

**Cyanobacterial Toxin (Microcystins):
Occurrence, Accumulation and Effects on Freshwater Clam**

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Abstract

Increasing of human population and the consequent intensification of agricultural and industrial activities along with deficient water management have led to enhancement of eutrophication and cyanobacterial blooms (CYBs) in freshwater bodies. Occurrence of toxic CYBs in freshwater environments is a global problem and public health concern due to produce secondary metabolites with toxic properties, named cyanotoxins. Among various cyanotoxins known, microcystins (MCs) are the most widespread in freshwaters. While MCs have been associated with many aquatic animal deaths as well as chronic effects in humans, bioaccumulation and adverse effects of sub-chronic exposure at environmentally relevant concentrations are not yet fully understood. Consuming water or food contaminated with MCs poses risks to human health. To minimize these risks, the World Health Organization (WHO) recommends a value of $1 \mu\text{g L}^{-1}$ for total MC for drinking water guideline and a chronic tolerable daily intake (TDI) of $0.04 \mu\text{g kg}^{-1}$ body weight per day for human consumption.

Episodes of toxic CYBs have recently been well documented in subtropical and temperate regions. However, information on toxic cyanobacteria and their toxins from tropical regions like Southeast Asia is limited. Dau Tieng Reservoir provides drinking water for millions of people in southern Vietnam. Although CYBs have recently reported, cyanobacterial toxins are not considered as an important parameter of water quality in Vietnam. Therefore, during excessive proliferation of cyanobacteria, local people may be facing health risks caused by cyanotoxins.

This work focused on (1) isolated cyanobacteria and their toxins in Dau Tieng Reservoir. (2) Investigated the accumulation and elimination of free MC and covalently bound MC (Co-MC) in the edible clam *Corbicula leana* under laboratory conditions. (3) Evaluated oxidative stress and toxic effects caused by various cyanobacterial biomass including toxic, non-toxic *Microcystis* intact cells and a natural cyanobacterial crude extract (CCE) containing MCs in

the clam tissues. And, (4) calculated potential health risks associated with consumption of the clam contaminated with MCs.

A total of 68 cyanobacterial strains belonging to 5 genera: *Microcystis* (59 strains), *Dolichospermum* (4 strains), *Arthrospira* (2 strains), *Pseudanabaena* (2 strains) and *Cylindrospermopsis* (1 strain) have been characterized from Dau Tieng Reservoir. Investigation these strains revealed the co-existence of toxic and non-toxic genotypes. In which *Microcystis aeruginosa* was bloom-forming species and toxin producer. The MC concentrations from bloom samples and cultures were as high as 669 and 2,129 $\mu\text{g g}^{-1}$ dry weight (DW), respectively.

In the aquatic environment, MCs present not only in ambient water but also contaminate in aquatic animals via bioaccumulation through food web. Aquatic animals may take up and accumulate MCs via the two main routes: uptake dissolved toxins via a transdermal route or intake of toxic cyanobacterial cells via ingestion. In this study, the accumulation and depuration of MC in clam *C. leana* were investigated in the two main routes by using both toxic cells (toxic *Microcystis*, for via ingestion) and CCE containing MCs (for via uptake from dissolved fraction). Results showed that clam *C. leana* was able to accumulate a considerable amount of MCs via both ways, ingest toxic cyanobacteria and/or via uptake from dissolved fraction in water column. The clam *C. leana* accumulated up to $12.7 \pm 2.5 \mu\text{g g}^{-1}$ DW of free and $4.2 \pm 0.6 \mu\text{g g}^{-1}$ DW of Co-MC when feed with toxic cells, and $3.4 \pm 0.63 \mu\text{g g}^{-1}$ DW of free and $0.3 \pm 0.013 \mu\text{g g}^{-1}$ DW of Co-MC when exposed to CCE containing MCs. Results also show that although free MC was quickly took up and rapidly excreted after 1 – 3 days of exposure and depuration, the Co-MC was still detectable after 10 days of depuration.

Both toxic, non-toxic cyanobacteria cells and/or CCE containing MCs caused many toxic effects on clam tissues. They induced the detoxification and antioxidant enzymes in various organs of *C. leana*. The activity of superoxide dismutase (SOD), catalase (CAT), and

glutathione *S*-transferases (GST) in the gills and mantle increased. However, CAT and GST activity was significantly inhibited in the foot and only slightly changed in the remaining tissues when treated clams with CCE. In contrast, GST activity inhibited significantly in the gills, foot and remaining tissues while CAT and SOD activities elevated significantly in the gills and mantle whereas they were almost no change in foot and other tissues when exposed the clams to toxic and non-toxic *Microcystis*.

These results suggested that both toxic, non-toxic cyanobacteria and CCE caused oxidative stress in the clam tissues, but did not kill the clam. At the same time, the animal would both improve their antioxidant abilities and metabolize the toxin to combat these adverse effects. However, toxic effects are only temporary in both cases and that prolonged exposure may lead to the adaptations to cope with deleterious effects. Consequently, in toxin-free water, both of the antioxidant enzymes and detoxification enzyme showed adaptive responses at several time points whereby enzyme activity was induced and then returned to control levels. In other words, clams are temporarily affected by toxic and non-toxic cyanobacteria but later show signs of resistant to cyanotoxins.

Consumption of food contaminated with MCs could be potentially cancer promotion. My results showed that the total MC contents in clams exceed the TDI of $0.04 \mu\text{g kg}^{-1}$ of body mass per day. It suggested that *C. leana* represents a health risk to consumers. Consumption of this clam should be limited when there are high concentrations of toxic cyanobacteria present in the water from which it is harvested. They need detoxification process before marketing.

Contents

Chapter 1

Introduction	1
1.1. Background	1
1.1.1. Cyanobacteria	1
1.1.2. Bloom-forming cyanobacteria and causes	2
1.1.3. Cyanobacterial hepatotoxin: Microcystins	3
1.1.4. Microcystin synthetases	4
1.1.5. Occurrence of hepatotoxic blooms	4
1.2. Previous studies on accumulation and effects of cyanotoxins	6
1.2.1. Accumulation	6
1.2.2. Toxicity and effect of microcystins	7
1.3. Aims of this study	8
1.4. Research contents	9

Chapter 2

Occurrence of toxic cyanobacterial blooms and their toxins in Dau Tieng Reservoir,

Vietnam	13
2.1. Introduction	13
2.2. Materials and methods	15
2.2.1. Sites and sampling	15

2.2.2. Morphological characterization	16
2.2.3. DNA extraction.....	16
2.2.4. PCR amplification.....	17
2.2.5. Microcystins extraction and analysis	18
2.3. Results.....	18
2.3.1. Isolation and morphological characteristics	18
2.3.2. Microcystin producers	21
2.3.3. Microcystin production.....	22
2.4. Discussion	22
2.5. Summary	28

Chapter 3

Accumulation and effects of cyanobacterial crude extract containing microcystins on the edible clam *Corbicula leana*

39

3.1. Introduction.....	39
3.2. Materials and methods	41
3.2.1. Rearing the organisms	41
3.2.2. Preparation of cyanobacterial crude extract.....	42
3.2.3. Experimental set up	42
3.2.4. Extraction and analysis of MCs in incubation water	43
3.2.5. Extraction and analysis of free MC in clam	44
3.2.6. Extraction of total MC in clam	44
3.2.7. GC-MS analysis	45
3.2.8. Enzyme extraction and measurement	46

3.2.9. Recovery experiment	46
3.2.10. Statistical analyses	47
3.3. Results.....	47
3.3.1. Microcystins concentration in incubation water	47
3.3.2. Uptake and depuration of free- and Co-MC	47
3.3.3. Biotransformation enzyme.....	48
3.3.4. Antioxidant enzyme activities	48
3.4. Discussion	49
3.5. Summary	55

Chapter 4

Accumulation and effects of toxic and non-toxic cyanobacteria on the edible clam

<i>Corbicula leana</i>	64
4.1. Introduction.....	64
4.2. Materials and methods	65
4.2.1. Culture of toxic, non-toxic <i>Microcystis</i> and green alga.....	65
4.2.2. Collection and maintenance of clams	65
4.2.3. Clearance rate	65
4.2.4. Feeding experiment.....	66
4.2.5. Extraction and analysis of MCs in incubation water	67
4.2.6. Extraction and analysis of free MC in clam	68
4.2.7. Extraction of total MC in clam	68
4.2.8. GC-MS analysis	68
4.2.9. Enzyme extraction and measurement	68

4.2.10. Statistical analyses	68
4.3. Results.....	69
4.3.1. Clearance rate	69
4.3.2. Microcystin concentrations in incubation water	69
4.3.3. Uptake and depuration of free- and Co-MC	69
4.3.4. Biotransformation enzyme.....	70
4.3.5. Antioxidant enzyme activities	70
4.4. Discussion	71
4.5. Summary	77

Chapter 5

General conclusions and recommendations.....	86
5.1. Conclusions.....	86
5.2. Recommendations.....	88
Acknowledgements.....	90
References	91

List of abbreviations

Abbreviations and definitions

4-PB	4-phenylbutyric acid
Adda	3-amino-9-methoxy-2,6,8-trimethyl-10-phenyldeca-4,6-dienoic acid
ANOVA	one-way analysis of variance
BW	body weight
CAT	catalase
CCE	cyanobacterial crude extract
Co-MC	covalently bound microcystin
CR	clearance rate
CTAB	cetyltrimethyl ammonium bromide
CYB(s)	cyanobacterial bloom(s)
DAD	diode array detector
D-MeAsp	D-erythro-b-methylaspartic acid
DNA	deoxyribonucleic acid
DTE	dithioerythritol
DW	dry weight
EDI	estimated daily intake
EDTA	ethylenediaminetetraacetic acid
FW	fresh weight
GC/MS	gas chromatography–mass spectrometry
GSH	glutathione
GST(s)	glutathione <i>S</i> -transferase(s)
HPLC	high-performance liquid chromatography
LD ₅₀	lethal dose, 50%
MC(s)	microcystin(s)
MC-LR	microcystin which has leucine and arginine in positions R ₁ and R ₂ , respectively (see Figure 1–2)
MC-LY	microcystin which has tyrosine and arginine in positions R ₁ and R ₂ , respectively (see Figure 1–2)
MC-RR	microcystin which has arginine and arginine in positions R ₁ and R ₂ , respectively (see Figure 1–2)
<i>mcy</i>	microcystin synthetase gene cluster

Mdha	N-methyldehydroalanine
me4-PB	methyl 4-phenylbutyric acid
meMMPB	methyl 2-methyl-3-methoxy-4-phenylbutyric acid
MeOH	methanol
MMPB	2-methyl-3-methoxy-4-phenylbutyric acid
MXR	multixenobiotic resistance
NIES	National Institute for Environmental Studies
NRPS	non-ribosomal peptide synthesis
OATP(s)	organic anion transporting polypeptide(s)
PCR	polymerase chain reaction
PDA	photodiode array detector
PKS	polyketide synthesis
PP1	protein phosphatase 1
PP2A	protein phosphatase 2A
PPFD	photosynthetic photon flux density
PPs	protein phosphatase
RNA	ribonucleic acid
ROS	reactive oxygen species
rRNA	ribosomal ribonucleic acid
RSD	relative standard deviations
SD	standard deviations
SEM	soil extract medium
SIM	selected ion monitoring
SOD	superoxide dismutase
TDI	tolerable daily intake
TE	tris-EDTA buffer solution
TN	total nitrogen
TP	total phosphorus
UV	ultraviolet
WHO	World Health Organization
WW	wet weight

Chapter 1

Introduction

1.1. Background

1.1.1. Cyanobacteria

Cyanobacteria (also known as blue-green algae) belong to the kingdom Monera (Prokaryota), division Eubacteria, class Cyanobacteria (Stanier and van Niel, 1941). The class includes about 150 genera and approximately 2,000 species (Hoek *et al.*, 1995; Duy *et al.*, 2000). Cyanobacteria are photosynthetic prokaryotes and common in limnic systems where they can exist as solitary, free-living cells or as colonies or filaments (Catherine *et al.*, 2013). They also can be found in marine environments, terrestrial habitats or even surviving in extreme environments of Antarctica or hot springs (Zanchett and Oliveira-Filho, 2013). Unlike photosynthetic bacteria, however cyanobacteria possess chlorophyll-a in common with photosynthetic eukaryotes, and they liberate oxygen during photosynthesis. Cyanobacteria are considered as an important contributor to the formation of the Earth's atmosphere and nitrogen fixation (Hoek *et al.*, 1995).

The cyanobacteria were traditionally classified by morphology into five sections, referred to by the numerals I – V: Chroococcales, Pleurocapsales, Oscillatoriales, Nostocales and Stigonematales (Hoek *et al.*, 1995). In which, group I (Chroococcales) comprises solitary and colonial unicellular cyanobacteria, for example, *Microcystis*, *Synechococcus* and *Gloeocapsa*. Group II (Pleurocapsales) consists of unicellular to pseudo-filamentous, thallus-forming cyanobacteria, with cells capable of multiple, as well as binary, fission, for example, *Pleurocapsa*. In Pleurocapsales, the cells have the ability to form internal spores (baeocytes). Group III (Oscillatoriales) comprises filamentous cyanobacteria without cell differentiation, for example, *Oscillatoria*, *Lyngbya* and *Phormidium* whereas Group IV (Nostocales) consists of filaments marked by cell differentiation to produce akinetes and heterocysts, for example,

Anabaena, *Nostoc* and *Cylindrospermopsis*. And group V (Stigonematales) comprises cell-differentiating cyanobacteria with more complex multicellular organization and includes species with truly branched trichomes, for example, *Mastigocladus* and *Stigonema* (Knoll, 2008).

1.1.2. Bloom-forming cyanobacteria and causes

Increasing of human population and the consequent intensification of agricultural and industrial activities has led to enhancement of eutrophication creating conditions favored cyanobacteria blooms (CYBs) in freshwater bodies (Figueiredo *et al.*, 2004).

There is no international definition for what a CYB is, however, this phenomenon is generally considered as an excessive production of cyanobacteria biomass over a short period of time (several weeks). In fact, blooms of cyanobacteria are often mono-specific (or nearly so) (Merel *et al.*, 2013). During the bloom, generally, a green layer or scum of cyanobacteria will form on surface water visible to the un-aided eye (Figure 1–1). Bloom-forming cyanobacteria often contain gas vesicles and are capable of floating up, enabling them to form a dense surface blooms where they can take advantage of high levels of irradiance to optimize photosynthesis (Paerl and Paul, 2012). Most of cyanobacteria prefer living in warm aquatic habitat, which therefore resulting in blooms mostly happening in summer (Havens, 2008).

Generally, the formation of CYBs is regulated by a combination of three primary environmental factors (Merel *et al.*, 2013). The first one is water temperature, many species of cyanobacteria preferring warmer conditions (20°C or above). Consequently, climate change and global warming may increase the frequency and magnitude of CYBs by favoring cyanobacteria among other phytoplankton species (Arheimer *et al.*, 2005; Wiedner *et al.*, 2007; Heisler *et al.*, 2008; Paerl and Huisman, 2009; El-Shehawy *et al.*, 2012; Kosten *et al.*, 2012; O’Neil *et al.*, 2012; Paerl and Paul, 2012; Reichwaldt and Ghadouani, 2012). The second environmental factor influencing CYBs is light intensity. Although several species of cyanobacteria can be considered hetero- or chemo-trophic, most species need a minimum of

light availability for photosynthesis (Merel *et al.*, 2013). Many cyanobacteria cannot survive high light intensities over longer periods. This may limit their distribution to more turbid and eutrophic habitats. However, some species are extremely flexible in their response to light exposure because buoyancy regulation enables them to find light conditions that are optimal for their growth (Chorus and Bartram, 1999). And the third factor leading to bloom formation is the trophic status of the aquatic system. Nitrogen and phosphorus are two nutrients that are most essential for the growth and survival of cyanobacteria. Thus, CYBs mainly occur in eutrophic water bodies and well correlate with the concentration of TN and TP (Downing *et al.*, 2001; Heisler *et al.*, 2008; El-Shehawy *et al.*, 2012).

1.1.3. Cyanobacterial hepatotoxin: Microcystins

CYBs are often toxic because they produce a variety of secondary metabolites, known as cyanotoxins. Among these, hepatotoxin microcystins (MCs) form the main family since they are the most frequently studied and the most widespread. MCs are produced by various species within the genera *Dolichospermum* (planktic *Anabaena*), *Microcystis*, *Oscillatoria*, *Planktothrix*, *Nostoc*, *Aphanizomenon*, *Arthrospira*, *Lyngbya*, *Pseudanabaena* and *Anabaenopsis* in freshwaters (Chorus and Bartram, 1999).

MCs contain seven peptide-linked amino acids, with the two terminal amino acids of the linear peptide being condensed (joined) to form a cyclic compound. The general structure is: cyclo-(D-alanine-R1-D-MeAsp-R2-Adda-D-glutamate-Mdha) in which R1 and R2 are variable L amino acids, D-MeAsp is D-erythro-β-methylaspartic acid, and Mdha is N-methyldehydroalanine (Duy *et al.*, 2000). The R1, R2 variable amino acids for MC-LR, MC-RR and MC-YR are leucine (L), arginine (R) and tyrosine (Y) (Figure 1–2). The amino acid Adda, (2S,3S,8S,9S)-3-amino-9-methoxy-2,6,8-trimethyl-10-phenyldeca-4,6-dienoic acid, is the most unusual structure in this group of cyclic peptide toxins. There are over 90 structure variants have so far been reported and the three most common are MC-LR, -RR and -YR (Pearson *et al.*, 2010).

1.1.4. Microcystin synthetases

MCs are synthesized by the thiotemplate mechanism characteristic for non-ribosomal peptide synthesis (NRPS), polyketide synthesis (PKS) and fatty acid synthesis (Kurmayer and Christiansen, 2009). The MC biosynthesis gene cluster (*mcy*) contains peptide synthetases, polyketide synthases and tailoring enzymes that are encoded by ten (in *Microcystis*, *Anabaena*) or nine (in *Planktothrix*) genes (Figure 1–3, Nishizawa *et al.*, 1999; Tillett *et al.*, 2000; Christiansen *et al.*, 2003; Rouhiainen *et al.*, 2004; Kurmayer and Christiansen, 2009).

The *mcy* gene was the first complex metabolite gene cluster to be fully sequenced from a cyanobacterium. In *M. aeruginosa* PCC7806, the *mcy* gene spans 55 kb and comprises 10 genes arranged in two divergently transcribed operons (*mcyA–C* and *mcyD–J*). The larger of the two operons, *mcyD–J*, encodes a modular PKS (*mcyD*), two hybrid enzymes comprising NRPS and PKS modules (*mcyE* and *mcyG*), and enzymes putatively involved in the tailoring (*mcyJ*, *F*, and *I*) and transport (*mcyH*) of the toxin. The smaller operon, *mcyA–C* encodes three NRPS (*mcyA–C*). Interestingly, the arrangement in the *mcy* cluster was found to be different in the organisms *Microcystis*, *Anabaena* and *Planktothrix* (Figure 1–3, Kurmayer and Christiansen, 2009; Pearson *et al.*, 2010). These fundamental studies have afforded insight into the evolution of cyanotoxin biosynthesis, and have additionally provided much of the groundwork for current PCR-based cyanobacterial detection methods (Neilan *et al.*, 2008).

1.1.5. Occurrence of hepatotoxic blooms

In recent centuries toxic CYBs have been reported worldwide and intensively reviewed on literature (Paerl *et al.*, 2001; Figueiredo *et al.*, 2004; Havens, 2008; Blaha *et al.*, 2009; Cheung *et al.*, 2013; Merel *et al.*, 2013). The most dominant bloom forming cyanobacterial genera in freshwaters are: *Microcystis*, *Dolichospermum*, *Aphanizomenon*, *Oscillatoria*, *Cylindrospermopsis*, *Phormidium* and *Nostoc* (Figueiredo *et al.*, 2004).

CYBs have been reported from many lakes and reservoirs in Europe, such as Lale Vela Portuguese, Lake Tuusulanjärvi in Finland, Lake Grand-Lieu, Saint-Caprais reservoir in

France, El Atazar reservoir in Spanish, ponds Liège in Belgium, lakes in southwestern Germany, lakes of northern Poland, all used for recreational or drinking purposes. They have been found to have hepatotoxic blooms, mainly associated with the dominance of *M. aeruginosa* and in some cases *Aphanizomenon*, *Dolichospermum* and *Oscillatoria* (Vasconcelos *et al.*, 1996; Vezie *et al.*, 1998; Wirsing *et al.*, 1998; Hummert *et al.*, 2001b; Vasconcelos *et al.*, 2001; Frank, 2002; Barco *et al.*, 2004; Mankiewicz *et al.*, 2005).

Many lakes used for drinking water from America, Canada and United States have also suffered with *M. aeruginosa* blooms that sometime have MC contents higher than the WHO guideline (Campos *et al.*, 1999; Amé *et al.*, 2003; Rinta-Kanto *et al.*, 2009; Ruiz *et al.*, 2013) and related to human exposed and animal deaths (Puschner *et al.*, 1998; Nasri *et al.*, 2008).

In Africa, occurrence of *Microcystis* and *Oscillatoria* blooms with production of MCs has been recorded in River Nile from Egypt, in Lake Victoria from Uganda, Lake Lalla Takerkoust from Morocco, Lake Oubeira in Algeria, Dam Lebna in Tunisia, dam Hartbeespoort and Roodeplaat in South African (Oudra *et al.*, 2002; Sabour *et al.*, 2002; Haande *et al.*, 2007; El-Herry *et al.*, 2008; Nasri *et al.*, 2008; Nyakairu *et al.*, 2010; Okello *et al.*, 2010; Conradie and Barnard, 2012).

The occurrence of severe *Microcystis*, *Dolichospermum* and *Cylindrospermopsis* blooms associated with MCs and other cyanobacterial toxins seems to be occur very frequent in Australia (Figueiredo *et al.*, 2004; Kemp and John, 2006; Mitrovic *et al.*, 2011; Al-Tebrineh *et al.*, 2012).

In Asian countries, intensive blooms of cyanobacteria (mainly *Microcystis*, *Dolichospermum* and *Planktothrix*) have been reported from Lake Taihu, Lake Chaohu, Lake Dianchi, Guanting Reservoir in China (Chen and Xie, 2005a; Dai *et al.*, 2008; Xu *et al.*, 2008; Chen *et al.*, 2009; Krüger *et al.*, 2010; Ma *et al.*, 2014), from Lake Kasumigaura, Lake Biwa, Lake Sagami, Isahaya Bay in Japan (Park *et al.*, 1993a; Park *et al.*, 1993b; Park *et al.*, 1998a; Tsujimura *et al.*, 2000; Ozawa *et al.*, 2005; Umehara *et al.*, 2012). CYBs associated with MCs

have also been found from eutrophic aquaculture ponds and water reservoirs in Taiwan (Lee *et al.*, 1998), many lakes from Korea (Park *et al.*, 1998b), from Laguna de Bay, the largest freshwater lake in the Philippines (Cuvin-Aralar *et al.*, 2002), as well as Kranji Reservoir in Singapore (Te and Gin, 2011), Lake Thanh Cong, Tri An, Dau Tieng and Nui Coc Reservoirs in Vietnam (Hummert *et al.*, 2001a; Dao *et al.*, 2010; Duong *et al.*, 2014).

CYBs are now global environmental problems and public concerns. Therefore, it is necessary to make more efforts to minimize the impacts of CYBs and their toxins in aquatic ecosystems.

1.2. Previous studies on accumulation and effects of cyanotoxins

1.2.1. Accumulation

The ability of MCs to accumulate in a wide range of aquatic animals, including zooplankton, bivalves, gastropods, fish and macrocrustaceans in both laboratory and field studies is well known from literature (for reviews: Ibelings and Chorus, 2007; Smith *et al.*, 2008; Martins and Vasconcelos, 2009; Ferrão-Filho and Kozlowsky-Suzuki, 2011).

Zooplankton is reported the best bioaccumulator of MCs, reaching value over 1,000 $\mu\text{g g}^{-1}$ dry weight (DW). This leads to transport of MCs through the food chains because zooplankton community is one of the most important links between the primary producers and higher aquatic consumers such as fish (Ferrão-Filho *et al.*, 2002; Sotton *et al.*, 2014).

Gastropods and bivalves may be among the most threatened groups of aquatic organisms in the presence of toxic cyanobacteria blooms because they are sessile filter-feeders (Martins and Vasconcelos, 2009). Freshwater as well as marine gastropods and bivalves are able to accumulate cyanobacteria toxins via ingestion of toxic cyanobacteria or uptake MCs dissolved in water column (Ibelings and Chorus, 2007). The highest concentrations of MCs in gastropods and bivalves were 436 and 630 $\mu\text{g g}^{-1}$ DW in hepatopancreases, respectively (Ozawa *et al.*, 2003; Yokoyama and Park, 2003).

In contrast, larger crustaceans (*i.e.*, *Macrobrachium nipponensis*) seem to be the less efficient accumulator of MCs with a maximum concentration of only $12 \mu\text{g g}^{-1}$ DW (Chen and Xie, 2005b).

