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## Cell free *Microcystis aeruginosa* spent medium affects *Daphnia magna* survival and stress response

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### Abstract :

Primary consumers in freshwater ecosystems, such as the zooplankton organism *Daphnia magna*, are highly affected by cyanobacteria, both as they may use it as a food source but also by cyanobacterial metabolites present in the water. Here, we investigate the impacts of cyanobacterial metabolites focussing on the environmental realistic scenario of the naturally released mixture without crushing cyanobacterial cells or their uptake as food. Therefore, *D. magna* were exposed to two concentrations of cell free cyanobacterial spent medium from *Microcystis aeruginosa* PCC 7806 to represent higher and lower ecologically-relevant concentrations of cyanobacterial metabolites. Including microcystin-LR, 11 metabolites have been detected of which 5 were quantified. Hypothesising concentration and time dependent negative impact, survival, gene expression marking digestion and metabolism, oxidative stress response, cell cycle and molting as well as activities of detoxification and antioxidant enzymes were followed for 7 days. *D. magna* suffered from oxidative stress as both catalase and glutathione S-transferase enzyme activities significantly decreased, suggesting enzyme exhaustibility after 3 and 7 days. Moreover, gene-expressions of the 4 stress markers (glutathione S-transferase, glutathione peroxidase, catalase and thioredoxin) were merely downregulated after 7 days of exposure. Energy allocation (expression of Glyceraldehyde-3-phosphate dehydrogenase) was increased after 3 days but decreased as well after 7 days exposure. Cell cycle was impacted time dependently but differently by the two concentrations, along with an increasing downregulation of myosin heavy chain responsible for cell arrangement and muscular movements. Deregulation of nuclear hormone receptor genes indicate that *D. magna* hormonal steering including molting seemed impaired despite no detection of microviridin J in the extracts. As a consequence of all those responses and presumably of more than investigated molecular and physiological changes, *D. magna* survival was impaired over time, in a concentration dependent manner. Our results confirm that besides microcystin-LR, other secondary metabolites contribute to negative impact on *D. magna* survival and stress response.

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## Highlights

► Cell free *M. aeruginosa* spent medium affected *Daphnia* survival and physiology ► Medium with higher concentration of cyanobacterial metabolites was more detrimental ► Other secondary metabolites, besides microcystin-LR highly likely had negative impact on *Daphnia*

**Keywords** : zooplankton, cyanobacteria, secondary metabolites, PCC7806, oxidative stress, transcriptomics

**44 Abbreviations**

45 MC-LR: microcystin-LR

46 des-MC-LR: des-microcystin-LR

47 CP: cyanopeptolin

48 AC: aerucyclamide

49 CP-A: cyanopeptolin A

50 AC-A: aerucyclamide A

51 AC-D: aerucyclamide D

52 LC: cyanobacterial spent medium diluted with the BG11 in the ratio 1:400

53 HC: cyanobacterial spent medium diluted with the BG11 in the ratio 1:40

54

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56

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76

**77 Declaration of interests**

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79  The authors declare that they have no known competing financial interests or personal  
80 relationships that could have appeared to influence the work reported in this paper.

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86 Due to eutrophication in freshwater ecosystems, cyanobacterial proliferation frequently  
87 results in blooms that potentially produce bioactive or toxic metabolites that harm the  
88 environment and humans (Heisler *et al.*, 2008). *Microcystis* is one of the most widespread  
89 cyanobacterial genus in freshwaters, with *Microcystis aeruginosa* being one of the most  
90 commonly detected and investigated (Svirčev *et al.*, 2019). Like other cyanobacteria,  
91 *Microcystis* produces a diverse range of secondary metabolites that have been shown to  
92 impact life traits and physiology of aquatic organisms including zooplankton such as  
93 *Daphnia* (Lürling and van der Grinten, 2003; Merwe and Sebbag, 2012). One of the most  
94 detected toxins produced by cyanobacteria is microcystin (MC), with more than 250 variants  
95 described so far (Mowe *et al.*, 2015; Svirčev *et al.*, 2019). Microcystins change the  
96 phosphorylation state of proteins by inhibiting 1 and 2A protein phosphatases, thus  
97 disrupting pathways involving phosphorylation (MacKintosh *et al.*, 1990; Trinkle-Mulcahy  
98 and Lamond, 2006; Zurawell *et al.*, 2005). Furthermore, microcystins trigger oxidative stress  
99 in aquatic organisms (Amado and Monserrat, 2010).

100 Besides microcystins, *Microcystis sp.* produces a wide range of intracellular and  
101 extracellular secondary metabolites such as aeruginosins, cyanopeptolins, cyclamides,  
102 microginins and microviridins (Welker and Von Döhren, 2006), that have various negative  
103 effects on *Daphnia* physiology (Rohrlack *et al.* 2001, Bister *et al.* 2004, Ishida *et al.* 2007,  
104 von Elert *et al.* 2012). Similar to microcystins, cyanopeptolins (CP) are synthesized through  
105 non-ribosomal metabolic pathways, by non-ribosomal peptide synthetases (NRPSs) and  
106 polyketide synthase (PKS) (Welker and Von Döhren, 2006). CP are widely distributed and  
107 diverse compounds with more than 82 variants described so far (Gademann *et al.* 2010).  
108 Aeruginosins are synthesized non-ribosomally and they can inhibit trypsin-type serine proteases  
109 (Ishida *et al.* 2000, 2007). CPs and aeruginosins are potent inhibitors of the serine proteases  
110 trypsin and chymotrypsin, that are among the main digestive enzymes in *Daphnia* (von Elert  
111 *et al.* 2005; Gademann and Portmann 2008; Elkobi-Peer *et al.* 2013). Microviridins are one of  
112 the largest oligopeptides produced in cyanobacteria, with 13 to 14 amino acids (1600-1900 Da),  
113 contrasting to the other groups, they are ribosomally synthesized tricyclic depsipeptides. They  
114 are produced by different cyanobacterial genera, including *Microcystis sp.*, however, the natural

115  
116 Microviridin J has been identified as causing fatal molting disruption in *Daphnia pulicaria*  
117 via inhibition of *Daphnia* proteases, thus leading to the death of the animals (Kaebernick *et*  
118 *al.*, 2001; Rohrlack *et al.*, 2004). Cyclamides are cyclic hexapeptides with cytotoxic  
119 properties to crustacea (Ishida *et al.*, 2000; Portmann *et al.*, 2008). Cyanopeptides can occur  
120 in high frequency comparable to MC concentrations in aquatic environments and thus may  
121 pose problems for drinking water purification from surface water reservoirs (Beverdors *et*  
122 *al.*, 2018, 2017; Janssen, 2019; Natumi and Janssen, 2020). Concentrations of  
123 cyanopeptolines ( $< 7 \text{ ug/L}^{-1}$ ), anabaenopeptins ( $< 1 \text{ ug/L}^{-1}$ ) and microginins ( $< 1 \text{ ug/L}^{-1}$ ) have  
124 been reported in surface waters (Beverdors *et al.*, 2017), however, more research is needed  
125 regarding their diversity and concentration in aquatic environments. Furthermore, their effect  
126 on organisms as a single compound or in a mixture are not investigated in detail.

127 Nevertheless, it has been suggested that in natural conditions some oligopeptides may be  
128 even more harmful than MCs and other cyanotoxins to certain zooplankton species, in  
129 particular as digestion inhibitors are active at much lower concentrations than the classical  
130 cyanotoxins (Von Elert *et al.*, 2004). Digestive enzyme inhibition would cause starvation,  
131 impair growth and reproduction, eventually leading to slow death (Von Elert *et al.*, 2004).

