

1 **Mitigating antibiotic pollution using cyanobacteria: removal**
2 **efficiency, pathways and metabolism**

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17 **ABSTRACT**

18 The occurrence of pharmaceuticals and personal care products (PPCPs) in wastewater
19 poses huge environmental threats, even at trace concentrations, and novel approaches
20 are urged due to the inefficiencies of conventional wastewater treatment plants,
21 especially when processing contaminants at high concentrations. Meanwhile, another
22 widespread problem in the aquatic domain is the occurrence of harmful algal blooms
23 (HABs) which cause serious damage to the ecosystem, but have rarely been investigated
24 for possible valorization. This study investigated the possibilities, mechanisms, and

25 effects of toxin release of using a harmful cyanobacterial species, *Microcystis*
26 *aeruginosa* (*M. aeruginosa*), in order to remove the widely used drug, tetracycline, at
27 high concentration. The results were compared with the performance obtained by the
28 use of the hitherto generally-selected chlorophyte alga *Chlorella pyrenoidosa* (*C.*
29 *pyrenoidosa*) for tetracycline concentrations of 10-100 mg L⁻¹. *M. aeruginosa* exhibited
30 a much more effective and rapid tetracycline removal (over 98.0% removal in 2 days)
31 than did *C. pyrenoidosa* (36.7%-93.9% in 2 days). A comprehensive kinetic
32 investigation into probable removal pathways indicated that, theoretically, bio-
33 remediation dominated the process by *M. aeruginosa* (71.6%), while only accounting
34 for 20.5% by *C. pyrenoidosa*. Both microalgae promoted the hydrolysis of tetracycline
35 under conditions of increased pH and inhibited abiotic photolytic reactions by the
36 shading effect to the water column, when compared with control experiments. Although
37 identical degradation by-products were identified from treatments by both microalgal
38 species, distinct by-products were also confirmed, unique to each treatment. Moreover,
39 the growth of *M. aeruginosa* biomass exhibited strong tolerance to tetracycline
40 exposure and released significantly lower levels of microcystin-LR, compared with the
41 control systems. This study supports the possibility of reusing HABs species for the
42 effective remediation of antibiotics at high concentrations. We have further suggested
43 possible mechanisms for remediation and demonstrated control of toxin release.

44 **Keywords:** Harmful Algal Blooms (HABs), Microalgae, Micropollutants, Microcystin
45 control, PPCPs.

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49 **1. Introduction**

50 Pharmaceuticals and personal care products (PPCPs) have been extensively
51 detected in aquatic systems, and pose serious hazards to human health and ecology even
52 at trace levels (Suárez et al., 2008). The global consumption of antibiotics alone has
53 been estimated at 100-200k tons (Qian et al., 2012), however, 25%-75% of the
54 consumed antibiotics are excreted from living systems and contaminate natural waters
55 (Sarmah et al., 2006). Such antibiotics are barely removed in conventional wastewater
56 treatment plants (WWTPs) due to their antibacterial properties (Wang et al., 2013).
57 Tetracycline (Fig. S1.) is the second most widely-used antibiotic, often employed for
58 the treatment of many different bacterial infections as diverse as severe acne, food
59 poisoning, and sexually transmitted diseases. The presence of residual tetracycline at
60 trace levels in the environment as a whole might lead to further development of
61 antibiotic-resistant bacteria, which, in turn, would be a major health problem. Worse
62 still, tetracycline exposure at high concentrations generates the equally serious
63 environmental problem of acute toxicity to the aquatic and edaphic organisms (Daghrir
64 and Drogui, 2013). To date, more attention has been paid to the investigation of
65 tetracycline removal at low concentrations, e.g. $\mu\text{g/L}$ (Kim et al., 2005), however,
66 tetracycline could be present at levels up to 200 mg L^{-1} in pharmaceutical wastewater
67 (Song et al., 2019). The acute toxicity effect from such high concentrations of
68 tetracycline raises significant challenges to conventional wastewater treatment methods.
69 Previous studies have indicated that WWTPs can only achieve up to 30% removal of
70 this drug (Watkinson et al., 2009), which may be attributed to the toxic effects of
71 tetracycline on the bacterial population present in aerobic sludge (Halling-Sørensen,
72 2001), especially with exposure at high concentration. Thus, development of technology

73 for the effective and economic mitigation of tetracycline at high concentrations is
74 urgently required.

75 Various approaches, such as flocculation (Fu et al., 2015), advanced oxidation
76 (Hou et al., 2016), and adsorption (Gao et al., 2012), have been proven to effectively
77 remove tetracycline from wastewater at high concentrations. However, such methods
78 require increasing dosage of additional chemicals with rising concentration of
79 tetracycline. Consequently, the large scale application of such techniques is still
80 hindered by their relatively high costs and the potential problem of secondary pollutants
81 (Tang et al., 2016). Microalgal technology has been recognised as an eco-friendly, and
82 cost-effective method for water treatment, including removal of emerging contaminants
83 (Matamoros et al., 2016). A further advantage of this technique is the potential reuse of
84 the algal biomass (Pan et al., 2018). Therefore, microalgal species with high economic
85 value, such as *Chlorella pyrenoidosa* (*C. pyrenoidosa*; Sun et al., 2011), have hitherto
86 been mostly selected for wastewater treatment. Cyanobacteria, although the most well-
87 known species responsible for harmful algal blooms (HABs) in eutrophic waters (Zhang
88 et al., 2018), is often neglected because of the production of toxic microcystins as by-
89 products of metabolism (Hitzfeld et al., 2000). From the perspective of wastewater
90 treatment, its characteristics of rapid growth, high nutrient uptake capability, and low
91 requirement for a favourable environment (e.g. temperature and pH), could make
92 cyanobacteria an ideal microalgae species, if the release of unwanted toxins could be
93 controlled during the process (Rzymiski et al., 2014).

94 Microalgal technology has been demonstrated to effectively remove tetracycline
95 under low initial concentration levels ($<2 \text{ mg L}^{-1}$) (Norvill et al., 2017; de Godos et al.,
96 2012). However, studies on microalgal technology for the treatment of wastewater
97 containing high concentrations of tetracycline, have been rarely investigated.

98 Furthermore, some microalgal species exhibit a Gram-negative-bacteria-like prokaryotic
99 structure, in which cases tetracycline could generate biphasic hormetic effects, *i.e.*
100 inhibition at high doses and stimulation at low doses (Wan et al., 2015). Thus, a high
101 initial concentration of the drug may lead to a dramatically low removal performance,
102 an effect which has rarely been thoroughly investigated. Therefore, research on the
103 removal, by microalgae, of high concentrations of tetracycline from PPCPs-polluted
104 wastewater is needed and is still challenging.

105 Considering the application of different microalgal species, full-scale microalgae
106 treatment systems, e.g., tubular photo-bioreactor and raceway ponds, have been
107 successfully applied for the treatment of various wastewaters, such as municipal
108 wastewater (Rawat et al., 2011) and livestock effluent (Wang et al., 2016). Nevertheless,
109 the major concern of using cyanobacteria to replace other commonly-used microalgae
110 species, e.g., *C. pyrenoidosa*, is the potential risk of toxin release during algal death and
111 cell lysis (Paerl and Otten, 2013). A previous study has demonstrated the significant
112 decrease of microcystin production and release from cyanobacteria on exposure to
113 tetracycline up to 10 mg L⁻¹ (Ye et al., 2017). This effect may have been due to the
114 blocking of peptide synthesis, controlling the production of microcystin-LR (Ye et al.,
115 2017) and a corresponding enhancement in the production of reactive oxygen species
116 (ROS) (Yang et al., 2013) due to the presence of tetracycline. However, release of
117 toxins from cyanobacteria under higher tetracycline concentrations (>10 mg L⁻¹) has
118 rarely been investigated. Release of toxins from cyanobacteria mainly occurs during
119 algal death and cell lysis. Thus, the monitoring of algal cell vitality and the
120 measurement of toxin production during the process is essential in order to evaluate the
121 safety envelope of the treatment technology.

122 The mechanisms of antibiotics removal, including pathways and metabolism, by
123 different microalgal species, always vary. It is generally agreed that comprehensive
124 pathways, i.e. photolysis, hydrolysis, cation-binding, adsorption, bioaccumulation and
125 biodegradation, may simultaneously contribute to the removal of antibiotics from the
126 environment (Xiong et al., 2017a). It has been found that photodegradation mainly
127 contributed to tetracycline removal (Norvill et al., 2017), however, de Godos *et al.*
128 (2012) reported that biosorption and photodegradation are both predominant pathways
129 for tetracycline removal during treatment by different microalgae. Thus, quantitative
130 investigation of removal pathways is vitally important for the understanding of
131 cyanobacteria-based treatment of tetracycline. Moreover, Halling-Sørensen *et al.* (2002)
132 have highlighted that anhydrotetracycline (ATC) and 4-epianhydrotetracycline (EATC)
133 could be major by-products of metabolism, and which may be more toxic than the
134 parent compound, during remediation in aqueous conditions (Halling-Sørensen et al.,
135 2002). Thus, identification of the by-products of degradation is also important in order
136 to systematically understand remediation mechanisms (Halling-Sørensen et al., 2002)
137 and potential environmental impacts.

138 In this study, we investigated the potential use of harmful cyanobacteria to
139 effectively and safely remediate wastewater containing high concentration of
140 tetracycline, and elucidated the probable mechanisms of removal. The removal
141 efficiencies of tetracycline by the cyanobacteria, *Microcystis aeruginosa* (*M.*
142 *aeruginosa*), were compared with the treatment by representative wastewater treatment
143 microalgal species *C. pyrenoidosa* at relatively high initial concentrations (10-100 mg
144 L⁻¹) of the drug. Different pathways and degradation by-products of tetracycline aided
145 the elucidation of likely removal mechanisms. Algal biomass growth and cell vitality
146 were characterised to estimate possibilities for biomass reuse. Moreover, levels of toxic

147 microcystin-LR, released from *M. aeruginosa*, was monitored, in order to assess water
148 reuse/discharge safety.

149 **2. Materials and methods**

150 *2.1 Materials*

151 Two species of microalgae strains, *M. aeruginosa* and *C. pyrenoidosa*, were
152 purchased from the freshwater algae culture collection at the Institute of Hydrobiology
153 (FACHB), Wuhan, China, and cultivated in BG11 media (Table S1) prior use.
154 Tetracycline was obtained from J&K Scientific Ltd., Beijing, China. Microcystin-LR
155 standard (SB05-287-2012) was purchased from the National Standard Material Center
156 of China (Beijing, China). All reagents used were of analytical grade and ultrapure
157 water (18 M Ω ·cm) was used in all experiments.

158 *2.2 Experimental operation*

159 The removal performance of tetracycline by the two microalgal species was
160 evaluated under different initial tetracycline concentrations. An appropriate volume of a
161 tetracycline solution in ultra-pure water was added into each BG11 culture medium,
162 resulting in three different concentrations of 10, 50, and 100 mg L⁻¹. Three control
163 groups were set up to elucidate the removal of tetracycline by natural degradation
164 (photolysis and hydrolysis) and binding to divalent cations (calcium, magnesium, cobalt)
165 present in the BG11 culture media. The groups comprised 1) BG11 medium with
166 tetracycline, but without microalgae under irradiation, was set as a light control, 2)
167 BG11 medium with tetracycline, but without microalgae and irradiation, was set as a
168 dark control, and 3) pure water with tetracycline, but without microalgae and irradiation,
169 was set as a chemical control. To clarify the removal of tetracycline by natural
170 degradation (photolysis and hydrolysis) and binding to divalent cations (calcium,

171 ~~magnesium, cobalt) present in the BG11 culture medium, a culture medium with~~
172 ~~tetracycline but without microalgae was set as the light control, whereas a sample of~~
173 ~~BG11 culture media with microalgae, but without tetracycline addition, was set as the~~
174 ~~microalgal control.~~ Media with microalgae addition are hitherto referred to as *treatment*
175 *groups*.

176 The treatments were conducted in Erlenmeyer flasks (1L) with 500 mL working
177 volume. Different microalgae species have distinct cell sizes and growth rates, therefore,
178 previous studies usually conducted wastewater treatment experiments under similar
179 initial algal biomass concentrations in order to allow the results to be directly
180 comparable (Arbib et al., 2014). To better compare the tetracycline removal
181 performance, the two species were separately pre-cultured until the late exponential
182 phase. Afterwards, both microalgal species were inoculated into corresponding flasks to
183 achieve an identical optical density (OD680) of 0.103 ± 0.016 , which represented the
184 same biomass concentrations (7.12×10^6 cell mL⁻¹ *M. aeruginosa* and 7.50×10^5 cell
185 mL⁻¹ *C. pyrenoidosa*). All flasks were placed in an incubator maintained at 28 ± 1 °C and
186 illuminated by white light (full-spectrum white LED; Ledvance GmbH, Garching,
187 Germany; intensity 1600 lux; light:dark ratio of 12:12h). All flasks were swirled
188 manually three times (5 mins each) each day. The experimental setup with the initial
189 tetracycline concentration of 50 mg L⁻¹ was selected for comprehensive study into the
190 possible removal pathways. ~~In addition, a dark control group (flasks wrapped in~~
191 ~~aluminium foil), which contained only tetracycline in growth media without algae, was~~
192 ~~prepared in order to determine abiotic hydrolysis and cation binding of tetracycline.~~
193 Each group was set up in triplicate and operated for 13 days. In total, 36 treatments were
194 conducted for the investigation.