Fish may be accumulated MCs via ingestion of toxic cyanobacteria or contaminated food and to a lesser extent via uptake of dissolved toxins (Sotton *et al.*, 2014). MCs were found to accumulate in different organs of freshwater fish and the highest concentrations (up to $874 \mu\text{g g}^{-1}$ DW) often found in the liver (Ibelings *et al.*, 2005).

The MCs concentrations accumulated in aquatic organisms depends on species, exposure routes, target organs as well as the MCs concentration from surrounding water. This bioaccumulation of MCs in food chains is a public concern for human health. However, most previous studies have reported only the concentration of the accumulation of free MC and did not adequately consider the content of MCs covalently bound to protein phosphatases (PPs), which may represent a considerably part of the MCs burden (Lance *et al.*, 2010; 2014).

1.2.2. Toxicity and effect of microcystins

MCs are cyclic heptapeptides because they target liver cells, and its cellular uptake requires organic anion transporter polypeptides (OATPs) activity (Fischer *et al.*, 2005). Once in hepatocytes, they are potent inhibitors of eukaryotic protein phosphatases PP1 and PP2A by interacting with the catalytic subunits of these enzymes (MacKintosh *et al.*, 1990; Duy *et al.*, 2000). While PPs serve as a regulator to maintain homeostasis in the cell, inhibition of PPs leads to hyperphosphorylation, causing severe cell damage (Eriksson *et al.*, 1990; Dawson, 1998). This is a major post-translational modification which can result in excessive signaling and may lead towards cell proliferation, cell transformation and tumor promotion (MacKintosh *et al.*, 1990; Apeldoorn *et al.*, 2007; Amado and Monserrat, 2010).

Besides inhibition of PPs, oxidative stress, produced by reactive oxygen species (ROS) such as superoxide anion ($\text{O}_2^{\bullet-}$), hydrogen peroxide (H_2O_2) and hydroxyl radical ($\text{HO}\bullet$) may play an important role in the pathogenesis of MCs toxicity in various organisms (Pašková *et*

al., 2008; Gonçalves-Soares *et al.*, 2012; Paskerová *et al.*, 2012; Pavagadhi *et al.*, 2012; Galanti *et al.*, 2013).

As a preventive step to protect the public health from adverse effects, WHO recommends a provisional guideline value of $1 \mu\text{g L}^{-1}$ for MC-LR concentration in drinking water in 1998, and a chronic tolerable daily intake (TDI) of $0.04 \mu\text{g kg}^{-1}$ body mass per day for human consumption (Chorus and Bartram, 1999).

Although MCs are present in surface water bodies worldwide, there is still little study on the toxicity of complex cyanobacterial crude extract (CCE) containing MCs or intact toxic-cells. Water from CYBs contain not only MCs but a complex hazardous compounds such as microviridins, micropeptins, oscillapeptins, or lipopolysacchardsides that can evoke more pronounced toxic effects than MCs or other well-recognized cyanotoxins (Buryšková *et al.*, 2006; Falconer, 2007; Palíková *et al.*, 2007; Smutná *et al.*, 2014). Therefore, it is necessary to consider and evaluate the effects of complex cyanobacterial biomasses or intact toxic-cells, especially at the environmentally relevant concentration on aquatic organisms.

1.3. Aims of this study

To reduce the impacts of CYBs on public health, it is important to characterize toxins in waters sources and mitigate their effects on aquatic animals. Testing toxicity of different MCs sources by using animal models is an important step toward understanding how they will interact in human health. Therefore, the aims of this study are:

- 1) Identify MCs producers and characterize MCs production/profiles of CYB samples from Dau Tieng Reservoir, which has been supplying drinking water for millions of people in southern Vietnam.

- 2) Investigate accumulation/depuration of free MC, Co-MC and adverse effects from CCE containing MCs on the edible clam *Corbicula leana*.

3) Investigate accumulation/depuration of free MC, Co-MC and adverse effects of toxic and non-toxic cyanobacteria *Microcystis* on the clam *C. leana*. And, determination human health risks associated with consumption of the animal contaminated with MCs.

1.4. Research contents

In order to understand occurrence, accumulation/depuration and effects of MCs, a series of experiments both in field and laboratory have been conducted in this study. The contents for this thesis consist 5 chapters and are summarized as follows:

Chapter 1: Introduction of research background, previous studies and objectives.

Chapter 2: Reported the identification and characterization a total of 68 cyanobacterial strains isolated from Dau Tieng Reservoir, determined their toxin profiles, toxic abilities and detected the MC concentrations of CYBs collected from this reservoir.

Chapter 3: In order to understand the toxicity of cyanobacterial cell lysis containing MCs (often occur at the end of a bloom), I collected toxic cyanobacterial biomass from water blooms in Kasumigaura Lake. The samples were then used to expose to the clam *C. leana*. The uptake and depuration of free- and Co-MC were investigated. And adverse effects on various tissues caused by this biomass in *C. leana* were evaluated through changes of antioxidant and detoxification enzymes.

Chapter 4: In order to understand the toxicity of toxic *Microcystis* (one of the most cyanobacteria frequently causes bloom throughout the world), I cultured the toxic *M. aeruginosa* (strain NIES-1086) and non-toxic *M. aeruginosa* (strain NIES-101); both were then used to expose to clam *C. leana*. And again, the uptake, depuration of free- and Co-MC as well as adverse effects on various tissues in clam *C. leana* were investigated by comparison with the green alga *Chlorella vulgaris* (strain NIES-2170).

Chapter 5: General conclusions and recommendations.



Lake Kasumigaura, Japan; August 2013

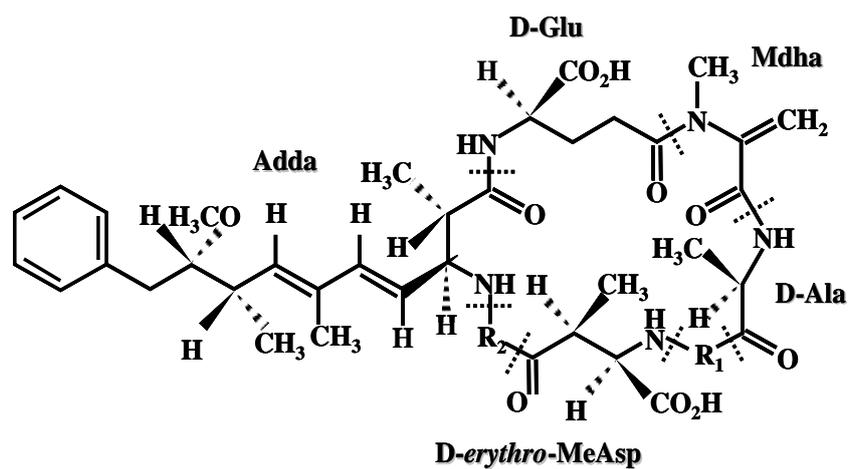


Dau Tieng Reservoir, Vietnam; July 2011



Lake Chao Hu, China; June 2008 (photo from www.researchgate.net)

Figure 1–1. Blooms of cyanobacteria.



	R ₁	R ₂
microcystin-RR	arginine	arginine
microcystin-LR	leucine	arginine
microcystin-YR	tyrosine	arginine

Figure 1–2. Chemical structure of microcystin-LR, -RR, and -YR.

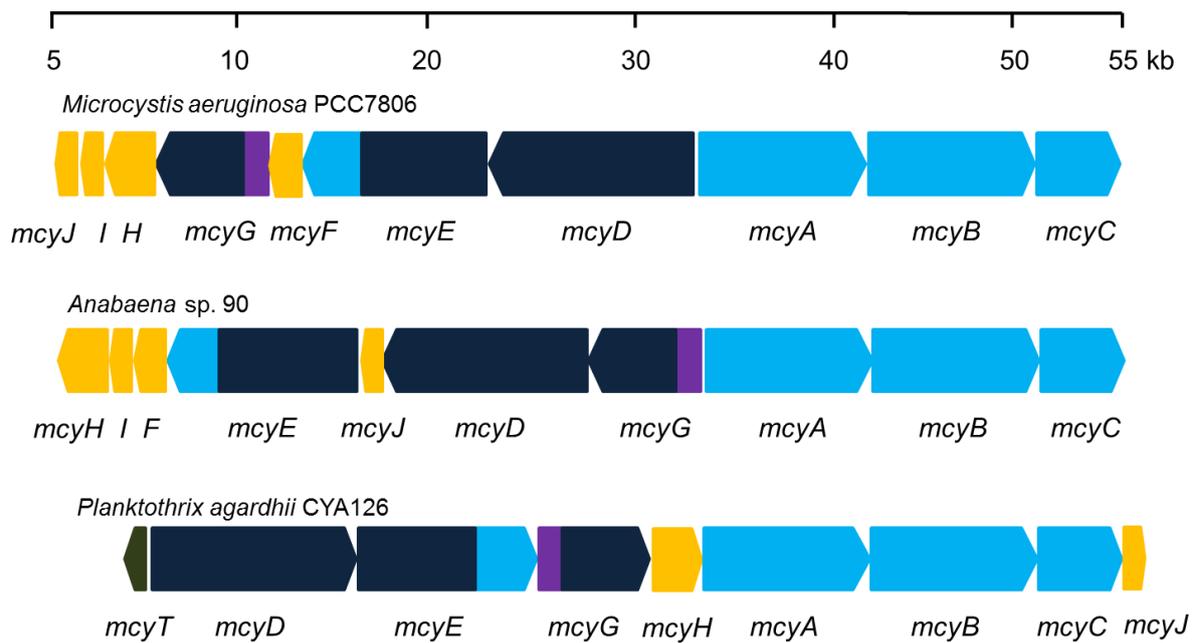


Figure 1–3. Structural organization of the *mcy* gene clusters in *Microcystis*, *Anabaena* and *Planktothrix* (modified from Pearson *et al.*, 2010).

Chapter 2

Occurrence of toxic cyanobacterial blooms and their toxins in Dau Tieng Reservoir, Vietnam

2.1. Introduction

Cyanobacteria are notorious for their ability to produce a variety of toxic secondary metabolites called cyanotoxins, which can be especially problematic during CYBs (Sivonen, 1996). The common occurrence of high concentrations of cyanotoxins associated with CYBs in drinking, recreational, and irrigation water bodies poses a serious hazard for wild and domestic animals as well as humans (Pouria *et al.*, 1998; Carmichael *et al.*, 2001; Stewart *et al.*, 2008).

Among cyanotoxins, MCs are the most prominent cyanobacterial hepatotoxins in freshwater (Chorus and Bartram, 1999). Morphological methods have traditionally been used to monitor and characterize cyanobacteria. However, blooms of cyanobacteria usually consist of toxic and non-toxic strains (Neumann *et al.*, 2000). Morphological characteristics cannot be used as the basis for differentiation of toxic and non-toxic strains because many strains of cyanobacteria appear to be identical under the microscope. The presence or absence of the *mcy* gene cluster has been widely used as a means for distinguishing the two genotypes and has recently been used to reveal the presence of MC-producing cyanobacteria in both environmental samples and axenic cultures (Nishizawa *et al.*, 2000; Tillett *et al.*, 2000; Bittencourt-Oliveira, 2003; Hisbergues *et al.*, 2003; Kurmayer and Kutzenberger, 2003; Hotto *et al.*, 2005; Pedro *et al.*, 2011). However, because the conclusions of most of these studies have been based on only one gene/operon, the results have sometimes been unreliable in cases of homology and mutation on the *mcy* gene. The amplification of several genes responsible for synthesis of MC in both the NRPS and PKS modules may be a more appropriate way to detect potentially toxic cyanobacteria.

Episodes of toxic CYBs have recently been rather well documented in subtropical and temperate regions (Te and Gin, 2011). However, information on toxic cyanobacteria and cyanotoxins from tropical regions like Southeast Asia is limited. In Vietnam, few investigations of toxic cyanobacteria and their toxins have been undertaken within the last decade. The most commonly cited potentially toxic cyanobacterial species has been *M. aeruginosa*, which has been reported from Lake Thanh Cong (Hummert *et al.*, 2001a), the Huong River (Nguyen *et al.*, 2007b), and Tri An Reservoir (Dao *et al.*, 2010). Other potentially toxic species such as *M. botrys* and *M. wesenbergii* have also been reported (Nguyen *et al.*, 2007b). Recently, Nguyen *et al.* (2012) collected, morphologically characterized, and classified *Microcystis* strains in the middle and north of Vietnam, but provided no information on MC concentrations. In those studies, a small number of strains was isolated and characterized for MC production. There is still little understanding about the potential toxin production of other common species belonging to the genera *Anabaena* (*Dolichospermum*), *Arthrospira*, *Cylindrospermopsis*, and *Pseudanabaena*.

Dau Tieng Reservoir has been supplying drinking water for millions of people in southern Vietnam. Nutrient enrichment, especially phosphorus and nitrogen, has led to conditions that favor cyanobacterial growth in the reservoir. However, there is still lack of data relevant to polymorphism of *mcy* genes, toxic and non-toxic genotypes, and toxin profiles from toxin producers. This study aimed to collect cyanobacterial assemblages, including samples from blooms, and to isolate numerous strains for investigation. Identification of cyanobacterial species was based on microscopic observations. MC concentrations in both isolated strains and bloom samples were quantified by high performance liquid chromatography (HPLC). The ability of isolated strains to produce MCs was elucidated with *mcyA*, *mcyB*, and *mcyD* molecular markers.

2.2. Materials and methods

2.2.1. Sites and sampling

Dau Tieng Reservoir is located in southern Vietnam, about 85 km northwest of Ho Chi Minh City. The reservoir is located within a quadrat bounded by 11°12'–12°00'N, 106°10'–106°30'E. Its maximum depth, mean depth, surface area, and volume are 24 m, 3 m, 264 km², and 1.08×10^8 m³, respectively (Figure 2–1). Dau Tieng Reservoir serves multiple purposes. It is a source of drinking and irrigation water, a recreational resource, a means of flood control, and an attraction to tourists (Vietnam-MOSTE, 2001). The reservoir falls into the eutrophic category according to the classification scheme described by Ye *et al.* (2009) that associates eutrophy with total phosphorus concentration of 25–100 µg L⁻¹ and total nitrogen concentration of 600–1500 µg L⁻¹ (unpublished data).

I used a conical plankton net with a mesh size of 25 µm to collect cyanobacterial samples monthly during July–October 2011 and March–May 2012 at both shallow- (DT3 and DT5) and deep- (DT1, DT2 and DT4) water sites (Figure 2–1). The sites included one location commonly used for recreation (DT1); two locations used intensively for fish and duck farming (DT2 and DT4); and two sites near stream mouths (DT3 and DT5). The characteristics of the water at the sampling sites were determined in situ during sampling and included pH (model 744 pH meter, Metrohm, Herisau, Switzerland), temperature (WTW Oxi197i, Metrohm, Weilheim, Germany), and water transparency (Secchi disk). The values of these parameters were used as metrics of the abiotic characteristics of the sites where the cyanobacteria were collected. Samples for isolation of cyanobacteria were maintained under viable conditions, and samples for identification were fixed with Lugol's solution in the field (Sournia, 1978). Samples of the scum from blooms were collected in July and August 2011 at the lake shore, filtered onto GF/C glass fiber filters (Whatman, Kent, England), dried at 45°C overnight, and stored at –80°C prior to MCs analysis.

2.2.2. Morphological characterization

Cyanobacteria were observed at 800 × magnification under a microscope Olympus BX51 equipped with a digital camera and DP71 software (Olympus, Tokyo, Japan). Taxonomic classification was based on the system of (Komárek and Anagnostidis, 1989; Komárek and Anagnostidis, 1999; Komárek and Anagnostidis, 2005). Descriptions of cyanobacteria were based on observations of both preserved and cultured samples.

Cyanobacterial isolation and cultivation: Cyanobacteria were isolated by micropipetting and washing. A single cyanobacterial trichome or colony was isolated by micropipetting, washed, and transferred into cyanobacterial growth medium (Belcher and Swale, 1988). Cyanobacteria were grown in MA medium (Ichimura, 1979). All cultures were grown on a 12:12 light:dark cycle at a temperature of 28°C and light intensity of 20 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$. Biomasses of cyanobacterial cultures were harvested onto GF/C glass fiber filters (Whatman, Kent, England) and processed as described above.

2.2.3. DNA extraction

DNA was extracted by the method of Hisbergues *et al.* (2003) with minor modifications. Briefly, 2 mL of fresh culture was harvested by centrifugation (10,000 × *g*, 15 min, 4°C). Cell pellets were suspended in 567 μL TE buffer (50 mM Tris/HCl, 40 mM EDTA, pH 8.0). An aliquot of 30 μL of 10% SDS (sodium dodecyl sulfate) and proteinase K (final concentration: 100 $\mu\text{g mL}^{-1}$ in 0.5% SDS) was then added and incubated for 60 min at 37°C. Then 5 M NaCl (100 μL) and CTAB/NaCl solution (10% CTAB in 0.7 M NaCl) (80 μL) were added, and the samples were incubated for 10 min at 65°C. DNA was then extracted twice with 780 μL phenol:chloroform:isoamyl alcohol (25:24:1 v/v). After centrifugation for 5 min at 6,000 × *g* at 4°C, the supernatant was collected and transferred to a fresh tube. DNA was then precipitated by the addition of a volume of isopropanol equal to 0.6 times the volume of the supernatant, followed by centrifugation for 20 min at 20,000 × *g* at 4°C. The precipitated

DNA was rinsed with 1 mL of 70% ethanol and dried under vacuum. The final DNA sample was rehydrated in 20 μ L of 1 \times TE buffer (10 mM Tris and 1 mM EDTA [pH 8.0]). Quantitation was done by absorbance (GeneQuant pro, Cambridge, England) at 260 nm using a Sub-Micro quartz cuvette (NSG, New York, USA).

2.2.4. PCR amplification

Two peptide synthetase gene fragments, *mcyA* and *mcyB*, (297 bp and 78 bp, respectively) were amplified using primer pairs *mcyA*-Cd1F/*mcyA*-Cd1R (Hisbergues *et al.*, 2003) and *mcyB*-30F/*mcyB*-108R (Kurmayer and Kutzenberger, 2003). The fragment of the *mcyA* gene has previously proven to be suitable for detection of MC-producing cells of the genera *Dolichospermum*, *Microcystis*, and *Planktothrix* (Hisbergues *et al.*, 2003). The polyketide synthase fragment (*mcyD*, 297 bp) was amplified using primer pair *mcyD*-F2/*mcyD*-R2 (Kaebernick *et al.*, 2000). To detect the presence of cyanobacterial DNA, the CYA primer pair (Urbach *et al.*, 1992) was used to amplify a 1200 bp fragment of the 16s rRNA gene common to all cyanobacteria. For each sample, four separate PCRs were conducted. DNA of *M. aeruginosa* NIES-102 and *M. aeruginosa* NIES-1086, both of which produce MCs (Yasuno *et al.*, 1998), were used for positive controls. As a negative control, I used DNA extracted from a non-toxic strain, *M. aeruginosa* NIES-101 (Baeka *et al.*, 2009). All PCR reactions were prepared in a volume of 20 μ L containing 2 μ L of 10 \times Ex-Taq Buffer, 200 μ M of each dNTP, 0.5 μ L of each primer (10 μ M), 0.5 U of Ex-Taq polymerase (Takara Bio Inc., Shiga, Japan), and 20–25 ng of template DNA. If any strain was positive for one *mcy* marker but not for others, each template DNA was diluted and used for PCR again, but with 10, 25, 50, and 100 ng DNA to confirm the results. Amplification was performed in a Veriti 200 Thermal Cycler (Applied Biosystems, Foster City, California, USA) according to the protocols summarized in Table 2–1. PCR products were examined on 1.5% or 2.5% (w/v) agarose gels stained with ethidium bromide. The images were obtained under ultraviolet (UV)

transillumination and digitalized with a Canon Digital EOS Kis X2 system (Canon Inc., Tokyo, Japan).

2.2.5. Microcystins extraction and analysis

The filters containing cells (about 20 mg of dried cells) were cut into small pieces (1–2 mm²) with scissors. Extraction of MCs was conducted as described by Barco *et al.* (2005) with minor modifications. Briefly, MCs were first extracted in 5 mL of 100% aqueous methanol (MeOH) by shaking for 60 min followed by two 60-min extractions in 3 mL of 75% (vol/vol) aqueous MeOH. Each extraction step was followed by sonication (1 min, 150W) and centrifugation (1,800 × *g*, 4°C, 30 min). The supernatants of all extractions from each sample were pooled, dried at room temperature, re-dissolved in 0.5 mL MeOH (100%) and centrifuged at 6,000 × *g* at 4°C for 5 minutes. The supernatant was passed through a Minisart RC4 filter membrane (0.2 µm pore size, Sartorius Stedim Biotech, Göttingen, Germany), and kept at –20°C prior to reversed-phase HPLC analysis.

A reverse-phase HPLC with UV-visible photodiode array (PDA) detector (Shimadzu 10A series, Kyoto, Japan) was equipped with a silica-based, reverse-phase C₁₈ column (Waters SunFire™ 5 µm, 3 × 250 mm, Milford, Massachusetts, USA) and maintained at 40°C. The samples were separated with a mobile phase consisting of methanol: 0.05 M phosphate buffer (pH 2.5; 50:50 v/v) at a flow rate of 0.58 mL min⁻¹. MC congeners were detected by UV detection at 238 nm and identified on the basis of both their retention time and characteristic UV spectra. Microcystins (MC-LR, MC-RR, and MC-YR) purchased from Wako Pure Chemical Industries, Ltd. (Chuoku, Osaka, Japan), were used as standards. The HPLC system had a detection limit of 0.1 µg L⁻¹.

2.3. Results

2.3.1. Isolation and morphological characteristics

Microscopic examination of the July and August 2011 CYB samples revealed the dominance of *Microcystis* (mainly *M. aeruginosa*) and the less frequent occurrence of other genera *Dolichospermum* (*Anabaena*), *Arthrospira*, *Planktothrix*, *Pseudanabaena*, and *Cylindrospermopsis*. During the blooms, which lasted for several weeks, the pH and water temperature of all sites were in the ranges of 8.3–9.1 and 29.0–31.0°C, respectively. Identification of individual *Microcystis* colonies revealed the occurrence of three species: *M. aeruginosa*, *M. botrys*, and *M. wesenbergii*. I successfully isolated 68 cyanobacterial strains from the cyanobacterial samples (collected from July–October 2011 and March–May 2012) and maintained them in cultures. Those 68 strains were representatives of eight species that belonging to three orders of cyanobacteria, Chroococcales (59), Nostocales (5) and Oscillatoriales (4) (Table 2–2). A taxonomic breakdown of the eight isolated species is as follows:

Order CHROOCOCCALES

Family MICROCYSTACEAE

Microcystis aeruginosa (Kützing) Kützing 1846

Colonies of this species were embedded in a colourless mucilage that varied in shape from more or less spherical to strongly irregular assemblages of sub-colonies (Figures 2–2a, b). The individual cells were more or less spherical, with aerotopes present. The cells were 4–6 µm in diameter and separated from each other, even in dense colonies. The colonial form of this species was not maintained, and the colonies were mostly separated as single and/or double cells in culture.

Microcystis botrys Teiling 1942

The colonies of this species were composed of more or less spherical sub-colonies, with densely packed cells in the centre of colonies (Figure 2–2c). Sub-colonies were 50–150 µm in diameter. The colonial form of this species was maintained in cultures during its exponential

phase. The mucilage was colourless and surrounded clusters of cells. Cells were dark in colour, 5.5–8.0 µm in diameter, and had many aerotopes.

Microcystis wesenbergii (Komárek) Komárek in Kondrateva 1968

This species formed elongate, often lobate, clathrate, and sometimes spherical colonies that were commonly composed of sub-colonies with a distinct refractive mucilage edge (Figure 2–2d). In nature, a sub-colony of this species was 15–100 µm in diameter and contained from a few (2–3) to many (> 150) cells, depending on the age of the colony. Cells were more or less evenly spread throughout the colony, 5.5–8.5 µm in diameter, with many spherical aerotopes.

Order NOSTOCALES

Family NOSTOCACEAE

Dolichospermum nygaardii (Cronberg & Komárek) Wacklin, L.Hoffmann & Komárek 2009

Trichomes were solitary, planktic, with regular coils 30–40 µm in width. The distance between coils was 10–25 µm. Cells were spherical, 5.5–6.5 µm in diameter with aerotopes (Figures 2–3 a–c). Heterocytes were spherical, slightly bigger than the vegetative cell, and 6–6.5 µm in diameter. Akinetes were oval or somewhat kidney-shaped, solitary, distant from heterocytes, with dimensions of 7–10 × 11.5–19 µm. The akinetes were only observed in the cultures. Usually only one heterocyte or akinete was present on each trichome.

***Dolichospermum* sp.**

Trichomes were solitary, planktic, with coils of 30–35 µm in width. The distance between coils was 7.5–10 µm. (Figures 2–3 d–g). Cells were oval, 6.5–8.5 µm broad, 7–10 µm long, with aerotopes. Heterocytes were spherical, somewhat larger than the vegetative cells, and 7.5–10 µm in diameter. Akinetes were not observed in either field samples or cultures.