132 Among the freshwater zooplankton species, *Daphnia* graze on phytoplankton including  
133 cyanobacteria, thereby connecting the primary production to the consumers within the  
134 aquatic food web (Ger *et al.*, 2016). Dominance of nutritionally inadequate phytoplankton,  
135 such as cyanobacteria, which lack important sterols and fatty acids necessary for *Daphnia*  
136 growth and development, can represent an obstacle in efficient carbon transfer to higher  
137 trophic levels (Martin-Creuzburg *et al.*, 2008). During their lifetime, however, *Daphnia* are  
138 able to develop tolerance to cyanobacterial metabolites, as a physiological response to  
139 bioactive compounds (Gustafsson and Hansson, 2004; Ortiz-Rodríguez *et al.*, 2012; Sarnelle  
140 and Wilson, 2005). Several mechanisms have been described so far, such as *Daphnia*'s  
141 ability to remodel their digestive enzymes (Schwarzenberger *et al.* 2012, von Elert *et al.*  
142 2012), or increase of antioxidant and biotransformation enzyme activity (Dao *et al.*, 2013;  
143 Ortiz-Rodríguez and Wiegand, 2010; Sadler and von Elert, 2014a). When exposed to  
144 cyanobacterial metabolites that are chymotrypsin and trypsin inhibitors, *Daphnia* switch to

145  
146 (Schwarzenberger *et al.* 2012, von Elert *et al.* 2012). The antioxidative enzymatic defenses  
147 include catalase (CAT), superoxide dismutase (SOD), glutathione-peroxidase (GPx), while  
148 glutathione S-transferase (GST) is the detoxification mechanism (Ighodaro and Akinloye,  
149 2018; Pflugmacher *et al.*, 1998). *Daphnia* can reduce oxidative stress caused by  
150 cyanobacterial metabolites by increasing CAT activity (Ortiz- Rodríguez and Wiegand,  
151 2010; Wojtal-Frankiewicz *et al.* 2014). Similar increased activity of antioxidant SOD and  
152 CAT enzyme providing cellular protection against ROS is found in a study where *Daphnia*  
153 *magna* was fed with *Microcystis* diet (Lyu *et al.*, 2016b). *Daphnia* can reduce the toxicity of  
154 microcystin by increasing the activity of GST catalysing the biotransformation via  
155 conjugation to glutathione (Dao *et al.* 2010; Ortiz-Rodríguez *et al.*, 2012; Miles *et al.* 2016).

156 Furthermore, studies in *Daphnia* have shown that cyanobacterial metabolites can affect  
157 expression of genes involved in digestive system (Asselman *et al.*, 2014; Drugă *et al.*, 2016;  
158 Schwarzenberger *et al.*, 2012), cell cycle (De Coninck *et al.*, 2014b; Giraudo *et al.*, 2017;  
159 Tong *et al.*, 2017), and oxidative stress (De Coninck *et al.*, 2014b; Lyu *et al.*, 2016a;  
160 Rhiannon *et al.*, 2011). However, characterizing transcriptional responses of *Daphnia* to  
161 cyanobacterial toxins so far focussed merely on effect of microcystin or cyanobacterial media  
162 without considering other bioactive molecules that might be present apart from microcystin  
163 (Asselman *et al.*, 2012; De Coninck *et al.*, 2014a; Drugă *et al.*, 2016; Lyu *et al.*, 2016b).

164 Besides being affected by grazing on cyanobacteria, zooplankton can also be affected by  
165 naturally produced cyanobacterial metabolites released in water (Barrios *et al.*, 2015;  
166 Ferrão-Filho *et al.*, 2014; Smutná *et al.*, 2014). Nevertheless, most of the studies investigate  
167 impact of cyanobacteria on *Daphnia* grazing on them, or exposure to extracts obtained by  
168 crushing cyanobacterial cells (from a culture or from a field sample), or to purified  
169 compounds (Dao *et al.*, 2013; Esterhuizen-Londt *et al.*, 2016; Peng *et al.*, 2018). Hence, it is  
170 of interest to investigate if *Daphnia* are impaired by the presence of cyanobacterial  
171 metabolites naturally released during cyanobacterial normal growth, without necessarily  
172 feeding on them, or crushing cells. Furthermore, knowing the composition and concentration  
173 of metabolites present in the medium, naturally released as a product of cyanobacterial

174  
175 cyanobacterial metabolites.  
176 Therefore, the aim and novelty of this study is *Daphnia* exposure to cell free cyanobacterial  
177 spent medium obtained from a two weeks culture of exponentially growing *M. aeruginosa*,  
178 containing metabolites naturally released during that time. In addition, we detected and  
179 quantified cyanobacterial metabolites present in the medium, beside commonly investigated  
180 microcystin. We monitored markers of stress response in order to predict *Daphnia*  
181 physiological phenotypes as a response to cyanobacterial spent medium. We analyzed the  
182 effects of cell free cyanobacterial spent medium that contained a quantified mixture of  
183 compounds on i) *Daphnia* survival, ii) activity of enzymes involved in oxidative stress and  
184 detoxification and iii) expression of candidate genes involved in digestion, growth and  
185 development, detoxification and oxidative stress response. We hypothesize a negative impact  
186 on *Daphnia* survival, a trigger of CAT and GST activities, as well as expression of genes  
187 involved in *Daphnia* growth and development, digestion, detoxification and oxidative stress.  
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190  
191192 **2.1. Culture conditions**

193

194 **2.1.1. *Microcystis aeruginosa* PCC 7806**

195

196 An axenic microcystin (MC) producing *M. aeruginosa* strain PCC 7806 was obtained  
197 from the Pasteur Culture collection of Cyanobacteria in Paris, France  
198 (<https://research.pasteur.fr/en/team/collection-of-cyanobacteria/>). The strain was grown in  
199 100% cyanobacterial BG11 medium (SIGMA), under a 14h:10h light:dark regime using  
200 daylight white fluorescent tubes (Toshiba, 15 W, FL15D) with 20  $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$   
201 illumination at a constant temperature of  $20\pm 1^\circ\text{C}$  (Sanyo incubator). The culture was  
202 maintained in exponential growth phase, while the axenicity was regularly evaluated as  
203 described in (Briand et al., 2012).

204

205 **2.1.2. *Daphnia magna***

206

207 The *D. magna* clone was obtained from the PEARL INRA 1036 U3E. As the exposure to  
208 cyanobacterial metabolites was realized via *M. aeruginosa* PCC 7806 spent medium, the *D.*  
209 *magna* clone was acclimated to BG11 medium (SIGMA). Before performing experiments we  
210 compared osmolarity of BG 11 medium with the osmolarity of commonly used Artificial  
211 *Daphnia* medium, Elendt M4 and Elendt M7. Osmolarity of BG 11 medium was similar to  
212 that of these *Daphnia* media, thus not affecting *Daphnia* survival. During the first three  
213 weeks *D. magna* were slowly acclimated and adjusted to the cyanobacterial BG 11 medium  
214 that was used in all the experiments, by gradually increasing the % of BG11 medium until it  
215 reached 100% in the end of the acclimation period. After the acclimation period *D. magna*  
216 were grown in 100% of BG11 medium for a month, before neonates (< 36h old) were used in  
217 the experiment. During the acclimation and cultivation period no irregularities in *Daphnia*  
218 survival, eating, movement and growth were noticed, suggesting that *D. magna* were  
219 successfully acclimated to the medium (Bojadzija Savic et al., 2020). *D. magna* were grown  
220 and cultivated in the aquarium at a constant temperature of  $20^\circ\text{C}$ , light intensity of 15  $\mu\text{mol}$   
221  $\text{photons m}^{-2} \text{ s}^{-1}$  having a day/night cycle of 14h:10h (Sanyo MIR 154) and daily renewal of



222 *Scenedesmus communis* originating from lake Grand Lieu, France, that was isolated in our  
223 laboratory (University of Rennes 1).