195 2.3 Sampling and analysis

196 *2.3.1 Sampling*

197 The pH of each treatment suspension was measured daily directly in the flask
198 using a PHB-600R pH meter (Omega Engineering, Norwalk, USA). In addition,
199 samples (0.2 mL) were taken daily for algal cell counting, while another sample (2 mL)
200 was taken from each flask at 0, 2, 4, 6, 16 and 24 hours, and then daily until day 13, for
201 determination of tetracycline concentration, by ultrahigh-performance liquid
202 chromatography (Waters Acquity UPLC, Waters Corp., Milford, USA) as described
203 later. Samples for investigation into possible tetracycline removal pathways,
204 microcystin-LR production, and detection of degradation by-products, were also taken
205 on the corresponding days.

206 *2.3.2 Tetracycline analysis and removal pathways*

207 Thus, tetracycline removal kinetics by natural hydrolysis, photolysis, and cation-
208 binding were determined by sampling at hour 0, 2, 4, 10, 16, and daily from day 1 to
209 day 11. The chemical control group could be categorised as the abiotic hydrolysis of
210 tetracycline. The difference between tetracycline removal in the dark and in the
211 chemical control groups was considered to represent tetracycline removal caused by
212 cation-binding. Meanwhile, differences between tetracycline removal in light and dark
213 control groups enabled estimation of abiotic photolysis process. The sampling methods
214 for tetracycline distribution (in water, via bio-adsorption, and via bio--accumulation) are
215 described in Text S1.1. The light control theoretically enable estimation of tetracycline
216 removal through photolysis, hydrolysis, and cation binding processes. Meanwhile, the
217 dark control was conducted to simulate the theoretical tetracycline removal through
218 hydrolysis and cation binding processes. Each 2 mL water sample was centrifuged
219 (4500 rpm for 15 min) in order to separate the algae and supernatant, with the latter
220 being subsequently used for the determination of tetracycline concentration remaining

221 ~~in water. The sample was further passed through a membrane filter (0.22 µm) prior to~~
222 ~~injection into the UPLC. Notably, at 24, 240 and 312 hours, additional samples (5 mL)~~
223 ~~were taken from the flasks and centrifuged as described previously. After complete re-~~
224 ~~suspension and homogenization with ultrapure water (5 mL), each algal pellet was~~
225 ~~washed and re-centrifuged, the supernatant being analysed for bio-adsorbed tetracycline.~~
226 ~~The algal pellet was then homogenized into a methanol and dichloromethane mixture (5~~
227 ~~mL; 2:1, v/v). After further treatment by freeze thawing with liquid nitrogen (x3),~~
228 ~~samples were centrifuged and the supernatant quantified as the intracellular~~
229 ~~bioaccumulated tetracycline fraction.~~ The analysis parameters for UV detection of
230 tetracycline by Acquity UPLC-PDA (Diode Array Detector) are detailed in S1.1.

231 *2.3.3 Detection of degradation by-products*

232 Filtered water samples (supernatant phase, 0.22 µm membrane filter), from
233 treatments spiked with an initial tetracycline concentration of 50 mg L⁻¹, were used to
234 identify tetracycline degradation by-products by analysis with an Acquity UPLC
235 coupled with a Waters Xevo G2 ToF-MS detector (Waters Corp., Milford, USA). Only
236 samples collected at 24 and 312 hours were processed. The working parameters for the
237 Acquity UPLC are described in the supporting information (Text S1. 2) and the working
238 parameters of the ToF-MS were: mass range 50-1200 Da, scan time 1.5 sec, collision
239 energy 6V, collision energy ramp 15 to 30 V, cone voltage 40 V, positive polarity.

240 *2.3.4 Microcystin-LR measurement*

241 The most toxic microcystin compound, microcystin-LR, was detected by UPLC-
242 UV in both intracellular and extracellular fractions in the samples collected at 10, 60
243 and 240 hours from the treatment groups with an initial tetracycline concentration of 50
244 mg L⁻¹. Specifically, 50 mL sample was initially centrifuged (4800 rpm for 15 min).
245 The supernatant thus produced was then used for the quantification of released

246 microcystin-LR after pre-concentration by SPE (Oasis R MCX 6cc, 500mg, Waters
247 Corp., Milford, USA). The SPE was initially activated with 100% methanol (10 mL),
248 followed by a wash-out of ultrapure water (20 mL, 3 mL min⁻¹). A gradient
249 concentration of methanol (0-20%, v/v) was utilized for the wash-out of impurities and
250 methanol (3 mL, 35% v/v) for elution of the microcystin-LR. After collection, the eluent
251 was evaporated under dry nitrogen to 1.2 mL.

252 The algal pellet was also analysed for intracellular microcystin-LR. Briefly, after
253 washing three times with ultrapure water, the pellet was dissolved with methanol (80%
254 v/v) and freeze-thawing with liquid nitrogen (x3) in order to fragment the algal cells,
255 and to extract the microcystin-LR. Finally, 1 mL sample was concentrated by
256 evaporation under dry nitrogen at room temperature. The working parameters of
257 Acquity UPLC for microcystin-LR detection are described in S.1.3.

258 *2.4 Microalgal growth monitoring*

259 Cell densities of both microalgae species were monitored daily using a
260 hemocytometer. After sampling on day 1, 3, 6, and 10, cell pigments were detected and
261 calculated as described in S1.4.

262 *2.5 Calculation and statistical analysis*

263 The Pseudo-first-order kinetic model (1) was used to simulate the removal,
264 desorption and decline of accumulated tetracycline: degradation removal, adsorption and
265 accumulation of tetracycline based on equation (1) and (2):

$$266 \ln(C_0/C) = k \times t \quad (1)$$

267 Meanwhile, according to (Choi et al., 2020), the concentration changes
268 through adsorption and accumulation by microalgae was simulated with modified
269 pseudo-first-order kinetic model (2):

270
$$\ln(1-C_0/C) = -k \times t \quad (2)$$

271 where, C_0 is the concentration of tetracycline at time $t=0$ and C is the tetracycline at
272 time $t=t$; k represents the pseudo-first-order kinetic rate constant; t is the time.

273 SPSS 19.0 (IBM Corporation, Armonk, USA) and Origin 8.5 (OriginLab,
274 Northampton, USA) were used to analyse and to plot the data, respectively. One-way
275 ANOVA and Tukey's multiple comparison test were used to compare ($p<0.05$) water
276 quality parameters between different treatment systems at each sampling point.

277 **3. Results and Discussion**

278 *3.1 Tetracycline removal efficiency and kinetics*

279 Tetracycline is a chemically reactive compound which can be degraded through
280 photolysis and/or hydrolysis processes (Yi et al., 2016; Jiao et al., 2008). This
281 characteristic supports the observation that the tetracycline degraded in all control
282 groups, even without addition of microalgae. In this study, *C. pyrenoidosa* was selected
283 as a representative, widely-investigated, and safe microalgal species for wastewater
284 treatment (Sun et al., 2011). The comparison of tetracycline removal efficiencies
285 between *M. aeruginosa* and *C. pyrenoidosa* could contribute to a better understanding
286 of the advantages or drawbacks for treatment of wastewater, containing high
287 concentrations of tetracycline, by the newly proposed HABs species over conventional
288 microalgae species. For *C. pyrenoidosa* treatments (Fig. 1a), from an initial
289 concentration of 10 mg L^{-1} , the tetracycline concentration significantly decreased to
290 0.65 mg L^{-1} (93.9% removal) by day 2 and then reached 0.01 mg L^{-1} (99% removal) on
291 day 11. However, the *M. aeruginosa* treatments showed a much faster removal rate, and
292 achieved 0.01 mg L^{-1} (99% removal) at day 2 which was furthermore maintained until
293 day 11 (Fig. 1a). Previous studies have indicated that higher tetracycline concentration

294 might hinder microalgae growth (Ye et al., 2017) and therefore affect drug removal.
295 This observation is supported in this study by the *C. pyrenoidosa* groups, at the higher
296 initial concentration of 50 mg L⁻¹ (Fig. 1b), where tetracycline concentrations decreased
297 faster than those in the control group, until day 4 after which it maintained at 0.7 mg L⁻¹
298 (98.6% removal rate) and performed similarly to the control. The growth of the algal
299 biomass may act to decrease the light penetration in the water and thus affect photolysis
300 and/or hydrolysis removal of tetracycline. Thus, at the initial concentration of 100 mg L⁻¹,
301 the tetracycline removal in *C. pyrenoidosa* groups became similar, or even less
302 effective, when compared to the control (Fig. 1c).

303 The *M. aeruginosa* groups consistently exhibited significantly superior
304 performance for tetracycline removal at high initial concentrations of 50 and 100 mg L⁻¹,
305 where the similar tendencies of rapid removal over 98.0% were achieved within 1 and 2
306 days, respectively (Fig. 1b and c). *M. aeruginosa*, as a typical cyanobacterial alga,
307 demonstrated a rapid reproduction rate, which, however, could lead to the appearance of
308 serious harmful algal blooms within several days in eutrophic lakes (Paerl and Otten,
309 2013). The existence of *M. aeruginosa* has been observed worldwide, regardless of
310 temperature and pH variance of the water (Paerl and Otten, 2013), which may indicate
311 its high tolerance against any antibiotic effects. The results demonstrated that the
312 harmful cyanobacteria, *M. aeruginosa*, could rapidly and effectively remove
313 tetracycline within limitations of initial concentration. Previous studies indicated that, in
314 algal ponds, only 69±1% tetracycline was removed from an initial concentration of 2
315 mg L⁻¹ (de Godos et al., 2012), and 93% tetracycline was eliminated from an initial
316 concentration of 0.1 mg L⁻¹ in 4 days (Norvill et al., 2017). Comparatively, the *M.*
317 *aeruginosa* demonstrated a much higher and faster removal capacity of tetracycline over
318 a wide range of initial concentrations, up to 100 mg L⁻¹.

319 Tetracycline removal is widely indicated by studies to follow the pseudo-first-
320 order kinetics in high-rate algal pond (HRAP) systems (de Godos et al., 2012, Norvill et
321 al., 2017). The results of tetracycline removal in this study also exhibited good
322 correspondence with the pseudo-first-order kinetic model (Fig. 1, Table 1, $R^2 > 0.94$).
323 Generally, elevation of levels of tetracycline significantly decreased the removal rates
324 (k). ~~Meanwhile, the light controls (including photolysis, hydrolysis and cation binding~~
325 ~~processes) achieved 1.7 times higher k value than did the dark controls (including~~
326 ~~hydrolysis and cation-binding processes), indicating the significance of photolysis to~~
327 ~~tetracycline removal.~~ Except for the *C. pyrenoidosa* with 100 mg L⁻¹ tetracycline, in
328 which the growth of microalgae probably inhibited the photolysis of tetracycline and
329 generated lower removal rates than the control, all other groups of both microalgae
330 species achieved greater removal rates than the control. This indicated a significant
331 promotion of the presence of microalgae on tetracycline removal than the natural
332 removal processes contributed by hydrolysis, photolysis, and cation-binding, especially
333 with *M. aeruginosa* (5.1-12.1 times higher than the control). The results further
334 demonstrated that, overall, *M. aeruginosa* exhibited significantly higher removal rates,
335 at all tetracycline levels, than did the *C. pyrenoidosa* ($p < 0.05$), indicating a better
336 general tetracycline removal ability of *M. aeruginosa* than the *C. pyrenoidosa*.
337 Compared with previous studies, the pseudo-first-order kinetic rate results also showed
338 statistically better tetracycline removal kinetic achieved by *M. aeruginosa* (0.17-0.077,
339 10-100 mg L⁻¹ tetracycline) than that achieved by the HRAP (0.091-0.038, 0-88 mg TSS
340 L⁻¹ biomass, 2 mg L⁻¹ tetracycline; (de Godos et al., 2012) and photolysis/hydrolysis
341 processes (0.0014-0.0065, 20-100 mg L⁻¹ tetracycline; Yi et al., 2016; Jiao et al., 2008).

342 3.2 Tetracycline removal pathways

343 The experiment at the initial tetracycline concentration of 50 mg L⁻¹ was further
344 explored in order to understand the contributions from each pathway of removal.
345 Considering the abiotic removal of tetracycline, processes of cation-binding, photolysis,
346 and hydrolysis all contributed to the removal of tetracycline, acting however, at
347 different levels (Fig. 2a-b, and S2a-b). The results from the chemical control group
348 indicated that divalent cations present in the BG11 medium (Table S1), such as calcium,
349 magnesium, and cobalt, could bind with tetracycline to form low solubility complexes
350 (Pala-Ozkok et al., 2019), which contributed to a relatively constant tetracycline
351 removal in the range of 1.42-4.08 mg L⁻¹ (2.8-8.0%, Fig. S2a). Meanwhile, abiotic
352 photolysis achieved a significant higher (p<0.05) removal rate (k=0.029) than did
353 abiotic hydrolysis (k=0.0069, Table S2).

