeostasis has to be clarified.

Bibliography

- Ahlert, C. (2013). Microcystin-einfluss auf proteine des calvin-benson-zyklus. Master's thesis, University of Potsdam.
- Alexova, R., Haynes, P. A., Ferrari, B. C., and Neilan, B. A. (2011). Comparative protein expression in different strains of the bloom-forming cyanobacterium *microcystis aeruginosa*. *Molecular and Cellular Proteomics*, 10(9).
- Alfonso, M., Perewoska, I., and Kirilovsky, D. (2001). Redox control of ntca gene expression in *synechocystis* sp. pcc 6803. nitrogen availability and electron transport regulate the levels of the ntca protein. *Plant Physiology*, 125(2):969–981.
- Allahverdiyeva, Y., Ermakova, M., Eisenhut, M., Zhang, P., Richaud, P., Hagemann, M., Cournac, L., and Aro, E.-M. (2011). Interplay between flavodiiron proteins and photorespiration in *synechocystis* sp. pcc 6803. *Journal of Biological Chemistry*, 286(27):24007–24014.
- Allahverdiyeva, Y., Mustila, H., Ermakova, M., Bersanini, L., Richaud, P., Ajlani, G., Battchikova, N., Cournac, L., and Aro, E.-M. (2013). Flavodiiron proteins flv1 and flv3 enable cyanobacterial growth and photosynthesis under fluctuating light. *Proceedings of the National Academy of Sciences*.
- Anderson, L. E. (1971). Chloroplast and cytoplasmic enzymes ii. pea leaf triose phos-

- phate isomerases. *Biochimica et Biophysica Acta (BBA) - Enzymology*, 235(1):237 – 244.
- Azuara, M. P. and Aparicio, P. J. (1983). In vivo blue-light activation of chlamydomonas reinhardii nitrate reductase. *Plant Physiology*, 71(2):286–290.
- Bailey, S. and Grossman, A. (2008). Photoprotection in cyanobacteria: Regulation of light harvesting. *Photochemistry and Photobiology*, 84(6):1410–1420.
- Benjamini, Y. and Yekutieli, D. (2001). The control of the false discovery rate in multiple testing under dependency. *Annals of statistics*, pages 1165–1188.
- Bersanini, L., Battchikova, N., Jokel, M., Rehman, A., Vass, I., Allahverdiyeva, Y., and Aro, E.-M. (2014). Flavodiiron protein flv2/flv4-related photoprotective mechanism dissipates excitation pressure of psii in cooperation with phycobilisomes in cyanobacteria. *Plant Physiology*, 164(2):805–818.
- Billini, M., Stamatakis, K., and Sophianopoulou, V. (2008). Two members of a network of putative na⁺/h⁺ antiporters are involved in salt and ph tolerance of the freshwater cyanobacterium synechococcus elongatus. *Journal of Bacteriology*, 190(19):6318–6329.
- Börner, T. and Dittmann, E. (2005). Molecular biology of cyanobacterial toxins. In Huisman, J., Matthijs, H. C. P., and Visser, P. M., editors, *Harmful Cyanobacteria*, volume 3 of *Aquatic Ecology Series*, pages 25–40. Springer Netherlands.
- Briand, J. F., Jacquet, S., Bernard, C., and Humbert, J. F. (2003). Health hazards for terrestrial vertebrates from toxic cyanobacteria in surface water ecosystems. *Veterinary Research*, 34(4):361–377.
- Bricker, T. M., Zhang, S., Laborde, S. M., Mayer, P. R., Frankel, L. K., and Moroney, J. V. (2004). The malic enzyme is required for optimal photoautotrophic growth of synechocystis sp. strain pcc 6803 under continuous light but not under a diurnal light regimen. *Journal of Bacteriology*, 186(23):8144–8148.

- Carmichael, W. W. and An, J. (1999). Using an enzyme linked immunosorbent assay (elisa) and a protein phosphatase inhibition assay (ppia) for the detection of microcystins and nodularins. *Natural Toxins*, 7(6):377–385.
- Christiansen, G., Kurmayer, R., Liu, Q., and Börner, T. (2006). Transposons inactivate biosynthesis of the nonribosomal peptide microcystin in naturally occurring planktothrix spp. *Applied and Environmental Microbiology*, 72(1):117–123.
- Christiansen, G., Molitor, C., Philmus, B., and Kurmayer, R. (2008). Nontoxic strains of cyanobacteria are the result of major gene deletion events induced by a transposable element. *Molecular Biology and Evolution*, 25(8):1695–1704.
- Dai, G.-Z., Qiu, B.-S., and Forchhammer, K. (2014). Ammonium tolerance in the cyanobacterium *synechocystis* sp. strain pcc 6803 and the role of the *psba* multigene family. *Plant, Cell and Environment*, 37(4):840–851.
- Dalle-Donne, I., Aldini, G., Carini, M., Colombo, R., Rossi, R., and Milzani, A. (2006). Protein carbonylation, cellular dysfunction, and disease progression. *Journal of cellular and molecular medicine*, 10(2):389–406.
- Del Giorgio, P. A. and Cole, J. J. (1998). Bacterial growth efficiency in natural aquatic systems. *Annual Review of Ecology and Systematics*, 29(1):503–541.
- DeVries, S. E., Galey, F. D., Namikoshi, M., and Woo, J. C. (1993). Clinical and pathologic findings of blue-green algae (*microcystis aeruginosa*) intoxication in a dog. *Journal of Veterinary Diagnostic Investigation*, 5(3):403–408.
- Dittmann, E., Fewer, D. P., and Neilan, B. A. (2013). Cyanobacterial toxins: biosynthetic routes and evolutionary roots. *FEMS Microbiology Reviews*, 37(1):23–43.
- Dittmann, E., Neilan, B. A., Erhard, M., vonDohren, H., and Börner, T. (1997). Insertional mutagenesis of a peptide synthetase gene that is responsible for hepatotoxin production in the cyanobacterium *microcystis aeruginosa* pcc 7806. *Molecular Microbiology*, 26(4):779–787.

- Dokulil, M. and Teubner, K. (2000). Cyanobacterial dominance in lakes. *Hydrobiologia*, 438(1-3):1–12.
- Doorn, J. A. and Petersen, D. R. (2002). Covalent modification of amino acid nucleophiles by the lipid peroxidation products 4-hydroxy-2-nonenal and 4-oxo-2-nonenal. *Chemical Research in Toxicology*, 15(11):1445–1450. PMID: 12437335.
- Dunn, I. G. (1967). Diurnal fluctuations of physicochemical conditions in a shallow tropical pond. *Limnology and Oceanography*, 12(1):pp. 151–154.
- Dziallas, C. and Grossart, H.-P. (2011). Increasing oxygen radicals and water temperature select for toxic microcystis sp. *PLoS ONE*, 6(9):e25569.
- Eriksson, J. E., Gronberg, L., Nygard, S., Slotte, J. P., and Meriluoto, J. A. O. (1990a). Hepatocellular uptake of h-3 dihydromicrocystin-lr, a cyclic peptide toxin. *Biochimica Et Biophysica Acta*, 1025(1):60–66.
- Eriksson, J. E., Toivola, D., Meriluoto, J. A. O., Karaki, H., Han, Y. G., and Hartshorne, D. (1990b). Hepatocyte deformation induced by cyanobacterial toxins reflects inhibition of protein phosphatases. *Biochemical and Biophysical Research Communications*, 173(3):1347–1353.
- Falkner, G., Horner, F., Werdan, K., and Heldt, H. W. (1976). pH changes in the cytoplasm of the blue-green alga anacystis nidulans caused by light-dependent proton flux into the thylakoid space. *Plant Physiology*, 58(6):717–718.
- Fastner, J., Flieger, I., and Neumann, U. (1998). Optimised extraction of microcystins from field samples - a comparison of different solvents and procedures. *Water Research*, 32(10):3177–3181.
- Fewer, D. P., Halinen, K., Sipari, H., Bernardova, K., Manttari, M., Eronen, E., and Sivonen, K. (2011). Non-autonomous transposable elements associated with inactivation of microcystin gene clusters in strains of the genus anabaena isolated from the baltic sea. *Environmental Microbiology Reports*, 3(2):189–194.