Cylindrospermopsis raciborskii (Woloszynska) Seenayya & Subba Raju in Desikachary 1972

Trichomes were solitary, straight, or slightly curved. Cells were cylindrical, 4–5.5 µm wide, and 7–13 µm long (Figures 2–3 h–j). The terminal heterocytes were long and conical, 3–6 µm wide, and 6–14 µm long. The akinetes was one or two cells distant from terminal heterocytes and sometimes occurred in pairs. They were long ovals, 5–8 µm wide and 13–19.5 µm long. Akinetes were observed in both field samples and cultures.

Order OSCILLATORIALES

Family PHORMIDIACEAE

Arthrospira massartii Kufferath 1914

Trichomes were greyish-blue-green, planktic, solitary, spiral, with indistinct cross walls. They were not constricted at cross walls and were tapered slightly at the ends (Figures 2–3 k–n). The distance between coils of spiral trichomes was 20–40 µm, and the trichomes had a coiled diameter of 35–45 µm. Cells were 2.5–3 µm long and 4.5–6 µm wide, with aerotopes. Apical cells were tapered and rounded.

Family PSEUDANABAENACEAE

Pseudanabaena limnetica (Lemm.) Komárek 1974

Trichomes were solitary, planktic, straight or slightly curved, and not tapering toward the ends (Figure 2–4). Cells were pale blue-green, cylindrical, without aerotopes, 1.5–2 µm wide and 3–6.5 µm long, and constricted at the cross wall. Apical cells were bluntly rounded.

2.3.2. Microcystin producers

The ability to produce MCs of all strains was determined by using three molecular markers: *mcyA*, *mcyB*, and *mcyD*. Results of the *mcy* gene analysis MC-producing ability, as determined by *mcyA* showed that among 59 strains of *Microcystis*, all three toxin genes *mcyA*, *mcyB*, and *mcyD* were present in 25 strains (42% of the *Microcystis* strains). Twelve *Microcystis* strains were positive for *mcyA* and *mcyB* but negative for *mcyD*; the 22 remaining *Microcystis* strains (37% of the *Microcystis* strains) were negative for all *mcyA*, *mcyB*, and

mcyD genes. None of the strains of *Dolichospermum*, *Arthrospira*, *Pseudanabaena* and *Cylindrospermopsis* were positive for an *mcyA*, *mcyB*, or *mcyD* amplicon. All strains were positive with 16S rRNA (Figure 2–5).

Within the genus *Microcystis*, relationships between morphospecies and MC genotypes as well as between morphospecies and MC production were apparent. Colonies of *M. aeruginosa* had the greatest potential for MC production. In contrast, no strains assigned to *M. botrys* and *M. wesenbergii* yielded fragments of *mcy* genes in the PCR amplification products, the indication being that these strains were non-toxic.

2.3.3. Microcystin production

Results of HPLC analysis indicated that 25 cultured strains (37% of all isolates) contained MCs. The total concentration of MCs from toxic isolated strains ranged from 39 to 2,129 $\mu\text{g g}^{-1}$ DW. The MCs content of these strains was quite variable, the highest concentration being found in strain M.ae–42 and the lowest concentration in strain M.ae–25. The predominant MC variant in these strains was MC-RR. It was present in most of the toxic strains, followed by MC-LR and MC-YR (Figure 2–6).

Two bloom samples collected in July and August contained three MCs, MC-LR, MC-RR and MC-YR (Figure 2–7). The concentration of MCs in those samples ranged from 521 to 669 $\mu\text{g g}^{-1}$ DW. The MC-RR concentration was high in the first sample but much lower in the second one. In contrast, the concentrations of MC-YR and MC-LR were low in the first sample (8% and 6%, respectively) but much higher (22% and 23%, respectively) in the second. In both bloom samples, MC-RR was the dominant congener (Table 2–3).

2.4. Discussion

There is still little known about the tropical cyanobacterial microflora (Cronberg and Komárek, 2004); this is especially true in the case of Vietnam. Like many other cyanobacterial species, *Microcystis* spp. are distributed throughout the world and can be

found in habitats ranging from freshwater to brackish water (Komárek and Anagnostidis, 1999; Cronberg and Annadotter, 2006). The species *M. aeruginosa* and *M. botrys* are common in Vietnam (Pham, 1969; Phung *et al.*, 1992; Duong, 1996; Nguyen *et al.*, 2007b; Dao *et al.*, 2010). In my study, *M. aeruginosa* was dominant in bloom samples from the Dau Tieng Reservoir; an observation that is consistent with previous records from Vietnam (Nguyen *et al.*, 2007b; Dao *et al.*, 2010). In general, cell sizes of *Microcystis* spp. were slightly larger in the Dau Tieng Reservoir than in some other freshwater environments in Vietnam (Nguyen *et al.*, 2007b; Dao *et al.*, 2010).

The genus *Dolichospermum* (formerly known as planktic species of *Anabaena*) comprises more than 40 species that are distributed worldwide (Cronberg and Annadotter, 2006; Wacklin *et al.*, 2009). *Dolichospermum nygaardii* is a tropical cyanobacterial species that has previously been recorded only in Africa (Cronberg and Komárek, 2004). Morphologically, it was more or less similar to *D. flos-aquae*. However, the coiling characteristics and akinete shapes of cultivated strains were more similar to those of *D. nygaardii* (Komárek and Zapomelova, 2007). Therefore, I preferred to identify it as *D. nygaardii*, but I recommend further molecular investigations of this strain, such as 16S rRNA gene sequencing, for confirmation of the identity of this species. I also suggest molecular characterization for species identification of the *Dolichospermum* sp. because of the absence of information about its akinetes from the field samples and cultures. My investigation recorded *D. nygaardii* for the first time in Vietnam.

About ten species of *Cylindrospermopsis* have been described (Cronberg and Annadotter, 2006), and *C. raciborskii* is the most commonly recorded and investigated (Falconer and Humpage, 2005). In Vietnam, this species was initially identified as *Anabaenopsis raciborskii* Woloszynska in some freshwater bodies in northern Vietnam (Duong, 1996) but subsequently updated with the current name by Nguyen *et al.* (2007b). This species has also been reported from the Tri An Reservoir in southern Vietnam (Dao *et al.*,

2010). However, the occurrence of *C. raciborskii* in this water body reflects in part the wide distribution of this harmful species in Vietnamese waters, especially drinking water supplies. The cell size and especially the cell length of *C. raciborskii* isolated from the Dau Tieng Reservoir are greater than the size and length of cells from the Tri An Reservoir or Hue localities (Nguyen *et al.*, 2007b; Dao *et al.*, 2010).

The genus *Arthrospira* comprises about ten species that occur mainly in tropical and semi-tropical regions (Cronberg and Annadotter, 2006). In Vietnam, I have found four *morphotypes* of this genus, including *A. gigantea*, *A. platensis*, *A. jeneri* and *A. massartii* (Pham, 1969; Phung *et al.*, 1992; Duong, 1996; Nguyen *et al.*, 2007b). The dimensions of trichomes and cells of this species in my study and in a previous investigation (Nguyen *et al.*, 2007b) are comparable. The genus *Pseudanabaena* consists of about 30 species (Komárek and Anagnostidis, 2005). However, few species of this genus have been described from Vietnam. *Pseudanabaena limnetica* was first identified as *Oscillatoria limnetica* Lemm. from the Mekong Delta in Vietnam (Pham, 1969); it has also been recorded from the Tri An Reservoir (Dao *et al.*, 2010) and now (my study) from the Dau Tieng Reservoir. Both *A. massartii* and *P. limnetica* are properly characterized as cosmopolitan species (Komárek and Anagnostidis, 2005).

The cyanobacterial biota from the Dau Tieng Reservoir consists of several potentially toxic species, including species of *Microcystis*, *Dolichospermum*, *Planktothrix*, *Pseudanabaena* and *Cylindrospermopsis*. My results are consistent with those of Joung *et al.* (2011) and Neumann *et al.* (2000) that cyanobacterial population exists as a mixture of toxic and non-toxic genotypes. *Arthrospira* and *Pseudanabaena* are not well known in terms of toxin production, but some reports of their toxicity have been published (Iwasa *et al.*, 2002; Ballot *et al.*, 2004; Nguyen *et al.*, 2007b). *Cylindrospermopsis* isolated from water bodies in the cities of Hue and Pleiku in the middle and central highlands of Vietnam have been reported to produce cylindrospermopsin (Nguyen *et al.*, 2010). Because I found no *mcy* gene

fragments and detected no production of MCs in my samples of *Arthrospira*, *Dolichospermum*, *Pseudanabaena*, and *Cylindrospermopsis* strains, I concluded that *Microcystis* was the major MCs producer in the Dau Tieng Reservoir. Nevertheless, there is no information for these strains concerning the presence of other toxins such as cylindrospermopsin, saxitoxins, and anatoxin-a; their potential presence warrants further investigation.

PCR-based detection of genes involved in the synthesis of MCs (*mcyA-J*) is the cornerstone of rapid detection techniques and has been successfully applied for early detection of the mass occurrence of potentially toxic cyanobacterial (Bittencourt-Oliveira, 2003; Rantala *et al.*, 2006; Martins *et al.*, 2009; Gkelis and Zaoutsos, 2014). The use of *mcyA*, *mcyB*, and *mcyD* for assessment of MC toxigenicity has previously been described (Hisbergues *et al.*, 2003; Hotto *et al.*, 2005; Rinta-Kanto *et al.*, 2005; Vasconcelos *et al.*, 2010; Kumar *et al.*, 2011). Microscopic and PCR results revealed that the different morphospecies varied considerably with respect to the proportion of genotypes that produced MCs. In general, non-toxic strains do not contain *mcy* genes. However, some strains may have fragments or mutant forms of *mcy* genes. Consequently, the *mcy* genes of these strains can be amplified with *mcy* primers, although the strains are not able to produce toxins (Kaebernick *et al.*, 2000; Dittmann *et al.*, 2001; Tillett *et al.*, 2001; Martins *et al.*, 2009; Vasconcelos *et al.*, 2010). Homology or down regulation of the *mcy* gene region or the presence of adenylation domains with other loci or even the presence of a cluster of *mcy* genes in some non-toxic *Microcystis* strains may also lead to such discrepancies (Janse *et al.*, 2004). In this study, I used three *mcy* genes from both NRPS and PKS domains for screening toxigenicity. Strains showing positive results for all three *mcyA*, *mcyB*, and *mcyD* genes generated at least one variant of MC, including MC-RR. However, several non-toxic strains were positive for the two molecular markers *mcyA* and *mcyB*. The same observations have been reported in cyanobacterial samples collected from Portuguese water bodies (Martins *et al.*, 2009) and

Central Mexico water bodies (Vasconcelos *et al.*, 2010). In contrast, Gkelis and Zaoutsos (2014) detected MCs in water samples from Greece, where the *mcyA* gene region was not amplified. Therefore, it is evident that *mcy* genes differ with respect to their ability to predict MC toxigenicity. My results indicate that *mcyD*, which encodes for parts of both the β -ketoacyl synthase and the acyltransferase domains (Rantala *et al.*, 2004), is one of the best molecular markers for determination of potential toxicity of cyanobacteria. The *mcyA* gene has been reported from *Microcystis* strains isolated from localities near Hue in Vietnam (Nguyen *et al.*, 2007a). However, my study is the first to apply *mcyB* and *mcyD* for the analysis of the toxicity of cyanobacterial strains from Vietnam. The combination of HPLC and PCR provides a robust tool for reliably characterizing lakes in terms of MCs. The HPLC assay measures the actual level of toxin production, whereas PCR provides an estimate of the potential for toxin biosynthesis.

The presence of MCs from cultures was revealed with the three variants MC-RR, MC-LR, and MC-YR, among which MC-RR was the dominant congener. MC production and yield varied considerably among strains. The most highly toxic strains were strains of *M. aeruginosa*. The cyanobacterial population of the Dau Tieng Reservoir is thus a mosaic of genotypes, the various strains being genetically different, with distinct toxicity potential and toxic ability. From the Dau Tieng Reservoir, MCs have been reported in a mixed *Microcystis* culture, the highest concentration being $128 \mu\text{g L}^{-1}$ (only MC-LR present) (unpublished data). Together with the MC-LR reported previously, I also identified MC-RR and MC-YR, but the most common variant in this reservoir was MC-RR. The MC concentrations in the bloom samples ($521\text{--}669 \mu\text{g g}^{-1}$ DW) were within the range of concentrations reported for the Tri An Reservoir ($450\text{--}640 \mu\text{g g}^{-1}$ DW) by Dao *et al.* (2010).

MCs are highly water soluble and more than 90% of the total amount is contained within the cells in healthy cyanobacterial populations. However, dying and decaying cyanobacteria may release MCs into the water (Chorus and Bartram, 1999). The lower the

concentration of intracellular MC at the end of blooms might indicate that release of MC from cells into their environment occurred during the senescence and the decomposition periods of *Microcystis* cells. My data agreement with those of (Park *et al.*, 1998a) that high concentrations of intracellular MC were found during the exponential growth phase of the blooms.

Risks associated with exposure to MCs present in surface waters and reservoirs worldwide are a serious concern from the standpoint of human health because of the potent hepatotoxicity of MCs and their tendency to promote tumors (Chorus and Bartram, 1999). The Dau Tieng Reservoir is a eutrophic body of water that receives nutrients from a large drainage area as well as the runoff from fish farms, duck farms, cattle ranches and other agricultural activities, especially during the dry season (unpublished data). MCs have been reported in the raw water (unpublished data), although the occurrence of blooms has not been observed previously. A succession of blooms was first observed along the southern shore of this reservoir during the summer of 2011 (Figure 2–1). I strongly recommend further investigations to elucidate the cause of these blooms.

Local authorities have not yet addressed the public health risks associated with the presence of cyanobacterial toxins in drinking water in Vietnam. There are no facilities for removal of MCs from drinking water, nor is monitoring being conducted to detect MCs in drinking water. Dau Tieng Reservoir supplies drinking water for million people in southern Vietnam. Both raw and tap water from this reservoir were found to contain MCs. MC concentration in raw water was sometimes higher than the WHO guideline value of $1.0 \mu\text{g L}^{-1}$ (unpublished data). The concentrations of MCs in tap water corresponded to the concentrations in the reservoir (unpublished data). Hence, during periods of high MCs concentrations in the reservoir, local residents may suffer from hepatotoxic effects via their daily consumption of MC-contaminated drinking water. Monitoring of toxic cyanobacterial abundance and the concentrations of their toxins as well as further investigations of the

toxicity of the Dau Tieng Reservoir water are strongly recommended to reduce impacts on humans and ecosystems.

2.5. Summary

In this chapter, cyanobacterial assemblages, isolated strains, and bloom samples from the Dau Tieng Reservoir were used for species identification, MC synthetase gene analysis, and MC determination. Microcystin concentrations in both isolated strains and bloom samples were quantified by high performance liquid chromatography, whereas toxic and nontoxic strains were distinguished by three molecular markers: *mcyA*, *mcyB*, and *mcyD*.

I isolated and characterized a total of 68 cyanobacterial strains belonging to 5 genera: *Microcystis* (59 strains), *Dolichospermum* (4 strains), *Arthrospira* (2 strains), *Pseudanabaena* (2 strains) and *Cylindrospermopsis* (1 strain). Cyanobacterial populations from the reservoir consisted of toxic and nontoxic genotypes. *Dolichospermum nygaardii* was morphologically identified and described for the first time in Vietnamese waters. The results also showed that *mcyD* is the best molecular marker for determination of toxicogenic strains. *Microcystis* included toxic and nontoxic genotypes. The MC concentrations from bloom samples and cultures were as high as 669 and 2,129 $\mu\text{g g}^{-1}$ DW, respectively. These results argue strongly for the implementation of a monitoring program for cyanobacteria and their toxins in the water to minimize potential health risks to animal and human populations.

Table 2–1. Primers used for PCR amplification.

Target	Primer set	Sequence (5'–3')	Reference
Cyanobacteria	CYA-F	ACGGGTGAGTAACRCGTRA	Urbach <i>et al.</i>
	CYA-R	CTTCAYGYAGGCGAGTTGCAGC	1992
<i>Microcystis</i> , <i>Anabaena</i> and <i>Planktothrix</i>	<i>mcyA</i> -Cd1F	AAAATTAAAAGCCGTATCAAA	Hisbergues <i>et al.</i>
	<i>mcyA</i> -Cd1R	AAAAGTGTTTTATTAGCGGCTCAT	2003
<i>Microcystis</i>	<i>mcyB</i> -30F	CCTACCGAGCGCTTGGG	Kurmayer and Kutzenberger
	<i>mcyB</i> -108R	GAAAATCCCCTAAAGATTCCTGAGT	2003
<i>Microcystis</i>	<i>mcyD</i> -F2	GGTTCGCCTGGTCAAAGTAA	Kaebnick <i>et</i>
	<i>mcyD</i> -R2	CCTCGCTAAAGAAGGGTTGA	<i>al.</i> 2000

Table 2–2. Cyanobacterial strains examined in this study.

Orders, genera, and species	Number of isolated strains
Chroococcales	
<i>Microcystis aeruginosa</i>	52
<i>Microcystis botrys</i>	5
<i>Microcystis wesenbergii</i>	2
Nostocales	
<i>Dolichospermum nygaardii</i>	2
<i>Dolichospermum</i> sp.	2
<i>Cylindrospermopsis raciborskii</i>	1
Oscillatoriales	
<i>Arthrospira massartii</i>	2
<i>Pseudanabaena limnetica</i>	2

Table 2–3. Microcystin concentrations (mean \pm SD, n = 4) in two bloom samples from Dau Tieng Reservoir.

Date collected	MC-RR	MC-YR	MC-LR	Total $\mu\text{g g}^{-1}$ DW
20/07/2011	582.9 \pm 37.5	51.2 \pm 15.4	39.3 \pm 14.9	668.9 \pm 24.8
06/08/2011	286.0 \pm 14.8	115.7 \pm 5.3	118.8 \pm 13.5	520.5 \pm 22.5

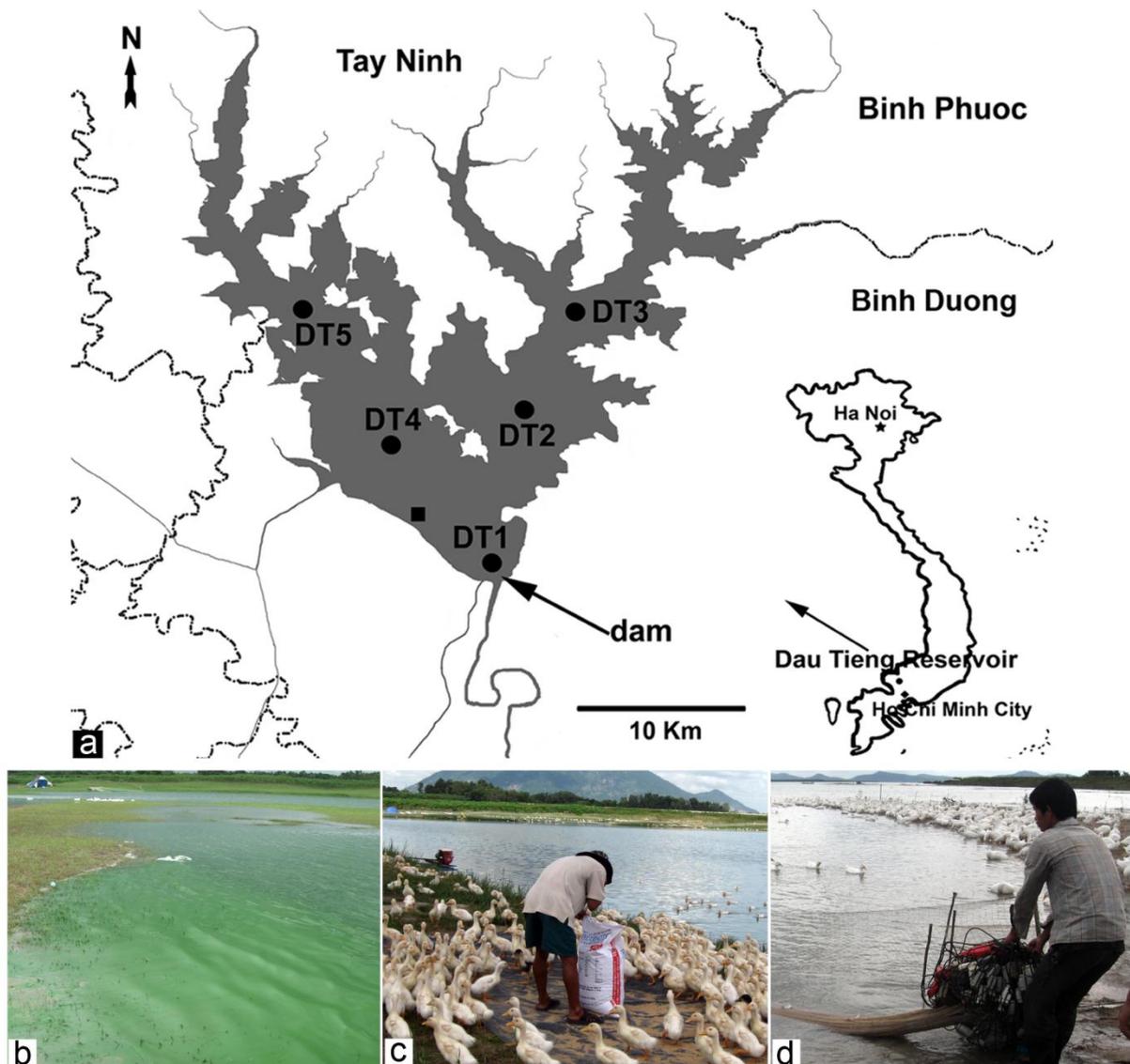
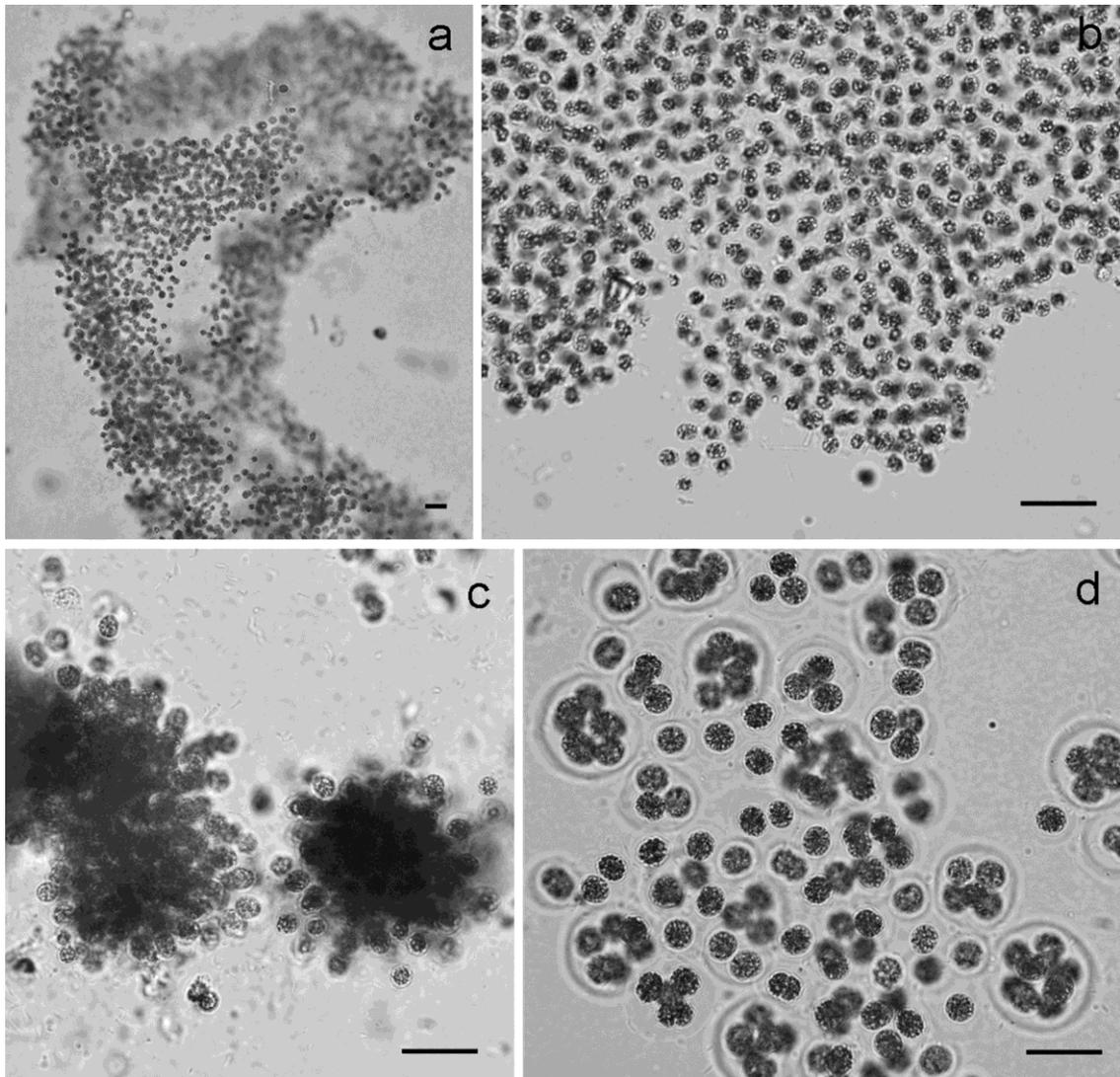


Figure 2–1. Map of the Dau Tieng Reservoir (a). The round black dots indicate locations where cyanobacteria were sampled for culture work. DT3 ($11^{\circ}27'24''\text{N}$; $106^{\circ}22'37''\text{E}$) and DT5 ($11^{\circ}25'48''\text{N}$; $106^{\circ}15'52''\text{E}$) represented shallow-water sites; DT1 ($11^{\circ}19'34''\text{N}$; $106^{\circ}20'36''\text{E}$), DT2 ($11^{\circ}23'38''\text{N}$; $106^{\circ}21'20''\text{E}$) and DT4 ($11^{\circ}22'21''\text{N}$; $106^{\circ}17'11''\text{E}$) represented deep-water sites. Black square indicate location where bloom occurred (b). Duck farming on the reservoir (c). And (d) a fisherman is catching fish with his fishing net.



