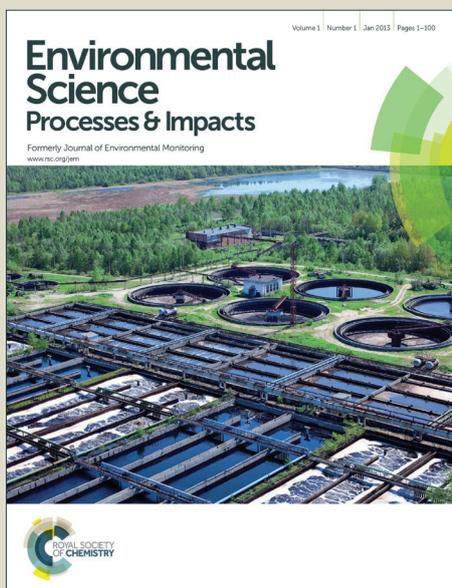


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Environmental Impact Statement

Oil spills and the dispersant application increase the concentration of dissolved petroleum hydrocarbons in water column which are potentially toxic to marine ecosystem. In this paper, simulated bioremediation experiments on oil spill-polluted marine shoal were conducted in open custom-designed devices. The impact of different substrates on microalgae followed a decreasing order: the microbial consortium plus Tween-80 > the microbial consortium > Tween-80. The acute toxicity effects of different substrates on microalgae illustrated that the microalgae in the biotreated seawater was recruited significantly during 96 h, suggesting the oil spill-polluted seawater quality was obviously improved by the bioremediation. The simulation and assessment of the ecological response to enhanced bioremediation can facilitate the better management of future oil spill restoration.

1 **Bioremediation of oil spill polluted marine intertidal zone and its toxicity effect**
2 **on microalgae**

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9 **Abstract:** Custom-designed device with 0.6 m (*L*)×0.3 m (*W*)×0.4 m (*H*) and a
10 microbial consortium were applied to simulate bioremediation on oil spill-polluted
11 marine intertidal zone. After the bioremediation, the removal efficiency of *n*-alkanes
12 and polycyclic aromatic hydrocarbons homologues in crude oil evaluated by GC-MS
13 were higher than 58% and 41% respectively. Besides, the acute toxicity effects of
14 crude oil on three microalgae, i.e. *Dicrateria sp.*, *Skeletonema costatum* and
15 *Phaeodactylum tricornerutum*, varied with concentration. The effects of microbes and
16 surfactant treated water on three microalgae followed a decreasing order: the
17 microbial consortium plus Tween-80 > the microbial consortium > Tween-80. During
18 96 h, the cell densities of the three microalgae in treated seawater increased from 4.0
19 ×10⁵, 1.0×10⁵ and 2.5×10⁵ cells•mL⁻¹ to 1.7×10⁶, 8.5×10⁵ and 2.5×10⁶ cells•
20 mL⁻¹ respectively, which illustrated that the quality of seawater contaminated by crude
21 oil was significantly improved by the bioremediation.

22 **Keywords:** bioremediation, marine oil pollution, microalgae, toxicity effect

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23 assessment

24 **1 Introduction**

25 Petroleum is one of the most important energy resources and raw materials for
26 the chemical industry. Rising global energy demand has resulted in an increase in the
27 extraction and transportation of crude oil in the sea, making marine environments
28 especially susceptible to increased risk of crude oil spills. The latest examples of
29 large-scale marine oil spills are the “Deepwater Horizon” blowout in Gulf of Mexico
30 on 20th April 2010 and the oil pipeline explosion in Dalian, China on 16th July 2010.
31 Therefore, huge quantities of spilled oils and petroleum products might enter the sea
32 leading to serious environmental problems and extensive damages to marine life,
33 human health and ecological resources and systems.¹⁻²