- Francis, G. (1878). Poisonous australian lake. *Nature*, 18:11–12. Letters to Editor.
- Gerbersdorf, S. U. (2006). An advanced technique for immuno-labelling of microcystins in cryosectioned cells of *microcystis aeruginosa* pcc 7806 (cyanobacteria): Implementations of an experiment with varying light scenarios and culture densities. *Toxicon*, 47(2):218 – 228.
- Ginn, H. P., Pearson, L. A., and Neilan, B. A. (2010). Ntca from *microcystis aeruginosa* pcc 7806 is autoregulatory and binds to the microcystin promoter. *Applied and Environmental Microbiology*, 76(13):4362–4368.
- Hackenberg, C., Engelhardt, A., Matthijs, H., Wittink, F., Bauwe, H., Kaplan, A., and Hagemann, M. (2009). Photorespiratory 2-phosphoglycolate metabolism and photoreduction of o₂ cooperate in high-light acclimation of *synechocystis* sp. strain pcc 6803. *Planta*, 230(4):625–637.
- Havens, K. E. (2008). Cyanobacteria blooms: effects on aquatic ecosystems. In Hudnell, H., editor, *Cyanobacterial Harmful Algal Blooms: State of the Science and Research Needs*, volume 619 of *Advances in Experimental Medicine and Biology*, pages 733–747. Springer New York.
- Helman, Y., Tchernov, D., Reinhold, L., Shibata, M., Ogawa, T., Schwarz, R., Ohad, I., and Kaplan, A. (2003). Genes encoding a-type flavoproteins are essential for photoreduction of o₂ in cyanobacteria. *Current Biology*, 13(3):230 – 235.
- Hoiczyk, E. and Hansel, A. (2000). Cyanobacterial cell walls: News from an unusual prokaryotic envelope. *Journal of Bacteriology*, 182(5):1191–1199.
- Huege, J., Krall, L., Steinhauser, M.-C., Giavalisco, P., Rippka, R., de Marsac, N. T., and Steinhauser, D. (2011). Sample amount alternatives for data adjustment in comparative cyanobacterial metabolomics. *Analytical and bioanalytical chemistry*, 399(10):3503–3517.

- Huisman, J., Sharples, J., Stroom, J. M., Visser, P. M., Kardinaal, W. E. A., Verspagen, J. M. H., and Sommeijer, B. (2004). Changes in turbulent mixing shift competition for light between phytoplankton species. *Ecology*, 65(4):2960–2970.
- Humbert, J.-F., Barbe, V., Latifi, A., Gugger, M., Calteau, A., Coursin, T., Lajus, A., Castelli, V., Oztas, S., Samson, G., Longin, C., Medigue, C., and de Marsac, N. T. (2013). A tribute to disorder in the genome of the bloom-forming freshwater cyanobacterium *microcystis aeruginosa*. *PLoS ONE*, 8(8):e70747.
- Ito, E., Takai, A., Kondo, F., Masui, H., Imanishi, S., and Ichi Harada, K. (2002). Comparison of protein phosphatase inhibitory activity and apparent toxicity of microcystins and related compounds. *Toxicon*, 40(7):1017 – 1025.
- Jähnichen, S., Ihle, T., Petzoldt, T., and Benndorf, J. (2007). Impact of inorganic carbon availability on microcystin production by *microcystis aeruginosa* pcc 7806. *Applied and Environmental Microbiology*, 73(21):6994–7002.
- Jochimsen, E. M., Carmichael, W. W., An, J., Cardo, D. M., Cookson, S. T., Holmes, C. E., Antunes, M. B., de Melo Filho, D. A., Lyra, T. M., Barreto, V. S. T., Azevedo, S. M., and Jarvis, W. R. (1998). Liver failure and death after exposure to microcystins at a hemodialysis center in Brazil. *New England Journal of Medicine*, 338(13):873–878.
- Jöhnk, K. D., Huisman, J., Sharples, J., Sommeijer, B., Visser, P. M., and Stroom, J. M. (2008). Summer heatwaves promote blooms of harmful cyanobacteria. *Global Change Biology*, 14(3):495–512.
- Kaebernick, M., Neilan, B. A., Börner, T., and Dittmann, E. (2000). Light and the transcriptional response of the microcystin biosynthesis gene cluster. *Applied and Environmental Microbiology*, 66(8):3387–3392.
- Kaebernick, M., Rohrlack, T., Christoffersen, K., and Neilan, B. A. (2001). A spontaneous mutant of microcystin biosynthesis: genetic characterization and effect on daphnia. *Environmental Microbiology*, 3(11):669–679.

- Kaplan, A., Volokita, M., Zenvirth, D., and Reinhold, L. (1984). An essential role for sodium in the bicarbonate transporting system of the cyanobacterium *Anabaena variabilis*. *FEBS Letters*, 176(1):166 – 168.
- Kardinaal, W. E. A., Tonk, L., Janse, I., Hol, S., Slot, P., Huisman, J., and Visser, P. M. (2007). Competition for light between toxic and nontoxic strains of the harmful cyanobacterium *Microcystis*. *Applied and Environmental Microbiology*, 73(9):2939–2946.
- Kaya, K. and Sano, T. (1999). Total microcystin determination using erythro-2-methyl-3-(methoxy-d3)-4-phenylbutyric acid (mmpb-d3) as the internal standard as the internal standard. *Analytica Chimica Acta*, 386(1):107–112.
- Kehr, J. (2009). *Characterisation of the lectin microvirin from Microcystis aeruginosa PCC 7806 and new insights into the role of microcystin*. PhD thesis.
- Kelly, G. and Latzko, E. (1976). Inhibition of spinach-leaf phosphofructokinase by 2-phosphoglycollate. *{FEBS} Letters*, 68(1):55 – 58.
- Kinney, J., Axen, S., and Kerfeld, C. (2011). Comparative analysis of carboxysome shell proteins. *Photosynthesis Research*, 109(1-3):21–32.
- Kirkwood, A., Nalewajko, C., and Fulthorpe, R. (2006). The effects of cyanobacterial exudates on bacterial growth and biodegradation of organic contaminants. *Microbial Ecology*, 51(1):4–12.
- Klähn, S. and Hagemann, M. (2011). Compatible solute biosynthesis in cyanobacteria. *Environmental Microbiology*, 13(3):551–562.
- Knoop, H., Zilliges, Y., Lockau, W., and Steuer, R. (2010). The metabolic network of *Synechocystis* sp. pcc 6803: Systemic properties of autotrophic growth. *Plant Physiology*, 154(1):410–422.
- Kohl, J.-G. and Nicklisch, A. (1988). *Ökophysiologie der algen*. Akademie- Verlag Berlin.