Figures 2–2. Photographs (a, b) *Microcystis aeruginosa*; (c) *Microcystis botrys*; (d) *Microcystis wesenbergii*. Photos were taken from preserved samples. Scale bars = 20 μ m.

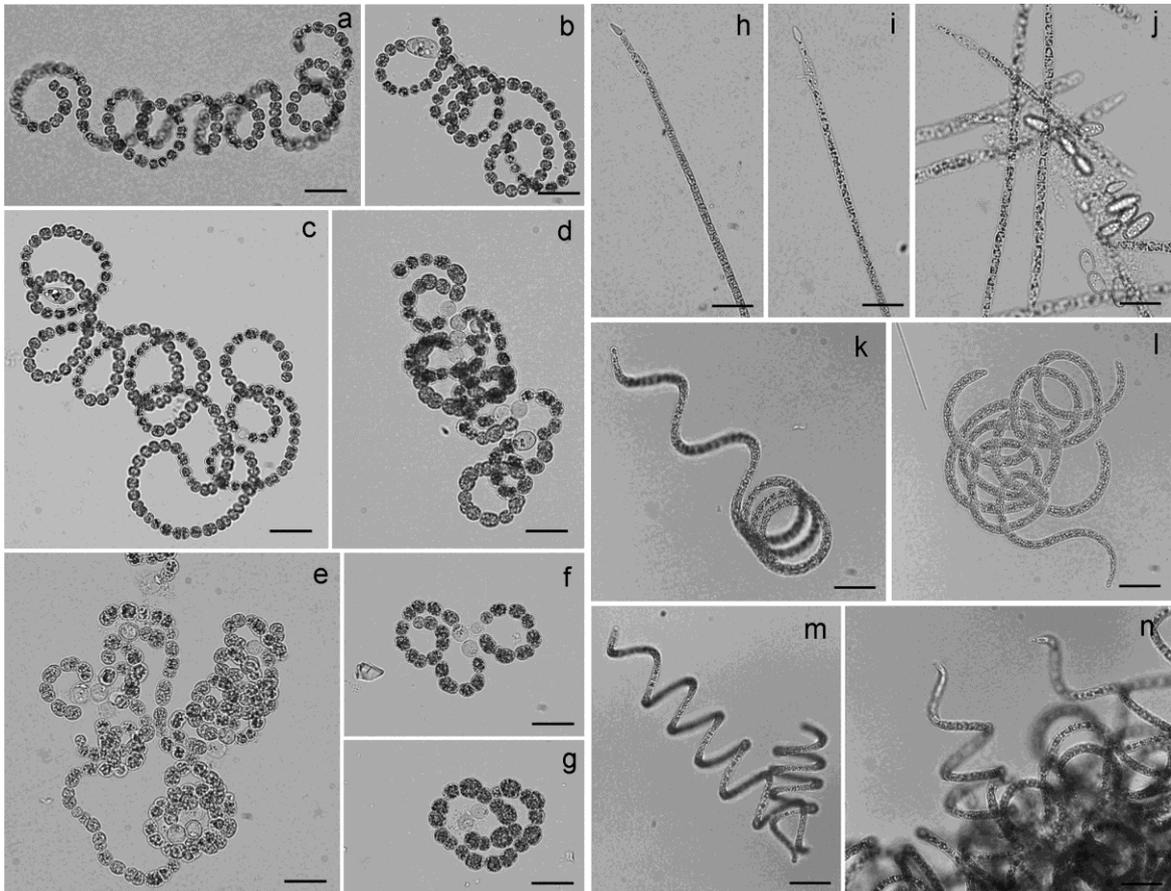


Figure 2–3. Photographs of (a–c) *Dolichospermum nygaardii*; (d–g) *Dolichospermum* sp.; (h–j) *Cylindrospermopsis raciborskii*; (k–n) *Arthrospira massartii*. Photos were taken from cultured samples. Scale bars = 20 μm .

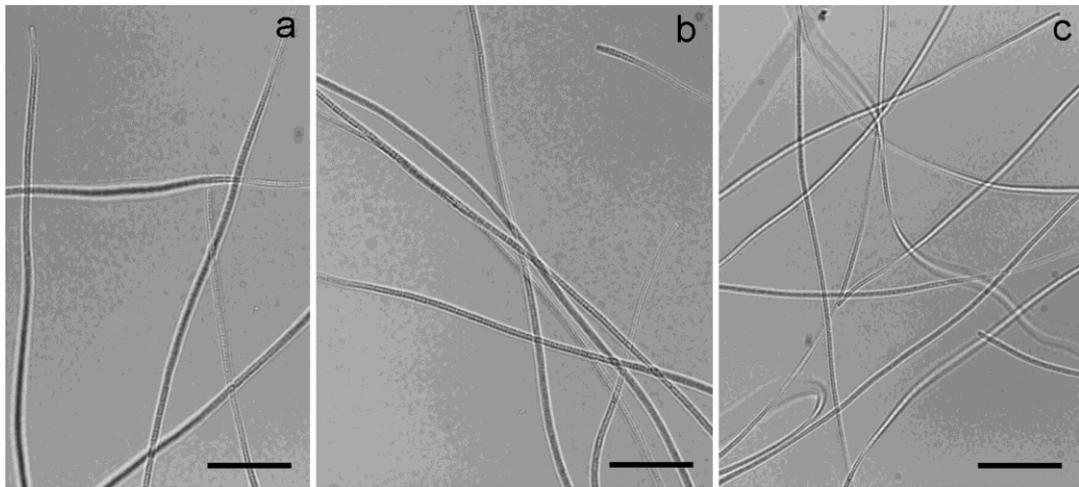


Figure 2-4. Photographs of (a-c) *Pseudanabaena limnetica*. Photos were taken from cultured samples. Scale bar = 20 μm .

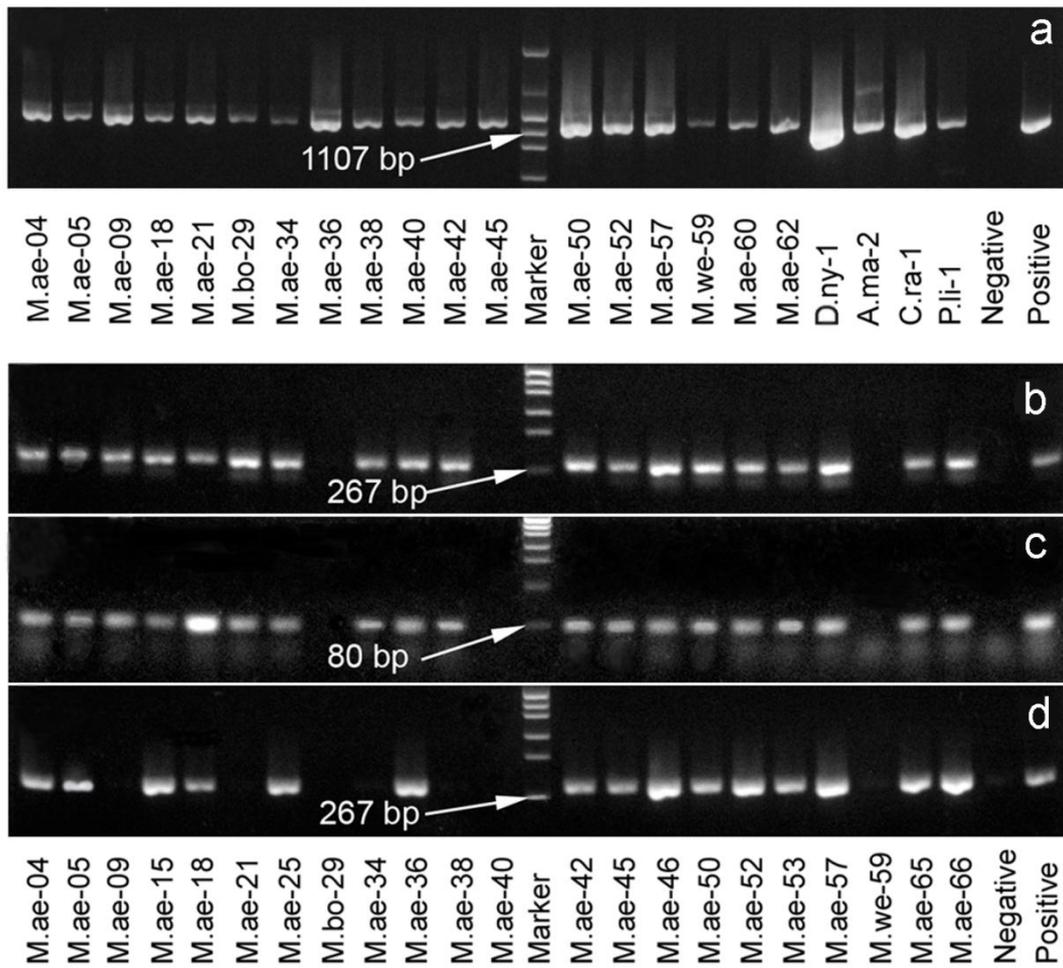


Figure 2–5. Photographs of 1.5% agarose gels (*mcyA* 297 bp, *mcyD* 297 bp, and 16S rRNA 1200 bp) and 2.5% agarose gel (*mcyB* 78 bp) stained with ethidium bromide showing the PCR products amplified by using (a) 16S rRNA, (b) *mcyA*, (c) *mcyB*, and (d) *mcyD* primer pairs. Molecular marker: PHY marker; negative control: NIES-101; positive control: NIES-1086. For 16S rRNA amplification, a sample containing no DNA template was used as the negative control. M.ae: *Microcystis aeruginosa*; M.bo: *Microcystis botrys*; M.we: *Microcystis wesenbergii*; D.ny: *Dolichospermum nygaardii*; A.ma: *Arthrospira massartii*; C.ra: *Cylindrospermopsis raciborskii* and P.li: *Pseudanabaena limnetica*. D.ny, A.ma, C.ra and P.li are not showed in *mcy* production figures (b, c and d) because they are non-toxic species and all negative with *mcy* gene.

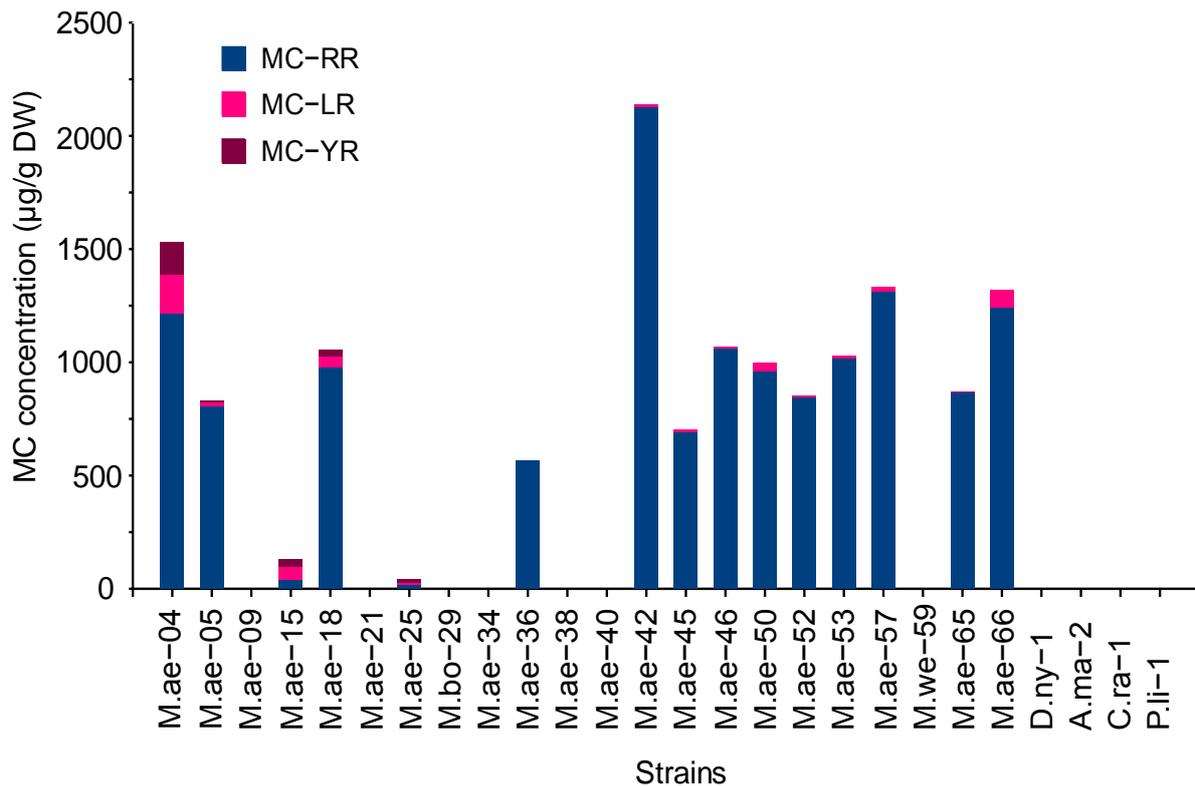


Figure 2–6. Microcystin profiles detected from isolated strains. M.ae: *Microcystis aeruginosa*; M.bo: *Microcystis botrys*; M.we: *Microcystis wesenbergii*; D.ny: *Dolichospermum nygaardii*; A.ma: *Arthrospira massartii*; C.ra: *Cylindrospermopsis raciborskii*; P.li: *Pseudanabaena limnetica*.

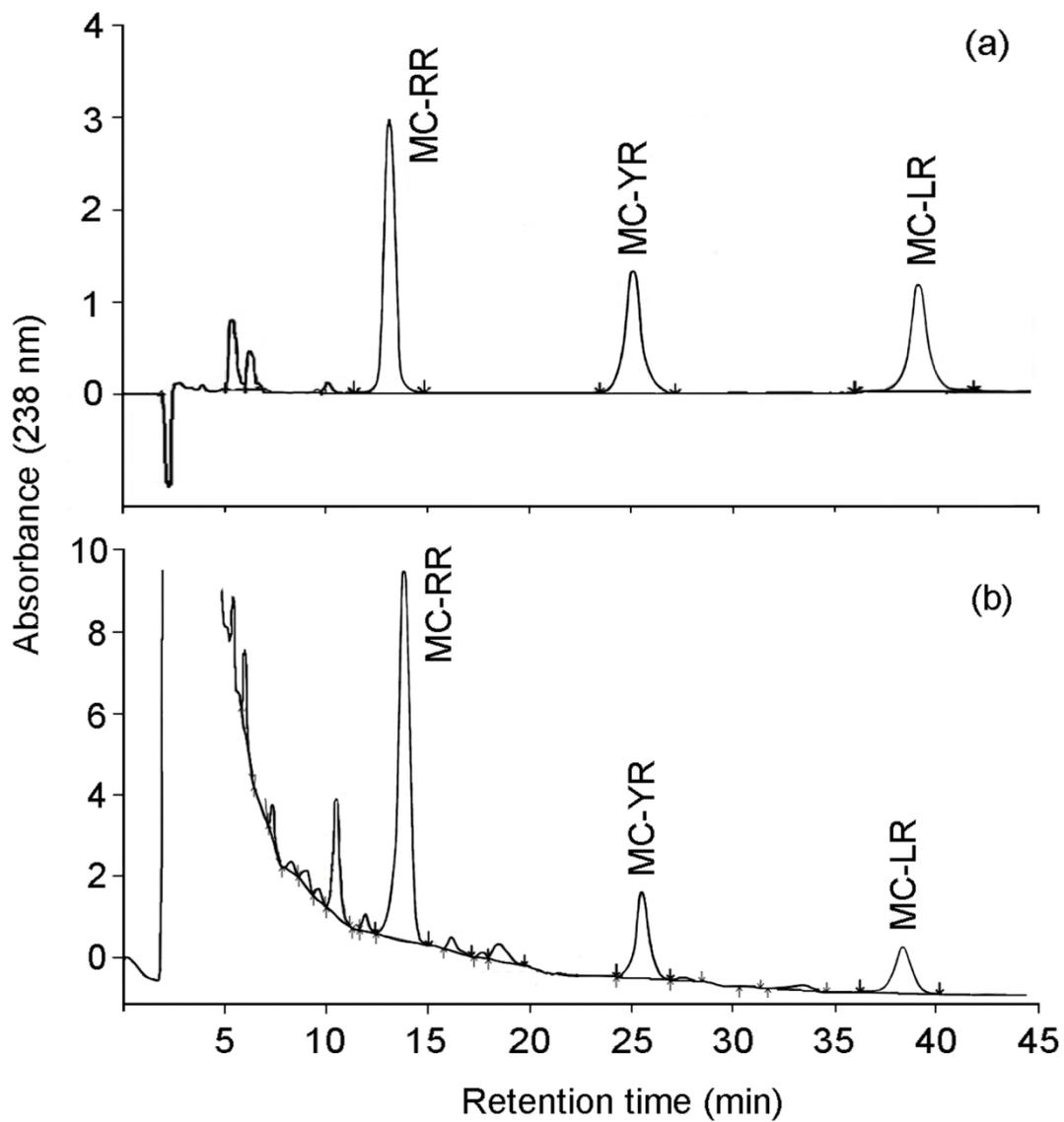


Figure 2–7. HPLC-chromatograms of (a) microcystin standards, and (b) bloom sample from Dau Tieng reservoir.

Chapter 3

Accumulation and effects of cyanobacterial crude extract containing microcystins on the edible clam *Corbicula leana*

3.1. Introduction

The occurrence of CYBs in eutrophic lakes, reservoirs and recreational waters has become a global environmental and public health concerns. These blooms produce a wide range of toxic secondary metabolites, especially MCs, the most widespread and occur in up to 75% of CYB incidents (Chorus and Bartram, 1999). MCs are intracellular but may rapidly and massively be released by cell lyses due to natural senescence, herbicides or physical stress (Issam *et al.*, 2010). Concentrations of dissolved MC from traces up to 1,800 $\mu\text{g L}^{-1}$ have been reported in many inland waters worldwide (Chorus and Bartram, 1999; Te and Gin, 2011). Therefore, aquatic animals may be subchronic exposed to high concentration of dissolved MCs for a period of time (Ibelings and Chorus, 2007). These dissolved toxins can be responsible for toxic effects observed in both animals and humans and are actually associated with massive deaths of aquatic animals (Chorus and Bartram, 1999).

MCs target liver cells, and their cellular uptake requires the activity of OATPs (Fischer *et al.*, 2005). Once in the cell, they can accumulate as free form of MC or specifically interact with protein phosphatases (PP1 and PP2A) in a two-step mechanism involving a rapid and reversible binding potentially followed several hours later by covalent binding; they can thus accumulate as covalently bound MC (Co-MC) with hyperphosphorylation and tumour-promoting abilities (MacKintosh *et al.*, 1990; Amado and Monserrat, 2010; Lance *et al.*, 2010). Moreover, MCs induced the production of ROS in various tissues of aquatic organisms (Pinho *et al.*, 2005; Burmester *et al.*, 2012; Gonçalves-Soares *et al.*, 2012; Turja *et al.*, 2014) leading to oxidative stress.

The cellular system of defense against MC toxicity comprises enzymatic antioxidant and detoxification enzymes, such as superoxide dismutase (SOD), catalase (CAT) and glutathione *S*-transferases (GSTs). SOD and CAT are antioxidant enzymes. SOD catalyzes the dismutation of superoxide anion ($O_2^{\bullet-}$) into oxygen and H_2O_2 , whereas CAT catalyzes the conversion of two molecules of H_2O_2 into two molecules of water and one of oxygen (Lushchak, 2011). The mechanism of MC detoxification in aquatic organisms involves GSTs, members of the phase II detoxification enzyme family that catalyze conjugation of MCs with glutathione (GSH) (Pflugmacher *et al.*, 1998). This conjugation is generally considered the primarily route of MC detoxification in aquatic organisms; it results in the formation of compounds that are more polar and thus more easily excreted (Kondo *et al.*, 1992; Pflugmacher *et al.*, 1998; Wiegand *et al.*, 1999; Beattie *et al.*, 2003; Campos and Vasconcelos, 2010). Furthermore, many aquatic species are able to survive in polluted environments by increasing their use of a multixenobiotic resistance (MXR) mechanism (Bard, 2000). The overexpressed membrane and intracellular transporters, such as P-glycoprotein, that pump unmetabolized and metabolized toxins directly out of the cell have been found in various organisms (Bard, 2000; Amé *et al.*, 2009; Faria *et al.*, 2011). This MXR mechanism is responsible for resistance to cyanotoxin bioaccumulation or insensitivity to natural toxins in mussels (Contardo-Jara *et al.*, 2008; Amé *et al.*, 2009; Campos *et al.*, 2014).

Nevertheless, toxic cyanobacteria and cyanotoxins, especially MCs, can have negative impacts on aquatic organisms. Bivalves usually insert themselves into sediments on the beds or shores of lakes or rivers and filter small particles via their gills. These sessile filter feeders are therefore seriously affected by the presence of toxic cyanobacterial colonies during CYBs or after the blooms have begun to decay. Increased attention is being paid to the accumulation and effects of MCs in bivalves, because humans consume these organisms (Ibelings and Chorus, 2007). Unlike the case in fish and mammals, there have been relatively few studies of the biological effects of cyanotoxins in bivalve mollusks (Gérard *et al.*, 2009; Sabatini *et al.*,

2011). MC accumulation in bivalves has been reported both in the field and in the laboratory studies (for a review see Martins and Vasconcelos, 2009). Previous studies, however, have not adequately considered MCs that are covalently bound to PPs, which may represent a considerable part of the MC burden (Lance *et al.*, 2010; 2014).

The toxicology and ecotoxicology of MCs have been investigated in detail (Duy *et al.*, 2000; Wiegand and Pflugmacher, 2005). However, toxicologists have focused only on isolating MCs (Beattie *et al.*, 2003; Li *et al.*, 2003; Kist *et al.*, 2012) or using purified MCs (Cazenave *et al.*, 2006; Contardo-Jara *et al.*, 2008; Pavagadhi *et al.*, 2012; Sun *et al.*, 2012) in toxicity studies; the toxicity of the complex CCE has not been evaluated to the same extent. Several recent findings indicate that water from CYBs contain not only MCs but a mixture of hazardous substances that can evoke more pronounced toxic effects than can MCs or other well-recognized cyanotoxins alone (Pietsch *et al.*, 2001; Burýšková *et al.*, 2006; Falconer, 2007; Palíková *et al.*, 2007; Smutná *et al.*, 2014). It would therefore be value to evaluate the effects of these complex cyanobacterial biomasses on aquatic organisms.

In this chapter, I examined the effects of a crude extract of CYBs containing MCs on the freshwater edible clam *C. leana*, as well as the accumulation and depuration of MCs by this species. My aims were to increase food safety and to reveal the clam's system of defense against MCs via the capacity of the antioxidant or detoxification enzymes CAT, SOD and GST in various organs (gills, foot, mantle and remaining tissues). Finally, evidences for the clam's resistance to cyanotoxins were also discussed.

3.2. Materials and methods

3.2.1. Rearing the organisms

Freshwater clam *C. leana* P. (Figure 3–1) was collected at a freshwater fisheries experimental station in Oita Prefecture, Japan, and transported alive to the laboratory. The clams were introduced into sufficient aerated 50-L aquatic aquariums containing

dechlorinated tap water and 5-cm sand layer as the substrate. Before the experiments, clams were kept at a density of below 100 individual per 50 L and acclimatized for 1 month at a photosynthetic photon flux density (PPFD) of $20 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ under a 12:12 light:dark photoperiod. The water temperature was $22 \pm 1^\circ\text{C}$, the pH 7.5 ± 0.3 , and the dissolved oxygen concentration $7.9 \pm 0.6 \text{ mg L}^{-1}$. All of the incubation water was renewed every 3 days. The clams were fed daily with the green alga *C. vulgaris* at a concentration of $2 \times 10^3 \text{ cell mL}^{-1}$ cultivated in soil extract medium (SEM) (Kong *et al.*, 2012). The wet weight (WW) of individual clams was $5.14 \pm 0.72 \text{ g}$ and the shell length was $2.12 \pm 0.53 \text{ cm}$.