224  
225 Sufficient food that 100 *Daphnia* (According to OECD guidelines for testing of  
226 chemicals 202) that should be available daily in the medium is equivalent to  $2.8 - 5.6 \times 10^8$   
227 cells/mL of *S. communis*. *Daphnia* are usually maintained in medium that is not appropriate  
228 for algal growth (Elendt M4, Elendt M7- OECD guidelines for testing of chemicals),  
229 therefore when *S. communis* are introduced to *Daphnia* medium, they are consumed before  
230 growing in high densities. However, in our cultures *Daphnia* were adjusted to BG11 medium  
231 that was also used for *S. communis* culture. Hence, it allowed *S. communis* to grow and reach  
232 high densities (10x higher than the initial one, within one week) while being consumed by  
233 *Daphnia*. As high density of *S. communis* disrupts normal *Daphnia* functioning; its  
234 concentration had to be adjusted to  $2.8 - 5.6 \times 10^7$  cells/mL to maintain equilibrium between  
235 growth and consumption. In order to keep the *S. communis* culture in more accessible form  
236 for consumption, in particular by neonates (i.e. unicellular /in pairs instead of four cells  
237 having long spikes), *Scenedesmus* culture was diluted every few days before feeding.

238

## 239 **2.2. Experimental design**

240

241 All experiments were performed in 5 replicates in 2 L aquariums and lasted for 3 and 7  
242 days. All *Daphnia* were fed daily with *S. communis*, whose density was monitored and  
243 adjusted daily. For the control, 150 *D. magna* neonates (< 36h old) per aquarium were raised  
244 in BG11.

245 For the treatment, the cyanobacterial spent media was prepared in the following way: from an  
246 exponentially growing *M. aeruginosa* PCC 7806 culture, centrifuged cells were transferred  
247 in fresh sterile BG 11 medium to remove extracellular metabolites. From the pellet, a  
248 cyanobacterial culture of  $2 \times 10^5$  cells/mL initial density was grown for two weeks, reaching a  
249 cell density of  $1 \times 10^6$  cell/mL. From that culture, cell free cyanobacterial spent medium was  
250 collected by filtering through 0.2  $\mu\text{m}$  sterile cellulose nitrate filter. *D. magna* were exposed to  
251 two concentrations of cyanobacterial spent medium: a) diluted with the BG11 in the ratio  
252 1:40 (thereafter called HC for high concentration) and b) 1:400 (thereafter called LC for low

254 MC-LR in our experiments (final concentration of MC-LR: LC: 0.5 µg/L, HC: 5 µg/L), as  
255 dissolved MC ranges in the environment between 0.2 and 11 µg/L (Lahti *et al.*, 1997;  
256 Pawlik-Skowrońska *et al.*, 2008; Rastogi *et al.*, 2015; Su *et al.*, 2015).

257 *D. magna* neonates (150 per treatment) were exposed to 2 L of these two concentrations.  
258 At the end of the exposure (3 days and respectively 7 days), *D. magna* samples  
259 (biotransformation, oxidative stress, energetic profiles) were taken by collecting them over a  
260 mesh, briefly rinsed with fresh BG11 media, and after removal of the excess media, snap  
261 frozen in liquid nitrogen and stored at -80°C until analysis.

262

### 263 **2.3. Cyanobacterial secondary metabolites analysis**

264

265 Cyanobacterial secondary metabolites previously known to be produced by this  
266 particular strain PCC7806 (Briand *et al.*, 2016; Rohrlack *et al.*, 2004; Sadler and von Elert,  
267 2014b) were monitored after 2 weeks growth phase from initially  $2 \times 10^5$  cells/mL to  $1 \times 10^6$   
268 cells/mL. Cyanobacterial cells were separated from the supernatant by centrifugation. Cell  
269 free spent medium was filtered through 0.2 µm filter and 1 mL was lyophilized. Extraction of  
270 lyophilized material was done in 0.5 ml 50% methanol and processed as described in  
271 Bojadzija Savic *et al.*, 2019. Waters Acquity Ultra-High Performance Liquid  
272 Chromatography coupled to a Xevo quadrupole time of flight mass spectrometer was used  
273 for the metabolites analysis. Cyanobacterial peptides were detected using extracted ion  
274 chromatograms for the respective specific masses of the different compounds (Bojadzija  
275 Savic *et al.*, 2019). Microcystin-LR (MC-LR), Microcystin-des-LR (des-MC-LR),  
276 cyanopeptolin A (CP-A), and aerucyclamide A (AC-A) and D (AC-D) were quantified using  
277 linear relationship between peak area (MC-LR and des-MC-LR at 238 nm, CP-A at 220 nm,  
278 and AC-A at 237 nm and AC-D at 240 nm) and known concentrations of the toxin standards.  
279 The microcystin-LR standard was purified as previously described (Edwards *et al.*, 1996).  
280 CP-A standard and AC-A and AC-D standard were purified using preparative HPLC  
281 (Biotage Parallelex Flex, Cardiff, UK) and Flex V3 software for instrument control and data  
282 acquisition as described in (Bojadzija Savic *et al.*, 2020). Detection and quantification of the  
283 cyanobacterial peptides was done by MassLynx v4.1 software.

284

### 285 **2.3. *D. magna* survival**

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287  
288 (identified as not moving and decaying *Daphnia* on the bottom of the aquarium) with results  
289 expressed in percentages of total individuals at the start of the exposure.

290

## 291 **2.4. Enzyme extraction and measurement**

292

293 Fifty *Daphnia* were resuspended and homogenized in 1 mL of ice cold extraction buffer  
294 (0.1 M phosphate buffer pH 6.5, glycerol, 1 mmol EDTA, and 1.4 mmol dithioerythritol)  
295 using Lysing Beads-Matrix E (MPbio) in the Vibro-mill MM200, (RETSCH) for 3 min at the  
296 frequency of 25 Hz to break the cells, followed by centrifugation (10,000 g, 10 min, 4°C,  
297 Sigma 3K18C). The supernatant was used for enzyme measurements using a  
298 spectrofluorometer (SAFAS Monaco Xenius XC, Monaco). Catalase (CAT) activity was  
299 assayed by measuring the rate of disappearance of H<sub>2</sub>O<sub>2</sub> at 240 nm (Chang and Kao, 1997).  
300 GST was assayed at 340 nm using 1-chloro-2, 4-dinitrobenzene (CDNB) as substrate. SOD  
301 activity was determined using a photochemical assay based on the reduction of nitro blue  
302 tetrazolium (NBT) according to total Superoxide Dismutase (T-SOD) assay kit  
303 (Hydroxylamine method, SIGMA KIT), however SOD activity in our experiments remained  
304 below the level of detection. All enzyme activities were related to the protein content in the  
305 extract, measured according to Bradford (1976).