- Kolodny, N. H., Bauer, D., Bryce, K., Klucsevsek, K., Lane, A., Medeiros, L., Mercer, W., Moin, S., Park, D., Petersen, J., Wright, J., Yuen, C., Wolfson, A. J., and Allen, M. M. (2006). Effect of nitrogen source on cyanophycin synthesis in *synechocystis* sp. strain pcc 6308. *Journal of Bacteriology*, 188(3):934–940.
- Komarek, J. and Anagnostidis, K. (1998). In *Suesswasserflora von Mitteleuropa; Bd. 19 Cyanoprocarvota Teil 1 Croococcales*. Gustav Fischer Verlag Jena.
- Kondo, F., Ikai, Y., Oka, H., Okumura, M., Ishikawa, N., Harada, K., Matsuura, K., Murata, H., and Suzuki, M. (1992). Formation, characterization, and toxicity of the glutathione and cysteine conjugates of toxic heptapeptide microcystins. *Chemical Research in Toxicology*, 5(5):591–596.
- Kopka, J., Schauer, N., Krueger, S., Birkemeyer, C., Usadel, B., Bergmüller, E., Dörmann, P., Weckwerth, W., Gibon, Y., Stitt, M., et al. (2005). The golm metabolome database. *Bioinformatics*, 21(8):1635–1638.
- Krall, L., Huege, J., Catchpole, G., Steinhauser, D., and Willmitzer, L. (2009). Assessment of sampling strategies for gas chromatography–mass spectrometry (gc–ms) based metabolomics of cyanobacteria. *Journal of Chromatography B*, 877(27):2952–2960.
- Kühl, M., Glud, R. N., Ploug, H., and Ramsing, N. B. (1996). Microenvironmental control of photosynthesis and photosynthesis-coupled respiration in an epilithic cyanobacterial biofilm1. *Journal of Phycology*, 32(5):799–812.
- Kurmayer, R. and Kutzenberger, T. (2003). Application of real-time pcr for quantification of microcystin genotypes in a population of the toxic cyanobacterium *microcystis* sp. *Applied and Environmental Microbiology*, 69(11):6723–6730.
- Latifi, A., Ruiz, M., and Zhang, C.-C. (2009). Oxidative stress in cyanobacteria. *FEMS Microbiology Reviews*, 33(2):258–278.
- Le Ai Nguyen, V., Tanabe, Y., Matsuura, H., Kaya, K., and Watanabe, M. M. (2012). Morphological, biochemical and phylogenetic assessments of water-bloom-forming

- tropical morphospecies of microcystis (chroococcales, cyanobacteria). *Phycological Research*, 60(3):208–222.
- Legendre, P. and Legendre, L. (1998). *Numerical ecology*. Elsevier.
- Li, H., Sherman, D. M., Bao, S., and Sherman, L. A. (2001). Pattern of cyanophycin accumulation in nitrogen-fixing and non-nitrogen-fixing cyanobacteria. *Archives of microbiology*, 176(1-2):9–18.
- Luinenburg, I. and Coleman, J. (1990). A requirement for phosphoenolpyruvate carboxylase in the cyanobacterium *synechococcus* pcc 7942. *Archives of Microbiology*, 154(5):471–474.
- Lutolf, M. P., Tirelli, N., Cerritelli, S., Cavalli, L., and Hubbell, J. A. (2001). Systematic modulation of michael-type reactivity of thiols through the use of charged amino acids. *Bioconjugate Chemistry*, 12(6):1051–1056.
- Lyons, T. W., Reinhard, C. T., and Planavsky, N. J. (2014). The rise of oxygen in earth's early ocean and atmosphere. *Nature*, 506(7488):307–315.
- Madian, A. G. and Regnier, F. E. (2010). Proteomic identification of carbonylated proteins and their oxidation sites. *Journal of Proteome Research*, 9(8):3766–3780.
- Marcus, Y., Altman-Gueta, H., Finkler, A., and Gurevitz, M. (2003). Dual role of cysteine 172 in redox regulation of ribulose 1,5-bisphosphate carboxylase/oxygenase activity and degradation. *Journal of Bacteriology*, 185(5):1509–1517.
- Marcus, Y., Berry, J., and Pierce, J. (1992). Photosynthesis and photorespiration in a mutant of the cyanobacterium *synechocystis* pcc 6803 lacking carboxysomes. *Planta*, 187(4):511–516.
- Marin-Navarro, J. and Moreno, J. (2003). Modification of the proteolytic fragmentation pattern upon oxidation of cysteines from ribulose 1,5-bisphosphate carboxylase/oxygenase. *Biochemistry*, 42(50):14930–14938.

- Meissner, S., Fastner, J., and Dittmann, E. (2013). Microcystin production revisited: conjugate formation makes a major contribution. *Environmental Microbiology*, 15(6):1810–1820.
- Meissner, S., Steinhauser, D., and Dittmann, E. (2014). Metabolomic analysis indicates a pivotal role of the hepatotoxin microcystin in high light adaptation of microcystis. *Environmental Microbiology*, pages n/a–n/a.
- Metcalf, J. S., Bell, S. G., and Codd, G. A. (2001). Colorimetric immuno-protein phosphatase inhibition assay for specific detection of microcystins and nodularins of cyanobacteria. *Applied and Environmental Microbiology*, 67(2):904–909.
- Miller, A. G., Turpin, D. H., and Canvin, D. T. (1984). Na⁺ requirement for growth, photosynthesis, and pH regulation in the alkalotolerant cyanobacterium *Synechococcus leopoliensis*. *Journal of Bacteriology*, 159(1):100–106.
- Muller-Navarra, D. C., Brett, M. T., Park, S., Chandra, S., Ballantyne, A. P., Zorita, E., and Goldman, C. R. (2004). Unsaturated fatty acid content in seston and trophodynamic coupling in lakes. *Nature*, 427(6969):69–72.
- Nakagawa, M., Takamura, Y., and Yagi, O. (1987). Isolation and characterization of the slime from a cyanobacterium, *Microcystis aeruginosa* k-3a. *Agricultural and Biological Chemistry*, 51(2):329–337.
- Neilan, B. A., Pearson, L. A., Muenchhoff, J., Moffitt, M. C., and Dittmann, E. (2013). Environmental conditions that influence toxin biosynthesis in cyanobacteria. *Environmental Microbiology*, 15(5):1239–1253.
- Nogales, J., Gudmundsson, S., Knight, E. M., Palsson, B. O., and Thiele, I. (2012). Detailing the optimality of photosynthesis in cyanobacteria through systems biology analysis. *Proceedings of the National Academy of Sciences*, 109(7):2678–2683.
- Otsuka, S., Suda, S., Shibata, S., Oyaizu, H., Matsumoto, S., and Watanabe, M. M. (2001). A proposal for the unification of five species of the cyanobacterial genus

- microcystis kützing ex lemmermann 1907 under the rules of the bacteriological code. *International Journal of Systematic and Evolutionary Microbiology*, 51(3):873–9.
- Paerl, H. W. and Huisman, J. (2008). Blooms like it hot. *Science*, 320(5872):57–58.
- Paerl, H. W. and Otten, T. G. (2013). Harmful cyanobacterial blooms: Causes, consequences, and controls. *Microbial Ecology*, 65(4):995–1010.
- Paerl, H. W. and Ustach, J. F. (1982). Blue-green-algal scums - an explanation for their occurrence during fresh-water blooms. *Limnology and Oceanography*, 27(2):212–217.
- Pereira, S. R., Vasconcelos, V. M., and Antunes, A. (2013). Computational study of the covalent bonding of microcystins to cysteine residues - a reaction involved in the inhibition of the ppp family of protein phosphatases. *FEBS Journal*, 280(2):674–680.
- Pflugmacher, S., Wiegand, C., Oberemm, A., Beattie, K. A., Krause, E., Codd, G. A., and Steinberg, C. E. (1998). Identification of an enzymatically formed glutathione conjugate of the cyanobacterial hepatotoxin microcystin-lr: the first step of detoxication. *Biochimica et Biophysica Acta (BBA) - General Subjects*, 1425(3):527 – 533.
- Ploug, H., Adam, B., Musat, N., Kalvelage, T., Lavik, G., Wolf-Gladrow, D., and Kuypers, M. M. M. (2011). Carbon, nitrogen and o₂ fluxes associated with the cyanobacterium *Nodularia spumigena* in the baltic sea. *ISME J*, 5(9):1549–1558.
- Price, G. (2011). Inorganic carbon transporters of the cyanobacterial co₂ concentrating mechanism. *Photosynthesis Research*, 109(1-3):47–57.
- Price, G. D., Badger, M. R., Woodger, F. J., and Long, B. M. (2008). Advances in understanding the cyanobacterial co₂-concentrating-mechanism (ccm): functional components, ci transporters, diversity, genetic regulation and prospects for engineering into plants. *Journal of Experimental Botany*, 59(7):1441–1461.
- Rantala, A., Fewer, D. P., Hisbergues, M., Rouhiainen, L., Vaitomaa, J., Börner, T., and Sivonen, K. (2004). Phylogenetic evidence for the early evolution of microcystin