3.2.2. Preparation of cyanobacterial crude extract

CCE was prepared as previously reported by Pietsch *et al.* (2001) with minor modifications. Briefly, 4 kg wet weight of bloom material (mainly *Microcystis* spp., collected from Lake Kasumigaura, Japan by using plankton net) was frozen at -30°C for two days and then thawed at room temperature. After the material had thawed completely, it was ice-cooled and sonicated for 1 min (Taitec Ultrasonic 150W, Saitama, Japan). This freeze–thaw–sonicate cycle was repeated four times. The samples were then centrifuged at $3,000 \times g$ at 4°C for 30 min to remove cell debris. The CCE supernatant was collected and kept at -30°C until use.

Subsamples of CCE were used for MCs analysis. Briefly, the CCE was centrifuged at $6,000 \times g$ at 4°C for 15 min. The supernatant was collected, dried completely, and redissolved in 500 μL of 100% MeOH. The samples were analyzed by HPLC for MCs quantification. MC-RR, MC-LR and MC-YR (Wako, Osaka, Japan) were used as standards. The HPLC analysis showed that the CCE contained three MC congeners, namely MC-RR (53%) and MC-LR (45%), and the minor congener MC-YR (2%), at a total concentration of $7892 \mu\text{g L}^{-1}$.

3.2.3. Experimental set up

The clams were placed in eight aquariums (30 clams per aquarium) containing 2 L distilled water and a 2-cm sand layer as a substrate. Clams were allocated randomly to an

exposure and a control group. Light intensity and water conditions were the same as previously described.

In the exposure group, CCE containing MCs was added to each aquarium to a final concentration of $400 \mu\text{g MC-LR}_{\text{eq}} \text{L}^{-1}$ on day 0. The water and MC were completely replaced on day 5 of the 10-day exposure period. The clams were then collected and relocated into aquariums containing distilled water, toxin-free water; they stayed in these aquariums for 5 days of depuration. The experiment therefore lasted a total of 15 days (10 days of MCs exposure following by 5 days of toxin depuration). In the control group only the water was replaced on day 5. No food was provided during the uptake and depuration periods. Dead clams were removed and counted daily.

Six hours after the start of exposure and again on days 1, 3, 5, and 10 of the exposure period and days 11, 13, and 15 of the depuration period, 12 – 15 clams were sampled. For MC quantification the shells of 8 – 10 clams were immediately removed; 10 clams were collected only before the experiment from control group for MC control. The clams were then freeze-dried for 48 h and kept at -30°C until MC analysis. For measurement of enzyme activity, the clams (in both groups) were rinsed gently under dechlorinated tap water. The gills, mantle, and foot of three to five clams (pooled) and the remaining tissues (kept individually) were dissected on ice. The samples were then immediately frozen in liquid nitrogen and stored at -80°C until enzyme extraction.

3.2.4. Extraction and analysis of MCs in incubation water

I measured MC concentrations in the incubation water immediately after the start of exposure and then at the same sampling times as listed above. The incubation water (about 10 to 100 mL) was collected and filtered through GF/C filter. The filtrate was then passed through the Presep C18 (ODS) cartridge (Wako Pure Chemical Industries Ltd., Osaka, Japan) that had been preconditioned with 5 mL MeOH 100% and 10 mL ultrapure water; it was then

subjected to final elution with 3 mL MeOH 100% and dried completely. The MC fraction was then redissolved in 500 μ L MeOH 100% and kept at -30°C until HPLC analysis. MCs (-RR, -LR, -YR) were analyzed with an reversed-phase HPLC system equipped with a UV detector (Shimadzu 10A series, Shimadzu Corporation, Kyoto, Japan) by using the method as described in the 2.2.5 section.

3.2.5. Extraction and analysis of free MC in clam

Free MC was extracted as previously reported by Xie and Park (2007), with minor modifications. Briefly, freeze-dried tissues (about 100 to 150 mg per sample) were homogenized in 3 mL of BuOH:MeOH:H₂O (5:20:75, v/v/v) by using a homogenizer (Polytron, Kinematica AG, Littau-Luzern, Switzerland) and extracted three times with 5 mL of the same solution, each time for 24 h with shaking in darkness. After sonication for 1 min (Taitec Ultrasonic 150W, Saitama, Japan), the samples were centrifuged at $2,000 \times g$ at 4°C for 30 min. The supernatants were then combined, evaporated to 10 mL, diluted three times with ultrapure water and applied to an Oasis HLB cartridge (60 mg, Waters Corp., Milford, MA, USA) that had been preconditioned with 3 mL MeOH 100% and 10 mL ultrapure water. The column was first washed with 3 mL MeOH 20%, and then eluted with 3 mL MeOH 100%. This elution fraction was evaporated to dryness under reduced pressure at below 40°C . MCs were suspended in 500 μ L MeOH 100%; they were then kept at -20°C prior to reversed-phase HPLC analysis as described above. Duplicate samples with duplicate analysis were used in this determination ($n = 4$).

3.2.6. Extraction of total MC in clam

Total MC (free and Co-MC) was extracted as previously reported by Neffling *et al.* (2010) and Cadel-Six *et al.* (2014), with minor modifications. Briefly, freeze-dried tissues were homogenized and trypsinated with 3 mL of 500 $\mu\text{g mL}^{-1}$ of trypsin in Sorensen's phosphate buffer (pH 7.5) at 37°C for 3 h; this was followed by oxidation with 0.1 M KMnO_4

and 0.1 M NaIO₃ (pH 9.0) for 3 h at room temperature. The reaction was quenched with sodium bisulphite solution (40% w/v) until colorless at pH 2 with 10% sulphuric acid. After sample centrifugation (2,000 × g, 4°C, 30 min), the supernatant was collected, diluted five times with ultrapure water, and then applied to an Oasis HLB cartridge (60 mg, Waters Corp.) that had been preconditioned with 3 mL MeOH 100% and 10 mL ultrapure water. The column was first washed with 3 mL MeOH 20%, and then 2-methyl-3-methoxy-4-phenylbutanoic acid (MMPB) fraction, which is the product of MC oxidation, was eluted with 3 mL MeOH 80%. The elution fraction was evaporated to dryness and redissolved in 500 µL MeOH 100%. The MMPB was converted to its methyl ester (meMMPB) by using a 10% BF₃-methanol kit (Sigma-Aldrich, Tokyo, Japan) (Figure 3–2). The derivatized samples were dissolved in *n*-hexane and kept at –20°C prior to GC-MS analysis. The Co-MC content was thus estimated by subtracting the free MC from the total MC content. 4-phenylbutyric acid (4-PB) was used as an internal standard (Sano *et al.*, 1992; Tsuji *et al.*, 2001). MMPB-d₃ and MC-LR purchased from Wako Pure Chemical Industries (Osaka, Japan) were used as external standards.

3.2.7. GC-MS analysis

GC-MS analyses were performed on a DSQ II mass spectrometer linked to a Trace GC Ultra gas chromatograph system (Thermo Scientific, Waltham, MA, USA), equipped with an Rxi-5ms column (30 m × 0.25 mm ID, phase thickness 0.25 mm; Restek, Bellefonte, PA, USA). Helium was used as the carrier gas at a flow rate of 1.5 mL min⁻¹ (splitless mode). The program used for the analysis was 80°C for 1 min followed by an increase to 280°C at 8°C min⁻¹. The other conditions were as follows: ion source temperature 200°C, injection port temperature 230°C, detector temperature 250°C, and interface temperature 280°C. Methylated 4-PB (me4-PB) and meMMPB were detected by using selected ion monitoring (SIM) mode. Ions at 91 and 104 m/z were selected for me4-PB; and those at 75, 78, 91, 131, and 134 m/z

for meMMPB (Tsuji *et al.*, 2001; Suchy and Berry, 2012). Xcalibur software was used for quantitative analysis of these analytes. Duplicate samples with duplicate analysis were used in this determination (n = 4).

3.2.8. Enzyme extraction and measurement

Enzymes were extracted as previously reported by Wiegand *et al.* (2000) with minor modifications. Briefly, samples (gill, foot, mantle, remaining soft tissues) were homogenized in 0.1 M sodium phosphate buffer (pH 6.5) (1:5 w/v) containing 20% (v/v) glycerol, 1 mM ethylenediaminetetraacetic acid (EDTA), and 1.4 mM dithioerythritol (DTE), as a reducing agent and a protease inhibitor, in ice. The homogenate was centrifuged at $10,000 \times g$ at 4°C for 15 min to eliminate cell debris and the other fragments. The supernatant was used for enzyme activity measurements. I used a Fluoroskan Ascent fluorometer (Thermo Electron Corp., Milford, MA, USA) to detect the activities of GST (EC 2.5.1.18), SOD (EC 1.15.1.1), and CAT (EC 1.11.1.6) at wavelengths of 340, 460, and 540 nm, respectively, with GST, SOD, and CAT assay kits purchased from Cayman Chemical Company (Ann Arbor, MI, USA). All enzyme activities were calculated in terms of the protein content, as measured with a Quick Start Bradford protein assay kit purchased from Bio-Rad Laboratories (Hercules, CA, USA). Each enzymatic assay was performed in triplicate.

3.2.9. Recovery experiment

In order to determine the recovery ratio of MC contents extracted from clam tissues, the recovery experiment was conducted by spiking 100 mg lyophilised clam tissues with a CCE that contained of 1 μg of MCs (MC-LR_{eq}). Samples were prepared in quadruplicate. MC contents were then extracted and analysed as previous described. The recovery and relative standard deviation of the analytical method were calculated. The mean recovery for the clam tissues (n = 4) was 95.8% (relative standard deviations RSD = 4.9%) (data not shown).

3.2.10. Statistical analyses

Data on CAT, SOD, GST and MCs are presented as mean \pm SD. Differences between the exposure and control groups were tested for significance by using one-way analysis of variance (ANOVA). When the ANOVAs were significant, I used pairwise comparison by using Tukey's HSD Post-hoc test to detect significant differences between the exposure concentrations and the control. *P*-values less than 0.05 were considered statistically significant.

3.3. Results

3.3.1. Microcystins concentration in incubation water

MC concentrations in the control incubation water were under the detection limit (data not shown). I monitored MC concentrations in the incubation water during the first 5 days of uptake and during the depuration period. In the uptake experiment, MC was immediately and continuously cleared from the incubation water. After only 6 h the MC concentration in the water had decreased to $326.3 \pm 13.5 \mu\text{g L}^{-1}$; after 1 day it was $262.2 \pm 12.9 \mu\text{g L}^{-1}$, after 3 days $185.8 \pm 10.7 \mu\text{g L}^{-1}$, and after 5 days $121.1 \pm 3.1 \mu\text{g L}^{-1}$ (Figure 3–3). There was no release of the unmetabolized parent compound into toxin-free water during depuration period.

3.3.2. Uptake and depuration of free- and Co-MC

There were no deaths in either of the groups of animals during the experiments. The control samples contained no MCs at detectable concentrations (data not shown).

Extractable free MC accumulated in the clams during the uptake and depuration periods was presented in Figure 3–3. Typically, the free MC concentration in the whole clams increased rapidly after the start of exposure and peaked (at $3.4 \pm 0.63 \mu\text{g g}^{-1}$ DW) after about 1 day. It then gradually declined over the rest of the exposure period. The free MC content was well correlated with the concentration of MCs in the incubation water ($R = 0.65$, $P <$

0.01). The Co-MC concentration increased slowly during the uptake and depuration periods, peaking (at $0.31 \pm 0.013 \mu\text{g g}^{-1} \text{DW}$) on day 11. It gradually declined thereafter.

During the depuration period, free MC was quickly eliminated from the clam tissues and below the limit of detection by HPLC. In contrast, the Co-MC concentration was enhanced on the first day of depuration and then gradually declined, although Co-MC was still detectable at the end of the depuration period (Figure 3–3).

3.3.3. Biotransformation enzyme

I measured GST activity in various tissues of both the exposure and the control groups (Figure 3–4). GST activity in the gills was significantly greater in the exposure group than in the control group, but only on days 0.25, 1, 3, and 11. Significant elevation of GST was also observed on days 10 and 11 in mantle. In contrast, GST activity in the foot was significantly lower in the exposure group than in the control group on days 3, 5, 10, and 13, although it had returned to the control level by the end of the experiment. GST activity in the remaining tissues did not differ significantly over time between the two groups.

3.3.4. Antioxidant enzyme activities

I examined the effects of CCE containing MCs on SOD activity in the various clam tissues (Figure 3–5). SOD activity in the gills was significantly greater in the exposure group than in the control group on all measurement days in the exposure period except day 10. In the mantle this was also true for all measurement days in the exposure period except day 3. In contrast, in the foot there were no significant differences in SOD activity between the two groups at any time. In the remaining tissues SOD activity was significantly greater in the exposure group than in the control group, but only on days 0.25 and 5. Unlike the case with GST, during the depuration period there were no differences in SOD activity between the two groups in any of the tissues.

I then examined changes in CAT activity (Figure 3–6). CAT activity in the gills was significantly greater in the exposure group than in the control group, but only on days 0.25, 1,

and 3. In contrast, CAT activity in the foot was significantly lower in the exposure group than in the control group on days 5, 10, and 11 but thereafter returned to normal. There were no detectable trends in CAT activity in the mantle and the remaining tissues. CAT activity in the mantle was significantly greater in the exposure group than in the control group on days 0.25, 1, 10, and 11 but significantly lower at the end of the experiment, on day 15. In the remaining tissues, CAT activity was significantly greater in the exposure group than in the control group on day 1 but significantly lower than in the controls on day 13.

3.4. Discussion

In natural environment and under experimental conditions, concentration of dissolved MCs in water can be expected to be decreased by such processes as adsorption onto particulate materials, attachment to substrates, UV or photolysis degradation, and degradation by intracellular organic matter and bacteria (Harada and Tsuji, 1998; Grützmaier *et al.*, 2009; Ding *et al.*, 2010; Wörmer *et al.*, 2010; Shimizu *et al.*, 2011; Ma *et al.*, 2012; Shimizu *et al.*, 2012). In my experiment, the concentration of MCs in the incubation water had decreased by about 69% after 5 days of incubation. This result agreed well with the finding in another study that after 3 days of incubation the concentration of dissolved MC-LR had decreased by more than 50% (Contardo-Jara *et al.*, 2008). However, the natural degradation of MCs in complex CYB extracts is still unknown. My results may suggest that the degradation of MCs in CCE is a result of the combined effects of physical, chemical, and biological factors, including uptake by aquatic animals. However, the main contributors to toxin degradation remain unknown and need further investigation.

The extraction solvents used for extraction of MCs from animal tissues vary greatly in the literature (Msagati *et al.*, 2006; Smith and Boyer, 2009). The solvent selected in this study was successfully used also in bivalve *Anodonta woodiana*, *Cristaria plicata* and *Unio douglasiae* (Yokoyama and Park, 2002), fish *Silurus glanis*, *Carassius auratus* and *Cyprinus*

carpio (Xie *et al.*, 2007), gastropod *Sinotaia histrica*, *Lymnaea stagnalis* (Xie *et al.*, 2007; Lance *et al.*, 2010), with similar percentages of recovery.

I revealed here that toxin uptake by *C. leana* was lower than that by most other mussels and snails. The maximum levels of free MC measured in *C. leana* ($3.4 \pm 0.63 \mu\text{g g}^{-1}$ DW) were similar to the MC content in the mussel *Anodonta* sp. collected from Lake Kastoria, in Greece (Gkelis *et al.*, 2006), but they were much lower than those in other bivalve species e.g. $16 \mu\text{g g}^{-1}$ DW in *Mytilus galloprovincialis* (Amorim and Vasconcelos, 1999), $16.3 \mu\text{g g}^{-1}$ DW and $21 \mu\text{g g}^{-1}$ WW in *Dreissena polymorpha* (Pires *et al.*, 2004; Contardo-Jara *et al.*, 2008) and $70 \mu\text{g g}^{-1}$ DW in *Anodonta cygnea* (Eriksson *et al.*, 1989), during laboratory exposure. Different species no doubt have different capacities for toxin accumulation, uptake, and tolerance. The decline in extractable MC content in *C. leana* after day 1 of exposure could have been the result of either enhanced biliary excretion of MCs and their metabolites (Sahin *et al.*, 1996) or slow covalent addition of MCs to the catalytic subunit of PPs and other thiol-containing cellular proteins (MacKintosh *et al.*, 1995) such as GSH (Kondo *et al.*, 1992). Whereas the former mechanism (biliary excretion) would progressively reduce the amount of free MC in the animal, the covalent binding of MCs to PPs would prevent the MCs from being excreted. This interpretation is consistent with my results showing that the Co-MC concentration gradually increased with time.

Because MCs covalently bind to PPs and cannot be extracted from the covalent complex by using organic solvents, detection of MCs in animal tissues has been limited to free MC (for reviews see Ibelings and Chorus, 2007; Smith *et al.*, 2008; Martins and Vasconcelos, 2009). By using an oxidation procedure adapted from previously developed methods (Sano *et al.*, 1992; Harada *et al.*, 1996; Tsuji *et al.*, 2001; Lance *et al.*, 2010; Neffling *et al.*, 2010; Suchy and Berry, 2012), I provided evidence for the existence and accumulation of Co-MC in *C. leana* tissues (Figure 3–3). On average, 0.5% of total MC was bound in *C. leana* during the 15-day experiment (data not shown). However, the clam rapidly

eliminated the MC when cultured in toxin-free water. Williams *et al.* (1997b) reported that the total MC content in the mussels *Mytilus edulis* transferred to untreated saltwater dropped from 337 μg to 11 $\mu\text{g g}^{-1}$ FW in 4 days, after which time it was undetectable. Prepas *et al.* (1997) have also shown that MC concentrations significantly decrease within 6 days of depuration in the clam *Anodonta grandis simpsoniana*. Also, immediate uptake and rapid release of MC have been observed in *D. polymorpha* (Pires *et al.*, 2004; Contardo-Jara *et al.*, 2008), and *M. galloprovincialis* (Amorim and Vasconcelos, 1999). I found here that free MC rapidly began to be released when the clam was transferred to toxin-free water, but the percentage of bound MC increased (and reached 100% of the total MC content) during the depuration period (Figure 3–3). This increase may have occurred because the enhancement of the free MC binding to PPs. At the end of the 5-day depuration period, *C. leana* tissues still contained $0.15 \pm 0.01 \mu\text{g g}^{-1}$ DW of Co-MC. Although depuration is commonly judged to be rapid, it is equally clear that depuration is incomplete, even after a considerable period of time (Wiegand *et al.*, 1999; Ibelings and Chorus, 2007). Therefore, Co-MC level should be considered in predictions of risk to higher trophic organisms and humans.

The current study revealed the toxin uptake by *C. leana* from dissolved MCs is possible. Despite these relatively low levels, however, my results raise concern about chronic toxicity from a human health perspective, because human may be consuming clams contaminated with MCs, and consumption of food contaminated with MCs could promote liver cancer (Duy *et al.*, 2000). I used a coefficient of 100 to convert dry weight to wet weight in the case of this clam; my results showed that the total MC content in clams exceeded the TDI of $0.04 \mu\text{g kg}^{-1}$ of body mass per day (Figure 3–7). My results therefore suggest that *C. leana* represents a health risk to consumers when aquatic MC concentrations are high. They need detoxification process before marketing.

In this study, I investigated the defense system against MC toxicity in the clam that focused on GST activity. It is well known that the family of GST enzymes is the most

important group for MCs detoxification (Li *et al.*, 2008; Burmester *et al.*, 2012; Galanti *et al.*, 2013; Pereira *et al.*, 2013). I found an elevation in GST activity in the gills during the first 3 days of exposure, suggesting that there was an immediate response by the tissue to the CCE. This response can be due either to an increase in MC conjugation with GSH or to the detoxification of endogenous molecules such as membrane peroxides (Pinho *et al.*, 2005). The higher GST activity in the exposure group suggested that there was an increase in MC conjugation capability in the gills of these animals. The same defense system against MC toxicity has been reported in the gut and gills of *M. galloprovincialis* mussel (Vasconcelos *et al.*, 2007), in the gills of crabs exposed to an aqueous extract of the toxic cyanobacterium *M. aeruginosa* (Vinagre *et al.*, 2003; Pinho *et al.*, 2005), and in the gills and intestine of the catfish *Corydoras paleatus* exposed to high concentration of MC-RR (Cazenave *et al.*, 2006). The further increase in GST activity in the gills on day 11 in *C. leana* may have been the result of excessive GST synthesis, which was thereafter regulated in response to the lack of MCs in the depuration period. Higher GST activity in the gills, digestive glands and muscle during depuration period has been reported in mussel *M. galloprovincialis* after the termination of exposure to toxic *M. aeruginosa* (Fernandes *et al.*, 2009). A similar pattern has been reported in the freshwater snail *Bellamya aeruginosa* after the end of exposed to *M. aeruginosa* (Zhu *et al.*, 2011). Contrastingly to the gills, in the foot, mantle, and remaining tissues GST expression was inhibited or did not change after exposure. Decreased GST activity in these tissues may be related to GSH depletion in response to MC toxicity (Amado *et al.*, 2011; Sabatini *et al.*, 2011); it may also result in altered biochemical effects in organisms exposed to MCs (Malbrouck *et al.*, 2003). In contrast with my results Gélina *et al.* (2012) reported no increase of GST activity as well as lipid peroxidation in both liver and brain tissues of rainbow trout (*Oncorhynchus mykiss*) after exposure to cyanobacterial extracts.

CCE containing MCs induces ROS production, resulting in oxidative stress to organisms (Jos *et al.*, 2005; Burýšková *et al.*, 2006; Palíková *et al.*, 2007). These ROS

activate the expression of several antioxidant enzymes, including SOD and CAT, which constitute the major defensive system against ROS (Amado and Monserrat, 2010; Lushchak, 2011; Paskerová *et al.*, 2012). Exposure of the freshwater clam *Diplodon chilensis patagonicus* to toxic *Microcystis* leads to an increase in oxidative stress, as indicated by enhanced CAT and SOD activities (Sabatini *et al.*, 2011). Similarly, exposure of the mussel *M. edulis* to an extract of the cyanobacterial toxin nodularin leads to an increase in CAT activity (Kankaanpää *et al.*, 2007). Here, I found significant changes in both CAT and SOD enzyme activities in various tissues of *C. leana*. These findings indicate that there was an activation of the antioxidant defensive system as a direct or indirect response to ROS generation after exposure to CCE containing MCs. More specifically, the alterations that I found in antioxidant enzyme activity were likely caused mainly by the presence of MCs and partly by the presence of other compounds in the CCE (Dao *et al.*, 2013). Also, my results are consistent with the observations of Burmester *et al.* (2012), who found that SOD activity in two bivalves, *D. polymorpha* and *U. tumidus*, was elevated in various tissues after exposure with purified MC-LR or CCE.

Elevation of CAT activity and other antioxidant enzymes have been observed in the crab hepatopancreas after 48 h of exposure to MCs from CCE (Pinho *et al.*, 2005) or in shrimp (*Litopenaeus vannamei*) injected with MCs (Gonçalves-Soares *et al.*, 2012). In contrast, CAT activity was significantly reduced, and SOD activity unchanged, in the crab hepatopancreas after 7 day's exposure to a high-dose *M. aeruginosa* aqueous extract (Pinho *et al.*, 2005). Likewise, CAT activity in larvae of the bighead carp *Hypophthalmichthys nobilis* is significantly reduced upon MC-LR exposure, suggesting that CAT activity is inhibited by MC-LR (Sun *et al.*, 2013). In my clam, CAT activity in the mantle was significantly lower in the exposure group than in the control group at the end of the experiment, possibly because at that point the mantle was less efficient than gills and foot at neutralizing the impact of oxidative stresses. In contrast, the reduction in CAT activity in the foot toward the end of the

exposure period could have been due to the generation of superoxide radicals during oxidative stress; these molecules have been reported to inhibit CAT activity (Kono and Fridovich, 1982). Therefore, toxicity effects depend not only on the dose and kind of toxins, the routes of exposure, and the duration time of exposure, but also on the target organs, the state of the organisms, specific species as well as method of detection (Malbrouck and Kestemont, 2006; Pavagadhi *et al.*, 2012; Sun *et al.*, 2013).

Contrastingly, MXR in the freshwater mussel *D. polymorpha* is evidence of the insensitivity of bivalves to purified cyanobacterial toxins (Contardo-Jara *et al.*, 2008). My results also correspond to those of Fischer and Dietrich (2000), who observed no deaths, malformations, or growth inhibition in *Xenopus laevis* embryos exposed to purified MCs at up to 2,000 $\mu\text{g L}^{-1}$ for 96 h. Similarly, no developmental toxicity of MCs (at up to 20,000 $\mu\text{g L}^{-1}$) has been observed in the toad *Bufo arenarum* (Chernoff *et al.*, 2002). Antioxidant enzyme levels may be elevated in response to cellular oxidative stress in animal cells (Dias *et al.*, 2009; Turja *et al.*, 2014), and the increased rate of synthesis of these antioxidant enzymes could be a plausible explanation for the insensitivity following MC exposure in some experimental groups (Pavagadhi *et al.*, 2012). My results demonstrate that biochemical toxic effects in *C. leana* are only temporary and that prolonged exposure can lead to adaptations to cope with deleterious effects. The significant change in GST, SOD, and CAT activities that I found in *C. leana* probably reflect adaptation to oxidative conditions. However, in toxin-free water, both of the antioxidant enzymes and detoxification enzyme showed adaptive responses at several time points whereby enzyme activity was induced and then returned to control levels. The responses of antioxidant and detoxification enzymes might thus contribute to the MC and cyanotoxins tolerance of *C. leana*.