354 Results further indicated that the significantly higher removal rates of tetracycline
355 (p<0.05) achieved by microalgae (especially by *M. aeruginosa*) ~~may be~~ could be
356 contributed through bioadsorption, bioaccumulation and biodegradation processes ~~of~~
357 microalgae (Fig. 2c-d and S2c). ; but also by the impact of microalgal growth on abiotic
358 hydrolytic and photolytic processes. Thus, tetracycline removal in the dark control
359 groups was attributed to hydrolysis and cation binding reactions (without microalgal
360 influence). Moreover, the concentration difference between the light control groups and
361 the dark control groups could be recognised as the theoretical removal by photolysis
362 (without microalgal influence). From the control groups, it can be concluded that all
363 abiotic photolysis, abiotic hydrolysis and cation binding clearly contributed to
364 tetracycline removal (Fig. 2a and b). Throughout the whole experiment, Simultaneous
365 with the decline in concentration of tetracyclines in water, concentrations adsorbed and
366 accumulated by both microalgae increased to a peak (uptake stage) inside one (*M.*
367 *aeruginosa*) or two (*C. pyrenoidosa*) days. For the *C. pyrenoidosa* treatment groups, the

368 bioremediation (including bio-adsorption, bio-accumulation, and bio-degradation)
369 contribution of the algae was always observed to be lower ($<10.41 \text{ mg L}^{-1}$, less than
370 20.5% contribution) than those from abiotic photolysis, hydrolysis, and cation-binding.
371 However, *M. aeruginosa* could be considered more effective for tetracycline
372 bioremediation (39.02 mg L^{-1} , 71.6% contribution) providing a total removal efficiency
373 of 98% after only 24 hours (Fig. 1, 2a and b). ~~Specifically, for bioremediation, the~~
374 ~~distribution results of residual tetracycline indicated that rapid adsorption (0.84 mg L^{-1}~~
375 ~~by *M. aeruginosa* and 2.46 mg L^{-1} by *C. pyrenoidosa*) and bioaccumulation (0.23 mg~~
376 ~~L^{-1} by *M. aeruginosa* and 5.56 mg L^{-1} by *C. pyrenoidosa*) of tetracycline could be~~
377 ~~achieved from day 1 by both microalgal species (Fig. 2c and d).~~ Previous studies also
378 illustrated that tetracycline, owing to its hydrophilic nature, could be absorbed by the
379 algal cell (de Godos et al., 2012). The compound has also been found to translocate into
380 an algal cell through water and nutrient uptake pathways (Xiong et al., 2017a). However,
381 the amount of tetracycline existing on cell surfaces (bioadsorption) and intracellular
382 regions (bio-accumulation) in *M. aeruginosa* (1.07 mg L^{-1} , 2%) was much lower than
383 that in *C. pyrenoidosa* (8.02 mg L^{-1} , 16%) on day 1. Afterwards, a gradual decline
384 of concentrations from the peak was followed until day 13 (through either metabolization
385 or release). Both concentrations of bioadsorbed and bioaccumulated tetracycline
386 changed as a consequence of microalgal uptake and translocation, and could be well
387 described by the pseudo-first-order kinetic model ($R^2 \geq 0.90$, Table S2). Generally, in the
388 uptake stage of tetracycline, the rates of bio-adsorption by both microalgal species were
389 significantly higher than those of bio-accumulation ($p < 0.05$) and, overall, *M.*
390 *aeruginosa* achieved higher rates of bio-adsorption and bio-accumulation ($k = 0.66$ and
391 0.19 , respectively) than did *C. pyrenoidosa* ($k = 0.37$ and 0.12 , respectively, Table S2).
392 Nevertheless, *M. aeruginosa* promoted a shorter uptake stage of tetracycline when

393 compared to *C. pyrenoidosa*. In the declining stage of tetracycline, the desorption rates
394 of *M. aeruginosa* ($k=0.23$) were still significantly higher than that of *C. pyrenoidosa*
395 ($k=0.071$), however, both species achieved similar decrease rates of accumulated
396 tetracycline ($k=0.012$ and 0.011 , respectively, $p>0.05$). Considering the superior
397 tetracycline removal efficiency in *M. aeruginosa* treatment groups, the species
398 presented significantly higher tetracycline biodegradation either inside the algal cell or
399 by side effects outside the algal cell, when compared with *C. pyrenoidosa*.

400 Although the contributions of each pathway may vary, the results supported the
401 hypothesis that all possible pathways, such as hydrolysis (tetracycline molecule split by
402 chemically-catalysed addition of water), photolysis (light-activated oxidation), cation-
403 binding (tetracycline binding with divalent cations), biodegradation (decomposition of
404 tetracycline by microbial activity), bioadsorption (tetracycline passively concentrating
405 and binding onto microalgal cells) and bioaccumulation (accumulation of tetracycline in
406 the microalgae cells) (Yi et al., 2016; Jiao et al., 2008; Xiong et al., 2017b), have an
407 effect on tetracycline removal. It should be noted that among the confirmed pathways,
408 more than one mechanism can take place simultaneously and thus can influence each
409 other. For example, the growth of microalgal biomass could reduce the intensity of light
410 inside the water column and thus reduce tetracycline degradation by photolysis (de
411 Godos et al., 2012) (Fig. 1c). Consequently, the realistic photolysis kinetics of
412 tetracycline removal in both microalgal systems should be less than those of the
413 theoretical results (Fig. 2-a and b-c). Oppositely, it was observed that the inoculum and
414 growth of both *M. aeruginosa* and *C. pyrenoidosa* led to an increase in solution pH than
415 the controls. Moreover, the *M. aeruginosa* samples generally produced significantly
416 higher pH levels than did the *C. pyrenoidosa* groups ($p<0.05$, Fig. S3). Previous studies
417 have suggested a reduction in tetracycline hydrolysis half-life time by 2.68-3.27 -fold

418 with an increase of pH from 5 to 11 (22-25°C) (Yi et al., 2016). Thus, the realistic
419 hydrolysis of tetracycline under both microalgal treatments should be significantly
420 increased, above those theoretical hydrolysis kinetics (Fig. [2c2-a and b](#)). The higher
421 levels of pH in the *M. aeruginosa* groups could promote a higher tetracycline hydrolysis
422 compared to that from the *C. pyrenoidosa* groups. Additionally, the elevated
423 photosynthetic processes occurring in microalgal treatments (Fig. [S5-S4](#) and [S6S5](#)) may
424 increase both dissolved oxygen (DO) and pH, increasing the number of reactive oxygen
425 species (ROS) (Norvill et al., 2017), which, in turn, may also lead to the degradation of
426 tetracycline. ~~Moreover, the existence of microalgae and transition metals may lead to
427 more complex tetracycline removal pathways such as indirect oxidation induced by
428 microalgae secretions (Tian et al., 2019), photo-catalysis of transition metals (Wei et al.,
429 2020), and affect the hydrolysis as well as the photolysis. Further investigations into the
430 specific contributions of each tetracycline removal pathway and simulation of their
431 potential kinetics should be carried out in order to gain understanding into the
432 underlying mechanisms and thus help realize the implications.~~

433 3.3 Tetracycline degradation by-products

434 Water samples from both microalgal treatment groups were analysed by HPLC-
435 ToF-MS in order to determine potential degradation by-products and removal pathways.
436 Based on the results from the LC-ToF-MS analysis (Fig. [S3-S6](#) and [S4S7](#)) and a review
437 of extant literature, we have elucidated that both microalgal systems utilised a common
438 degradation pathway (named PI), but also used additional specific pathways unique to
439 each species.

440 The results indicated that the tetracycline degradation process proceeded mainly
441 by two reaction patterns, *i.e.* changes to functional groups (gain and loss), and ring-
442 opening reactions (Cao et al., 2016). Relevant structures and ESI-ToFMS spectra are

443 illustrated in Fig. S7. By-product 1 (m/z 415) was detected in the samples (Fig. 3, PI),
444 which indicated the removal of the N-methyl and C3 hydroxyl groups (Shen et al.,
445 2020). Further loss of the C6 hydroxyl group and the formation of a conjugated double
446 bond at C6-C5a position, resulted in the formation of by-product 2 (m/z 397) (Huang et
447 al., 2019). This molecule could be further degraded via loss of the amide group at
448 position C2 (Huang et al., 2019) and further demethylation of the secondary amine at
449 position C4 (Guo et al., 2018), forming by-product 3 (m/z 340). The ring-opening
450 reaction across C2 and C4a could lead to the formation of by-product 4 (m/z 284)
451 (Huang et al., 2019), while further ring fragmentation across C5a and C11a with
452 concurrent hydration could generate by-product 5 (m/z 183) (Zhou et al., 2020).
453 Notably, most by-products of the PI pathway (m/z 415, 397, 340, 284) were also found
454 in a tetracycline photo-catalysis degradation process mediated by a Bi₂WO₆-based
455 material (Shen et al., 2020; Huang et al., 2019). Meanwhile, the final product from PI
456 (m/z 183) was reported from an activated hydrogen peroxide oxidation process for
457 tetracycline degradation (Zhou et al., 2020). This final product (m/z 183) has been
458 evaluated by Zhou et al (2020) according to the Globally Harmonized System of
459 classification and labelling of chemicals (GHS) method, showing a significantly
460 reduced toxicity relative to the parent tetracycline (Zhou et al., 2020).

461 In addition to pathway PI, an additional scheme (PII) could be identified for
462 tetracycline degradation by *M. aeruginosa* (Fig. 3a), namely, occurrence of ring-
463 opening across the C1 and C4 positions, and fission of the double bond between C2 and
464 C3 to form the by-product 6 (m/z 163). A further loss of N-methyl resulted in the
465 formation of by-product 7 (m/z 149). Both tetracycline by-products 6 and 7 have been
466 previously reported from a degradation experiment via TiO₂ photo-catalysis (Niu et al.,
467 2013). Therefore, both degradation pathways (PI and PII) may include some processes

468 ~~of photo-catalysis degradation. This could be caused by the microalgae-induced indirect~~
469 ~~photo-degradation of antibiotics. It has been proved that, under irradiation, the~~
470 ~~extracellular organic matters (EOMs) released by microalgae could promote the~~
471 ~~formation of active species, which may lead to indirect photo-degradation of antibiotics~~
472 ~~(Tian et al., 2019). Moreover, the ferric ion (in BG11 medium) may further react with~~
473 ~~the EOMs to generate Fe(III)-carboxylate complexes, resulting in further augmentation~~
474 ~~of the antibiotic photolysis (Wei et al., 2020). The potential photo-catalysis degradation~~
475 ~~by-products 6 and 7 (m/z 163, 149) from pathway PII generated by *M. aeruginosa*~~
476 ~~were have been demonstrated to exhibit a decreased~~ toxicity compared to the parent
477 compound (Niu et al., 2013). However, a different degradation pathway (named PIII,
478 Fig. 3b) was identified in *C. pyrenoidosa* systems, where the double bond at the C11a-
479 C12 position was attacked by OH· to form by-product 8 (m/z 461). This molecule was
480 then further degraded to by-product 9 (m/z 459) via hydrogen abstraction at the C5-C5a
481 position (Ao et al., 2019). The by-products of PIII pathway (m/z 461, 459) were
482 reported from an activated peroxymonosulfate oxidation process (Ao et al., 2019).
483 Moreover, the by-products 8 and 9 from pathway PIII generated by *C. pyrenoidosa*,
484 even reduced its toxicity to algae (based on the GHS evaluation), but still demonstrated
485 the same level of toxicity to fish and daphnid according to previous studies (Pala-Ozkok
486 et al., 2019). Therefore, the defined degradation pathway from *M. aeruginosa* treatment
487 groups may be used to support the rapid rate of tetracycline removal and greater
488 efficiency compared with those from the *C. pyrenoidosa* groups. Further systematic
489 toxicity evolution experiments could help to ensure reductions in toxicity of the by-
490 products.

491 3.4 Microalgae biomass and vitality response

492 Microalgal-based wastewater treatment offers the advantage of, in addition to the
493 elimination of the pollutant, potential biomass re-utilization, *e.g.*, as biofuel, biochar, or
494 fertilizer (Kim et al., 2012; Miao et al., 2004). Therefore, during the experiment, we
495 further investigated changes occurring to the biomass, due to tetracycline exposure.
496 Between the two algal species, *M. aeruginosa* demonstrated a better tolerance and
497 growth recovery against tetracycline than did the *C. pyrenoidosa*. Specifically,
498 tetracycline generated an acute inhibition on the growth of *M. aeruginosa*, at all
499 concentrations, after one day incubation (Fig. 4a). However, the inhibition was
500 temporary, and growth fully recovered afterwards. No significant differences in cell
501 numbers were observed with the 10 and 50 mg L⁻¹ tetracycline solutions (4.36 x 10⁷
502 cells mL⁻¹ and 3.11 x 10⁷ cells mL⁻¹, respectively) which were also similar to the algal
503 cell numbers noted in microalgal control groups (4.19 x 10⁷ cells mL⁻¹, *p*>0.05) at day
504 11 (Fig. 4a). However, 100 mg L⁻¹ tetracycline slightly inhibited biomass growth of *M.*
505 *aeruginosa* (*p*<0.05) until day 11. Comparatively, all three concentrations of
506 tetracycline inhibited the growth of *C. pyrenoidosa* to a greater extent than the
507 microalgal control (1.74 x 10⁷ cells mL⁻¹), resulting in a final value of 1.87-9.58 x 10⁶
508 cells mL⁻¹ (Fig. 4b). The results agreed well with a previous study, which revealed the
509 inhibition, adaption, and hormesis effects of tetracycline on *M. aeruginosa* at
510 concentrations under 10 mg L⁻¹ (Ye et al., 2017). However, our study further extended
511 the tetracycline concentration to 100 mg L⁻¹, and proved a recovery ability of *M.*
512 *aeruginosa* at tetracycline concentrations under 50 mg L⁻¹.