- synthesis. *Proceedings of the National Academy of Sciences of the United States of America*, 101(2):568–573.
- Reynolds, C. S., Oliver, R. L., and Walsby, A. E. (1987). Cyanobacterial dominance: The role of buoyancy regulation in dynamic lake environments. *New Zealand Journal of Marine and Freshwater Research*, 21(3):379–390.
- Rippka, R., Deruelles, J., Waterbury, J. B., Herdman, M., and Stanier, R. Y. (1979). Generic assignments, strain histories and properties of pure cultures of cyanobacteria. *Journal of General Microbiology*, 111(1):1–61.
- Rohrlack, T., Dittmann, E., Börner, T., and Christoffersen, K. (2001). Effects of cell-bound microcystins on survival and feeding of daphnia spp. *Applied and Environmental Microbiology*, 67(8):3523–3529.
- Rohrlack, T., Dittmann, E., Henning, M., Börner, T., and Kohl, J.-G. (1999). Role of microcystins in poisoning and food ingestion inhibition of daphnia galeata caused by the cyanobacterium microcystis aeruginosa. *Applied and Environmental Microbiology*, 65(2):737–739.
- Runnegar, M., Berndt, N., Kong, S. M., Lee, E. Y. C., and Zhang, L. F. (1995). In-vivo and in-vitro binding of microcystin to protein phosphatase-1 and phosphatase-2a. *Biochemical and Biophysical Research Communications*, 216(1):162–169.
- Sandrini, G., Matthijs, H. C. P., Verspagen, J. M. H., Muyzer, G., and Huisman, J. (2014). Genetic diversity of inorganic carbon uptake systems causes variation in co₂ response of the cyanobacterium microcystis. *ISME J*, 8(3):589–600.
- Schatz, D., Keren, Y., Vardi, A., Sukenik, A., Carmeli, S., Börner, T., Dittmann, E., and Kaplan, A. (2007). Towards clarification of the biological role of microcystins, a family of cyanobacterial toxins. *Environmental Microbiology*, 9(4):965–970.
- Sevilla, E., Martin-Luna, B., Vela, L., Bes, M. T., Fillat, M. F., and Peleato, M. L.

- (2008). Iron availability affects mcyd expression and microcystin-Lr synthesis in *Microcystis aeruginosa* pcc7806. *Environmental Microbiology*, 10(10):2476–2483.
- Simon, R. D. and Weathers, P. (1976). Determination of the structure of the novel polypeptide containing aspartic acid and arginine which is found in cyanobacteria. *Biochimica et Biophysica Acta (BBA) - Protein Structure*, 420(1):165 – 176.
- Sivonen, K. and Jones, G. (1999). Chapter 3. cyanobacterial toxins. In Chorus, I. and Bartram, J., editors, *Toxic cyanobacteria in water- A guide to their public health consequences, monitoring and management*. UNESCO, WHO and UNEP by E&FN Spon.
- Sokal, R. and Rohlf, F. (1995). *Biometry: the principles and practice of statistics in biological research*. W.H. Freeman and Company, New York.
- Sommer, U., Adrian, R., De Senerpont Domis, L., Elser, J. J., Gaedke, U., Ibelings, B., Jeppesen, E., Luerling, M., Molinero, J. C., Mooij, W. M., van Donk, E., and Winder, M. (2012). Beyond the plankton ecology group (peg) model: Mechanisms driving plankton succession. *Annual Review of Ecology, Evolution, and Systematics*, 43(1):429–448.
- Spoof, L., Vesterkvist, P., Lindholm, T., and Meriluoto, J. (2003). Screening for cyanobacterial hepatotoxins, microcystins and nodularin in environmental water samples by reversed-phase liquid chromatography-electrospray ionisation mass spectrometry. *J Chromatogr A*, 1020(1):105–119.
- Stewart, I., Seawright, A., and Shaw, G. (2008). Cyanobacterial poisoning in livestock, wild mammals and birds – an overview. In Hudnell, H., editor, *Cyanobacterial Harmful Algal Blooms: State of the Science and Research Needs*, volume 619 of *Advances in Experimental Medicine and Biology*, pages 613–637. Springer New York.
- Straub, C., Quillardet, P., Vergalli, J., de Marsac, N. T., and Humbert, J.-F. (2011). A day in the life of *Microcystis aeruginosa* strain pcc 7806 as revealed by a transcriptomic analysis. *PLoS ONE*, 6(1):e16208.

- Su, Z., Olman, V., Mao, F., and Xu, Y. (2005). Comparative genomics analysis of ntca regulons in cyanobacteria: regulation of nitrogen assimilation and its coupling to photosynthesis. *Nucleic Acids Research*, 33(16):5156–5171.
- Suzuki, H. and Terada, T. (1988). Removal of dodecyl sulfate from protein solution. *Analytical Biochemistry*, 172(1):259 – 263.
- Tanigawa, R., Shirokane, M., Maeda, S.-i., Omata, T., Tanaka, K., and Takahashi, H. (2002). Transcriptional activation of ntca-dependent promoters of synechococcus sp. pcc 7942 by 2-oxoglutarate in vitro. *Proceedings of the National Academy of Sciences*, 99(7):4251–4255.
- Tchernov, D., Silverman, J., Luz, B., Reinhold, L., and Kaplan, A. (2003). Massive light-dependent cycling of inorganic carbon between oxygenic photosynthetic microorganisms and their surroundings. *Photosynthesis Research*, 77(2-3):95–103.
- Thomas, R. H. and Walsby, A. E. (1986). The effect of temperature on recovery of buoyancy by microcystis. *Journal of General Microbiology*, 132(6):1665–1672.
- Tibshirani, R., Walther, G., and Hastie, T. (2001). Estimating the number of clusters in a data set via the gap statistic. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 63(2):411–423.
- Tillett, D., Dittmann, E., Erhard, M., von Dohren, H., Borner, T., and Neilan, B. A. (2000). Structural organization of microcystin biosynthesis in microcystis aeruginosa pcc7806: an integrated peptide-polyketide synthetase system. *Chemistry & Biology*, 7(10):753–764.
- Toivola, D. M., Eriksson, J. E., and Brautigan, D. L. (1994). Identification of protein phosphatase 2a as the primary target for microcystin-1r in rat-liver homogenates. *Febs Letters*, 344(2-3):175–180.
- Tolbert, N. E. (1997). The c2 oxidative photosynthetic carbon cycle. *Annual Review of Plant Physiology and Plant Molecular Biology*, 48(1):1–25. PMID: 15012254.