Many aquatic organisms live and reproduce in contaminated waters, suggesting that they have ways to resist or tolerate contaminants (xenobiotics) in their environment (Cornwall *et al.*, 1995). Exposure to toxins can trigger the MXR mechanism, which serves as a first line

of defense against a broad spectrum of natural and man-made toxicants in the cells (Bard 2000; Eufemia and Epel, 2000; Faria *et al.*, 2011). Contardo-Jara *et al.* (2008) pointed out that the interactions of various defense mechanisms against MC toxicity in the freshwater mussel *D. polymorpha* are due to high constitutive level of P-gp and the reaction of MXR mechanisms; this explains the clams' survival success, even when they are exposed to high MC concentrations. Further studies are needed to give us an integrated view of toxin insensitivity and the MXR mechanism in the clam *C. leana*. To my knowledge, this is the first report of MC uptake by, and the biochemical responses of, this edible clam in the context of safe food production.

3.5. Summary

In this chapter the accumulation and effects of CCE containing MC on the edible clam *C. leana* were investigated. Toxic effects were evaluated through the activity of antioxidant and detoxification enzymes: CAT, SOD, and GSTs from gills, foot, mantle and remaining soft tissues. Clams were exposed to CCE containing $400 \mu\text{g MC-LR}_{\text{eq}} \text{L}^{-1}$ for 10 days and were then kept in toxin-free water for 5 days. Clam accumulated MCs (up to $3.41 \pm 0.63 \mu\text{g g}^{-1}$ DW of free- and $0.31 \pm 0.013 \mu\text{g g}^{-1}$ DW of Co-MC). The activity of SOD, CAT, and GST in the gills and mantle increased in MC-treated animals. In contrast, CAT and GST activity was significantly inhibited in the foot and mostly only slightly changed in the remaining tissues.

My findings in this chapter provide insights into the uptake of CCE containing MCs at high concentrations by *C. leana* and the consequent biochemical responses of the clam under laboratory conditions. Results highlight the involvement of antioxidant and biotransformation systems in detoxification of MCs. It explains the possible tolerance of *C. leana* continuously exposed to high level of MCs. In addition, it reveals that MCs accumulated by the clam via the uptake of dissolved MCs in water bodies is possible. My findings should also improve our

understanding of the impacts of MC-containing cyanobacteria dissolved in the water column on aquatic life under natural conditions. The results also showed that the total MC content in clams exceeded the TDI of $0.04 \mu\text{g kg}^{-1}$ of body mass per day. My results therefore suggest that *C. leana* represents a health risk to human when aquatic MC concentrations are high. They need detoxification process before marketing. Consumption of this clam should be limited when there are high concentrations of dissolved MC present in the water (especially after cells lyse at the end of the blooms). However, further research is required to deepen our understanding of the fate and transfer of MCs and the toxicity of other hazardous substances from CCE.



Figure 3–1. Photos of the clam *Corbicula leana*. (a) Whole external shell; (b) Soft tissues, arrow indicates cyanobacterial cells accumulated in soft tissues; and (c) the inner shell-side.

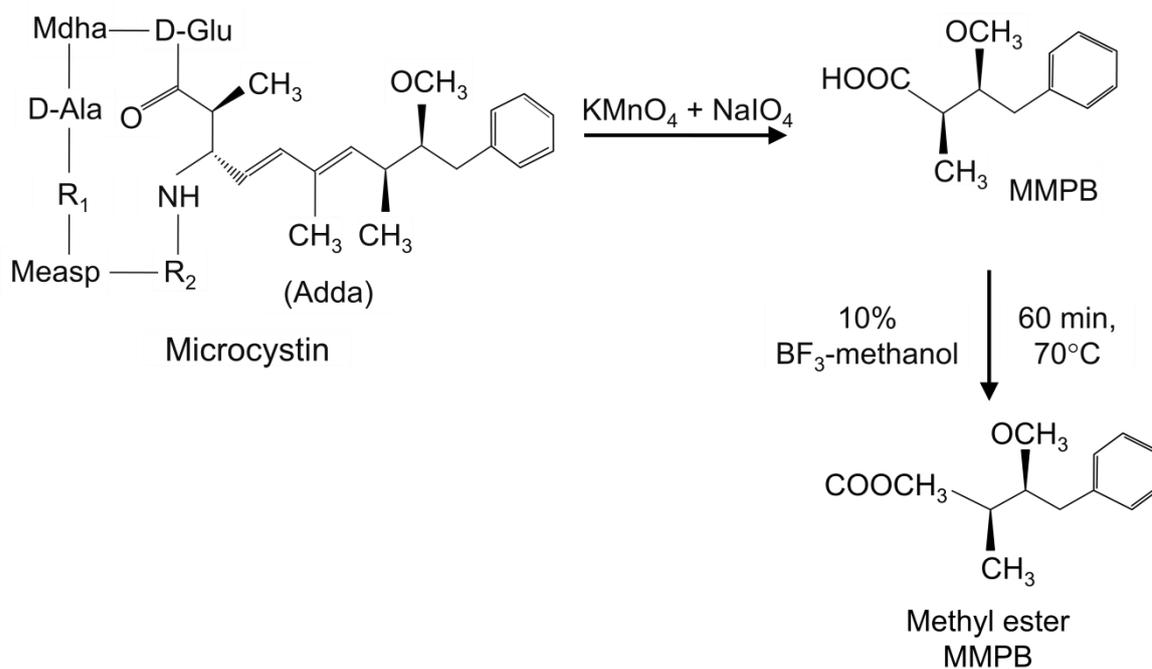


Figure 3–2. The oxidation of 3-amino-9-methoxy-2,6,8-trimethyl-10-phenyldeca-4,6-dienoic acid (Adda) in microcystins to the carboxylic acid 2-methyl-3-methoxy-4-phenylbutyric acid (MMPB) and its methyl ester (modified from Tsuji *et al.*, 2001).

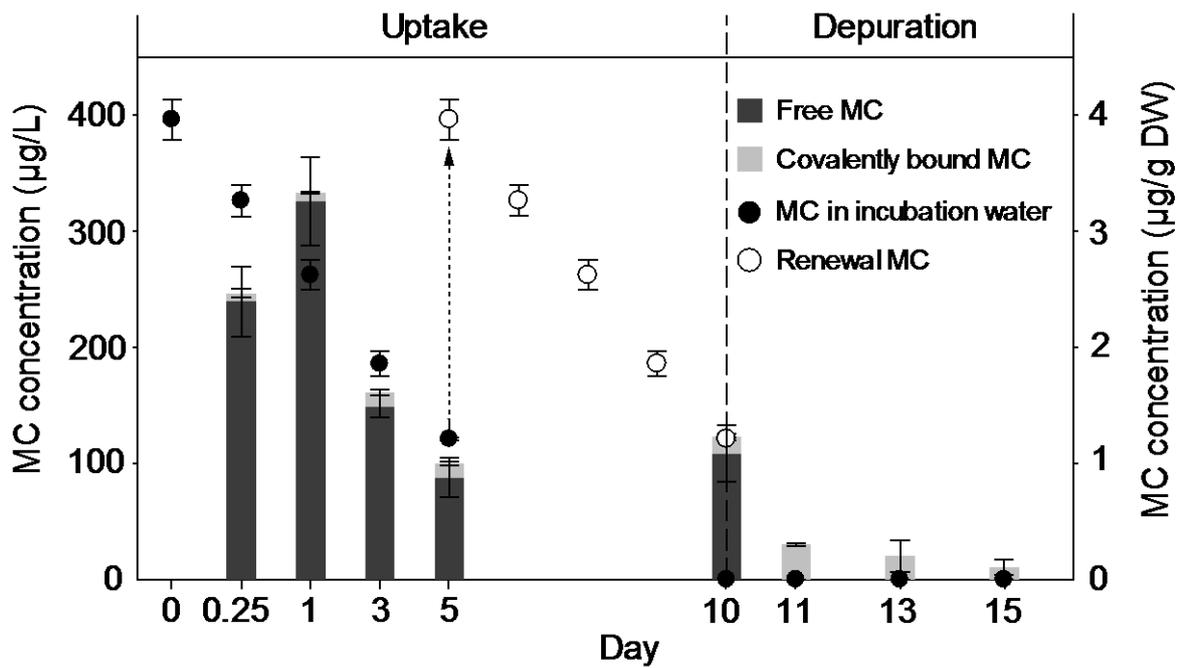


Figure 3–3. Concentrations of free microcystin (MC), covalently bound MC in *Corbicula leana*, and of MC in incubation water, during the uptake and depuration periods. Arrow indicates the time of renewal of the MC concentration and the water during the uptake period.

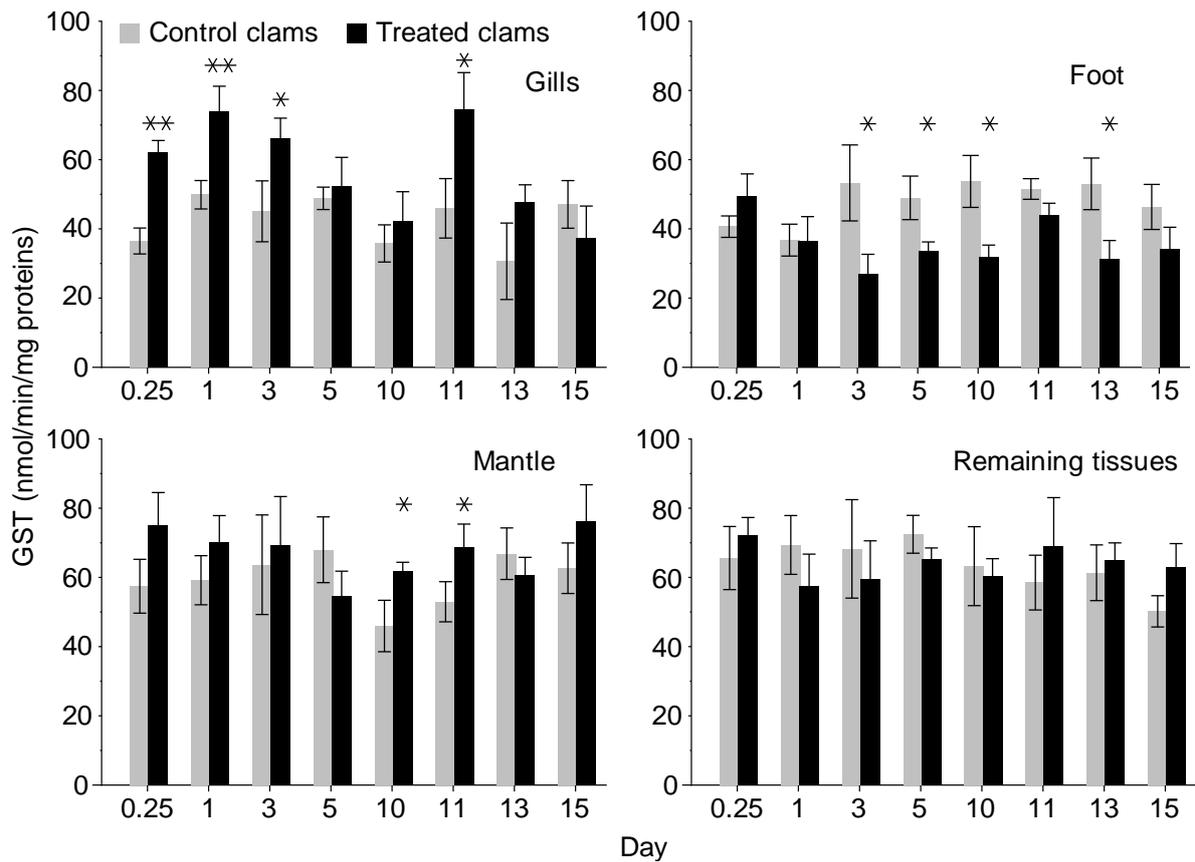


Figure 3–4. Production of glutathione *S*-transferase (GST) (nmol min⁻¹ mg⁻¹ proteins) in various tissues of *Corbicula leana* exposed to toxic cyanobacterial bloom crude extract. Asterisks indicate significant differences compared with controls at the respective time points (* $P < 0.05$, ** $P < 0.01$).

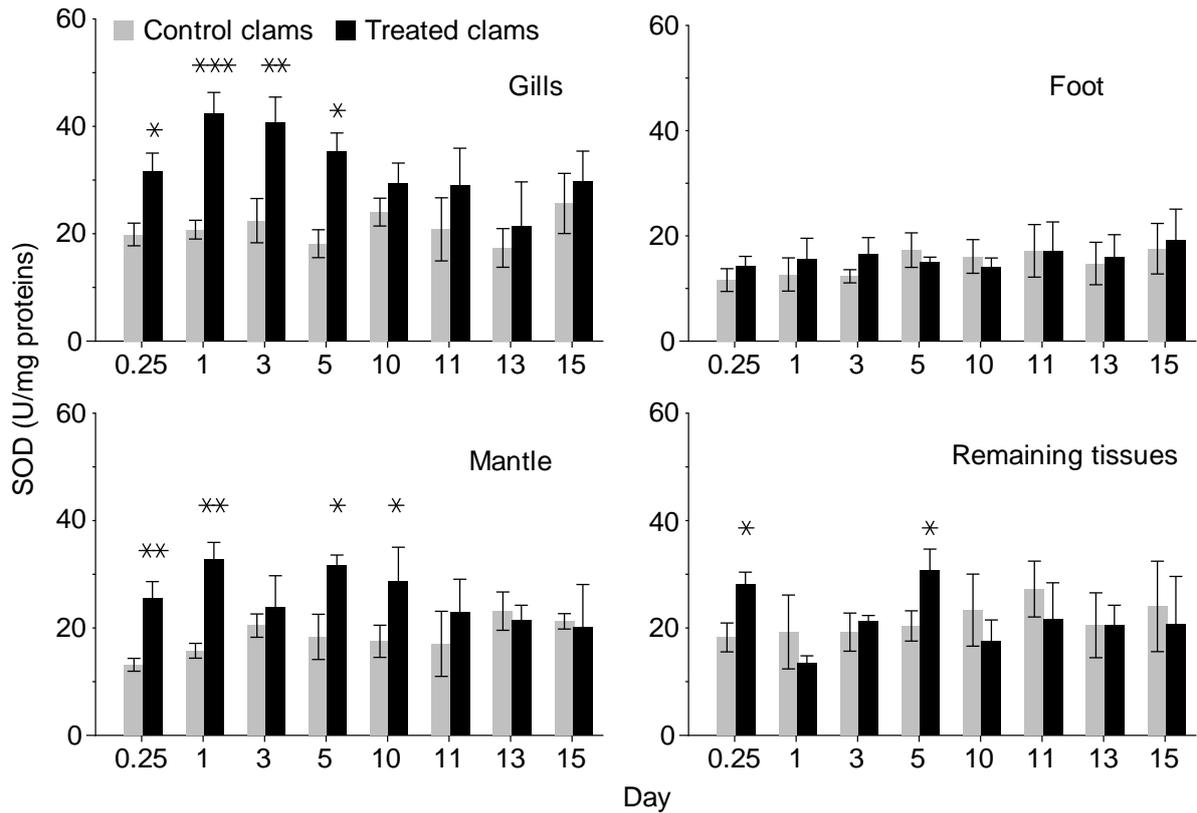


Figure 3–5. Production of the antioxidant enzyme superoxide dismutase (SOD) (U mg^{-1} proteins) in various tissues of *Corbicula leana* exposed to toxic cyanobacterial bloom crude extract. Asterisks indicate significant differences compared with controls at the respective time points (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$).

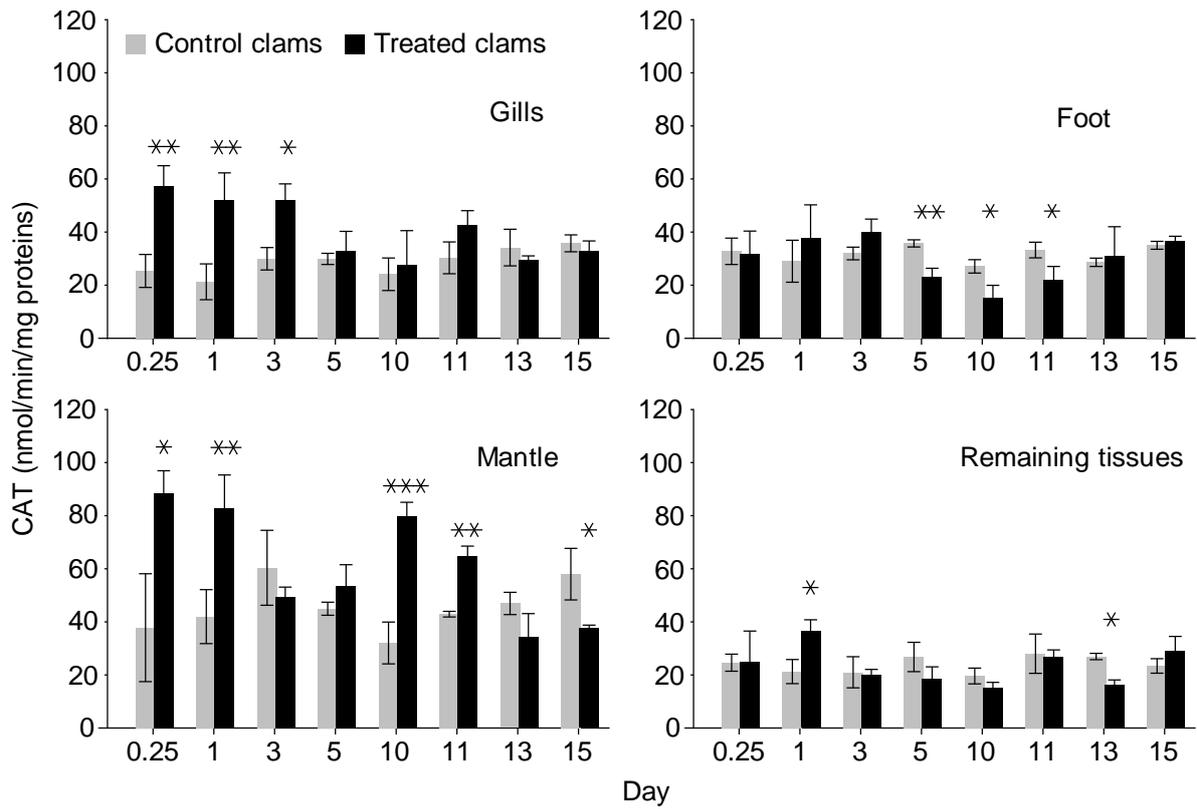


Figure 3-6. Production of the antioxidant enzyme catalase (CAT) ($\text{nmol min}^{-1} \text{mg}^{-1} \text{ proteins}$) in various tissues of *Corbicula leana* exposed to toxic cyanobacterial bloom crude extract. Asterisks indicate significant differences compared with controls at the respective time points (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$).

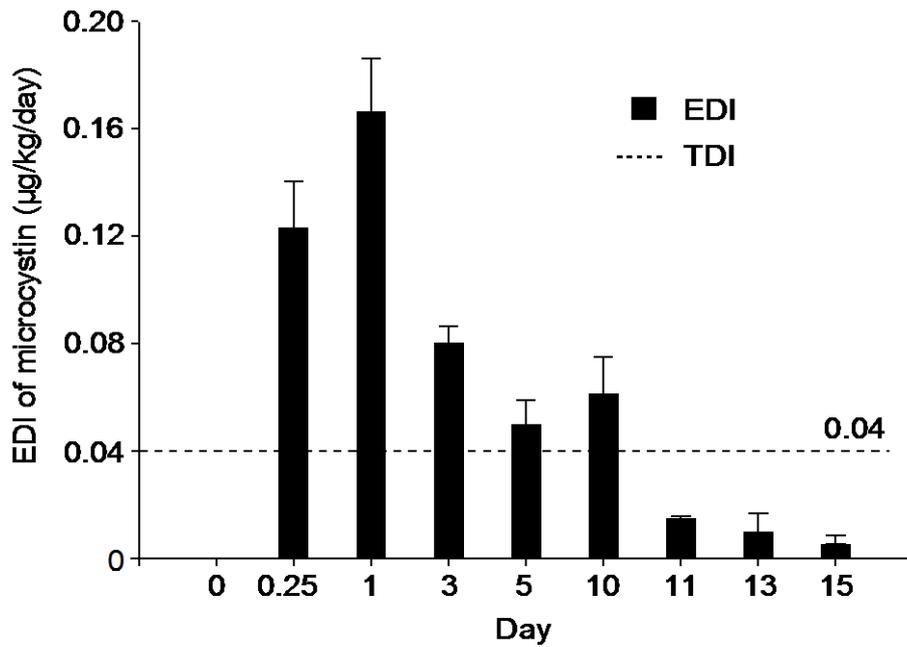


Figure 3–7. Estimated daily intake (EDI) of microcystin by a person (60 kg) consuming 300 g wet weight of *Corbicula leana* (Ibelings and Chorus, 2007). Horizontal line indicates the maximum tolerable daily intake (TDI) for humans ($0.04 \mu\text{g kg}^{-1}\text{day}^{-1}$), as proposed by the World Health Organization (WHO) (Chorus and Bartram, 1999).

Chapter 4

Accumulation and effects of toxic and non-toxic cyanobacteria on the edible clam

Corbicula leana

4.1. Introduction

Toxic cyanobacteria as well as MCs pronounce negative effects on aquatic animals, including zooplankton, fish, gastropods and bivalves (Amado and Monserrat, 2010; Paskerová *et al.*, 2012; Pavagadhi and Balasubramanian, 2013). In aquatic environment, animals may take up and accumulate cyanotoxins via the two main routes: From dissolved toxins via a transdermal route or ingestion via the in-take of toxic cyanobacterial cells (Ibelings and Chorus, 2007). High concentrations of cyanotoxins in water are likely to be short-lived due to a lysis of surface blooms. Thus, aquatic animal may be exposed to high dissolved MCs for short time periods. However, filter feeding organisms like mussels may directly graze on toxic cyanobacteria (Pires *et al.*, 2005). Previous studies have concluded that bivalves uptake of MCs via the food (ingestion) is the main route for accumulation (Yokoyama and Park, 2003).

In previous chapter, I reported the accumulation/depuration of free- and Co-MC, and potential adverse effects in *C. leana* via absorption/uptake caused by MC dissolved in ambient water column. In this chapter, I investigated the accumulation and elimination of free- and Co-MC in the same animal under laboratory experiments, but exposed to toxic and non-toxic cyanobacterial cells. An oral route of exposure was employed, in which clam (*C. leana*) was given a single oral dose of approximately $100 \mu\text{g L}^{-1}$ of MC-LR_{eq} via food supply (toxic *Microcystis*) for ten days, and then the clam was exposed to a non-toxic *Microcystis* for another 10 days. Moreover, I also performed a clearance rate (CR) experiment to test the hypothesis that whether *C. leana* filtered toxic and non-toxic *M. aeruginosa* and the green alga *C. vulgaris* at different rates. The MC concentrations (MC-RR, -YR and -LR) in the whole body of mussels and in incubation water were monitored during the experiment. In

addition, the changes of antioxidant enzymes CAT, SOD, and detoxification enzyme GST in various clam tissues (gills, foot, mantle and remaining tissues) were also examined. Finally, evidences for the clam's resistance to cyanotoxins were also discussed.

4.2. Materials and methods

4.2.1. Culture of toxic, non-toxic *Microcystis* and green alga

The toxic cyanobacterium *M. aeruginosa* (strain NIES-1086), non-toxic *M. aeruginosa* (strain NIES-101), and green alga *C. vulgaris* (strain NIES-2170) were ordered from the National Institute for Environmental Studies (NIES) collection (Tsukuba, Ibaraki, Japan). The toxic strain NIES-1086 produced MCs at a concentration of 15.21 fg cell⁻¹ as determined by HPLC. Toxic strain was cultured in MA medium and non-toxic strain in CB medium (Ichimura, 1979; Shirai *et al.*, 1989). The green alga was grown in SEM medium (Kong *et al.*, 2012). All culture was maintained at 24°C under a 12:12 light:dark photoperiod with white fluorescent lights at a PPFD of 30 μmol m⁻² s⁻¹. When the culture had reached the stationary phase, cells were harvested by centrifugation at 4,200 × g at 4°C for 30 min (Avanti HP-26XP, Beckman Coulter, Brea, CA, USA). Both cyanobacteria and green alga were cultured as single cells.

4.2.2. Collection and maintenance of clams

As described in the 3.2.1 section.