513 Additionally, the results of pigment concentration (chlorophyll-a and carotenoid)
514 and fluorescence signal intensity (Fv/Fm) analyses also agreed well with the impacts of
515 cell number, where all tetracycline concentrations generated an acute inhibition on
516 pigment accumulation and photosynthesis intensity (Fv/Fm). However, at tetracycline

517 concentrations under 50 mg L⁻¹, both algal species demonstrated stepwise recoveries in
518 varying degrees (Fig. S5 and S6). We concluded from these results, that *M. aeruginosa*
519 possessed a strong tetracycline removal capacity along with a higher tolerance to
520 tetracycline than did *C. pyrenoidosa*. Meanwhile, the successful recovery ability of *M.*
521 *aeruginosa* showed the potential for high biomass production, which could benefit re-
522 utilization upon completion of the treatment process.

523 3.5 Effect of tetracycline on microcystin release

524 As a species of cyanobacteria, *M. aeruginosa* poses a potential threat for
525 microcystin release, which may cause damage, in humans, to the liver and to the
526 nervous system (Hitzfeld et al., 2000). Consequently, we paid close attention to the
527 investigation of changes in both intercellular and released microcystin during the
528 treatment process. The study of toxin-release of *M. aeruginosa* is significant for
529 broadening the valorization of HABs species. The synthesis of microcystin is induced
530 by a mechanism protective against both abiotic and biotic stress (Babica et al., 2006)
531 and is often coupled with photosynthesis (Walls et al., 2018). Microcystin, however,
532 typically remains intracellularly, unless being released into the surroundings through
533 cell death and lysis, or as extracellular release (Paerl and Otten, 2013). In the present
534 study, at initial tetracycline concentrations of 10 and 50 mg L⁻¹, *M. aeruginosa* cells
535 analysed were in a growing or stable phase, reflected by cell growth curves (Fig. 4a).
536 Thus, intracellular microcystin-LR concentrations were generally higher than those
537 measured in the water (Fig. 5). For intracellular microcystin-LR, tetracycline inhibited
538 photosynthesis (Fig. S5a). It also exerted abiotic stress, which may have resulted in no
539 significant differences in intracellular microcystin-LR production being noted within 60
540 hours ($p > 0.05$, except the systems with 100mg L⁻¹ tetracycline), however, being
541 distinctly lowered over 240 hours (Fig. 5a, $p < 0.05$). This reduction of induced

542 microcystin-LR may be caused by the long-term damage caused by tetracycline on the
543 synthesis of peptide synthetases, which control microcystin-LR production (Ye et al.,
544 2017).

545 The microalgal control group simulated the development of *M. aeruginosa*
546 unexposed to tetracycline, where an accelerating growth and metabolism was observed
547 (Fig. 4a). The increasing death and lysis of the cells coupled with *M. aeruginosa* growth
548 could result in an elevated microcystin-LR release into the water (Fig. 5b). Notably, an
549 overall decreasing release of microcystin-LR into the water was detected due to
550 tetracycline exposure (in the tetracycline treated groups) compared to the microalgal
551 control (except at 10 hours with 10mg L⁻¹ tetracycline). This may be mainly due to the
552 reduced growth and metabolic activity of the microalgae, caused by tetracycline. The
553 rapid tetracycline removal ability of *M. aeruginosa*, which produced a removal rate of
554 over 98% in 24 hours (under 50 mg L⁻¹ tetracycline) or in 48 hours (up to 100 mg L⁻¹
555 tetracycline), indicated that an optimum, but safe, treatment time for the removal of
556 tetracycline could be set at 48 hours. Within this time, the effluent with initial
557 tetracycline concentrations < 50 mg L⁻¹ generated a microcystin-LR concentration lower
558 than 1 µg L⁻¹ (Fig.5b). Even for wastewater containing more concentrated tetracycline
559 (up to 100 mg L⁻¹), a low-level microcystin-LR concentration of 1.8 µg L⁻¹ was
560 detected in the final effluent, which was much lower than both the concentration in the
561 natural water (Christoffersen and Kaas, 2000) and the guideline concentration for
562 recreation or bathing water of Germany and Australia (< 10 µg L⁻¹) (Burch, 2008).

563 Summarily, for tetracycline concentrations in the range of 10-100 mg L⁻¹, both
564 intracellular and released microcystin-LR have been found to be reduced by varying
565 degrees. A previous study also confirmed the decrease of synthesized and released
566 microcystin-LR after tetracycline exposure (Ye et al., 2017). Regarding the effective

567 tetracycline removal ability even with low biomass (Fig. 1 and 4a), an appropriate
568 decrease of the initial amount of inoculum, and timely harvest of *M. aeruginosa* cells
569 may further ensure the effluent will conform to safe microcystin-LR levels according to
570 the natural water and recreation or bathing water regulations. In addition, the present
571 study also demonstrated the possibility of the long-term cultivation of low microcystin-
572 LR *M. aeruginosa* biomass by treatment with tetracycline. Nevertheless, real-time
573 monitoring facilities are needed for surveillance during the treatment and cultivation
574 process in order to ensure further water security. Moreover, due to the complexity of
575 real wastewater, where more complex compounds and other limiting factors may
576 challenge the performance of tetracycline removal as well as release of toxin, further
577 study is needed to investigate the efficacy and safety of the proposed approach with
578 realistic wastewater in scaled-up systems before implementation.

579 3.6 Insight into future implementation

580 Along with the rapid development of the microalgal technology, many full-scale
581 systems have been successfully applied for the treatment of various wastewaters, where
582 hydraulic retention times (HRTs) were normally several days (Rawat et al., 2011;
583 Wang et al., 2016). The current study demonstrated that *M. aeruginosa* could reduce
584 high concentrations of tetracycline (up to 100 mg L⁻¹) down to an acceptable level
585 (>98%) in 48 hours, which supported the feasibility of incorporating the process into
586 microalgal treatment systems. Normally, such wastewaters contain both macro nutrients,
587 e.g., N and P (Wang et al., 2016), and trace elements, e.g., metals (Rawat et al., 2011),
588 which could support the growth of microalgae and result in acceptable effluent to meet
589 discharge regulations (Wang et al., 2016). In some circumstances of wastewater with
590 limited available nutrients, such as hospital wastewater, the nutrients could be
591 compensated through the admixture of other high-nutritional wastewaters (Norvill et al.,

2017). Moreover, microalgae-based wastewater treatment could also provide additional benefits, such as biodiesel generation (Li et al., 2020), nutrient recovery (Chu et al., 2020), and greenhouse gas emission control (Rawat et al., 2011). The present investigation expanded the potential use of cyanobacteria for antibiotic removal at high concentrations. The present investigation has preliminarily demonstrated the potential feasibility of using cyanobacteria for antibiotic removal at high concentrations. HABs occur more frequently globally due to the problems of intensive eutrophication, which is detrimental to natural waters (Lyu et al., 2020). Meanwhile, wastewater contaminated with high concentrations of tetracycline, e.g., pharmaceutical wastewater, livestock industry wastes, and emergency releases from hospitals, brings potential resistance-risk to the ecology. It could further impair the action of the sludge bacteria of WWTPs (Halling-Sørensen, 2001), resulting in low amounts of the tetracycline removed after treatment (Watkinson et al., 2009). By using a typical harmful algal species, *M. aeruginosa*, for the treatment of wastewater contaminated with higher concentrations of tetracycline, the problems of eutrophication and of tetracycline resistance (Fig. 6) could be simultaneously addressed.

~~Accompany with the results of current study, *M. aeruginosa* could be promising for tetracycline treatment in wastewater. However, there are still gaps between the current study and the real implementation. the high tetracycline tolerance and efficient removal rate of *M. aeruginosa* further confirmed the feasibility of this concept, which achieved a much higher tetracycline removal rate than other investigated microalgal species (de Godos et al., 2012). In addition, tetracycline was observed to have inhibited the synthesis of microcystin-LR~~

In this study, tetracycline was observed to have inhibited the synthesis of microcystin-LR, and the effluent from the process could achieve a safe natural and

617 recreational water quality in respect of microcystin-LR. Notably, other trace organic and
618 inorganic matter released by microalgae may also lead to potential risks, such as the
619 formation of haloacetonitriles during further chlorine disinfection treatment (Pals et al.,
620 2011). However, this has long been a common challenge for the End-of-Pipe
621 technology of chlorine disinfection during the treatment of final wastewater effluents or
622 of drinking water (Pals et al., 2011), which was yet covered by this study. Therefore,
623 before the application of this treatment process, further investigations, e.g., the
624 treatment performance in real wastewater and comprehensive risk assessment are
625 needed. in realistic wastewater, and timely harvesting of the microalgal biomass for
626 reducing the risk of such toxic release (e.g., organic nitrogen, microcystin) are
627 significant for further investigations. and with a properly managed harvest of *M.*
628 *aeruginosa*, the effluent from the process could achieve a safe natural and recreational
629 water quality in respect of microcystin-LR.

631 **4. Conclusion**

632 The present study demonstrated the possibility of reusing harmful algal species
633 for effectively remediating high-concentration antibiotics. The harmful cyanobacterial
634 species, *M. aeruginosa*, provided superior, efficient and rapid capacity for tetracycline
635 removal, compared with *C. pyrenoidosa*, under a wide initial concentration range (10-
636 100 mg L⁻¹). Both microalgal species promoted tetracycline hydrolysis by raising the
637 water pH, however, biodegradation contributed to the major part of the removal by *M.*
638 *aeruginosa*. Both microalgae species shared a common tetracycline degradation
639 pathway, but also utilised unique species-specific pathways producing different
640 degradation by-products. The by-products showed no significant increase of toxicity
641 according to published references. The presence of the tetracycline could have

642 significantly inhibited the release of toxic microcystin-LR into the water, thus
643 promoting the relative safety of the final effluent after treatment. Notably, the current
644 study was carried out in the synthetic antibiotic-contaminated water, which provided
645 evidence-based insights into the proposed approach. However, further study is needed
646 in order to evaluate the performance with realistic wastewater in upscaled systems prior
647 to practical implementation.