- Tonietto, A., Petrizz, B., Araujo, W., Mehta, A., Magalhaes, B., and Franco, O. (2012). Comparative proteomics between natural microcystis isolates with a focus on microcystin synthesis. *Proteome Science*, 10(1):38.
- Towbin, H., Staehelin, T., and Gordon, J. (1979). Electrophoretic transfer of proteins from polyacrylamide gels to nitrocellulose sheets: procedure and some applications. *Proceedings of the National Academy of Sciences*, 76(9):4350–4354.
- Usher, K. M., Bergman, B., and Raven, J. A. (2007). Exploring cyanobacterial mutualisms. *Annual Review of Ecology Evolution and Systematics*, 38:255–273.
- Van de Waal, D. B., Verspagen, J. M., Finke, J. F., Vournazou, V., Immers, A. K., Kardinaal, W. E. A., Tonk, L., Becker, S., Van Donk, E., Visser, P. M., and Huisman, J. (2011). Reversal in competitive dominance of a toxic versus non-toxic cyanobacterium in response to rising co₂. *ISME J*, 5(9):1438 – 1450.
- Vazquez-Bermudez, M. F., Herrero, A., and Flores, E. (2002). 2-oxoglutarate increases the binding affinity of the ntcA (nitrogen control) transcription factor for the *Synechococcus glina* promoter. *FEBS Letters*, 512(1-3):71 – 74.
- Via-Ordorika, L., Fastner, J., Kurmayer, R., Hisbergues, M., Dittmann, E., Komarek, J., Erhard, M., and Chorus, I. (2004). Distribution of microcystin-producing and non-microcystin-producing microcystis sp in european freshwater bodies: Detection of microcystins and microcystin genes in individual colonies. *Systematic and Applied Microbiology*, 27(5):592–602.
- Whitton, B. A., Ward, D. M., Castenholz, R. W., Miller, S. R., Stal, L. J., Paerl, H. W., Oliver, R. L., David P. Hamilton, J. D. B., Ganf, G. G., Sejnohova, L., Marsalek, B., Cristiana Callieri, G. C., Stockner, J. G., Pentecost, A., Whitton, B. A., Albertano, P., Chunxiang Hu, K. G., Vincent, W. F., Quesada, A., Quesada, A., and Oren, A. (2012). Part 1, environments. In Whitton, B. A., editor, *Ecology of Cyanobacteria II*, pages 39–427. Springer Netherlands.

- Wiedner, C., Visser, P. M., Fastner, J., Metcalf, J. S., Codd, G. A., and Mur, L. R. (2003). Effects of light on the microcystin content of microcystis strain pcc 7806. *Applied and Environmental Microbiology*, 69(3):1475–1481.
- Wittig, I., Braun, H.-P., and Schagger, H. (2006). Blue native page. *Nat. Protocols*, 1(1):1754–2189.
- Yang, C., Hua, Q., and Shimizu, K. (2002). Metabolic flux analysis in synechocystis using isotope distribution from ^{13}C -labeled glucose. *Metabolic Engineering*, 4(3):202 – 216.
- You, L., Berla, B., He, L., Pakrasi, H. B., and Tang, Y. J. (2014). ^{13}C -mfa delineates the photomixotrophic metabolism of synechocystis sp. pcc 6803 under light- and carbon-sufficient conditions. *Biotechnology Journal*, 9(5):684–692.
- Young, F. M., Thomson, C., Metcalf, J. S., Lucocq, J. M., and Codd, G. A. (2005). Immunogold localisation of microcystins in cryosectioned cells of microcystis. *Journal of Structural Biology*, 151(2):208 – 214.
- Young, J. D., Shastri, A. A., Stephanopoulos, G., and Morgan, J. A. (2011). Mapping photoautotrophic metabolism with isotopically nonstationary ^{13}C flux analysis. *Metabolic Engineering*, 13(6):656 – 665.
- Zhang, S. and Bryant, D. A. (2011). The tricarboxylic acid cycle in cyanobacteria. *Science*, 334(6062):1551–1553.
- Zilliges, Y. (2007). *Molekulare Funktionsanalyse von Microcystin in Microcystis aeruginosa PCC 7806*. PhD thesis.
- Zilliges, Y., Kehr, J.-C., Meissner, S., Ishida, K., Mikkat, S., Hagemann, M., Kaplan, A., Börner, T., and Dittmann, E. (2011). The cyanobacterial hepatotoxin microcystin binds to proteins and increases the fitness of *Microcystis* under oxidative stress conditions. *PLoS ONE*, 6(3):e17615.