4.2.3. Clearance rate

The clearance rate (CR) experiment was performed to determine whether *C. leana* filtered toxic and non-toxic *M. aeruginosa* and the green alga *C. vulgaris* at different rates. Nine clams of the same shell size were gently scrubbed under tap water and allocated randomly to three groups of three. They were then incubated individually in 500-mL beakers with 300 mL of dechlorinated tap water, with constant aeration at a temperature of 22 ± 1°C

(Figure 4–1). Bakers with phytoplankton but no clam were used as controls. After 12 h of acclimation with no food, when each individual had its valves open, toxic *M. aeruginosa*, non-toxic *M. aeruginosa*, or *C. vulgaris* was added to the water to a final concentration of 2×10^6 cells mL⁻¹. This density is often found in water bodies (Davis *et al.*, 2009; Okello *et al.*, 2010; Sabart *et al.*, 2010). Water samples were taken at 1-h interval for 6 h. Cell density was estimated directly by using a Speirs-Levy Eosinophil counting slide under an Olympus light microscope, as described by Andersen (2005). CR, defined as the volume of water (mL) cleared with suspended particles per unit time (h) by each individual, was calculated according to the method of Coughlan (1969) as follows:

$$CR = \frac{V}{wt} \left(\ln \frac{C_o}{C_t} - \ln \frac{C'_o}{C'_t} \right)$$

In which *CR* is the clearance rate expressed in mL g⁻¹ wet weight (WW) h⁻¹. *V* is the water volume (300 mL), *w* is the whole body WW of the clam in gram, *t* is the duration course of the experiment in *h*, *C_o* is the cell density (cell L⁻¹) at *t* = 0 or one time step before *t* and *C_t* is the cell density at time *t*. *C'_o* is the cell density in the control baker at *t* = 0 and *C'_t* is the cell density at time *t*. The overall *CR* was calculated as the mean of the six consecutive measurements.

4.2.4. Feeding experiment

After acclimation, clams were placed in 8 aquariums (35 clams in each) containing 2 L of dechlorinated tap water and a 2-cm sand layer as a substrate, with constant aeration. Clams were allocated randomly to an exposure group and control group. Light intensity and water temperature were the same as previously described.

For MCs uptake, toxic *M. aeruginosa* cells were added to the aquarium to a final concentration of 100 µg MC-LR_{eq} L⁻¹ on days 0, 3, 5, and 7 of the uptake period which lasted for 10 days. This concentration of MC is often found in natural environment during blooms (Chorus and Bartram, 1999; Znachor *et al.*, 2006; Davis *et al.*, 2009). The clams were then

collected and relocated into aquariums containing dechlorinated tap water as a toxin-free water. They were kept in these aquariums for another 10 days as a depuration period. During the depuration, the toxic *M. aeruginosa* was completely replaced by non-toxic *M. aeruginosa* at a concentration of 6×10^6 cells mL⁻¹. The non-toxic *Microcystis* cells were completely renewed on days 0, 3, 5 and 7 of the depuration period, which corresponded to days 11, 13, 15, 17 and 20 of the experiment. The water was also completely replaced at the same times. The entire experiment therefore lasted for 20 days (10 days of exposure following by 10 days of depuration). The control group was incubated in dechlorinated tap water and fed three times a week with *C. vulgaris* at a concentration of 6×10^6 cells mL⁻¹. Dead clams were removed and counted daily.

On days 1, 3, 5, 7, and 10 (in the uptake period) and days 11, 13, 15, 17 and 20 (in the depuration period) I sampled randomly about 12 – 15 clams in assigned aquariums. For MC quantification 8 – 10 clams were rinsed gently under dechlorinated tap water. The shell was removed immediately and the remaining tissues were freeze-dried completely and kept at –30°C until MC extraction. Ten clams collected before the start of the experiment were used as controls. To measure enzyme activity, in both groups I first dissected the gills, foot, and mantle of three to five clams (pooled) and the remaining tissues (kept individually) on ice. The samples were immediately frozen in liquid nitrogen and stored at –80°C until enzyme extraction.

4.2.5. Extraction and analysis of MCs in incubation water

MCs (intracellular content) in the incubation water were monitored every day during uptake and on days 11, 13, 15, 17 and 20 in the depuration period. The incubation water (10 to 100 mL) was filtered through GF/C filters. The filters were then dried completely at 45°C and kept at –30°C. MCs extraction and analysis were performed as described in 2.2.5 section. The preliminary experiment showed that more than 99% of MCs concentration was

intracellular (data not shown). Therefore I ignored the extracellular MCs in the incubation water.

4.2.6. Extraction and analysis of free MC in clam

As previously described in the 3.2.5 section.

4.2.7. Extraction of total MC in clam

As previously described in the 3.2.6

4.2.8. GC-MS analysis

GC-MS analyses were performed on a GCMS-QP2010 Plus mass spectrometer linked to a GC-2010 gas chromatography system (Shimadzu, Kyoto, Japan) equipped with an Rxi-5ms column (30 m × 0.25 mm ID, phase thickness 0.25 mm; Restek, Bellefonte, PA, USA). Helium was used as the carrier gas, at a flow rate of 1.5 mL min⁻¹ in splitless mode. The program used for the analysis was 80°C for 1 min, followed by an increase to 280°C at 8°C min⁻¹. The other conditions were as follows: ion source temperature 200°C, injection port temperature 230°C, detector temperature 250°C and interface temperature 280°C. Methyl 4-PB (me4-PB) and meMMPB were detected by using SIM mode. Ions at 91 and 104 m/z were selected for me4-PB, and those at 75, 78, 91, 131, and 134 m/z were selected for meMMPB (Tsuji *et al.*, 2001; Suchy and Berry, 2012). GC-MS solution software was used for the quantitative calculation. Duplicate samples with duplicate analysis (yielded 4 measurements, n = 4) were used in this determination.

4.2.9. Enzyme extraction and measurement

As previously described in the 3.2.8 section.

4.2.10. Statistical analyses

As previously described in the 3.2.10 section.

4.3. Results

4.3.1. Clearance rate

In the control bakers the mean cell densities of all strains was almost constant over the course of the experiment. The CR of 2×10^6 cells mL⁻¹ of toxic *Microcystis* by *C. leana* was 16.0 ± 3.3 mL g⁻¹ WW h⁻¹; that of non-toxic *Microcystis* was 15.3 ± 3.2 mL g⁻¹ WW h⁻¹, and that of *C. vulgaris* was 7.0 ± 1.1 mL g⁻¹ WW h⁻¹ (Figure 4–2).

One-way ANOVA showed that the *Microcystis* CRs were significantly higher than that of green alga ($P < 0.03$). There was no significant different in CR between the toxic and non-toxic *Microcystis*. I observed that larger amount of pseudo-faeces were expelled in the bakers containing the toxic or non-toxic *Microcystis* than in the *C. vulgaris* beakers.

4.3.2. Microcystin concentrations in incubation water

Concentrations of MC in the control incubation water were under the detection limit (data not shown).

At the starting and renewal points, the concentrations of MC in the incubation water were 105 ± 4.7 µg MC-LR_{eq} L⁻¹. The MC concentrations in the incubation water slowly and continuously declined after each renewal. After 1 day the MC level had decreased to 96 ± 3.8 µg L⁻¹, after 2 days to 89 ± 4.1 µg L⁻¹, and after 3 days to 83 ± 1.5 µg L⁻¹ (Figure 4–3).

4.3.3. Uptake and depuration of free- and Co-MC

There were no deaths in the exposure or control groups during the experiments. The control samples contained no detectable MCs, whereas exposed clams showed substantially enhanced toxin accumulation. I monitored the changes in MC accumulation by the clams during the uptake and depuration periods (Figure 4–3). Typically, free MC concentrations rose rapidly after the start of exposure and peaked (at 12.7 ± 2.5 µg g⁻¹ DW) after about 3 days. The free MC content was relatively constant at the different time point during the uptake period. In contrast, the Co-MC concentration slowly increased during uptake period,

peaking at $4.2 \pm 0.6 \mu\text{g g}^{-1}$ DW on day 10. Free MC was quickly eliminated from the clam tissues in the depuration period and declined from 12.7 ± 2.5 to $5.7 \pm 0.3 \mu\text{g L}^{-1}$ after 24 h (day 11), then to $1.3 \pm 0.3 \mu\text{g L}^{-1}$ after 72 h (day 13). It was under the detection limit after 7 days of depuration, which corresponded to day 17 of the experiment. In contrast, Co-MC level was almost unchanged during the first 5 days of depuration. It then gradually declined but was still detectable at the end of the depuration period (Figure 4–3).

4.3.4. Biotransformation enzyme

I examined the effects of toxic and non-toxic *Microcystis* on GST activity in different organs in the exposure and control groups (Figure 4–4). Inhibition of GST activity in the gills was observed after exposure of the clam to toxic *Microcystis* for 5 days, and there was significant difference compared with the controls after 7 days and at the end of the experiment. A decrease in GST activity was also observed on days 10 and 15 in the foot and days 10 and 20 in the remaining tissues. In contrast, in the mantle, GST activity was significantly higher than in the controls on day 11, but there were no significant differences at other time points.

4.3.5. Antioxidant enzyme activities

I examined the effects of toxic and non-toxic cyanobacteria on SOD activity in the different clam tissues (Figure 4–5). In the gills, SOD activity was significant higher in the exposed clams than in the controls on days 5 and 10 (exposure period) and on days 11 and 15 (depuration period). There was also a significant elevation of SOD activity on days 1 and 5 in the foot and on days 10 and 17 in the mantle. However, SOD activity in the gills, foot and mantle eventually returned to control levels during exposure to non-toxic *Microcystis* at the end of the experiment (day 20). In the remaining tissues, SOD activity did not differ significantly from that in the controls, with the exception of a significant inhibition at the end of the experiment (day 20).

I examined changes in CAT activity in the different tissues (Figure 4–6). There were no definable trends. In the gills, CAT activity in the exposure group was significantly higher than in the controls on days 5, 7, and 15 but was significantly lower on day 20. Significant elevation of CAT activity in the exposure group was observed on day 13 in the foot and on days 5 and 11 in the mantle. In the remaining tissues there were no differences in CAT activity between the control and exposure groups over the course of the experiment.

4.4. Discussion

This study is the first to describe uptake and depuration in the edible clam *C. leana* grazing on toxic and non-toxic cyanobacteria *Microcystis* and on the green alga *C. vulgaris*. Although aquatic animals have been shown to select and ingest only non-toxic food in laboratory experiments (Zurawell *et al.*, 2005; Juhel *et al.*, 2006b), my results rejected the hypothesis that the clams would graze less efficiently on toxic strains than on non-toxic ones, because no significant difference in CRs was observed. My observations agreed well with the results of Pires and Donk (2002), Pires *et al.* (2005) and Gazulha *et al.* (2012) who reported no significant differences in CR between mussels grazing on toxic and on non-toxic *Microcystis*. The second hypothesis that clams would graze less efficiently on toxic strains than on green algae was rejected as well. In contrast, the clams had higher CRs on toxic *Microcystis* than on the green alga (Figure 4–2). I observed more pseudo-faeces were expelled by clams fed cyanobacteria than by those fed the green alga (data not shown); clams are able to sort captured material, ingesting the nutritious particles (*C. vulgaris*) and rejecting the unpalatable ones (*Microcystis*) as pseudo-faeces. Their pumping rates may therefore be enhanced when there is a relative abundance of unpalatable food. Similar observations have been reported by Pires *et al.* (2004) namely that mussels filter toxic *Microcystis* faster than the green algae *Nannochloropsis* and *Scenedesmus*. Efficient expulsion of toxic cells via pseudo-faeces has been described as a primary defense mechanism in zebra mussel *D. polymorpha*

when exposed to highly toxic cyanobacteria (Juhel *et al.*, 2006a). However, my observations contradict those of Pires *et al.* (2007) and Liu *et al.* (2009), in which the CR did not change significantly in the three mussels *Anodonta anatina*, *Dreissena polymorpha* and *Unio douglasiae* when they were provided with varying concentrations of cyanobacteria and green algae. Differently, Gazulha *et al.* (2012) reported that highest filtration rates of the golden mussel *Limnoperna fortunei* were registered when mussels fed on diatom *Nitzschia* instead of *Microcystis*. Possibly, CR may depend not only on the food type (including the MC content) and the mussel species but also the food concentration and physical parameters such as temperature, salinity, pH, and season (Riisgård *et al.*, 2003; Bontés *et al.*, 2007; Naddafi *et al.*, 2007; Pestana *et al.*, 2009; Hwang *et al.*, 2010; Riisgård *et al.*, 2011). My results supported that the CR is even higher in case of bloom occurred with one species of *Microcystis*. This characteristic indicated that mussels are capable of removing cyanobacteria from water, regardless of whether the cyanobacteria are toxic or not. Hence, mussels may be used as a biofilter for mitigating harmful CYBs in eutrophic shallow lakes.

Field and experimental studies have reported the accumulation and distribution of MCs in different bivalve species fed on toxic cyanobacteria cells or exposed to purified MCs. Commonly, the highest MC content is found in the hepatopancreas (Prepas *et al.*, 1997; Yokoyama and Park, 2003; Pires *et al.*, 2004; Chen and Xie, 2005a; Chen *et al.*, 2005; Chen and Xie, 2007; Contardo-Jara *et al.*, 2009; Fernandes *et al.*, 2009; Sabatini *et al.*, 2011). Despite intensive studies, the accumulation and distribution of free MC and Co-MC in bivalve gavaged with toxic cyanobacteria at environmentally relevant concentrations are not yet fully understood. My laboratory experiments revealed that free MC was accumulated by *C. leana* by 1 day after the start of exposure. The peak levels of free MC measured in *C. leana* (12.7 $\mu\text{g g}^{-1}$ DW) were similar to the MC concentration measured in the zebra mussel *D. polymorpha* (11 $\mu\text{g g}^{-1}$ DW; Pires *et al.*, 2004), and the freshwater mussel *Mytilus galloprovincialis* (10.5 $\mu\text{g g}^{-1}$ DW; Vasconcelos, 1995) during laboratory exposure. However,

even when data on accumulation in other bivalves are available (Watanabe *et al.*, 1997; Yokoyama and Park, 2003; Chen and Xie, 2005a; Vareli *et al.*, 2012) they are not suitable for comparison with mine, because most were obtained from measurement in individual tissues and not the whole body. In general, MC accumulation in aquatic animals is likely to be affected by a number of factors, such as the exposure route, exposure duration and exposure dose, target tissues as well as by the mussel species (Galanti *et al.*, 2013). Thus, laboratory studies, using different approaches, can contribute to understand the dynamic of cyanotoxins accumulation.

Because of the difficulties of extracting covalently linked MC, analysis of MCs in animal tissues has until now been limited to quantification of the free MC content (for reviews see Ibelings and Chorus, 2007; Martins and Vasconcelos, 2009; Ferrão-Filho and Kozłowski-Suzuki, 2011). By using an oxidation procedure adapted from previously developed methods (Tsuji *et al.*, 2001; Neffling *et al.*, 2010; Suchy and Berry, 2012; Cadel-Six *et al.*, 2014) I were able to detect Co-MC in *C. leana* tissues (Figure 4–3). On average, 3.2% (the number was calculated from mean percentages of the Co-MC contents from the MC concentrations in incubation water on days 1, 3, 5, 7 and 10) of total MC was bound in *C. leana* during the 10-day exposure period (data not shown). The existence of high content of Co-MC has been reported in several organisms such as fish (Williams *et al.*, 1997a; Suchy and Berry, 2012; Cadel-Six *et al.*, 2014), gastropods (Lance *et al.*, 2010; 2014) and mussels (Williams *et al.*, 1997b; Pires *et al.*, 2004).

Fortunately, my observations showed that clams rapidly eliminated the free MC content within several days when culture in toxin-free water, this has been reported elsewhere (Prepas *et al.*, 1997; Williams *et al.*, 1997b). Immediate uptake and rapid release of MCs were also observed in *D. polymorpha* (Pires *et al.*, 2004; Contardo-Jara *et al.*, 2008), and in *M. galloprovincialis* (Amorim and Vasconcelos, 1999). In contrast, the rate of elimination of Co-MC in *C. leana* was lower than that of free MC, and the clam's tissues still contained a

detectable amount of Co-MC after 10 days in toxin-free water. Therefore, to accurately assess the risks to humans, Co-MC in edible aquatic animals need to be quantified. Meanwhile, their toxicity and potential transfer to higher trophic levels remain unknown.

Freshwater mussels are among the most numerous macro-invertebrates in the world's streams, rivers, ponds, and lakes (Byrne *et al.*, 2000), where cyanobacteria frequently bloom. Consumption of bivalve mollusks is a potential route of human exposure to hepatotoxic MCs, especially in the case of mollusks harvested from lakes and reservoirs that routinely experience toxic CYBs (Chen and Xie, 2007; Song *et al.*, 2007; Funari and Testai, 2008; Dyble *et al.*, 2011; Mulvenna *et al.*, 2012; Cheung *et al.*, 2013). In this study, I used a linear equation $y = 0.0116x$ ($r^2 = 0.94$, $n = 30$), to convert the clam's whole-body wet weight to dry weight. Assuming that a 60-kg person consumes 100 g WW (~1.16 g DW) of the clam per day (Ibelings and Chorus, 2007), the maximum EDI during the accumulation period would be more than seven times the TDI guideline value (Figure 4–7), suggesting that *C. leana* poses high risks to human consumers. Consumption of this clam should be limited when there are high concentrations of toxic cyanobacteria present in the water from which it is harvested. My estimation was made for a healthy adult, and the risks for children, the elderly and sensitive individuals are likely to be higher.

Detoxification of MCs by aquatic animals occurs first via conjugation to GSH, a reaction catalyzed by GSTs (Kondo *et al.*, 1992; Pflugmacher *et al.*, 1998; Zhang *et al.*, 2012; Li *et al.*, 2014). Nevertheless, the responses of GST activity to MCs in mussels and other aquatic animals are variable (Vasconcelos *et al.*, 2007; Amado and Monserrat, 2010; Gélinas *et al.*, 2012; Paskerová *et al.*, 2012). It appears that the exposure time, route, composition of MCs, and target tissues all influence the GST response after exposure to MCs or toxic cyanobacteria. An increase in the activity of these enzymes can arise from an activation of existing enzymes or from de novo enzyme synthesis, whereas a decreased activity can be sign of saturation due to substrate inhibition caused by the presence of high toxin concentration

(Cazenave *et al.*, 2006; Hao *et al.*, 2008; Burmester *et al.*, 2012). Inhibition of GST activity has been observed in the mussel *U. tumidus* exposed to MC-LR or CCE (Burmester *et al.*, 2012). Similar results have been reported in the gills of the freshwater mussel *D. polymorpha* after exposure to MC-LR at $100 \mu\text{g L}^{-1}$ for 1 h; the highest MC content in whole mussel tissue was detected at this time point (Contardo-Jara *et al.*, 2008). In this study, I found significant inhibition of GST activity after 7 days of exposure in the gills and at two time points in the foot, but there was no inhibition in the mantle. This response of the detoxification system was synchronous with the increase in the rate of MC accumulation by the clam (Figures 4–3 and 4–4). Depression of GST activity may result from inhibition of GST synthesis as a result of the high levels of accumulation of MCs during the exposure period (Hao *et al.*, 2008; Li *et al.*, 2008). In contrast, Vasconcelos *et al.* (2007) and Fernandes *et al.* (2009) reported increase of GST activity in gills of the blue mussel (*M. galloprovincialis*) after exposure to toxic *Microcystis* for 24 h or 2 weeks. Increase of GST activity was also observed in the freshwater clam *D. chilensis patagonicus* after exposure to toxic *Microcystis* for 6 weeks (Sabatini *et al.*, 2011). Out of mussel group, Gavrilović *et al.* (2014) reported that GST activity in the gills of three cyprinids fish, *Rutilus rutilus* (roach), *Blicca bjoerkna* (white bream), and *Carassius gibelio* (Prussian carp), was inhibited during a CYB with high concentration of MCs. The same observations have been reported in the gills of zebrafish (*Danio rerio*) upon sub-chronic exposure to MC-LR (Chen *et al.*, 2012) and in the liver, gills, intestine, and brain of the catfish *Corydoras paleatus* exposed to dissolved MC-RR at concentrations from 0.5 to $10 \mu\text{g L}^{-1}$ for 24 h (Cazenave *et al.*, 2006). In another study (Cazenave *et al.*, 2008) observed an increase of GST activity in liver and brain of one-sided livebearer (*Jenynsia multidentata*) exposed to MC-LR at $1 \mu\text{g g}^{-1}$ but decreased when exposed to MC-LR at $0.1 \mu\text{g g}^{-1}$ for 24 h. On the contrary, the GST in zebra fish (*Danio rerio*) and tilapia fish (*Oreochromis* sp.) remained stable after exposure (Best *et al.*, 2002; Atencio *et al.*, 2009). Probably, CYBs or MCs, or both, can inhibit GST activity in a range of aquatic animals.

Toxic cyanobacteria and MCs could alter antioxidant systems and induce ROS production, resulting in the oxidative stress that has been well documented in aquatic species (Prieto *et al.*, 2007; Leão *et al.*, 2008; Amado and Monserrat, 2010; Chen *et al.*, 2012; Jiang *et al.*, 2012; Paskerová *et al.*, 2012; Sun *et al.*, 2013; Gavrilović *et al.*, 2014). SOD, CAT, and other molecules such as lipoic and dihydrolipoic acid are an essential components of antioxidative defense systems (Lushchak, 2011; Amado and Monserrat, 2010), and increase SOD and CAT activities in animal tissues plays an important role in eliminating excessive ROS (Li *et al.*, 2003; Jos *et al.*, 2005; Zhang *et al.*, 2013). In a recent study, Burmester *et al.* (2012) reported that SOD activity in *D. polymorpha* was elevated in most mussel tissues after exposure to MC-LR or CCE, or both, but CAT activity was barely affected. Increased SOD and CAT activities have been observed in the freshwater clam *D. chilensis patagonicus*, but only at 5 and 6 weeks after exposure to toxic *Microcystis* (Sabatini *et al.*, 2011). I found here that SOD and CAT activities in *C. leana* were elevated only at some points and in some tissues during the exposure and depuration periods (Figures 4–5 and 4–6). My results were partly in line with those of Burmester *et al.* (2012), who observed that SOD in *U. tumidus* was slightly induced during 7 days exposure to MC-LR or CCE, or both. Similar response of SOD activity was reported in *U. tumidus* after exposure to aquatic contaminations in the Fensch River for 15 and 30 days (Cossu *et al.*, 1997). In contrast, studies performed on crustaceans such as shrimp (*Palaemonetes argentinus*), on tilapia fish (*Oreochromis* sp.), on bighead carp (*Aristichthys nobilis*), and on loach (*Misgurnus mizolepis*) given intraperitoneal MC-LR injections or exposed to toxic cyanobacteria have shown significant elevations of antioxidant enzymes, especially in the liver (Li *et al.*, 2005; Prieto *et al.*, 2006; Li *et al.*, 2010; Galanti *et al.*, 2013). Probably, SOD and CAT play key roles in scavenging free radicals and ROS in fishes but play minor roles in mussels.

Although no MCs were present in the incubation water during the depuration period, SOD, CAT, and GST activities were still induced by the non-toxic *Microcystis*. This is

evidence that both toxic and non-toxic *Microcystis* cause oxidative stress in the clam and that MCs are not the only, or even the main, toxic compounds in cyanobacteria. Probably, other components of the complex cyanobacteria biomass contribute to this oxidative stress. However, these adverse effects are only temporary in the case of both toxic and non-toxic *Microcystis*, and prolonged exposure may lead to adaptation. I found here that although enzyme activity was induced it returned to control levels at later time points. In other words, clams are temporarily affected by toxic and non-toxic cyanobacteria. This resistance may occur because of an ability to efficiently expel toxic cyanobacteria cells without metabolising them (Fernandes *et al.*, 2009; Burmester *et al.*, 2012). In addition, recent evidence indicates that MXR mechanisms represent a general biological defense of many marine and freshwater mussels against environmental toxicants (Eufemia and Epel, 2000; Achard *et al.*, 2004; Contardo-Jara *et al.*, 2008; Faria *et al.*, 2011). Animal cells can trigger an MXR mechanism that serves as an efflux transporter against a broad spectrum of natural and man-made toxicants under stress conditions. This mechanism needs further investigation in *C. leana*.

4.5. Summary

In this chapter the accumulation and toxicity of toxic and non-toxic *Microcystis* in the edible clam *C. leana* were investigated. Treated clams were exposed to toxic *Microcystis* at 100 µg of MC (microcystin)-LR_{eq} L⁻¹ for 10 days. The experimental organism was then placed in toxin-free water and fed on non-toxic *Microcystis* for the following 10 days for depuration. CRs by *C. leana* of toxic and non-toxic *Microcystis* and of the green alga *Chlorella vulgaris* as a control were estimated. Toxic effects were evaluated through the activity of CAT, SOD and GST. Clam accumulated MCs (up to 12.7 ± 2.5 µg g⁻¹ DW of free- and 4.2 ± 0.6 µg g⁻¹ DW of Co-MC). My results suggest that although both toxic and non-toxic cyanobacteria caused oxidative stress by inducing the detoxification and antioxidant

defense system, the clam was quite resistant to cyanotoxins. The estimated MC concentration in *C. leana* was far beyond the WHO's provisional TDI ($0.04 \mu\text{g kg}^{-1} \text{ day}^{-1}$), suggesting that consuming clams harvested during cyanobacterial blooms carries a high health risk.