648 **Declaration of competing interest**

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

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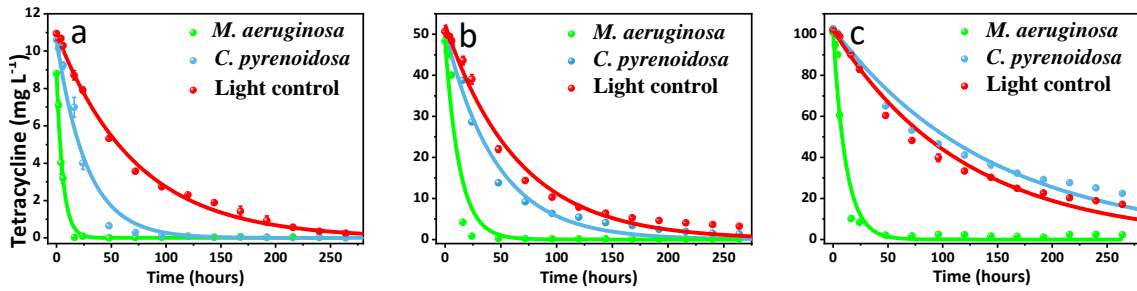
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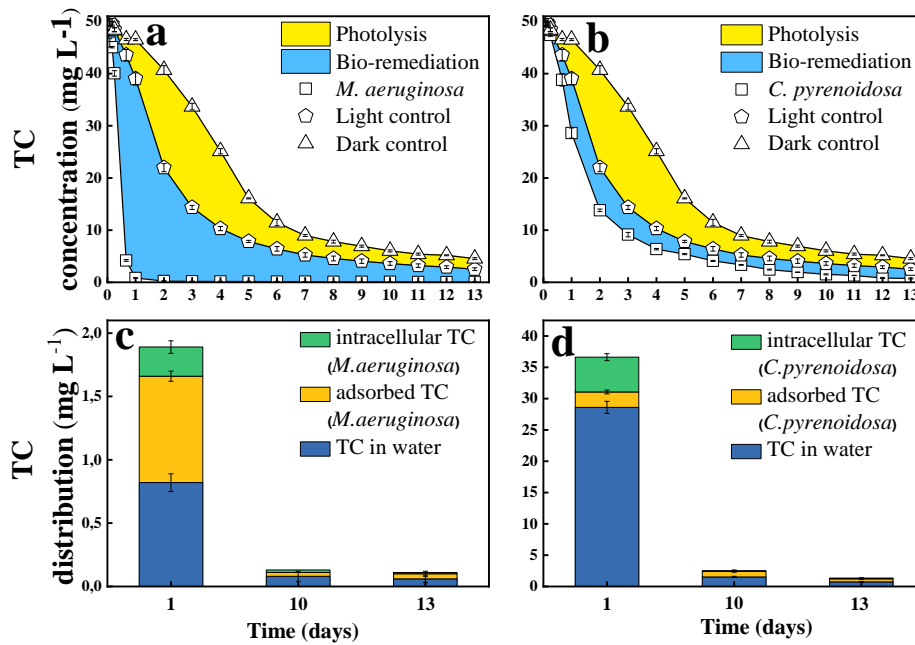
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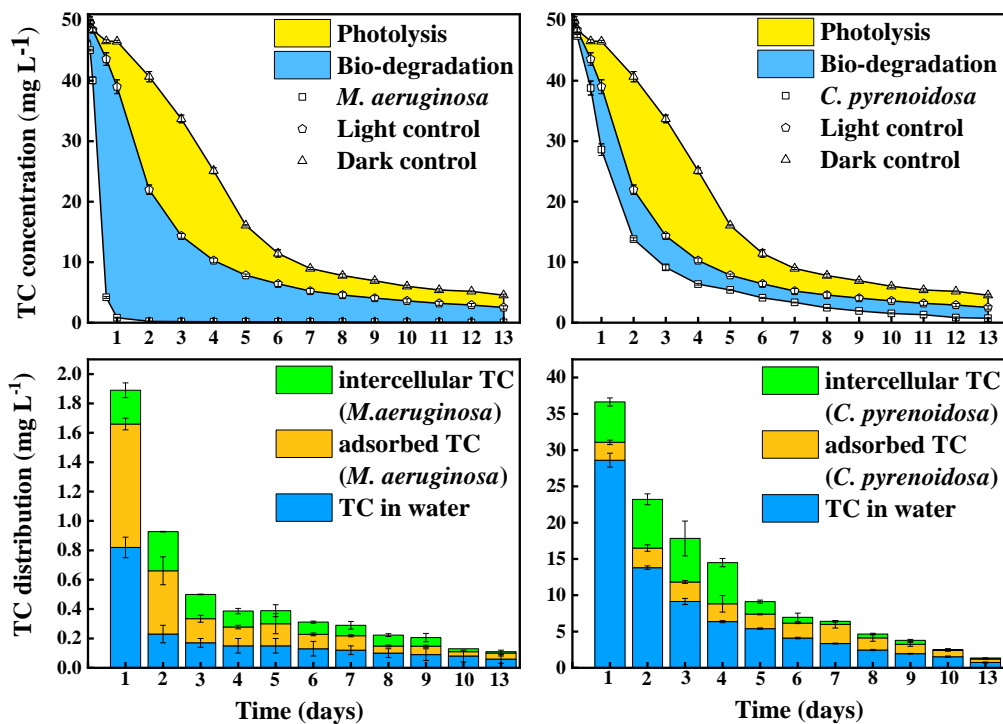
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Fig. 1. The dynamics of tetracycline concentration in blank control groups, and treatment groups of *M. aeruginosa* and *C. pyrenoidosa* at initial concentrations of 10 mg L⁻¹ (a), 50 mg L⁻¹ (b), and 100 mg L⁻¹ (c). The solid lines are simulated pseudo-first-order kinetic degradation models.

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835 **Fig. 2.** Theoretically different contributions (photolysis, hydrolysis & cation-binding and bio-
 836 remediation) towards tetracycline removal in (a) *M. aeruginosa*, and (b) *C. pyrenoidosa*
 837 treatment groups, and distribution (in water, adsorption by microalgae and bio-accumulation
 838 into microalgal cells) of residual tetracycline in (c) *M. aeruginosa*, and (d) *C. pyrenoidosa*
 839 treatment groups.

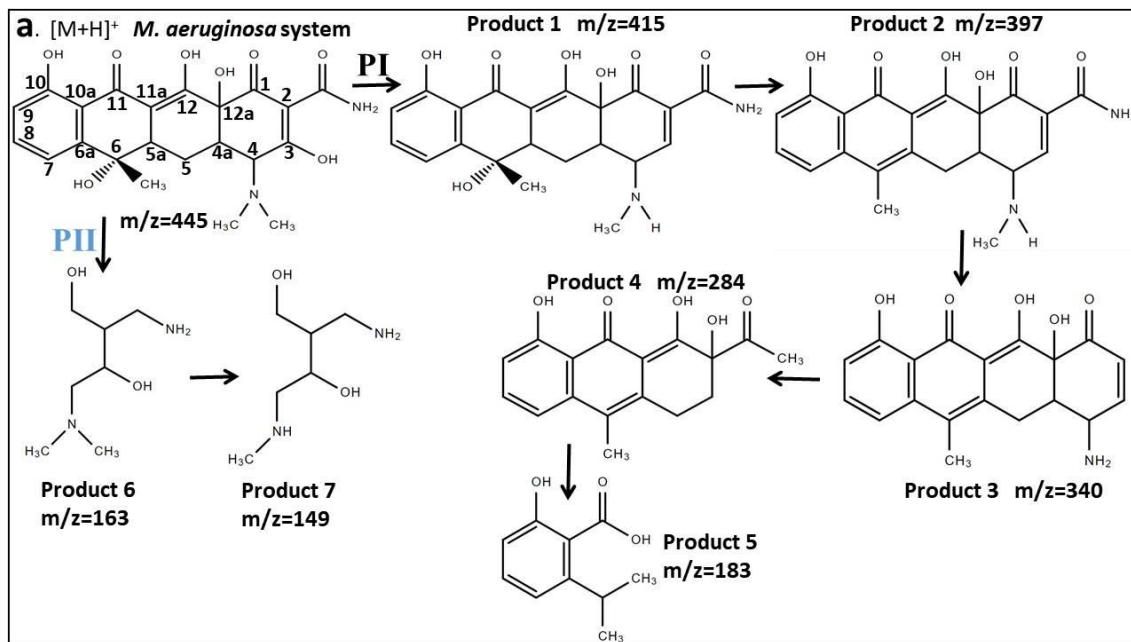
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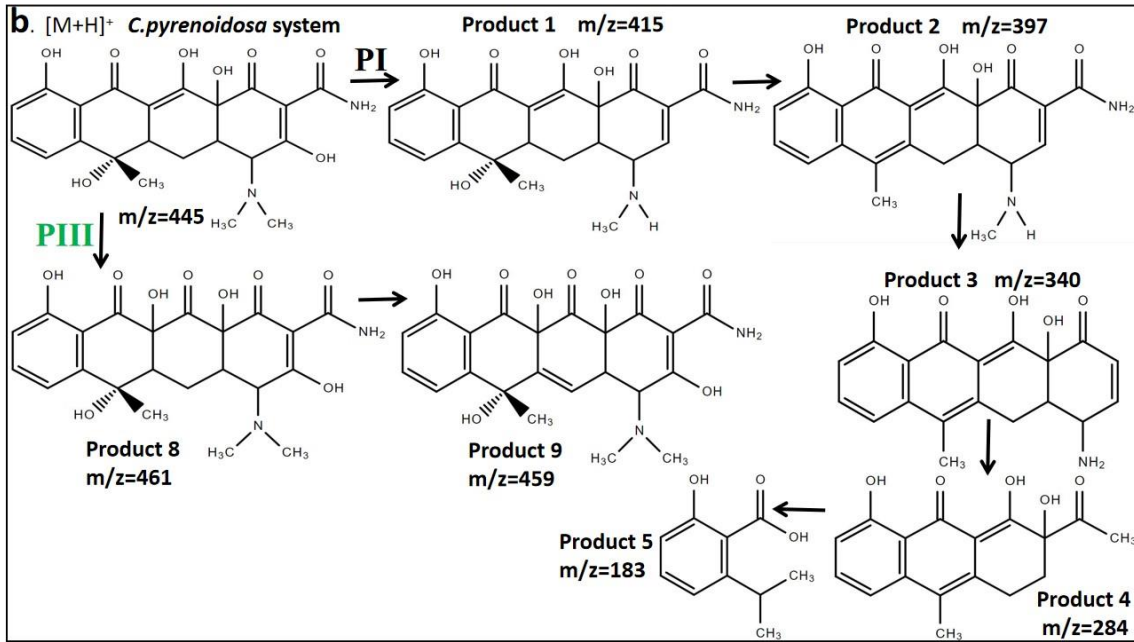
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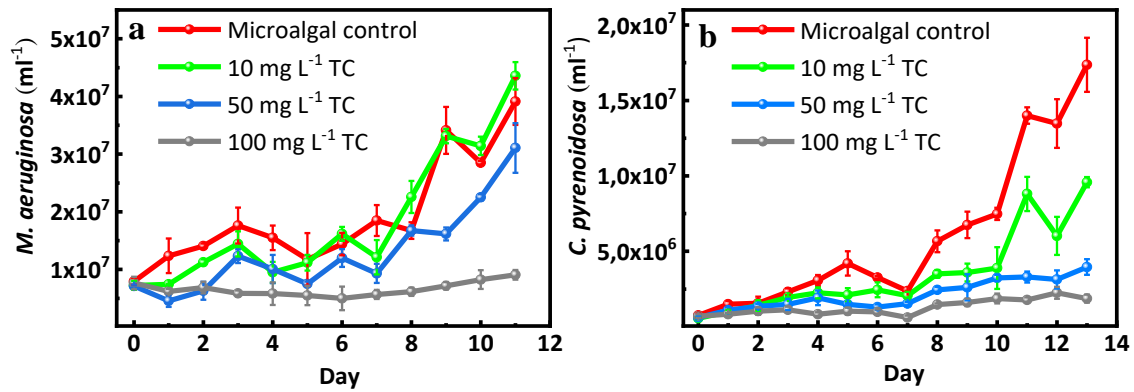


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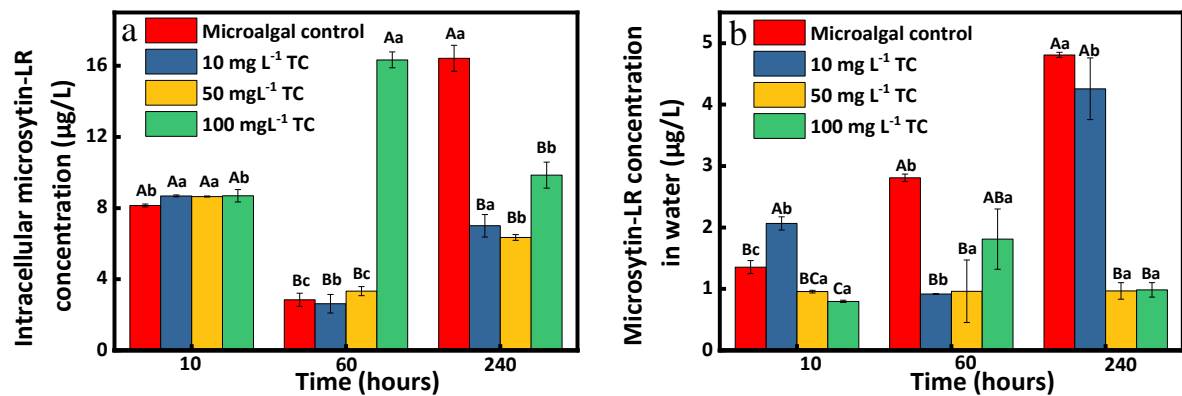
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854 **Fig. 3.** Tetracycline degradation by-products and potential pathways (PI, PII, and PIII) in (a) *M.*
855 *aeruginosa*, and (b) *C. pyrenoidosa* treatment groups.

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859 **Fig. 4.** Cell number growth under varying tetracycline concentrations for (a) *M. aeruginosa*, and
860 (b) *C. pyrenoidosa* treatment groups.

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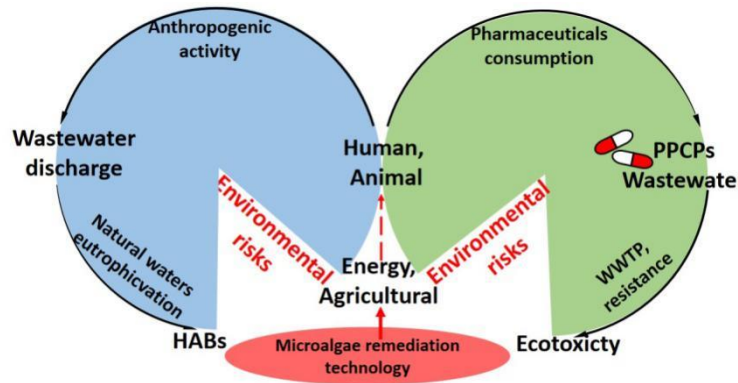
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863 **Fig. 5.** Microcystin-LR concentrations of (a) intracellular *M. aeruginosa*, and (b) released into
 864 water from *M. aeruginosa*. Different uppercase letters above the error bars in each figure
 865 represent significant difference ($p < 0.05$) among different treatment groups at the same
 866 sampling time. Different lowercase letters above error bars in each figure represent significant
 867 difference ($p < 0.05$) of the same treatment group over different sampling times.