306

## 307 **2.5. Candidate function gene expression**

308

### 309 **2.5.1. RNA extraction and reverse transcription**

310

311 RNA extraction and reverse transcription was done according to (Colinet *et al.* 2010)  
312 from the unexposed control and from *Daphnia* exposed to LC and HC after 3 and 7 days. For  
313 each condition and sampling time point, five RNA samples (i.e. biological replicates), each  
314 consisting of a pool of 50 *Daphnia*, were used. *Daphnia* were ground to fine powder in 1.5  
315 mL tubes placed in liquid nitrogen. Samples were mixed with lysis buffer (containing 1%  
316 β-mercaptoethanol) from RNA extraction kits (Qiagen) and crushed for 10 min to complete  
317 homogenization. RNA extraction and purification was performed following the  
318 manufacturer's instructions (Qiagen). Total RNA was eluted in 40 μL of DEPC-treated  
319 water. RNA was quantified and quality-checked with a Nanodrop 1000 (Thermo Scientific,  
320 Waltham, MA). Three hundred nanograms of total RNA was used in the reverse transcription  
321 to cDNA, using the SuperScript ® III First-Strand Synthesis System for RT-PCR

322 20°C until use.

324

### 325 2.5.2. Real-time PCR

326

327 We used primers of candidate genes involved in *Daphnia* energy  
 328 (glyceraldehyde-3-phosphate dehydrogenase: *gapdh*), digestive system (protease: *ct383*),  
 329 oxidative stress (glutathione S-transferase: *gst*, glutathione peroxidase: *gpx*, catalase: *cat*,  
 330 thioredoxin: *trx*), cell cycle (histone: *h2a*, myosin heavy chain: *mhcr1*) and molting (nuclear  
 331 hormone receptor: *hr3*, nuclear hormone receptor: *ftz-fl1*) that potentially could be affected by  
 332 cyanobacterial metabolites. We used  $\beta$ -actin as the reference gene. Oligonucleotide primers  
 333 were obtained from the previously published references (see **Table 1.** for details), having  
 334 efficiency between 92% and 105% (Giraud *et al.*, 2017; Houde *et al.*, 2013; Lyu *et al.*, 2014;  
 335 Rhiannon *et al.*, 2011; Schwarzenberger *et al.*, 2010; Tong *et al.*, 2017; Wang *et al.*, 2016).  
 336 Oligonucleotide primers were made by Integrated DNA Technologies, BVBA.

337

**Table 1.** Oligonucleotide primers used in the experiments.

Gene name	Symbol	Primer sequence 5'-3'	Amplicon size	Reference
Glyceraldehyd e-3-phosphate dehydrogenase	<i>gapdh</i>	F- TGCTGATGCCCAATGTTTGTGT R-GCAGTTATGGCGTGGACGGTTGT	132	(Giraud <i>et al.</i> , 2017)
Protease CT383	<i>ct383</i>	F- TTGGCACCTTCCACCGAAT R- TCATCAGGACTGGAGAAACGC	183	(Schwarzenberger <i>et al.</i> , 2010)
Glutathione S-transferase (NCBI: No. EFX81634.1)	<i>gst</i>	F- GGGAGTCTTTTACCACCGTTTC R- TCGCCAGCAGCATACTTGTT	150	(Wang <i>et al.</i> , 2016)
Glutathione peroxidase	<i>gpx</i>	F- AACGTTACGATGCCAGTTCC R- TCTTTCGAGCGGTTGAGATT	212	(Rhiannon <i>et al.</i> , 2011)
Catalase	<i>cat</i>	F- AGGTGCCTTTGGATACTTTGA R- TTGCGTATTCCTTGTCAGTC	495	(Lyu <i>et al.</i> , 2014)
Thioredoxin	<i>trx</i>	F- GTATCCACGCCAGTCCTTGTT R- TCCTTCCACTTTTCCTCCCTTA	129	(Liu <i>et al.</i> , 2019)
Histone 2A	<i>h2A</i>	F- CTGGTGCCCCTGTCTACCTA R- TAGGGAGGAGAACAGCCTGA	219	(Giraud <i>et al.</i> , 2017)
Myosin heavy chain	<i>mhcr1</i>	F - GATGCCGTTTCCGAGATGAG R - CTCGGCGGTCATGTGGTC	132	(Tong <i>et al.</i> , 2017)
Nuclear	<i>hr3</i>	F- AAGGTCGAGGATGAAGTGCG	81	(Giraud <i>et al.</i> ,

hormone receptor TRK3		R- AAAGACGCTACTATCGGGCG	2017)
Nuclear hormone receptor FTZ-F1	<i>ftz-f1</i>	F- TCTTACCGGACATTACGCC R- ACAGCCGTTGAGATGCTTGA	71 (Girauda <i>et al.</i> , 2017)
Beta-actin	<i>β-actin</i>	F- GCCCTCTTCCAGCCCTCATTCT R- TGGGGCAAGGGCGGTGATT	189 (Houde <i>et al.</i> , 2013)

338

339 Real-time PCRs were performed on the LightCycler 480 system. Reactions were performed  
 340 in 384-well LightCycler plates, using LightCycler 480 High Resolution Melting Master Mix  
 341 and the crossing point (Cp), equivalent to the cycle threshold (Ct), estimates were obtained  
 342 using the absolute quantification module in the software package. The PCR reactions were  
 343 performed in four replicates, containing 4 μL of cDNA sample, 2 μm each primer, and 6 μL  
 344 of the High Resolution Melting Master Mix. After 10 min at 95°C, the cycling conditions  
 345 were as follows: 60 cycles at 95°C for 10 s, 60°C for 15 s, and 72°C for 15 s. To validate the  
 346 specificity of amplification, a post amplification melt curve analysis was performed.  
 347 Amplicons were first denatured at 95°C for 1 min, and then cooled to 65 °C, and the  
 348 temperature was then gradually raised to 95°C). Fluorescence data were recorded  
 349 continuously during this period, and subsequently analyzed using the Tm calling module in  
 350 the LightCycler 480 software.

$$R = \frac{(E_{target})^{\Delta CP_{target}(control-treated\ sample)}}{(E_{reference})^{\Delta CP_{target}(control-treated\ reference)}}$$

351 Relative expression ratios (R) (i.e. fold change) were calculated using the efficiency  
 352 calibrated model of (Colinet *et al.*, 2010; Pfaffl, 2001). In the Pfaffl model, CP is the crossing  
 353 point (i.e. Ct) and E the efficiency of PCRs. qPCR CT values of all candidate genes have been  
 354 provided in **Supplementary 1**. The ratio of the target gene is expressed in treated samples  
 355 versus matched controls (calibrators), and normalized using the housekeeping reference  
 356 gene.

357

## 358 2.7. Statistical analyses

359

360 R Core Team (2013) was used to access statistical analysis of the obtained data. All data  
 361 are presented as mean ± standard deviation. Significant differences were determined at

362  $p < 0.05$ . We performed t-tests to determine the difference between CAT, GST activities, as  
363 well as gene expression between the control and treatment. Repeated-measures analysis of  
364 variance was done to determine the difference in *Daphnia* survival between Control/LC,  
365 Control/HC and LC/HC ). Repeated-measures analysis of variance is a mixed linear model  
366 with day, treatment (Control vs Treatment) and interaction between day and treatment  
367 considering the repeated measures on replicates (random effect). Normality of residuals was  
368 tested via Shapiro test (residuals normally distributed when  $p > 0.05$ ). Anova was performed to  
369 test the effects of the model. Pairwise comparison with correction for multiple comparison  
370 was performed to check significant differences between control and the two treatments,  
371 differences between LC and HC and if there was time dependency effect on control and  
372 treatment.