Appendix

Metabolomic data summary

Mass Spectral Feature			Metabolite Information										Z-Way ANOVA (Variance Analysis)										TukeyHSD - Tukey Honest Significant Differences (differences between the means)									
#	M/Z	Retention [s]	Metabolite	Class	Genotype (G)		Treatment (T)		G x T		Genotype (G)		Syn-Mut		Timepoint (T)		p-value (adjusted using Benjamini, Hochberg, and Yekutieli method (BY))		Mar x T		Mut x T		Syn x T									
					Mut-Mar	Syn-Mar	Syn-Mut	T0-T1	T0-T3	T1-T3	Mar-0-Mut:0	Mar-1-Mut:1	Mar-3-Mut:3	Mar-0-Syn:0	Mar-1-Syn:1	Mar-3-Syn:3	Mar-0-Mar:1	Mar-0-Mar:3	Mar-1-Mar:3	Mut-0-Mut:1	Mut-0-Mut:3	Mut-1-Mut:3	Syn-0-Syn:1	Syn-0-Syn:3	Syn-1-Syn:3							
1	160	186.26	Glyoxylate	Carboxylic acids	0.0003	0.3174	1	0.0003	0.0006	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05							
2	126	187.4	Unknown	Unknown	1E-07	0.0189	1	0.9395	2E-07	8E-05	0.0314	0.3457	1	0.0102	0.0006	0.0314	0.3457	1	0.0102	0.0006	0.0314	0.3457	1	0.0102	0.0006							
3	117	189.48	Lactate	Carboxylic acids	5E-05	1	1	0.0254	5E-05	1	1	1	1	0.9395	2E-07	8E-05	0.0314	0.3457	1	0.9395	2E-07	8E-05	0.0314	0.3457	1							
4	89	189.6	Unknown	Unknown	0.3624	1	1	1	0.4216	1	1	1	1	0.0254	5E-05	1	1	1	0.0254	5E-05	1	1	1	1	1							
5	85	194.17	Unknown	Unknown	0.0005	0.764	1	0.8717	0.0004	0.1535	1	1	1	0.8717	0.0004	0.1535	1	1	0.8717	0.0004	0.1535	1	1	1	1							
6	101	195.32	Unknown	Unknown	0.5097	1	1	1	0.5139	1	1	1	1	0.5097	1	1	1	1	0.5097	1	1	1	1	1	1							
7	161	203.25	Pyridine, 2-hydroxy-	Unknown	0.0731	0.6999	1	0.1412	1	1	1	1	1	0.1412	1	1	1	1	0.1412	1	1	1	1	1	1							
8	152	204.41	Unknown	Miscellaneous	0.0053	0.0009	1	1	0.9846	0.0041	1	1	1	0.9846	0.0041	1	1	1	0.9846	0.0041	1	1	1	1	1							
9	245	204.88	Unknown	Unknown	0.0421	0.9433	1	0.8784	0.0508	1	1	1	1	0.8784	0.0508	1	1	1	0.8784	0.0508	1	1	1	1	1							
10	144	206.06	Unknown	Unknown	0.0001	0.1004	0.0246	1	0.0009	0.0007	1	1	1	0.0009	0.0007	1	1	1	0.0009	0.0007	1	1	1	1	1							
11	177	206.27	Glycolate	Carboxylic acids	0.0023	0.0276	0.0019	1	0.002	0.3135	0.0448	0.3728	1	0.002	0.3135	0.0448	0.3728	1	0.002	0.3135	0.0448	0.3728	1	0.002	0.3135							
12	116	208.48	Alanine	Amino acids	7E-18	4E-15	3E-10	1	5E-12	4E-12	7E-11	6E-12	0.0081	1	5E-12	4E-12	7E-11	6E-12	0.0081	1	5E-12	4E-12	7E-11	6E-12	0.0081							
13	110	212.46	Unknown	Unknown	0.0018	0.6526	1	0.0104	0.0168	1	1	1	1	0.0104	0.0168	1	1	1	0.0104	0.0168	1	1	1	1	1							
14	89	216.65	Unknown	Unknown	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1							
15	174	222.35	Pyruvate	Carboxylic acids	0.6862	0.7088	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1							
16	102	227.96	Glycine	Amino acids	4E-06	0.0012	0.0582	1	3E-05	4E-05	0.015	0.0035	1	3E-05	4E-05	0.015	0.0035	1	3E-05	4E-05	0.015	0.0035	1	3E-05	4E-05							
17	153	228.44	Unknown	Unknown	0.0803	1	1	1	0.1592	0.2427	1	1	1	0.1592	0.2427	1	1	1	0.1592	0.2427	1	1	1	1	1							
18	140	233.99	Unknown	Unknown	0.4261	1	1	1	1	0.5441	1	1	1	1	0.5441	1	1	1	1	0.5441	1	1	1	1	1							
19	174	234.62	Unknown	Unknown	0.7042	1	1	1	1	0.7435	1	1	1	1	0.7435	1	1	1	1	0.7435	1	1	1	1	1							
20	177	245.83	Unknown	Unknown	2E-05	0.0313	1	1	2E-05	0.0049	0.0778	0.2143	1	1	2E-05	0.0049	0.0778	0.2143	1	1	2E-05	0.0049	0.0778	0.2143	1							
21	130	248.86	Butyrate, 2-amino-	Amino acids	6E-10	1E-15	2E-06	1	0.6895	1E-09	8E-07	3E-11	0	0.0015	1	0.6895	1E-09	8E-07	3E-11	0	0.0015	1	0.6895	1E-09	8E-07							
22	89	253.49	Unknown	Unknown	0.1868	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1							
23	184	254.45	Unknown	Unknown	0.3003	1	1	1	1	0.2983	1	1	1	1	0.2983	1	1	1	1	0.2983	1	1	1	1	1							
24	116	254.62	Unknown	Unknown	0.0415	1	1	1	0.7017	0.0541	1	1	1	0.7017	0.0541	1	1	1	0.7017	0.0541	1	1	1	1	1							
25	104	260.76	Unknown	Unknown	0.2678	1	1	1	1	0.2543	1	1	1	1	0.2543	1	1	1	1	0.2543	1	1	1	1	1							
26	147	264.46	Oxalate	Carboxylic acids	5E-07	1	1	1	1	4E-05	1E-06	1	1	1	4E-05	1E-06	1	1	1	4E-05	1E-06	1	1	1	1							
27	144	271.67	Valine	Amino acids	5E-05	8E-19	0.1804	1	0.6031	4E-05	0.0723	0	0	0.6031	4E-05	0.0723	0	0	0.6031	4E-05	0.0723	0	0	0.6031	4E-05							
28	131	273.85	Unknown	Unknown	4E-06	1E-11	1E-07	1	0.018	3E-06	0.1461	0.0664	1E-11	3E-07	1	0.018	3E-06	0.1461	0.0664	1E-11	3E-07	1	0.018	3E-06	0.1461							
29	140	275.46	Acetate	Carboxylic acids	0.3546	1	1	1	1	0.4278	1	1	1	1	0.4278	1	1	1	1	0.4278	1	1	1	1	1							
30	120	280.02	Unknown	Unknown	1E-07	1	1	1	0.001	8E-08	0.1093	1	1	0.001	8E-08	0.1093	1	1	0.001	8E-08	0.1093	1	1	1	1							
31	152	282.79	Pyridine, 3-hydroxy-	Miscellaneous	2E-10	7E-06	1	1	0.0066	1E-05	2E-10	0.0473	4E-06	0.2498	1	0.0066	1E-05	2E-10	0.0473	4E-06	0.2498	1	0.0066	1E-05	2E-10							
32	140	286.66	Unknown	Unknown	2E-06	0.0808	1	0.3043	0.0037	1E-06	1	1	1	0.3043	0.0037	1E-06	1	1	0.3043	0.0037	1E-06	1	1	1	1							
33	125	287.52	Unknown	Unknown	0.0002	1	1	1	0.071	0.0002	1	1	1	0.071	0.0002	1	1	1	0.071	0.0002	1	1	1	1	1							
34	89	288.01	Unknown	Unknown	8E-11	1	0.039	1	0.3684	2E-10	1E-07	1	1	0.3684	2E-10	1E-07	1	1	0.3684	2E-10	1E-07	1	1	1	1							
35	103	288.79	Unknown	Unknown	3E-05	0.0441	0.6713	1	0.1435	0.091	3E-05	0.0551	0.469	1	0.1435	0.091	3E-05	0.0551	0.469	1	0.1435	0.091	3E-05	0.0551	0.469							
36	144	289.12	Unknown	Unknown	5E-20	2E-17	7E-16	1	1	0	0	6E-10	0	4E-08	1	1	1	1	1	0	0	6E-10	0	4E-08	1							
37	205	291.9	Glycerol	Sugar alcohols	1E-13	1	1	1	1	0	0	1	1	1	0	0	1	1	1	0	0	1	1	1	1							
38	241	299.54	Unknown	Unknown	0.0049	3E-11	0.0057	1	0.0052	0.1521	7E-11	6E-08	0.1748	1	0.0052	0.1521	7E-11	6E-08	0.1748	1	0.0052	0.1521	7E-11	6E-08	0.1748							
39	158	304.98	Leucine	Amino acids	8E-15	8E-18	1E-08	1	0.3243	5E-12	1E-11	1E-11	8E-05	1	0.3243	5E-12	1E-11	1E-11	8E-05	1	0.3243	5E-12	1E-11	1E-11	8E-05							
40	117	305.92	Unknown	Unknown	9E-05	1	1	1	0.5559	0.1059	6E-05	1	1	0.5559	0.1059	6E-05	1	1	0.5559	0.1059	6E-05	1	1	1	1							
41	228	306.44	Unknown	Unknown	0.2029	1	1	1	1	1	0.1794	1	1	1	0.1794	1	1	1	1	0.1794	1	1	1	1	1							
42	166	308.41	Unknown	Unknown	0.5128	1	0.5408	1	1	1	0.4812	1	1	1	0.4812	1	1	1	1	0.4812	1	1	1	1	1							
43	198	309.12	Unknown	Unknown	0.3137	1	0.5401	1	0.3137	1	0.5401	1	1	0.3137	1	0.5401	1	1	0.3137	1	0.5401	1	1	1	1							
44	89	309.79	Unknown	Unknown	0.0001	1	0.096	1	0.0002	0.0052	1	1	1	0.0002	0.0052	1	1	1	0.0002	0.0052	1	1	1	1	1							
45	103	312.64	Acetone, 1,3-dihydroxy- (Dimer)	Monosaccharides	2E-09	0.1991	0.0193	1	0.0066	1E-09	0.0002	0.1758	1	0.0066	1E-09	0.0002	0.1758	1	0.0066	1E-09	0.0002	0.1758	1	0.0066	1E-09							
46	151	313.55	Unknown	Unknown	0.0617	0.0555	1	1	1	0.0678	1	1	1	1	0.0678	1	1	1	1	0.0678	1	1	1	1	1							
47	158	318.91	Isoleucine	Amino acids	0.3946	2E-22	0.0046	1	0.3869	1	0	0	4E-08	1	0.3869	1	0	0	4E-08	1	0.3869	1	0	0	4E-08							