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872 **Fig. 6.** Sustainable microalgae remediation strategy for addressing the environmental problems
 873 caused by pharmaceuticals and personal care products (PPCPs) and Harmful Algae Blooms
 874 (HABs).

875 **Table 1** Pseudo-first-order kinetic model fitting results of tetracycline removal.

Tetracycline removal	Initial tetracycline concentration (mg L ⁻¹)	k value	R ²
<i>M. aeruginosa</i>	10	$(1.7 \pm 0.1) \times 10^{-1}$	0.99
	50	$(7.7 \pm 1.3) \times 10^{-2}$	0.94
	100	$(8.6 \pm 1.0) \times 10^{-2}$	0.97
<i>C. pyrenoidosa</i>	10	$(3.6 \pm 0.3) \times 10^{-2}$	0.99
	50	$(2.2 \pm 1.1) \times 10^{-2}$	0.99
	100	$(7.0 \pm 0.3) \times 10^{-3}$	0.98
Control	10	$(1.4 \pm 0.0) \times 10^{-2}$	0.99
	50	$(1.5 \pm 0.1) \times 10^{-2}$	0.99
	100	$(8.4 \pm 0.4) \times 10^{-3}$	0.98

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879 **Supplementary information**

880 **Mitigating antibiotic pollution using cyanobacteria: removal**
881 **efficiency, pathways and metabolism**

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903 **S1. Materials and methods**

904 **S1.1 Sample preparation and tetracycline detection**

905 Standard tetracycline hydrochloride was purchased from J&K Scientific Ltd.,
906 Beijing, China. Prior to the determination, samples were filtered using a membrane
907 filter (0.22 μ m). The Acquity UPLC-PDA (Diode Array Detector) analysis parameters
908 for UV detection of tetracycline were as follows: wavelength 355nm (4.8 nm resolution),
909 sample temperature 10°C and column temperature 35°C. The following was used as the
910 mobile phase: 0.2% formic acid in ultrapure water (A) and acetonitrile (B). The eluent
911 flow rate was 0.4 mL min⁻¹. A gradient ratio of A 90%: B 10% to A 10%: B 90% was
912 applied over 4 min. 10 μ L of sample was taken for each injection. Before each
913 determination, the analytical precision was checked with three levels of tetracycline (0.5,
914 5, 50 mg L⁻¹). The results showed a relative standard deviation (RSD%) to be in the
915 range of between 4.3-8.7%.

916 Samples of treated wastewater (2mL) were taken at days-hours 1/6, 1/3, 1, 2, 4, 10,
917 20, 24, 36, and daily from day 2 to 13, and pre-treated by centrifugation at 8000 rpm for
918 15min, thus isolating the microalgae cells. The supernatant was then passed through a
919 membrane filter (0.22 μ m) for the detection of tetracycline concentration in water. After
920 re-suspension of the microalgae pellet into ultrapure water (5ml) and re-centrifugation,
921 the supernatant was measured in order to quantify the bio-adsorption of tetracycline.
922 The microalgal pellets were finally homogenised into a mixture of methanol and
923 dichloromethane (5ml; 2:1 v/v) followed by 40 minutes sonication (60kHz). After
924 subsequent centrifugation, the supernatant was analysed to determine the concentration
925 of bioaccumulated tetracycline.

926 **S1.2 Sample preparation and detection of tetracycline by-products**

927 A UPLC (Acquity UPLC I-Class, Waters Corp., Milford, USA) coupled with a
928 Xevo G2 ToF-MS (Waters Corp., USA) was utilised for the analysis of tetracycline
929 degradation products. Prior to analysis, samples were initially pre-concentrated by
930 treatment with SPE Oasis solid-phase extraction sorbents (Oasis R MCX 6cc (500mg)
931 LP extraction cartridges, Waters Corp., Milford, USA). For ToF-MS detection,
932 effluent A and B were 0.1% formic acid in ultrapure water and pure acetonitrile,
933 respectively. The flow speed was 0.4 ml min⁻¹, a gradient of flowing phase A and B
934 from initial ratio of 90% : 10% to 10% : 90% was set within 10 min and kept the final
935 ratio until 30 min. Mass spectrometry conditions were as follows: detection time 30min,
936 acquisition mass range 50 to 1200 Da, scan time 1.5 sec, collision energy 6V, collision
937 energy ramp from 15 to 30V, cone voltage 40 V, positive polarity, analyse mode
938 resolution, dynamic range normal.

939 **S1.3 Sample preparation and microcystin detection**

940 In this study, the most toxic microcystin compound, microcystin-LR (MC-LR),
941 was analysed for both intracellular and extracellular concentrations. Specifically, 50ml
942 of sample was centrifuged (4800rpm for 15min) and MC-LR in the supernatant was
943 initially concentrated by SPE (Oasis R MCX 6cc, 500mg, LP extraction cartridges;
944 Waters Corp., Milford, USA), 10ml 100% methanol was used to activate the SPE,
945 following by a wash-out of 20ml ultrapure water with a speed of 3ml min⁻¹. Afterwards,
946 the supernatant was flowing through the activated SPE with a speed of 1ml min⁻¹. 10ml
947 ultrapure water, 20ml 5%, 15% and 20% (v/v) methanol were utilized for the wash-out
948 of impurities, following by a speed of 1ml min⁻¹ 35% (v/v) 3ml methanol to elute the
949 MC-LR. The 3ml eluent was then flushed with nitrogen with a temperature of 25°C to
950 1.2ml. Final sample was further filtered with 0.22µm filter before the injection into the
951 UPLC.

952 For the intracellular MC-LR concentration, the pellet was first washed three times
953 with ultrapure water and then dissolved with 80% (v/v) methanol and freeze-thawing
954 with liquid nitrogen three times to break the microalgae cells and extract the
955 intracellular MC-LR, finally 1ml concentrated sample was achieved by nitrogen
956 flushing in room temperature. The samples were further filtered with 0.22µm filter
957 before the detection by Acquity UPLC. For the Acquity UPLC detection, For
958 microcystin-LR detection, 0.5% trifluoroacetic acid (A) and pure acetonitrile (B) were
959 used as mobile phases, with a gradient from A60%:B40% to A40%:B60%. The working
960 parameters were set as: flow rate 0.5 mL min⁻¹, 30 °C column temperature and 10 °C
961 sample temperature, detector wavelength 238 nm (1.2 nm resolution).

962 **S1.4 Sampling and pigments detection**

963 At day 1, 3, 6 and 10, cell pigments were firstly extracted with methanol (10 mL,
964 90% v/v), and the concentrations of chlorophyll and carotenoids were determined by
965 UV spectrophotometer (Varian Cary 50; Agilent Instruments, Santa Clara, USA)
966 measuring the absorbance at wavelengths of 665, 652 and 470nm. Based on the
967 equation (1-3) below, the concentrations were calculated:

$$968 \quad C_a = 16.82A_{665.2} - 9.28A_{652.4} \quad (S2)$$

$$969 \quad C_b = 36.92A_{652.4} - 16.54A_{665.2} \quad (S3)$$

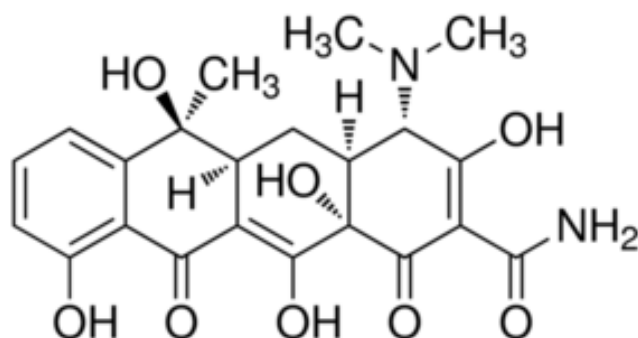
$$970 \quad C_{\text{carotenoid}} = \frac{1000A_{470} - 1.91C_a - 1.91C_b}{225} \quad (S4)$$

971 where, C_a and C_b (mg L⁻¹) are the concentrations of the chlorophyll-a and chlorophyll-b,
972 $C_{\text{carotenoid}}$ (mg L⁻¹) represents the concentration of carotenoid pigment.

973 **S1.5 Sampling and photosynthesis intensity detection**

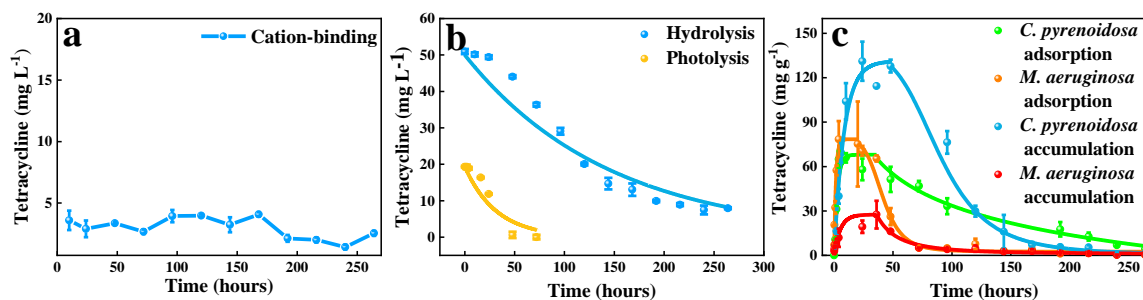
974 Samples of 1 mL was taken daily from each flasks for the photosynthesis intensity
975 detection. Photosynthesis intensity parameter Fv/Fm was measured using a FluorPen
976 (FP100, PSI spol.s.r.o., Drasov, Czechia), of which a 10 min dark adaption phase for
977 each sample was conducted before the measurement.

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980 **Fig. S1.** Molecular structure of tetracycline

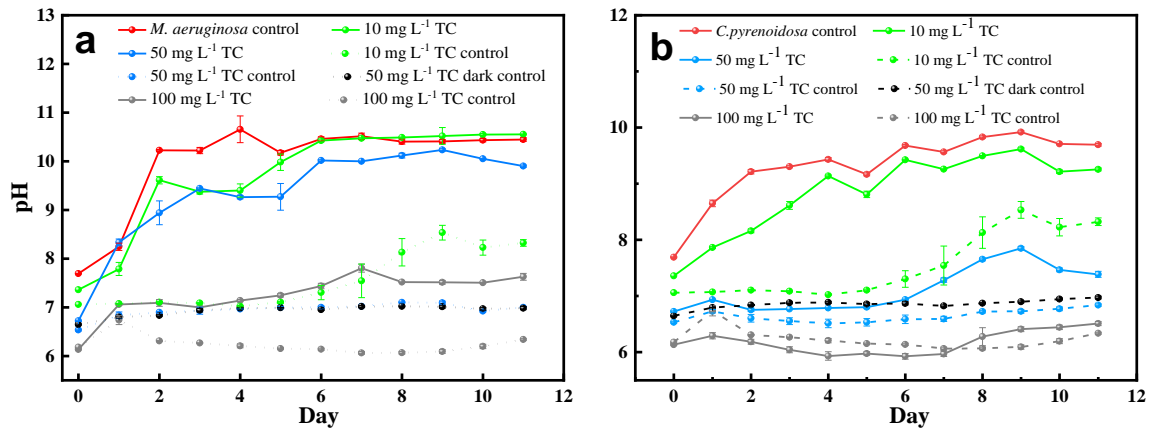


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982 **Fig.S2.** Kinetic study of different contributions towards tetracycline removal of (a)
983 ascent stage of bio-adsorption and bio-accumulation, (b) declining stage of bio-
984 adsorption and bio-accumulation, (c) hydrolysis and photolysis and (d) cation-binding.
985 The solid lines in (a), (b) and (c) are simulated pseudo-first-order kinetic degradation models.