373

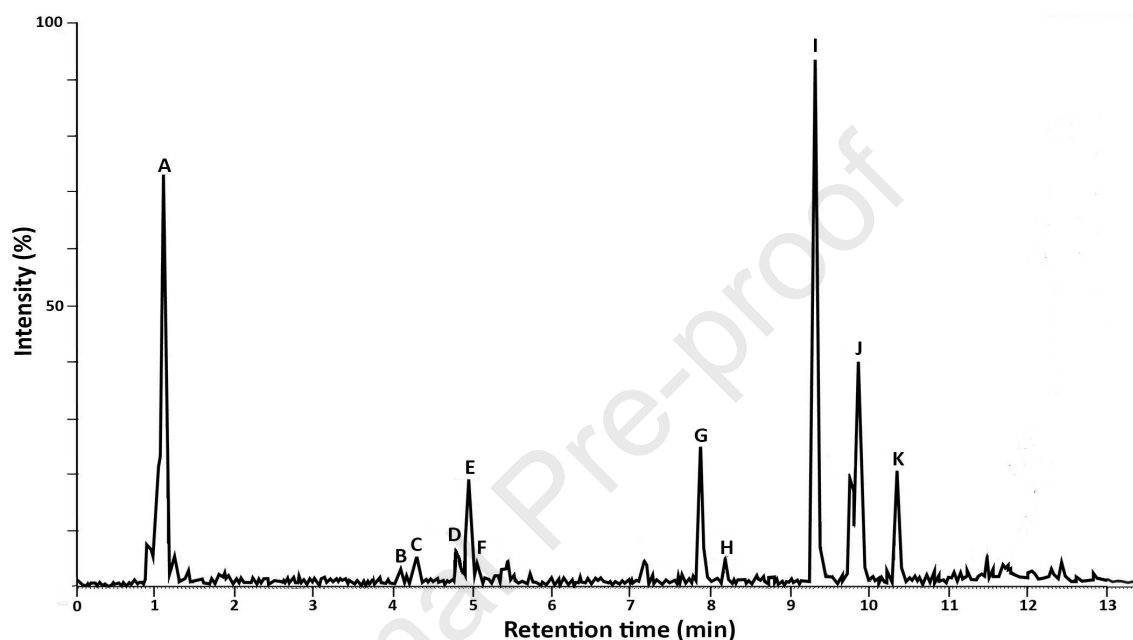
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376

377 **3.1. Composition of the two weeks old *M. aeruginosa* PCC7806 medium**

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379 In the media produced by exponentially growing *M. aeruginosa* PCC7806, 11  
 380 metabolites were detected after 2 weeks of cultivation. *M. aeruginosa* PCC 7806 produced  
 381 MC-LR and des-MC-LR, cyanopeptolins, CP (963A, A and B), aerucyclamides, AC (A,B,C  
 382 and D) and aeruginosins (684 and 602) (**Figure 1**).



383

384 **Figure 1.** Secondary metabolites detected in *M. aeruginosa* PCC 7806. (A) aeruginosin 684, (B)  
 385 cyanopeptolin B, (C) aeruginosin 602, (D) des-MCLR, (E) MC-LR, (F) CP A, (G) aerucyclamide D, (H)  
 386 cyanopeptolin 963A, (I) aerucyclamide A, (J) aerucyclamide C, (K) aerucyclamide B.

387

388 The concentrations of five extracellular metabolites (MC-LR, des-MC-LR, CP-A,  
 389 AC-D, AC-A) in *M. aeruginosa* PCC 7806 after 2 weeks growth phase from  $2 \times 10^5$  cells/mL  
 390 initially to  $1 \times 10^6$  cells/mL, and in dilutions HC and LC are shown in **Table 2**.

391

**Table 2.** Concentrations of extracellular metabolites in original medium of the 2 weeks *M. aeruginosa* PCC 7806 and its HC and LC dilutions

Extracellular metabolite	Original spent <i>M. aeruginosa</i> PCC 7806 medium ( $\mu\text{g/L}$ )	HC ( $\mu\text{g/L}$ )	LC ( $\mu\text{g/L}$ )
MC-LR	<b>218±21</b>	<b>5.45±0.53</b>	<b>0.55±0.05</b>
Des-MC-LR	<b>61±1</b>	<b>1.53±0.03</b>	<b>0.15±0.01</b>
CP-A	<b>135±11</b>	<b>3.38±0.28</b>	<b>0.34±0.03</b>
AC-D	<b>93±10</b>	<b>2.33±0.25</b>	<b>0.23±0.02</b>

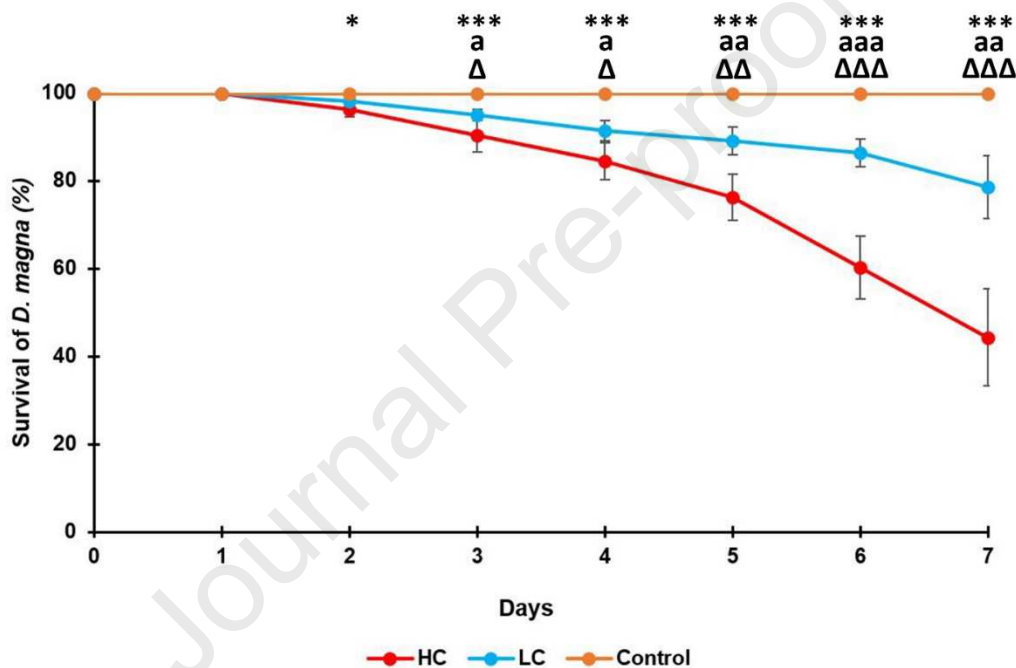
392

393 **3.1. *Daphnia* survival**

394

395 The high concentration of the cyanobacterial medium (HC) caused a significant decrease  
 396 in survival from day 2 onwards, compared with the control, while exposure to the low  
 397 concentration (LC) caused significant decrease after day 3. Both concentration levels  
 398 significantly decreased *Daphnia* survival over the course of the experiment. *Daphnia*  
 399 survival was significantly higher in LC exposure from day 3 onwards (80% survival after 7  
 400 days) compared with the HC exposure (40% survival after 7 days) (**Figure 2.**)

401



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**Figure 2.** *D.magna* survival when exposed to HC and LC. Control vs HC: \*; Control vs LC: a; HC vs LC: Δ. \*, a, Δ (p < 0.05), \*\*, aa, ΔΔ (p < 0.01), \*\*\*, aaa, ΔΔΔ (p < 0.01); repeated-measures analysis of variance