Materials

Chemicals

Chemical	Provider
Acetic acid	Carl Roth, Karlsruhe, Germany
Acetone	Carl Roth, Karlsruhe, Germany
Acetonitrile	Carl Roth, Karlsruhe, Germany
Ammonium sulphate	Carl Roth, Karlsruhe, Germany
APS	Carl Roth, Karlsruhe, Germany
BICINE	Carl Roth, Karlsruhe, Germany
Boric acid	VEB Laborchemie, Apolda, Germany
BSA	Carl Roth, Karlsruhe, Germany
Calcium chloride dihydrate	Serva, Heidelberg, Germany
Citric acid	Carl Roth, Karlsruhe, Germany
Cobalt(II+) dinitrate hexahydrate	Sigma-Aldrich, Munich, Germany
Copper sulphate pentahydrate	Sigma-Aldrich, Munich, Germany
Dipotassium hydrogen phosphate $\times 3\text{H}_2\text{O}$	Carl Roth, Karlsruhe, Germany
Disodium carbonate	Carl Roth, Karlsruhe, Germany
Disodium hydrogen phosphate	Carl Roth, Karlsruhe, Germany
DTT	Carl Roth, Karlsruhe, Germany
EDTA	Carl Roth, Karlsruhe, Germany
Ethanol	Carl Roth, Karlsruhe, Germany
Ferric ammonium citrate	Fluka, Buchs, Switzerland
Formaldehyde	Sigma-Aldrich, Munich, Germany
Glycerol	Carl Roth, Karlsruhe, Germany
Glycine	Carl Roth, Karlsruhe, Germany
HEPES	Carl Roth, Karlsruhe, Germany

Hydrogen chloride	Carl Roth, Karlsruhe, Germany
Hydrogen peroxide solution 30 %	Carl Roth, Karlsruhe, Germany
Iodoacetamide	ICN Biomedicals, Aurora, Ohio, USA
Iodoacetic acid	Applichem, Darmstadt, Germany
Isopropanol	Carl Roth, Karlsruhe, Germany
Magnesium Chloride	Carl Roth, Karlsruhe, Germany
Magnesium sulphate heptahydrate	Carl Roth, Karlsruhe, Germany
Manganese chloride tetrahydrate	ICN Biomedicals, Aurora, Ohio, USA
Methanol	Carl Roth, Karlsruhe, Germany
n-Propylgallate	Carl Roth, Karlsruhe, Germany
Phosphoric acid 85 %	Carl Roth, Karlsruhe, Germany
PMSF	Sigma-Aldrich, Munich, Germany
Potassium bicarbonate	Carl Roth, Karlsruhe, Germany
Potassium carbonate	Carl Roth, Karlsruhe, Germany
SDS	Carl Roth, Karlsruhe, Germany
Sodium chloride	Carl Roth, Karlsruhe, Germany
Sodium dihydrogen phosphate,	Carl Roth, Karlsruhe, Germany
Sodium hydroxide	Carl Roth, Karlsruhe, Germany
Sodium molybdate dihydrate	ICN Biomedicals, Aurora, Ohio, USA
Sodium nitrate	Carl Roth, Karlsruhe, Germany
TCA	Carl Roth, Karlsruhe, Germany
TEMED	Carl Roth, Karlsruhe, Germany
TFA	Sigma-Aldrich, Munich, Germany
Tricine	Carl Roth, Karlsruhe, Germany
TRIS	Carl Roth, Karlsruhe, Germany
Triton® X-100	Sigma-Aldrich, Munich, Germany
Tween® 20	Sigma-Aldrich, Munich, Germany
Urea	MP Biochemicals, Illkirch, France
Zinc sulphate heptahydrate	Merck, Darmstadt, Germany

Miscellaneous

Item	Provider
Agarose LE	Biozym Scientific, Oldendorf, Germany
Bacto™ Agar	Becton-Dickson, Sparks, MD, USA
PageRuler™ Prestained Protein Ladder	Fermentas, St. Leon-Rot, Germany
Rotiphorese® Gel 30	Carl Roth, Karlsruhe, Germany
Microcystin LR	Dr. K. Ishida, Jena
Microcystin standards	Enzo Life Sciences, Germany
Nodularin standard	DHI, Denmark
Lysozyme from chicken egg white	Serva, Heidelberg, Germany
Antibodies	
Anti-Microcystin-LR mAB MC10E7	Enzo® Life Sciences, Lörrach, Germany
Anti-RbcL form I, II pAB AS03 037	Agrisera AB, Vannas, Sweden
Sheep Anti-Mouse IgG-Peroxidase	GE Hethcare, Buckinghamshire UK
Goat Anti-Rabbit IgG-Peroxidase	Sigma-Aldrich, St. Louis, MO, USA
FITC-conjugated Goat Anti-Mouse IgG	Jackson-Dianova, Hamburg, Germany
Consumables	
Amicon®Ultra centrifugal filters	Millipore™ Cooperation, Cork, Ireland
Plastibrand® Cuvetts PS, 1.5-3 ml	Carl Roth, Karlsruhe, Germany
Rotiprotect® Nitril gloves	Carl Roth, Karlsruhe, Germany
Glass sample slides 76x26x1 mm	Carl Roth, Karlsruhe, Germany
Cover slides 40x25x0.13-0.16 mm	Carl Roth, Karlsruhe, Germany
Microtiter® Flat bottom 96 well micro plates, sterile	Greiner-bio one, Frickenhausen, Germany
PARAFilm "M" Distensible plastic sealing film	Pechiney Plastic Packaging, Chicago, IL, USA

Pipett tips, TipOne® 0.1-10, 1-200, 101-1250 μ l natural tips	Starlab, Ahrensburg, Germany
Safe Lock Tubes Polypropylene re- action tubes, 500 μ l	Eppendorf AG, Hamburg, Germany
Serological Pipettes 2 mL, 10 mL, 25 mL, sterile	Carl Roth, Karlsruhe, Germany
Syringe filter 4 mm, Acrodisc®, 0.45 μ m nylon membrane	PALL Life Sciences, USA
Syringe filter Whatman®, 0.2 μ m sterile	Whatman®, Maidstone, UK
Whatman® 3MM Filter Paper	Whatman® Paper, Maidstone, UK

Technical appliance

Item	Provider
PowerPack Basic/ HC	Bio-Rad, Hercules, CA, USA
Mini-PROTEAN® Tetra System	Bio-Rad, Hercules, CA, USA
Haereus Pico 21 Microcentrifuge	Thermo Fisher Scientific Inc. Waltham, MA, USA
Perfect Spin 24R Microcentrifuge	PeqLab Biotechnology GmbH, Germany
200R 21 Microcentrifuge	Hettich, Tuttlingen, Germany
Heraeus Multifuge 1S-R	Thermo Fisher Scientific Inc. Waltham, MA, USA
Sigma 6-16K	Sartorius AG, Göttingen, Germany
Vortex Genie 2™, G560E	Scientific Industries, Bohemia N.Y., USA
Cell mill	Retsch GmbH, Haan, Germany
IKAMAG®RET Magnetic stirrer	IKA GmbH & Co. Kg, Staufen, Germany
Variomag mono	Thermo Fisher Scientific Inc. Waltham, MA, USA
Mini Rotator PTR-25	Grant-bio, Shepreth, England
Stirring bars	Carl Roth, Karlsruhe, Germany
KM-2-SWIP-VARIO Shaker	Edmund Buhler, Germany