My experiments confirmed the transient bioaccumulation of free MC and Co-MC in *C. leana* after exposure to toxic cyanobacteria. Although free-MC was partially eliminated from the clams after transferring to MC-free water, the Co-MC would have still been contaminated in their tissues. Both toxic and non-toxic *Microcystis* caused oxidative stress, as shown by the induction of antioxidant and detoxification systems. However, my laboratory experiments suggested that GST activity did not play a major role in the elimination of MC. The clam may be able to efficiently expel toxic cyanobacteria cells or eliminate cyanotoxins without metabolising them. Alternative mechanisms, such as MXR, could be responsible for MC removal and resistance during exposure. These mechanisms need to be studied further.



Figure 4-1. Clearance rate experiment.

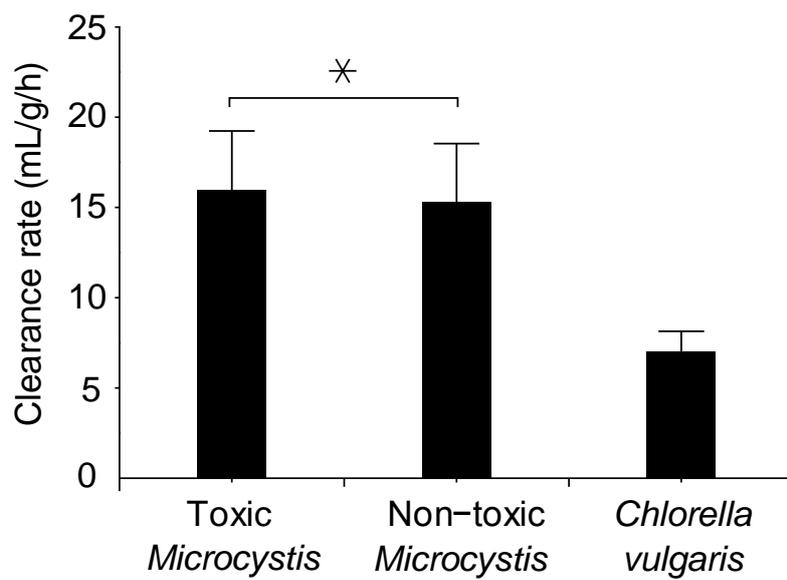


Figure 4–2. Mean (\pm SD) clearance rates (CRs) (in mL g⁻¹ wet weight h⁻¹ over 6 h) after feeding of *Corbicula leana* with toxic *Microcystis* (NIES-1086), non-toxic *Microcystis* (NIES-101), or the green alga *Chlorella vulgaris* (NIES-2170). Asterisk indicates significant difference ($P < 0.05$).

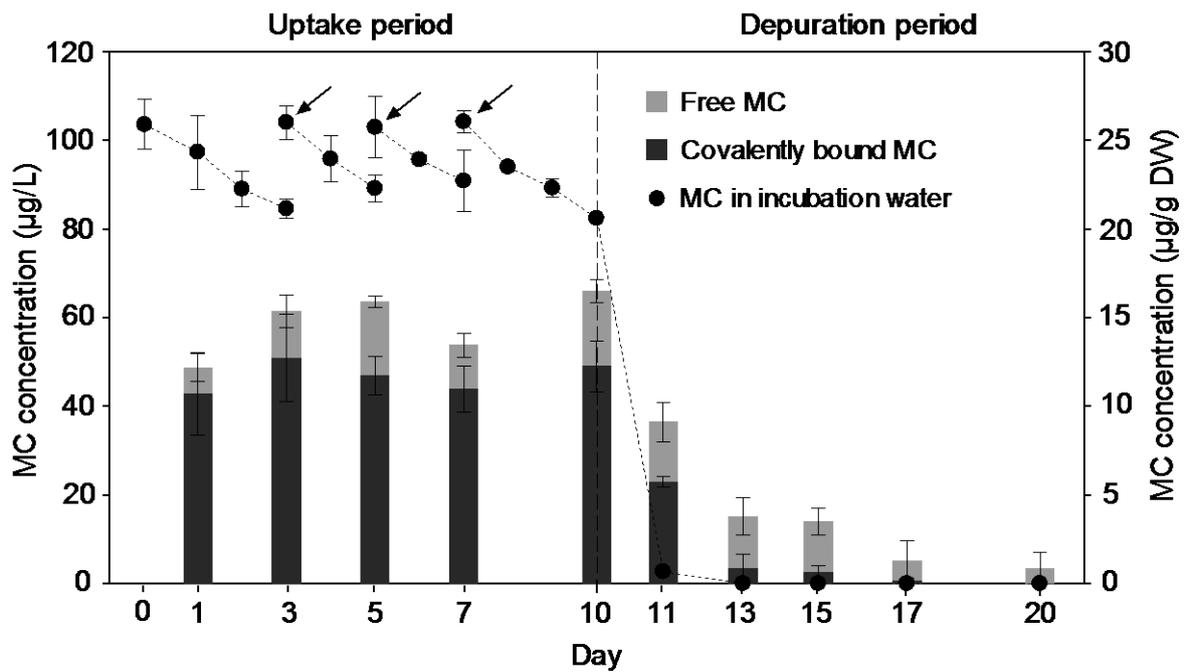


Figure 4-3. Concentrations of microcystin (MC) in incubation water, of free MC, and covalently bound MC accumulated in clams during the uptake and depuration periods. Arrows indicate points at which the MC and the water were renewed during the uptake period.

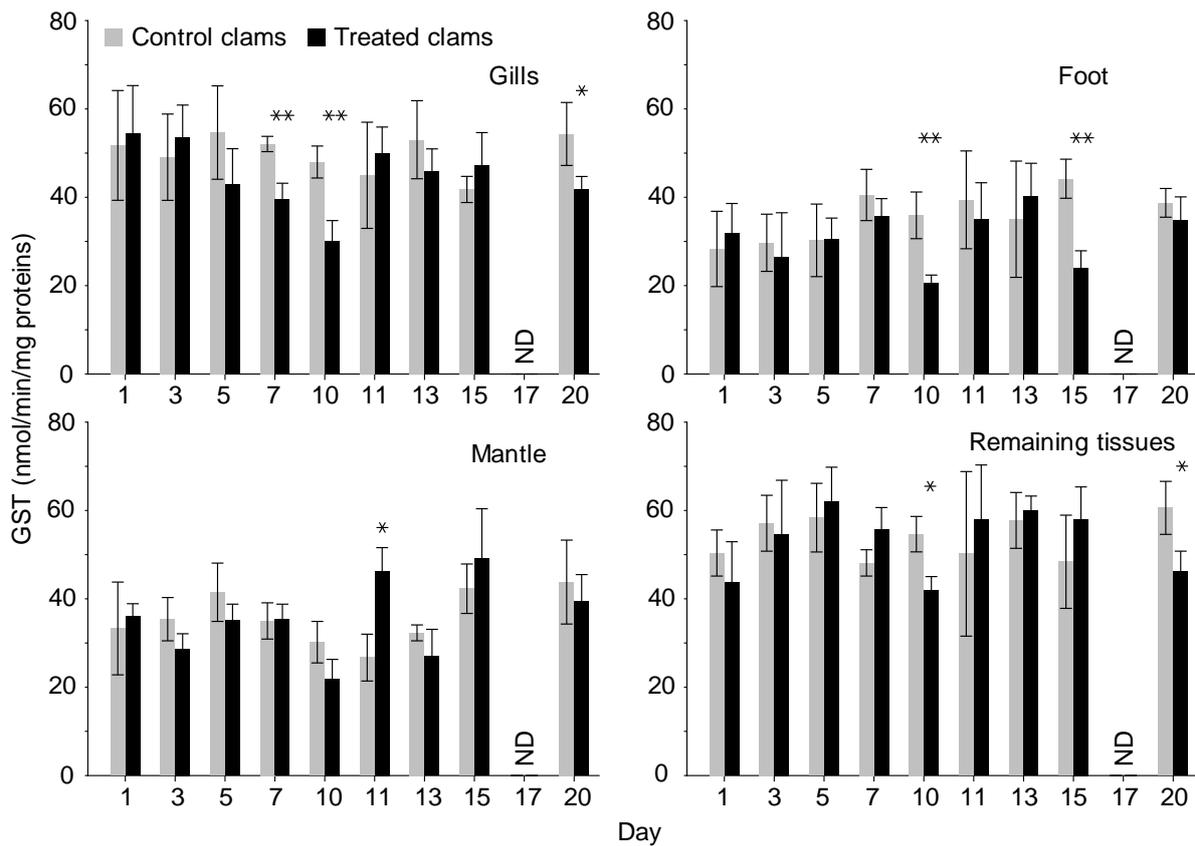


Figure 4-4. Changes in glutathione *S*-transferase (GST) activity (nmol min⁻¹ mg⁻¹ protein) in various tissues of clams fed with toxic *Microcystis* (days 0 to 10) or non-toxic *Microcystis* (days 11 to 20). Asterisks indicate significant differences compared with controls (fed with *Chlorella vulgaris*) at the respective time points (**P* < 0.05, ***P* < 0.01). ND: not detected.

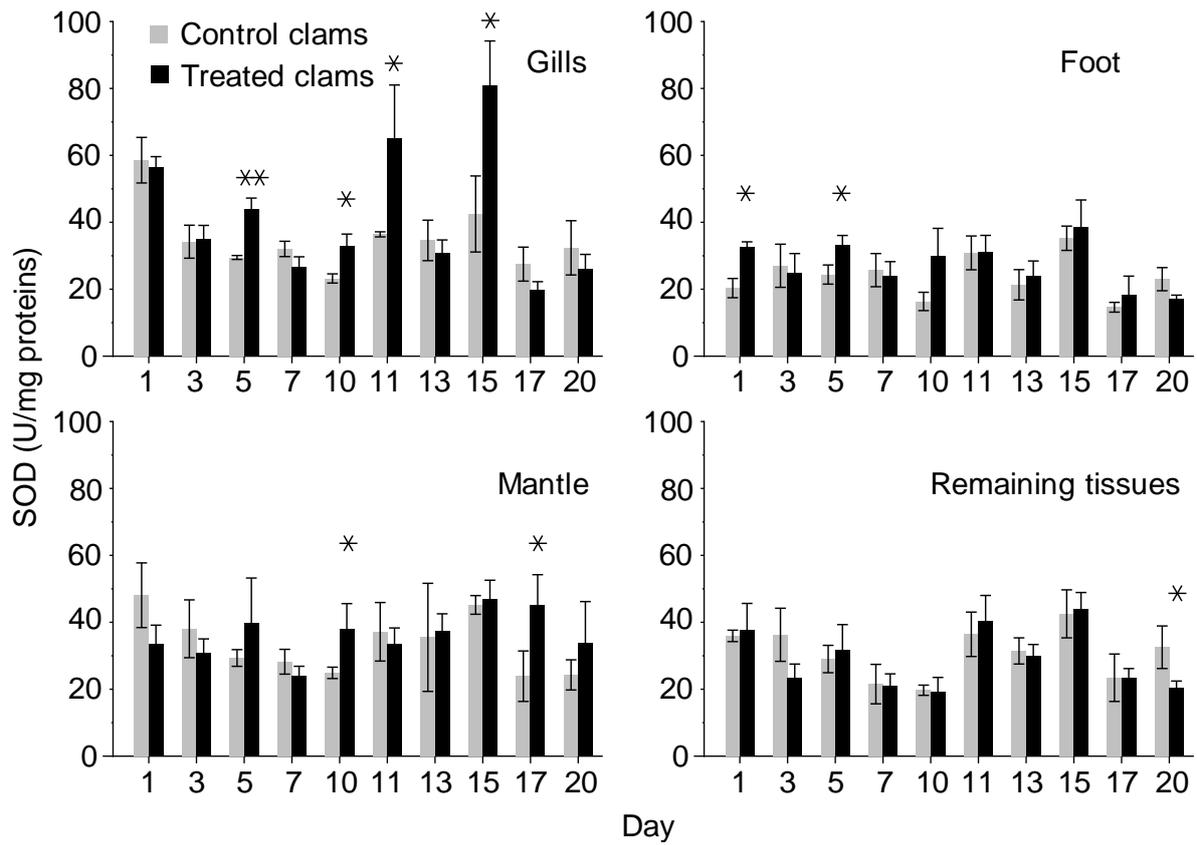


Figure 4–5. Changes in superoxide dismutase (SOD) activity (U mg^{-1} proteins) in various tissues of clams fed with toxic *Microcystis* (days 0 to 10) or non-toxic *Microcystis* (days 11 to 20). Asterisks indicate significant differences compared with controls (fed with *Chlorella vulgaris*) at the respective time points (* $P < 0.05$, ** $P < 0.01$).

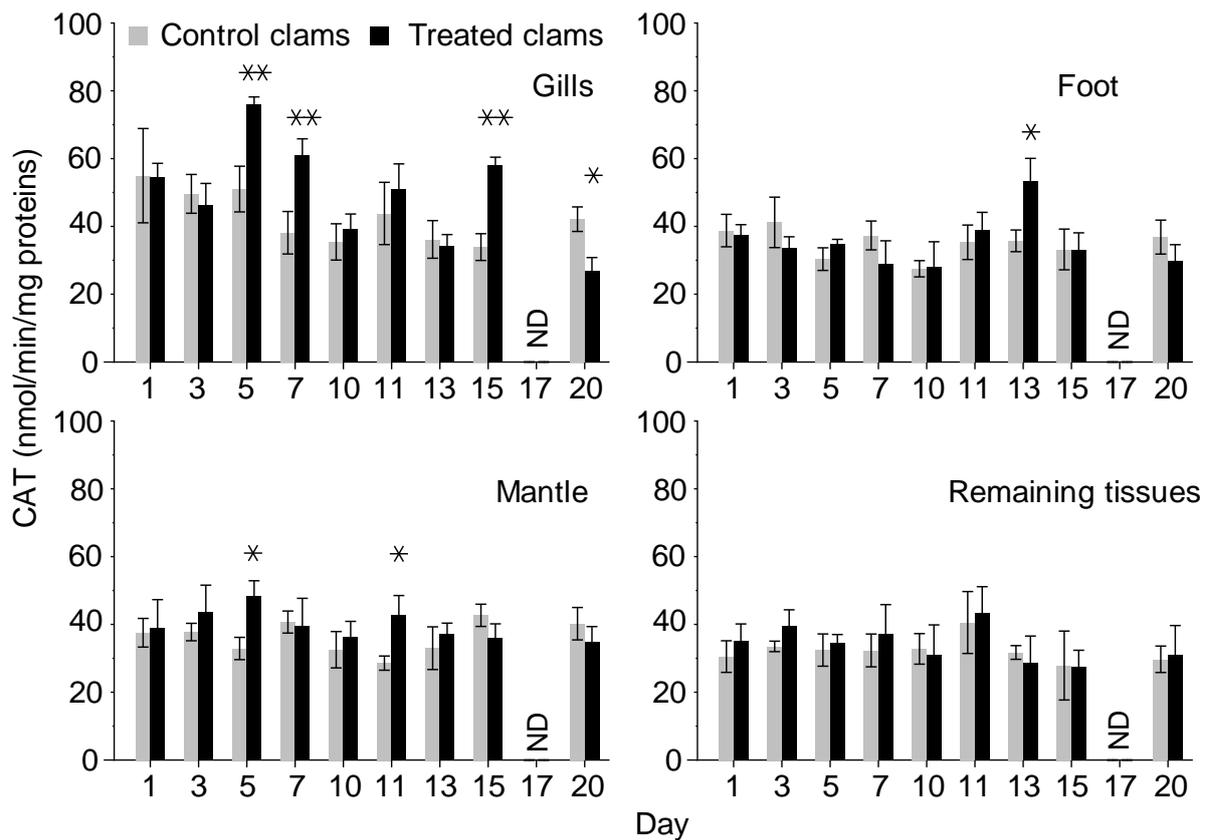


Figure 4–6. Changes in catalase (CAT) activity ($\text{nmol min}^{-1} \text{mg}^{-1} \text{protein}$) in various tissues of clams fed with toxic *Microcystis* (days 0 to 10) or non-toxic *Microcystis* (days 11 to 20). Asterisks indicate significant differences compared with controls (fed with *Chlorella vulgaris*) at the respective time points (* $P < 0.05$, ** $P < 0.01$). ND: not detected.

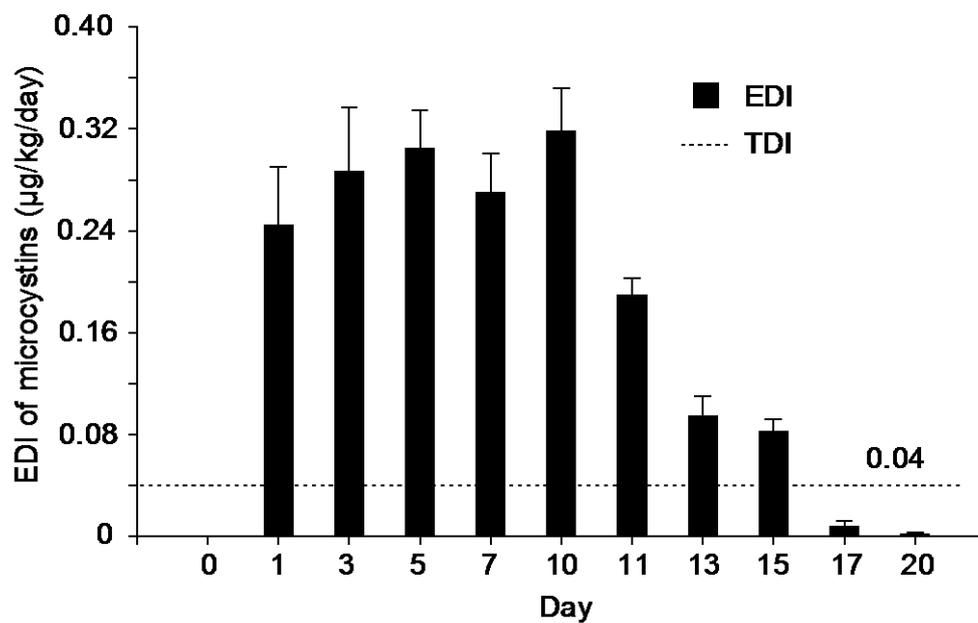


Figure 4–7. Estimated daily intake (EDI) of microcystins by a person (60 kg) consuming 100 g of clam wet weight per day (Ibelings and Chorus, 2007). Horizontal line indicates the maximum tolerable daily intake (TDI) of $0.04 \mu\text{g kg}^{-1} \text{day}^{-1}$, as proposed by the World Health Organization (WHO) (Chorus and Bartram, 1999).

Chapter 5

General conclusions and recommendations

5.1. Conclusions

Toxic CYBs and their toxins are a global threat to human health and aquatic biota. MCs are the most common cyanotoxins and can be produced wherever blooms of cyanobacteria occur in surface water. The worldwide occurrence of MC-producing blooms mainly dominated by *M. aeruginosa* strains is well established, although other species of *Microcystis* and of other genera such as *Dolichospermum*, *Arthrospira* and *Cylindrospermopsis* may co-dominate with *Microcystis*. Blooms of *Microcystis* are also the most common recorded in Vietnamese waters.

Cyanotoxins cause adverse effects on aquatic animals. Freshwater mussels are a fascinating group of animals that reside in the bottom of streams, rivers, and lakes. They play an important role in natural ecosystems by taking up phytoplankton, filtering organic matter and suspended particles from the water column and providing food for many types of fish and aquatic mammals. These filter feeders inhabit the littoral areas where cyanobacteria frequently form scums. They therefore are among the most threatened group of aquatic animals during CYBs or after blooms decay. This study reveals that MCs can be accumulated in the edible clam *C. leana* via both ingestion of toxic cells and/or via uptake of MCs dissolved in water column. MCs can be accumulated in the animal up to thousands ng g^{-1} DW but the actual concentration of MC accumulated may depend on the levels of MC dissolved in water column or in food seston, routes and time of exposure as well as target organs and species. It may be possible to correlate the toxin level in mussels with levels in the water column. MCs not only accumulated under unbound forms (free forms) but also covalently bound to PPs. However, the clam could metabolize effectively and/or eliminate MCs. Free MC was completely eliminated within a few days, whereas the elimination of Co-MC last for

weeks. Results on the presence of Co-MC in bivalve tissues illustrate the necessity to consider the total of MC content (free- and Co-MC) when assess the toxicity in aquatic animals and human health.

Toxic, non-toxic cyanobacteria as well as CCE containing MCs stimulated the detoxification and antioxidant enzymes in the mussel. CCE induced these systems to a greater extent but less bioaccumulation than the intact cells. Exposure of the mussel to natural CCE containing MCs caused significant changes in levels and activities of these enzymes, while exposure to toxic intact cells caused minor changes of these enzymes. These changes could potentially lead to chronic toxic effects on the clam. In addition, both toxic and non-toxic cyanobacterium caused oxidative stress in bivalves and that MCs are not the only, or even the main, toxic compounds in cyanobacteria. Probably, other components of the complex cyanobacteria biomass contribute to this oxidative stress. However, toxic effects are only temporary in all cases and that prolonged exposure may lead to the adaptations to cope with deleterious effects. Effectively eliminate free MC and adaptation in detoxification and antioxidant systems are evidences that there is an adaptive response in the detoxification system and possible tolerance of *C. leana* with continuous exposure to high levels of toxic cyanobacteria or to aqueous extract containing MCs.

Results of this study suggested that toxic, non-toxic cyanobacteria as well as CCE cause increasing of ROS contents in clam tissues leading oxidative stress, at the same time, the animal would both improve their antioxidant abilities and metabolize the toxin to overcome these adverse effects. It is likely that GST is not the only one involved in the elimination of MCs in clam. Other alternative mechanisms, like MXR could be responsible for partly MCs removal in clam tissues.

Humans are potentially exposed to harmful algal blooms from contact with toxic algal blooms via recreational activities, via oral uptake by drinking contaminated water or via ingestion food contaminated with cyanotoxins. This study reveals MCs from water or toxic

Microcystis cells, or both, can accumulate in edible clam *C. leana*. Moreover, my findings clearly demonstrate that consumption of the clam contaminated with MC poses a serious health risk for consumers. Cyanotoxins concentrations accumulated in bivalve were often highest during bloom period, which often occurs during summer or after cells lyse at the end of the blooms. Therefore, consumption risks may be reduced or avoided if the local government adjusts harvesting time. Additionally, bioaccumulation of cyanotoxins is expected to be higher in the tropics and may be transported to higher trophic levels; humans might be at high risks, especially in undeveloped countries where the control of toxins in food and in water supply is not well regulated.

5.2. Recommendations

In order to reduce the risk in humans and animals exposure to cyanobacterial toxins, it is necessary to have on-going monitoring of both CYBs and their toxins in surface water bodies. More studies on the impact of CYBs and their toxins in tropical regions should be carried out, since the incidence and persistence of these blooms are greater than that in temperate regions. Blooms of cyanobacteria in surface waters need to be regularly monitored due to their potential toxicity. Water treatment for removing cyanotoxins in drinking water is also important to mitigate effects from CYBs. Hence, more efficient and affordable on monitoring strategies and drinking water treatment should be developed to address these concerns.

It is important to predict the presence and occurrence of potential CYBs in water bodies. Although cyanotoxins and their toxicity have been well documented, predicting the occurrence of CYBs remains challenging. Climate change has been promoting the frequency and magnifying of blooms and altering toxin distribution to latitudes outside of their current range. Hence, future research should address on prediction the impact of climate change on bloom occurrence and challenge to mitigate the effects from CYBs.

The majority of studies in freshwater systems have focused only on MCs and other cyanotoxins has not been investigated to the same extent. It is likely that other cyanotoxins (e.g. anatoxins, saxitoxins, cylindropermopsin) have been presented in CYB waters, and these toxins should also be characterized in both water and aquatic animals. Also, special attention should be paid to other metabolites of cyanobacteria such as microviridins, micropeptins, oscillapeptins, lipopolysaccharides and β -Methylamino-L-alanine (BMAA).

Cyanotoxin concentrations should be characterized in all levels of the food web in order to gain further insight into the trophic transfer of cyanotoxins (particularly through the analysis of non-fish food web components). In addition, attention to the covalent complex MC bound to PPs, its toxicity and bioavailability for the next trophic level still require to be elucidated.

In particular, it remains unknown whether the resistance of bivalves to MCs may be a result of a higher efficiency in detoxification systems or to a decrease in uptake of MCs by the efflux systems, or both. Additional research is needed with respect to the insensitivity of bivalves toward MCs in natural aquatic environments. Studies are needed to investigate the MXR mechanism in bivalves that serves as a driver against a broad spectrum of natural and man-made toxicants in the cells. In aquatic ecosystems, it is likely that aquatic organisms are simultaneously exposed to multiple stresses not only natural toxins but also anthropogenic pollutants. Characterization of single and combine effects of these toxicants on aquatic animals under relevant condition are also necessary in future research.

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