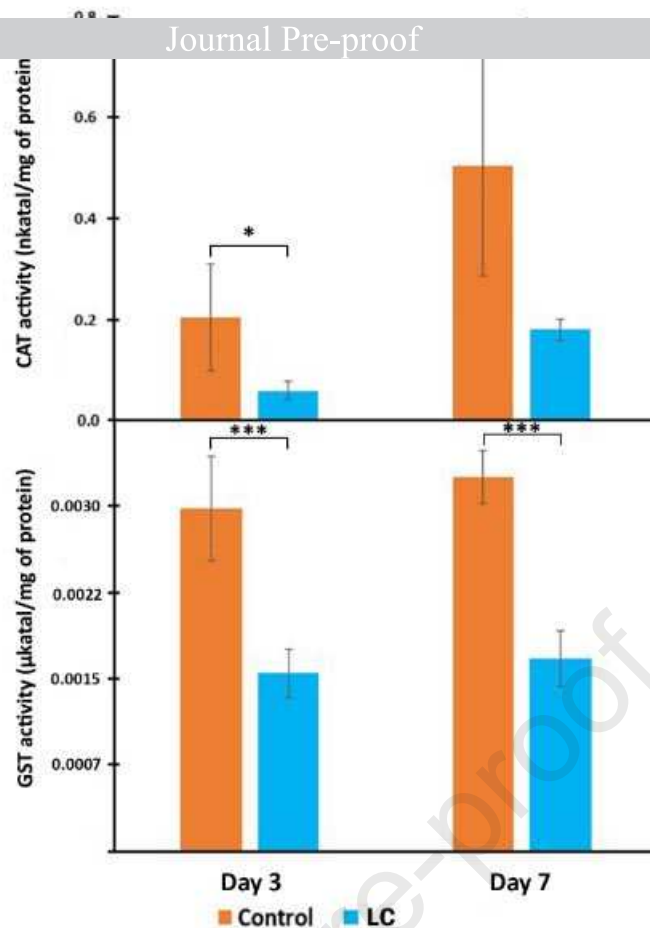
406 **3.2. Antioxidant and detoxification enzymes**

407

408 CAT activity was significantly lower on day 3 and day 7 in the LC exposure, compared  
 409 to the control. Similarly GST activity was significantly lower on day 3 and 7 in the treatment  
 410 exposed to LC, compared to the control. Due to the high mortality in the HC exposure, the  
 411 biomass of the remaining *Daphnia* was insufficient for enzyme analysis on both days (**Figure**  
 412 **3.**)

413





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**Figure 3.** CAT and GST activity in *D.magna* exposed to LC \* ( $p < 0.05$ ), \*\* ( $p < 0.01$ ), \*\*\* ( $p < 0.01$ ), t-test

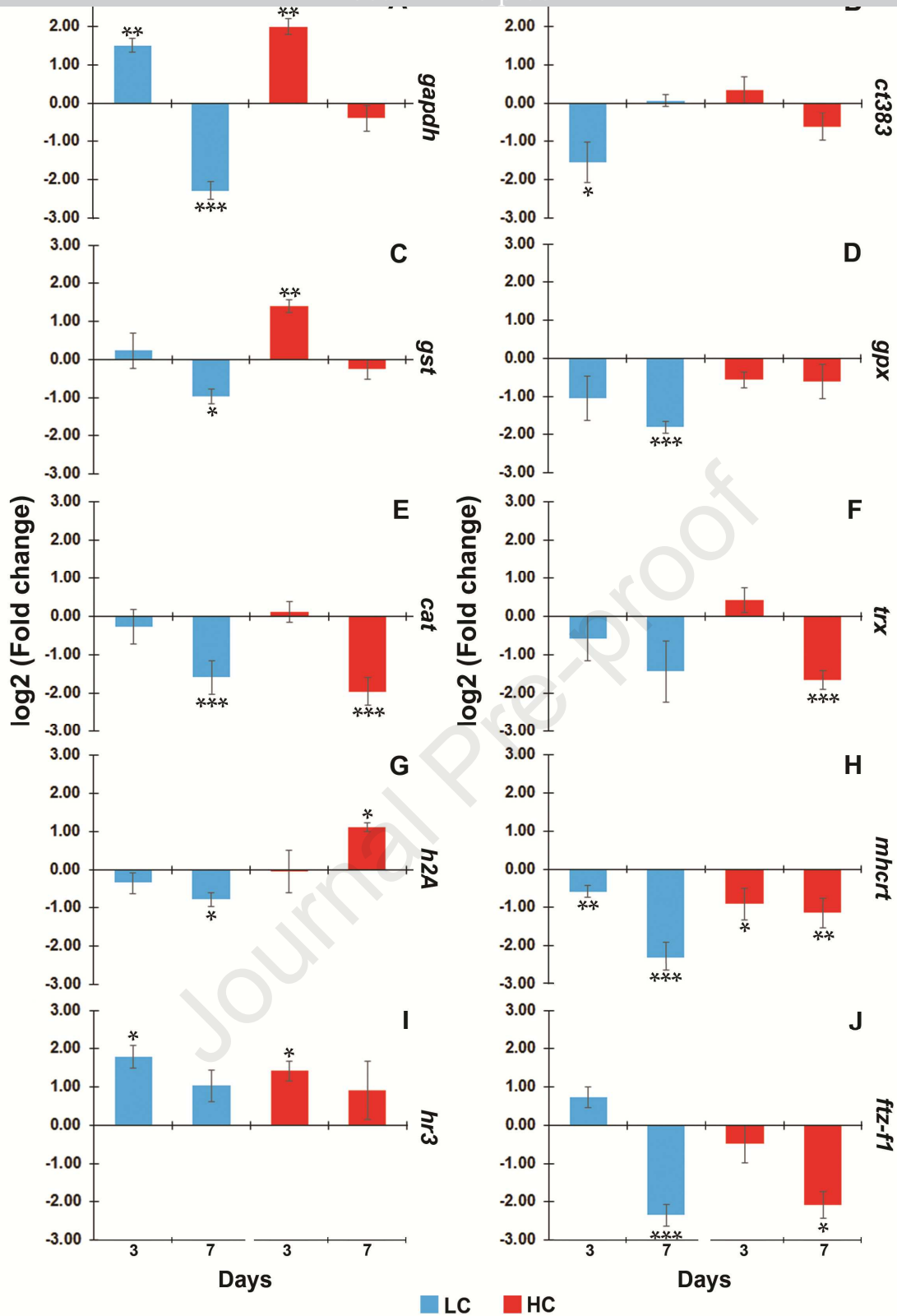
### 417 3.5. Selected genes expression

418

419 Glyceraldehyde 3-phosphate dehydrogenase (*gapdh*) was significantly overexpressed on  
420 day 3 when *Daphnia* were exposed to both HC and LC, but downregulated after 7 days,  
421 significant for LC (**Figure 4. A**). The gene coding for digestive enzyme Protease CT383  
422 (*ct383*) was significantly downregulated after 3 days exposure to LC (day 3) of *Microcystis*  
423 spent medium, but not in the other treatment (**Figure 4. B**). Concerning the oxidative stress  
424 and detoxification related genes, merely downregulation was observed. The only exception  
425 was the gene encoding for the detoxification enzyme Glutathione S-transferase (*gst*) which  
426 was significantly upregulated on day 3 when exposed to HC, while on day 7, *gst* was  
427 downregulated at LC treatment (**Figure 4. C**). Furthermore, Glutathione peroxidase (*gpx*)  
428 expression was significantly downregulated on day 7 after *Daphnia* exposure to LC (**Figure**  
429 **4. D**). Genes responsible for oxidative stress enzymes Catalase (*cat*) (**Figure 4. E**) and  
430 Thioredoxin (*trx*) (**Figure 4. F**) were downregulated on day 3 (LC) and day 7 (HC and LC).  
431 The response of the histone 2A (*h2A*) gene was the opposite of this, when exposed to HC and