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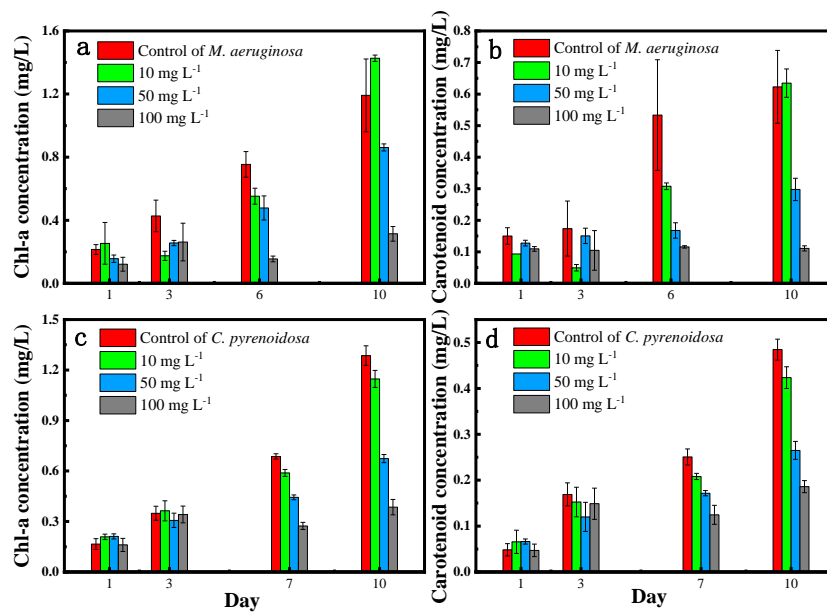
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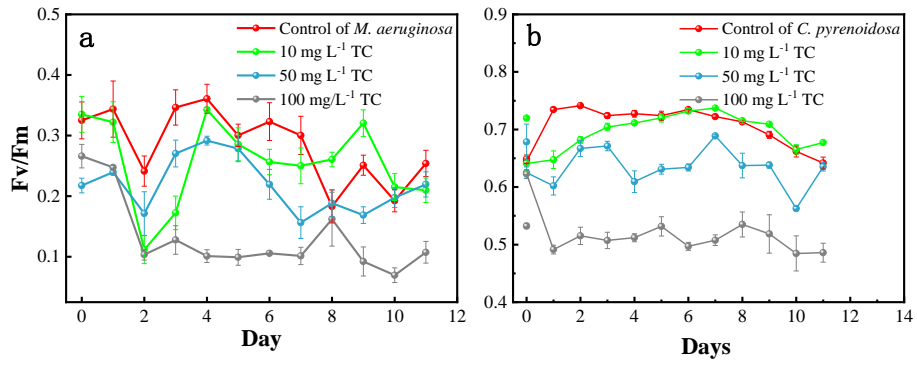
989 **Fig. S2S3.** pH changes under varying tetracycline concentrations in (a) *M. aeruginosa* treatment
 990 groups, and (b) *C. pyrenoidosa* treatment groups.

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993 **Fig. S4.** Chlorophyll-a concentration changes in (a) *M. aeruginosa* treatment groups,
 994 and (c) *C. pyrenoidosa* treatment groups, and Carotenoid concentration changes in (b)
 995 *M. aeruginosa* treatment groups and (d) *C. pyrenoidosa* treatment groups.



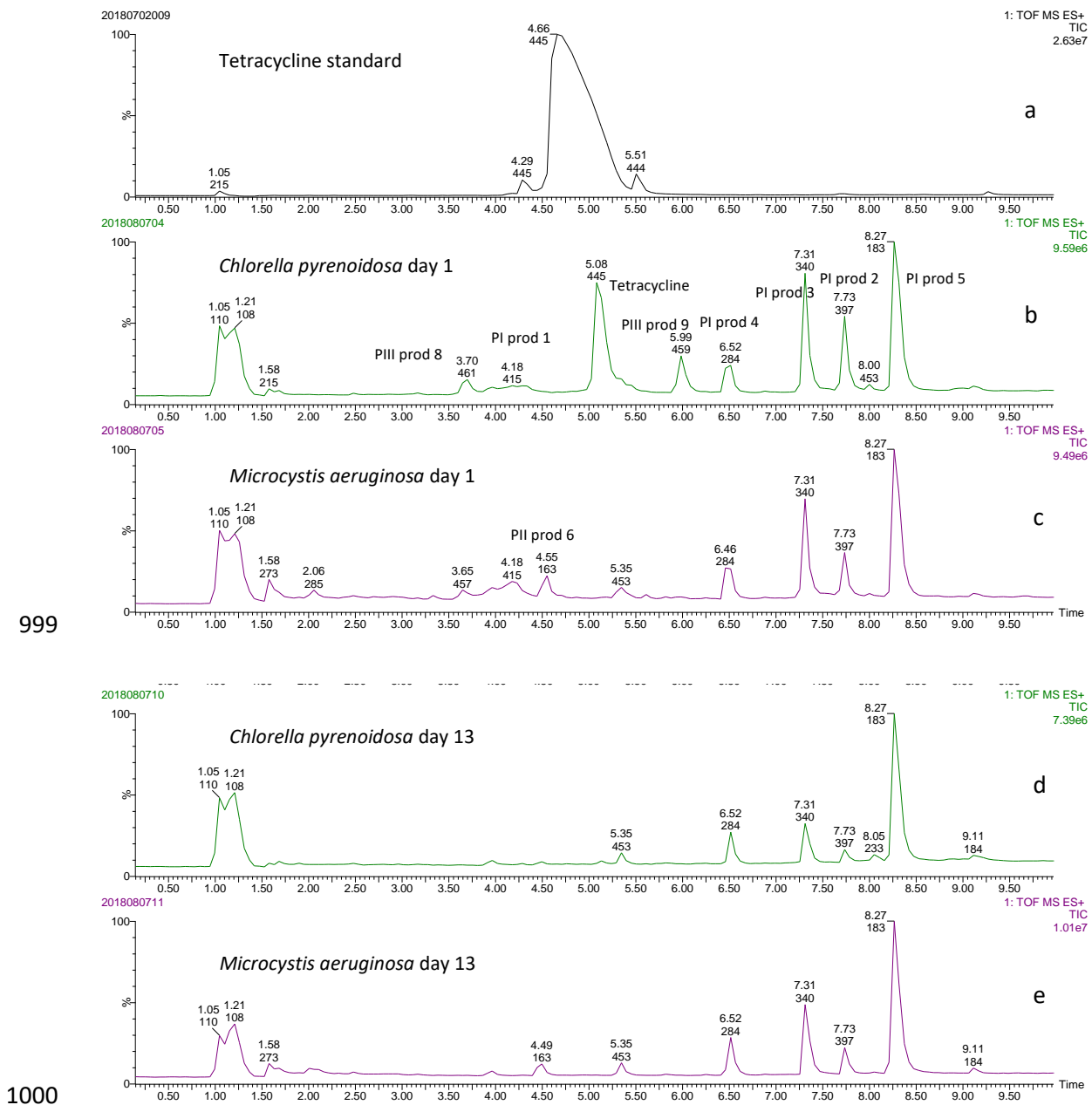
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Fig. S5. Fluorescence intensity changes of Fv/Fm under varying tetracycline concentrations in

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(a) *M. aeruginosa* treatment groups, and (b) *C. pyrenoidosa* treatment groups

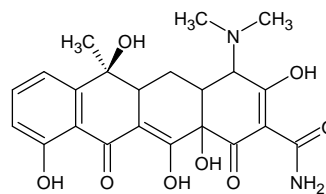
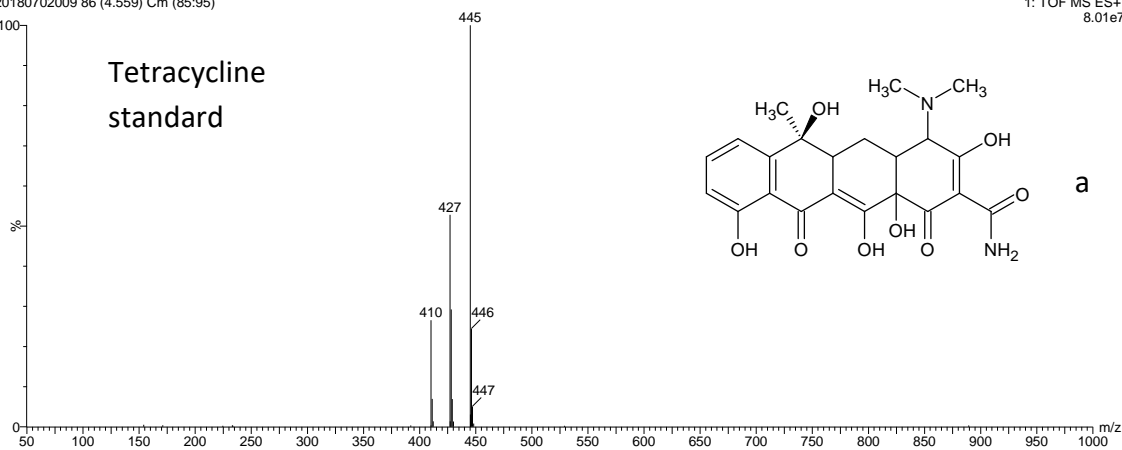


1001 **Fig. S3S6.** LC-ToFMS chromatograms of tetracycline (a) and degradation by-products from the
 1002 *C. pyrenoidosa* (b; day 1 & d; day 13) and *M. aeruginosa* (c; day 1 & e; day 13) treatment
 1003 groups. Chromatographic peak labels indicate retention time in minutes (top number) and base
 1004 peak mass (lower number). Peaks with the same retention time and base peak mass represent the
 1005 same compounds. Additional peak labels in chromatograms b and c indicate compound
 1006 identifications according to degradation pathways illustrated in Fig. 3.

20180702009 86 (4.559) Cm (85:95)

1: TOF MS ES+
8.01e7

Tetracycline
standard



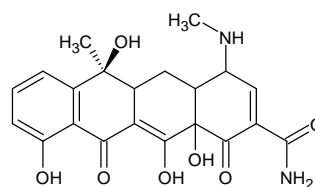
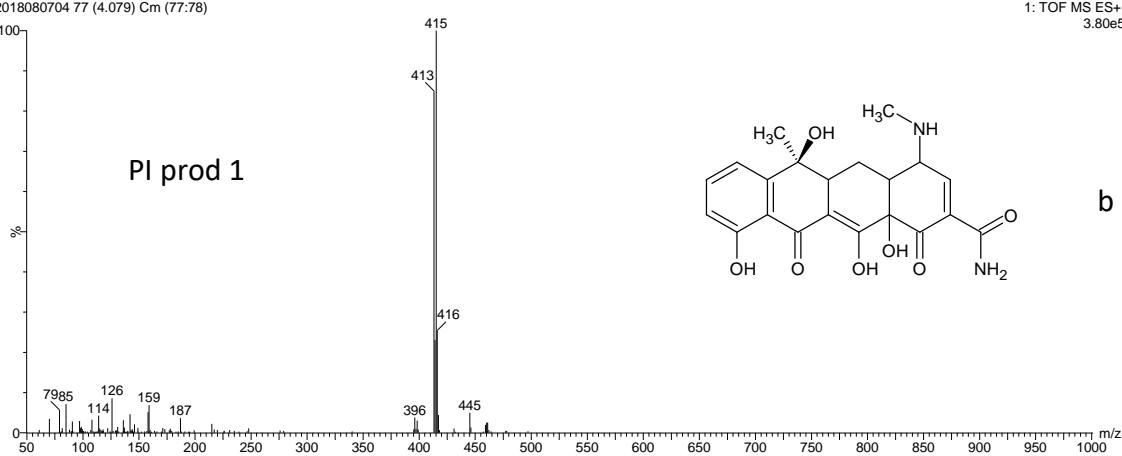
a

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2018080704 77 (4.079) Cm (77:78)

1: TOF MS ES+
3.80e5

PI prod 1



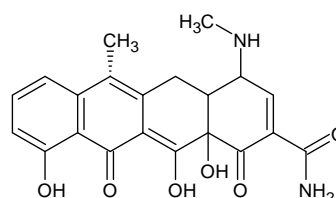
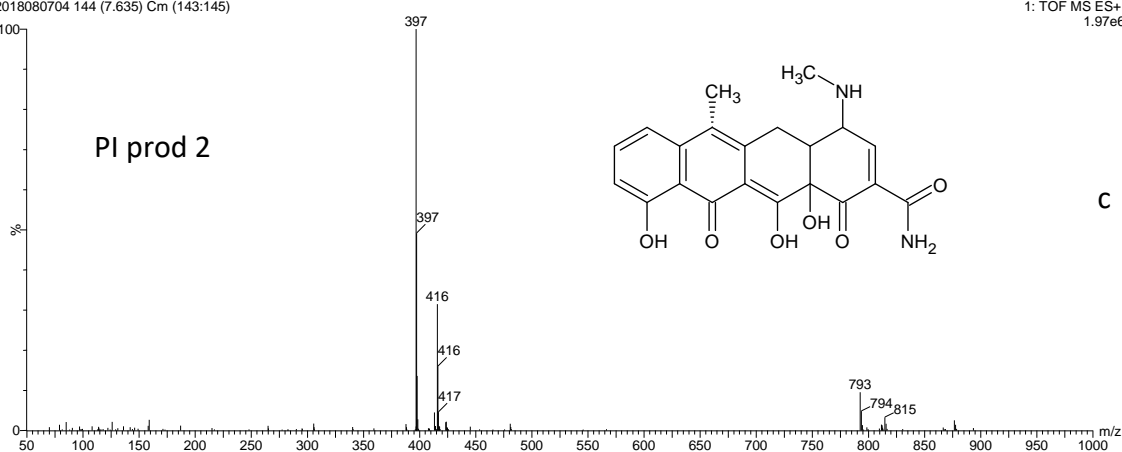
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2018080704 144 (7.635) Cm (143:145)