DOS-10L Shaker	NeoLab, Migge, Heidelberg, Germany
Sartorius Basic Balance	Sartorius AG, Göttingen, Germany
Kern 572-37 Balance	Kern & Sohn GmbH, Balingen, Germany
Thriller Thermo-shaker block	PeqLab Biotechnology GmbH, Germany
Heat block	PeqLab Biotechnology GmbH, Germany
PCE-PHD multi meter	PCE Deutschland GmbH, Meschede, Germany
FiveEasy™ FE 20 pH Meter	Mettler Toledo AG, Schwerzenbach, Switzerland
LE 409 pH Sond	Mettler Toledo AG, Schwerzenbach, Switzerland
Sonorex TK 52	Bandelin Electronic, Berlin, Germany
Sonopuls UW 3100	Bandelin Electronic, Berlin, Germany
Sonotrode MS 72	Bandelin Electronic, Berlin, Germany
UV-1800 Spectrophotometer	Shimadzu, Japan
Varioskan™ Flash Plate Reader	Thermo Fisher Scientific Inc. Waltham, MA, USA
Li-250 Spherical photometer	Li-COR, inc., Lincoln, NE, USA
ChemiDoc™ XRS+ Imager	BioRad, USA
Milli-Q Reference A ⁺	Merck Millipore, Darmstadt, Germany
SpeedVac Vacuum concentrator	Eppendorf, Hamburg, Germany
MZ 2C Vacuum Pump	Vacuubrand, Wertheim, Germany
PC 2004 Vario Vacuum Pump	Vacuubrand, Wertheim, Germany
ÄKTAprime plus™ FPLC	GE Healthcare, USA

HPLC

DGU-20 A5 Degasser	Shimadzu, Japan
CBM-20 A System controler	Shimadzu, Japan
LC-20 AD Liquid chromatograph	Shimadzu, Japan
SPD-M20A Diode array detector	Shimadzu, Japan
SIL-20 AD Auto injector	Shimadzu, Japan
Column oven CTO-10 ASVP	Shimadzu, Japan
Fraction Collector FRC-10 A	Shimadzu, Japan

SymmetryShield™RP18 capped 3.5 μm , 4.6 \times 100 mm C18 column	end-	Waters, Milford, MA, USA
Agilent 2900 series HPLC		Agilent, Waldbronn, Germany
Purospher STAR RP-18 capped 3 μm , 30 \times 4 mm	end-	Merck, Darmstadt, Germany
API 5500 QTrap MS		AB Sciex, USA
Microscopy		
AMG EVOS fl		Peqlab, Erlangen, Germany
Canon PowerShot A520		Canon, Tokyo, Japan
CM100 TEM		Philips, Eindhoven, The Netherlands
Wilozyt H500		Hund, Wetzler, Germany
Software		
ExPASy proteomics server		Swiss Institute of Bioinformatics
Image Lab™		BioRad, USA
ImageBrowser EX for Windows		Canon, Tokyo, Japan
ImageJ analysis software		Rasband WS. ImageJ, U.S. National Institutes of Health, Bethesda, Maryland, USA
Kyoto Encyclopedia of Genes and Genomes (KEGG)		Kyoto, Japan
ℒ _A T _E X		www.latex-project.org
LCsolution HPLC software		Shimadzu, Japan
Microsoft Office 2010		Microsoft®, Redmond, WA, USA
NCBI		National Center for Biotechnology Information, USA
Prime View FPLC software		GE Healthcare, USA
R 3.0.2		R Development Core Team, 2013
UV Probe spectroscopy software		Shimadzu, Japan
Windows 7 Professional OS		Microsoft®, Redmond, WA, USA

Publications

Zilliges, Y., Kehr, J.-C., **Meissner, S.**, Ishida, K., Mikkat, S., Hagemann, M., Kaplan, A., Börner, T., and Dittmann, E. (2011)

The cyanobacterial hepatotoxin microcystin binds to proteins and increases the fitness of *Microcystis* under oxidative stress conditions

PLoS ONE, 6: e17615

Meissner, S., Fastner, J., and Dittmann, E. (2013)

Microcystin production revisited: conjugate formation makes a major contribution

Environmental Microbiology, 15(6):1810–1820

Meissner, S., Steinhauser, D., and Dittmann, E. (2014)

Metabolomic analysis indicates a pivotal role of the hepatotoxin microcystin in high light adaptation of *Microcystis*

Environmental Microbiology, pages n/a–n/a

Deutsche Zusammenfassung

Effekte der Produktion von Microcystin in *Microcystis aeruginosa* PCC 7806

Cyanobakterien produzieren etwa 40 Prozent der primären Biomasse auf der Welt, aber auch giftige Peptide wie das leberschädigende Microcystin. Massenvorkommen, so genannte Blaualgenblüten, gefährden vielerorts regelmäßig die Trinkwasserversorgung. Diese Arbeit hatte zum Ziel, den Einfluss der Microcystinproduktion auf physiologische Abläufe in dem weit verbreiteten blütenbildenden Cyanobakterium *Microcystis aeruginosa* zu charakterisieren.

Zum einen, wurde hierfür der Einfluss der Beleuchtungsintensität auf die Produktion von Microcystin und dessen Bindung an zelluläre Proteine ermittelt. Hierzu wurden etablierte Quantifizierungstechniken mit biochemischen Methoden kombiniert. RubisCO, das Schlüsselenzym zur primären Kohlenstofffixierung, war ein Hauptinteraktionspartner von Microcystin. Hohe Beleuchtungsintensität erhöhte die Menge von an Proteine gebundenem Microcystin. Bis zu 60 Prozent des gesamten zellulären Microcystins lag an Proteine gebunden vor, d.h. es wurde durch Standardquantifizierungsmethoden nicht erfasst. Die Notwendigkeit, zur Quantifizierung des gesamten Microcystins die Proteinfraktion mit einzubeziehen, wurde auch in Freilandproben demonstriert. Die Entwicklung einer immunfluoreszenzbasierten Methode erlaubte die Unterscheidung von

toxischen und nichttoxischen *Microcystis* Kolonien in Freilandproben.

Die starklichtinduzierte Interaktion von Microcystin mit Proteinen deutete auf einen möglichen Einfluss des Sekundärmetabolits auf den Primärstoffwechsel von *Microcystis* hin. Um dieser Frage nachzugehen, wurde ein umfassender GC/MS-basierter Versuch durchgeführt, um die Akkumulation von Metaboliten im Microcystin produzierenden Stamm *Microcystis aeruginosa* PCC 7806 und dessen microcystinfreier *mcyB*-mutierten Variante vergleichen zu können. Es zeigte sich, dass Microcystin einen Einfluss auf die Akkumulation von 85 (17 Prozent) aller 501 detektierten Metabolite unter erhöhter Beleuchtungsstärke hatte. Besonders die vermehrte Synthese osmotisch aktiver Substanzen in der *mcyB* Mutante, verstanden als generelle Reaktion auf allgemeinen Stress, deutet auf eine Beteiligung von Microcystin in der metabolischen Justierung von *Microcystis* hin.

Die Parallelanalyse des Modellstamms *Synechocystis* PCC 6803 offenbarte grundsätzliche metabolische Unterschiede zwischen verschiedenen Cyanobakterienspezies. Demnach produzierte *Microcystis* vor allem Kohlehydrate und *Synechocystis* eher Aminosäuren. Die GC/MS-basierten Ergebnisse wurden durch elektronenmikroskopische Aufnahmen und die Quantifizierung von Speichermetaboliten gestützt. Innerhalb drei Stunden bewirkte Starklicht die Akkumulation von Glykogen in *Microcystis* auf ca. 8.5 Prozent des Frischgewichts, wohingegen *Synechocystis* mehr Cyanophycin produzierte. Die Ergebnisse zeigten, dass im Hinblick auf die biotechnologische Nutzung von Cyanobakterien, die Charakterisierung speziesspezifischer metabolischer Eigenschaften mehr Beachtung finden sollte.