433 exposed to HC or LC (**Figure 4. G**). HC and LC also had significant negative effect on gene  
434 expression of Myosin heavy chain (*mhcrt*) that was significantly underregulated on day 3 and  
435 7 (**Figure 4. H**). Cyanobacterial secondary metabolites affected two genes involved in the  
436 molting cycle: the Nuclear hormone receptor HR3 (*hr3*) and FTZ-F1 (*ftz-f1*). While the *hr3*  
437 was significantly upregulated on day 3 when exposed to both HC and LC (**Figure 4. I**)  
438 *ftz-*was significantly downregulated on day 7 when exposed to both HC and LC (**Figure 4. J**).  
439

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**Figure 4.** Effect of cyanobacterial media (LC and HC) on the relative gene expressions expressed as log<sub>2</sub>(fold change). Relative expressions in *D. magna* for: A) Glyceraldehyde 3-phosphate dehydrogenase (*gapdh*), B) Protease CT383 (*ct383*), C) Glutathione S-transferase (*gst*), D) Glutathione peroxidase (*gpx*) E) Catalase (*cat*), F) Thioredoxin (*trx*), G) histone 2A (*h2A*), H) Myosin heavy chain (*mhcr1*), I) Nuclear hormone receptor HR3 (*hr3*), J) Nuclear hormone receptor FTZ-F1 (*ftz-f1*). Gene expressions were normalized to the control condition for each sampling time. Replicates of culture are represented as a mean and error bars represent the standard deviations (n = 5). \* (p < 0.05), \*\* (p < 0.01), \*\*\* (p < 0.001), t-test

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450  
451 *Daphnia* are unselective phytoplankton filter feeders, and as such can be exposed to  
452 cyanobacterial metabolites by direct grazing on cyanobacteria as well as by uptake of  
453 metabolites released in the water. While previous studies have demonstrated the negative  
454 impacts of cyanobacterial medium (Lanaras and Cook 1994, Neumann *et al.* 2000, Dao *et al.*  
455 2010, 2013, Esterhuizen-Londt *et al.* 2016, Peng *et al.* 2018) on *Daphnia*, the novelty of this  
456 study was to connect responses from selected markers on the gene-level to enzymatic  
457 activities and to consequences for the survival of *D. magna* exposed to cyanobacterial  
458 cell-free spent medium. From the mixture of cyanobacterial metabolites in the medium we  
459 identified 11 and quantified 5.

460 As *M. aeruginosa* was grown in BG11, *D. magna* had to be acclimatised to this medium  
461 during several weeks before the experiment. Survival of the control group throughout the  
462 experiment was always high (>98%). These results are in line with the literature where  
463 non-treated *D. magna* survival was always high (close to 100%) in the first 8 days of  
464 experiments, although specific *D. magna* cultivation medium was used (Dao *et al.* 2010,  
465 Ortiz-Rodríguez *et al.* 2012), suggesting that BG 11 medium used in our study did not have  
466 impact on the *D. magna* survival. Apart from increased CAT activities no other changes were  
467 observed in the control group over the exposure time, we nevertheless suggest for further  
468 studies to compromise between both media by adding necessary minerals, e.g. calcium, using  
469 diluted BG 11, while keeping the osmolarity as we ensured in our exposures.

470 Cyanobacterial spent medium had a dose and time dependent negative impact on *D.*  
471 *magna* survival, verifying our hypothesis. The concentrations used (Table 2.) were  
472 detrimental thus preventing *D. magna* from acclimatisation during the exposure period.  
473 These detrimental effects within 7 days were not expected as these concentrations were  
474 chosen according to previous studies showing that survival of *D. magna* rapidly decreased  
475 during 3 weeks exposure to crude extract containing 50 µg/L of dissolved microcystin, while  
476 exposure to 5 µg/L did not impact *Daphnia* survival much (Dao *et al.*, 2010). Similar results  
477 were observed by Lürling and van der Grinten (2003) where exposure to 3.5 µg/L of  
478 dissolved microcystin showed no significant decrease in survival over 7 days. When exposed  
479 to crude extract or artificial mixtures of pure microcystins containing 60 µg/L of total MC

480  
481 appear to have an impact on *D. pulex* survival for 6 days (Esterhuizen-Londt *et al.*, 2016).  
482 Our results are, however, in line with studies exposing *D. magna* to *M. aeruginosa* containing  
483 1.4–9 µg/L of MC, where feeding was inhibited, followed by increase of mortality in the first  
484 week of the treatment (DeMott, 1999; Demott *et al.*, 1991; Ghadouani *et al.*, 2004; Rohrlack  
485 *et al.*, 2001). *D. laevis* (two clones) and *D. similis* exposed to five *Microcystis* extracts in  
486 which microcystins were detected (434 - 538 mg/g of lyophilized sample) suffered decreased  
487 survival, reproduction and disturbance in egg production after 48 h (Herrera *et al.* 2015).  
488 Crude extract obtained from *Microcystis* spp. had lethal effect on *D. magna* neonates, with  
489 LC50 (48 h) ranging from 168.3–442.7 mg microcystin (total) DW L<sup>-1</sup> (Pham, 2018).  
490 Susceptibility to microcystin is, however, not only species-specific, but *Daphnia* species can  
491 also show different responses within their clones (DeMott, 1999; Hairston *et al.*, 1999;  
492 Rohrlack *et al.*, 2001).

493 As both concentrations in our experiment caused mortality (20% for LC and 60% for  
494 HC) within the 7 days exposure, we suggest a high *D. magna* sensitivity to the other  
495 cyanobacterial metabolites present in the spent medium, as besides MC-LR and desmethyl  
496 MC-LR, cyanopeptolin-A, aerucyclamides A and D were quantified, and aeruginosins (602  
497 and 684), cyanopeptolins (B and 963) and aerucyclamides (B and C) detected. HC and LC of  
498 *Microcystis* spent medium downregulated a gene encoding the digestive enzyme protease,  
499 *ct383*, thus potentially interfered with *D. magna* digestion and as a consequence could  
500 contribute to the increasing mortality in a concentration and time dependent manner.  
501 Similarly, when *D. magna* were fed with MC-producing strain of PCC 7806 wild type, *ct383*  
502 was downregulated after 6 days, leading to reduced total chymotrypsin activity  
503 (Schwarzenberger *et al.*, 2010).

504 When fed with *Microcystis* strain UWOC MRC (a non-microcystin producing strain) a  
505 lethal molting disruption in *Daphnia* spp. has been observed, suggesting that cyanobacterial  
506 proteases, other than microcystin, could interfere with the molting cycle (Kaebernick *et al.*,  
507 2001). Despite the absence of microviridins J in our medium, known to impair the molting  
508 cycle in *Daphnia* via protease inhibition (Rohrlack *et al.*, 2004), upregulation of a gene  
509 coding for nuclear hormone receptor (*hr3*) followed by significant downregulation of *ftz-fl*

510  
511 observed. Our results suggest that other metabolites have a role in impairment of these  
512 pathways which may affect *Daphnia* molting.