1: TOF MS ES+
1.97e6

PI prod 2



c

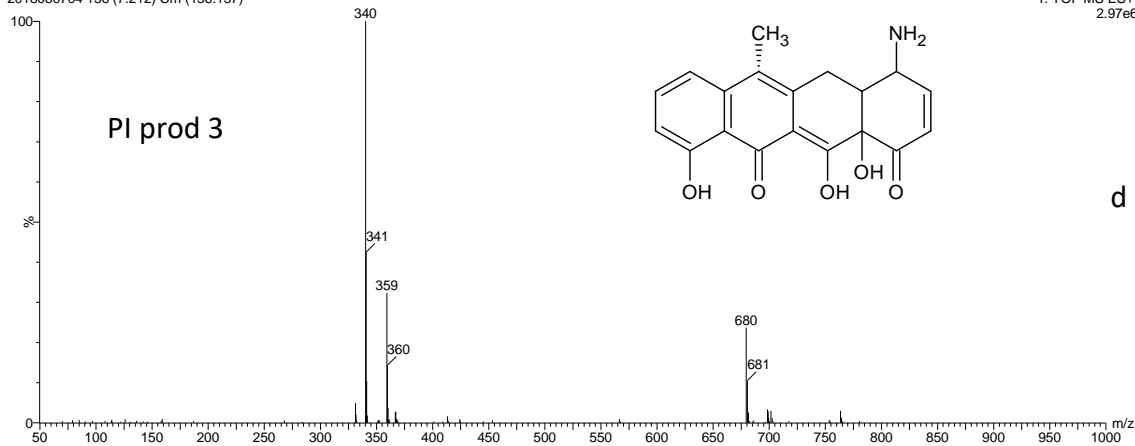
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2018080704 136 (7.212) Cm (136:137)

1: TOF MS ES+
2.97e6

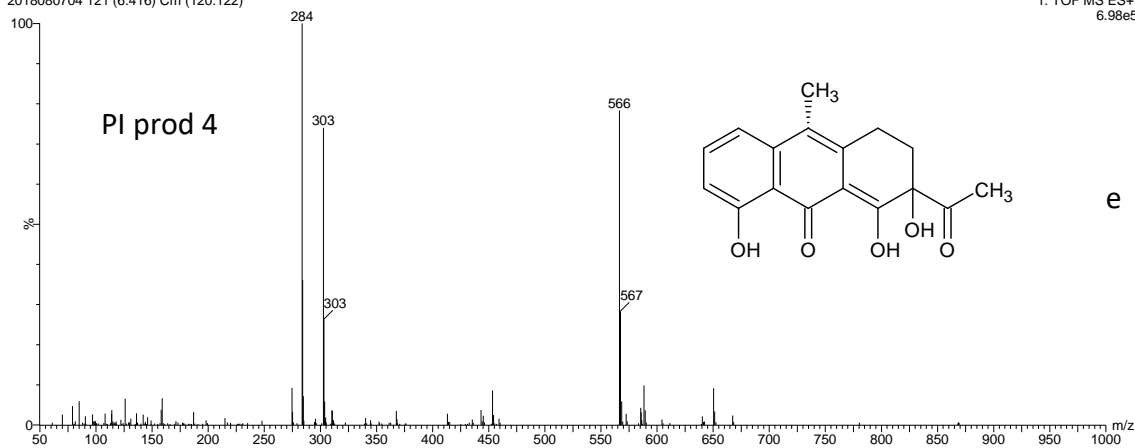


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2018080704 121 (6.416) Cm (120:122)

1: TOF MS ES+
6.98e5



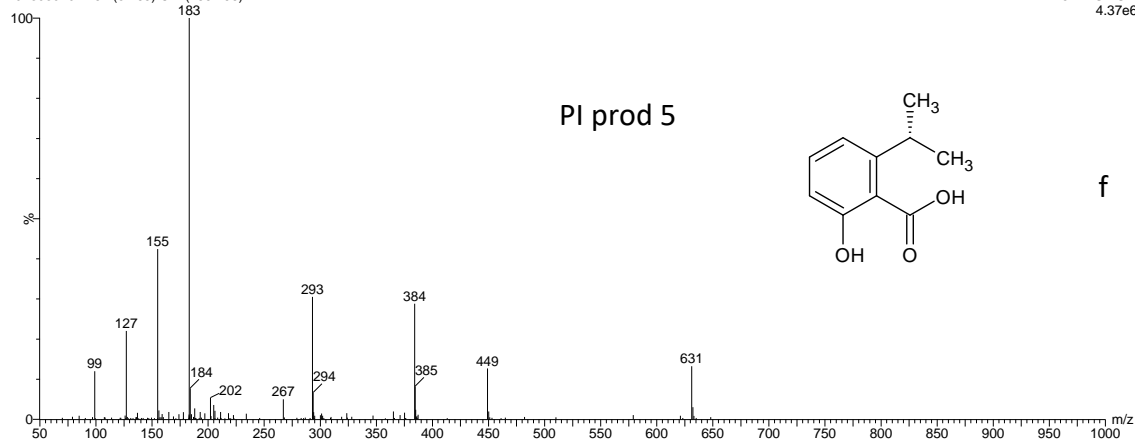
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2018080704 154 (8.165) Cm (153:156)

1: TOF MS ES+
4.37e6

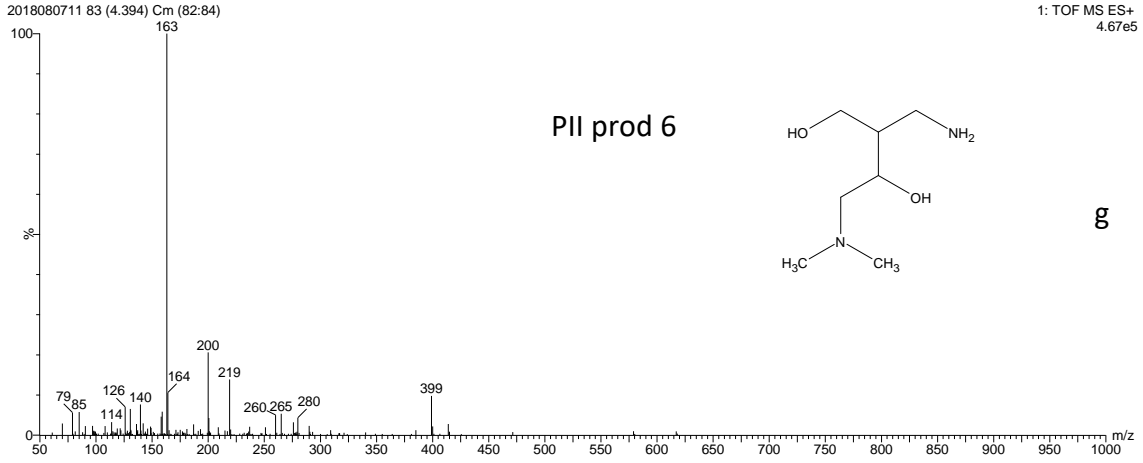


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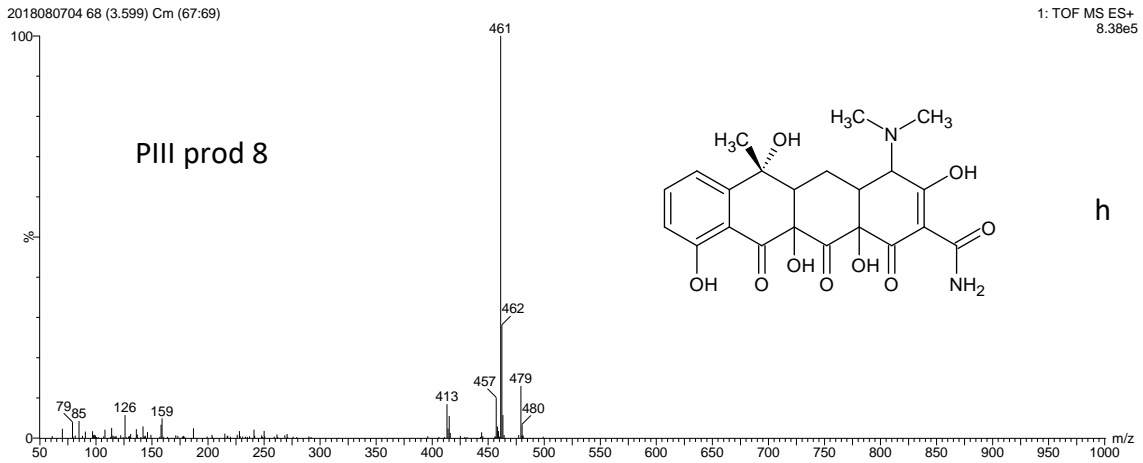
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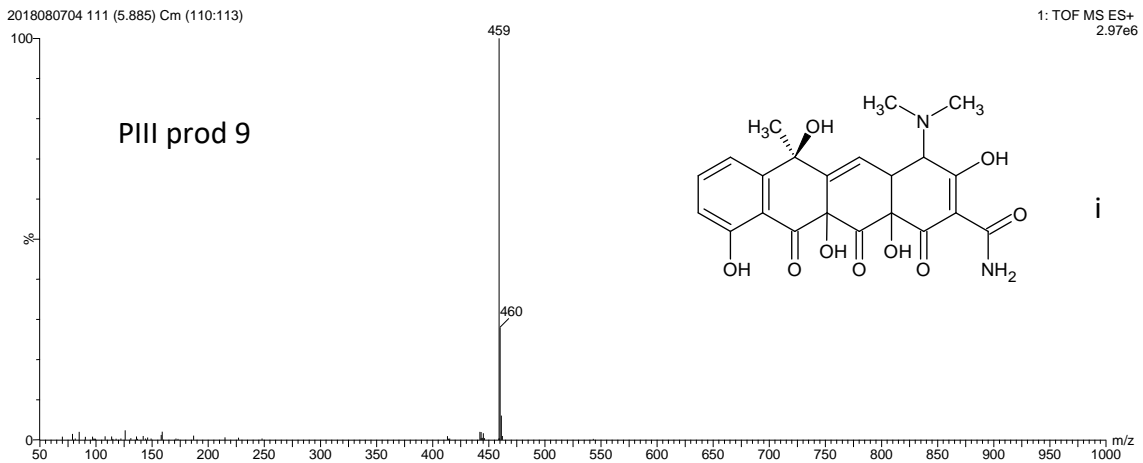


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1024 **Fig. S4-S7 a-i.** ESI-MS spectra of hypothesised tetracycline degradation products. In all cases
1025 the most intense signal represents the protonated molecular ion $[MH]^+$ for the compound
1026 suggested. Other peaks in the spectra may represent adduct ions, multimers, or other moieties
1027 originating from the chromatographic process.

1028 **Table S1** Composition of the BG11 growth medium

	Concentration (mg L ⁻¹)
NaNO ₃	1500
K ₂ HPO ₄	40
MgSO ₄ ·7H ₂ O	75
CaCl ₂ ·2H ₂ O	36
Citric acid	6
Ferric ammonium citrate	6
Na ₂ EDTA	1
Na ₂ CO ₃	20
H ₃ BO ₃	2.86
MnCl ₂ ·4H ₂ O	1.81
ZnSO ₄ ·7H ₂ O	0.22
Na ₂ MoO ₄ ·2H ₂ O	0.39
CuSO ₄ ·5H ₂ O	0.08
Co(NO ₃) ₂ ·6H ₂ O	0.05

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Table S2 Pseudo-first-order kinetic model fitting results of different removal pathways

<u>Different removal pathways</u>	<u>Initial tetracycline concentration (mg L⁻¹)</u>	<u>k value</u>	<u>R²</u>
<u>Hydrolysis</u>	<u>50</u>	<u>$(6.9 \pm 0.6) \times 10^{-3}$</u>	<u>0.94</u>
<u>Photolysis</u>	<u>50</u>	<u>$(2.9 \pm 0.7) \times 10^{-2}$</u>	<u>0.90</u>
<u>Adsorption by <i>M. aeruginosa</i></u>	<u>50</u>	<u>$(6.6 \pm 0.7) \times 10^{-1}$</u>	<u>0.98</u>
<u>Desorption by <i>M. aeruginosa</i></u>	<u>50</u>	<u>$(2.3 \pm 0.0) \times 10^{-1}$</u>	<u>0.97</u>
<u>Adsorption by <i>C. pyrenoidosa</i></u>	<u>50</u>	<u>$(3.7 \pm 0.8) \times 10^{-1}$</u>	<u>0.90</u>
<u>Desorption by <i>C. pyrenoidosa</i></u>	<u>50</u>	<u>$(7.1 \pm 0.8) \times 10^{-3}$</u>	<u>0.92</u>
<u>Accumulation by <i>M. aeruginosa</i> (uptake)</u>	<u>50</u>	<u>$(1.9 \pm 0.3) \times 10^{-1}$</u>	<u>0.93</u>
<u>Accumulation by <i>M. aeruginosa</i> (decline)</u>	<u>50</u>	<u>$(1.2 \pm 0.1) \times 10^{-2}$</u>	<u>0.92</u>
<u>Accumulation by <i>C. pyrenoidosa</i> (uptake)</u>	<u>50</u>	<u>$(1.2 \pm 0.1) \times 10^{-1}$</u>	<u>0.96</u>
<u>Accumulation by <i>C. pyrenoidosa</i> (decline)</u>	<u>50</u>	<u>$(1.1 \pm 0.2) \times 10^{-2}$</u>	<u>0.90</u>

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