513 Activity of anti-oxidative stress enzymes is a crucial defense mechanism against the  
514 induction of oxidative stress by microcystins (Amado and Monserrat, 2010). Through  
515 increased oxidative stress enzyme activities and detoxication, *D. magna* are able to enhance  
516 acclimation to cyanobacterial metabolites (Ortiz-Rodríguez *et al.*, 2012). CAT is a highly  
517 efficient antioxidant enzyme, responsible for reduction of H<sub>2</sub>O<sub>2</sub> concentrations in the cells  
518 (Fridovich, 1998). Elevated CAT activity can prevent oxidative damage caused by  
519 cyanotoxins thus provides oxidative protection for *Daphnia* (Wojtal-Frankiewicz *et al.*,  
520 2013). Increased CAT activity was observed in adults and neonates after 24 h when exposed  
521 to 100 µg/L pure MC-LR, while exposure to 5 µg/L MC-LR or less, CAT activity was similar  
522 to control (Ortiz-Rodríguez *et al.*, 2012). In our experiments, genes of antioxidant enzymes,  
523 *cat* and *trx*, were downregulated, confirming the results of the enzyme activity. The  
524 significant decrease in CAT activity on days 3 and 7, suggests that these enzymes were  
525 exhausted due to the presence of the mixture of cyanobacterial compounds in the  
526 concentrations applied. Similarly, CAT decreased in *D. magna* after being exposed to  
527 cyanobacterial crude extract (containing 60 µg/L total MC) during the whole exposure period  
528 of 72 h while the pure toxin MC-LR increased its activity (Esterhuizen-Londt *et al.* 2016).  
529 Even when *D. magna* were exposed to extracts from non-microcystin and  
530 non-cylindrospermopsin medium, their CAT decreased after day 1 and 7 (Dao *et al.*, 2013).  
531 In combination with the observed lethality, our results suggest that *D. magna* oxidative  
532 defence response was repressed in such way that oxidative damages may have occurred  
533 resulting in lethal effects.

534 In *D. magna* and *D. longispina*, increased GST activity can detoxify microcystin up to a  
535 certain concentration or exposure duration, which can also be transferred to the next  
536 generation (Ortiz-Rodrigues *et al.*, 2012; Wojtal-Frankiewicz *et al.* 2013, 2014). Despite the  
537 upregulation of *gst* within the first 3 days, our exposures, however, decreased GST activity,  
538 compared with the control on day 3 and day 7, where expression of *gst* gene was  
539 downregulated as well. Our GST results concern one or at maximum two out of on average 7

540  
541 have had a different response. Asselman *et al.* (2012) showed that sigma-class *gst* genes in *D.*  
542 *pulex* were upregulated when fed on MC-producing *M. aeruginosa* after 16 days. However,  
543 our results are in line with previous studies where short term exposure (48 h) to  
544 microcystin-producing *M. aeruginosa* PCC7806 increased *delta-gst* transcript levels, while  
545 long term exposure (15 days) downregulated them (Lyu *et al.*, 2016a). Similar decrease in  
546 GST activities were observed in *D. magna* exposed to cyanobacterial medium (containing 60  
547  $\mu\text{g/L}$  total MC) after 24 h and 72 h (Esterhuizen-Londt *et al.*, 2016). Furthermore, GST  
548 activity in *D. magna* decreased with increased MC-LR concentrations from 10 to 2000  $\mu\text{g/L}$   
549 (Chen *et al.*, 2005), suggesting enzymes exhaustibility as also seen in (Dao *et al.*, 2013).

550 Our results suggest that even lower concentrations of MC in the cyanobacterial medium,  
551 along with the other cyanobacterial metabolites can affect enzyme activity in a similar way  
552 like cyanobacterial medium containing higher microcystin concentrations. Besides  
553 cyanobacterial metabolites that were detected, cyanobacterial medium could contain  
554 undetected compounds that could potentially interfere with overall ecotoxicity (Smutná *et*  
555 *al.*, 2014) or inhibit enzymes activity, such as microcin SF608 that was shown to have  
556 inhibitory impact on GST (Wiegand *et al.*, 2002).

557 When *Daphnia* are in toxic environments, mobilization of detoxification and antioxidant  
558 defense mechanisms, as well as growth and development, comes with energetic cost (Calow,  
559 1991; McKee and Knowles, 1986; Pane *et al.*, 2004). For instance, *D. magna* exposed to  
560 nickel (Pane *et al.*, 2004) or the fungicide tebuconazole (McKee and Knowles, 1986) showed  
561 increased energy consumption, as glycogen and lipids levels were decreased. In our  
562 experiments energetic resources were instantly used, visible by the induction of *gapdh*  
563 (involved in glycolysis) at day 3. Upregulation of *gapdh* has been observed in *D. magna* in  
564 response to diet containing microcystins after 4 days of the experiment, suggesting that  
565 ingestion of microcystin induces glycolysis and protein catabolism (Schwarzenberger *et al.*,  
566 2009). Our results further suggest that severe depletion of energy affected also the muscular  
567 activity, as the myosin heavy chain was immediately and significantly downregulated in both  
568 experimental exposures (HC and LC). Depletion of energy in combination with  
569 downregulation of the myosin heavy chain could provide a mechanistic explanation of the

570  
571 *al.*, 2001; Ghadouani *et al.*, 2004).

572 The response of the histone 2A gene (*h2A*) (involved in normal cell cycle progression)  
573 may indicate two different cellular pathways, depending on the exposure concentration. The  
574 downregulation at LC hints on apoptotic processes, while the upregulation at HC exposure  
575 may imply cellular dysfunction occurring during necrotic processes, indicating a stronger  
576 negative effect of HC medium on *Daphnia*, that is in line with the higher mortality in this  
577 exposure. Activation of apoptotic pathways are positively correlated with the decline in  
578 *mhcr1* (Tong *et al.*, 2017) that was also observed in our study, suggesting apoptotic processes  
579 in *D. magna*, caused by cyanobacterial metabolites. Used concentrations of cyanobacterial  
580 metabolites in our exposures may have been too high for *Daphnia* to adapt, therefore use of  
581 lower concentration in future studies would provide deeper understanding of *Daphnia*'s  
582 molecular response to the cyanobacterial metabolites.

583

## 584 **5. CONCLUSION**

585

586 In conclusion, *D. magna* survival was strongly affected by cyanobacterial spent medium  
587 at both LC and HC, due to the combined effect of MC and the other secondary metabolites  
588 present. *D. magna* were not able to acclimate during the short exposure period. Medium with  
589 the highest tested concentration of cyanobacterial metabolites was the most detrimental as  
590 expected. Exposure to cyanobacterial compounds in the *M. aeruginosa* spent medium  
591 affected *D. magna* genes involved in i) digestion, thus mobilization of the limited internal  
592 energetic resources, ii) oxidative stress and detoxification, iii) muscular activity and iv) cell  
593 regulation including the molting process. We also observed consequences of cyanobacterial  
594 medium on detoxification and antioxidant capacities which were dose and in particular  
595 time-dependent indicating an exhaustion of the enzymes with high concentration or long  
596 exposure duration. Despite this, the concentrations were chosen based on available data of  
597 pure MCs or MCs in crude extracts causing low lethality, for following sublethal effects an  
598 even lower concentration is recommended.

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- Cell free *M. aeruginosa* spent medium affected *Daphnia* survival and physiology
- Medium with higher concentration of cyanobacterial metabolites was more detrimental
- Other secondary metabolites, besides microcystin-LR highly likely had negative impact on *Daphnia*

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**Declaration of interests**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:

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