34 Bioremediation which is economical and environmental friendly is considered to
35 be one available and effective technique to eliminate oil pollution from contaminated
36 environments and reduce damages caused by oil spills in comparison with other
37 physical and chemical methods.³⁻⁵ Crude oil is an extremely complex mixture
38 containing thousands of different hydrocarbon compounds such as *n*-alkanes,
39 aromatics, resins, asphaltenes and many other chemical compounds.⁶ Many
40 microorganisms are known to be able to attack and degrade some specific oil
41 components and/or certain classes of oil hydrocarbons.^{7,8} At present, about 70 genera
42 and more than 200 species of microorganisms have been found to utilize and degrade
43 one or more hydrocarbons. In addition, it has been reported that bioremediation can

44 remove oil hydrocarbons from oil contaminated environments successfully and
45 effectively.^{9, 10}

46 During a bioremediation process, oil biodegradation efficiency may be limited by
47 several factors such as substrate, oxygen, nutrient concentration, environment
48 sensitivity and the abundance of oil-degrading microorganisms themselves.¹¹
49 Bioaugmentation and biostimulation by adding microorganisms, nitrogen, phosphorus
50 and surfactant have been employed to improve and enhance bioremediation
51 efficiency.^{12, 13} However, most of the experiments have been performed in microcosm
52 and few studies have been dedicated to investigate bioremediation on marine intertidal
53 zone.^{14, 15} In order to study bioremediation performance of oil-degrading
54 microorganisms in natural circumstances, it is necessary to simulate the
55 bioremediation condition in amplified models.

56 Phytoplankton is one of primary producers, which sustains the pelagic food
57 chains in the aquatic ecosystems. One of the factors supporting the use of algae in
58 bioassays is their niche in the aquatic ecosystem.¹⁶⁻¹⁸ If these organisms are adversely
59 affected by a toxicant, the surrounding ecosystem may also be implicated, either
60 directly or indirectly, due to the lack of a food source. Thus, phytoplankton being
61 sensitive to any change of seawater quality is a good bioindicator. Extensive
62 investigations on toxicities of crude oil, polycyclic aromatic hydrocarbons (PAHs)
63 and metals to a variety of fish and mollusk species have been conducted.¹⁹⁻²¹
64 Pasternak and Kołwzan²² had reported that microtox toxicity changes during
65 biodegradation of carbazole by newly isolated methylotrophic strain

66 *methylobacterium sp.* GPE1 without microalgae. However, little attention has been
67 paid to the toxicity effect of a bioremediation process on marine microalgae and the
68 evaluation of the ecological response to bioremediation. In addition, previous studies
69 only covered the impact of oils on algae without biodegradation.^{16, 23}

70 In this paper, open custom-designed devices were employed to simulate oil-spill
71 bioremediation on marine intertidal zone. We also characterized the predominant
72 bacterial strains isolated from petroleum-contaminated marine sediments. This study
73 evaluated the hydrocarbon-utilizing capability of microbial consortium and surfactant
74 and their oil removal performance by bioaugmentation and biostimulation in
75 mesocosm on contaminated marine intertidal zone. In addition, the toxicity effects of
76 different substrates on *Dicrateria sp.*, *Skeletonema costatum* and *Phaeodactylum*
77 *tricornutum* in the bioremediation process were evaluated. This work will provide a
78 support for the practical applied feasibility of the microbial consortium by enhanced
79 bioremediation in marine oil-spill environment.

80 **2 Materials and methods**

81 **2.1 Materials**

82 2.1.1 Chemicals

83 All chemicals used in this work were analytical grade and obtained from various
84 commercial sources. The crude oil which was purchased from Shengli oilfield
85 (Dongying, Shandong, China) was dissolved in the hexane and filtered to remove
86 un-dissolved precipitate (such as colloids and asphaltenes), and it had a viscosity of
87 22.2 mPa·s (50 °C, 50 RPM) and a density of 0.855 g·cm⁻³.

88 2.1.2 Microbial consortium and microalgae

89 A microbial consortium was isolated from petroleum-contaminated sediments in
90 Bohai Sea and then was recultivated in the laboratory conditions using only oil as the
91 carbon source, which has enhanced the capacity of degrading crude oil. Previous
92 studies in our laboratory had shown that the microbial consortium exhibits strong
93 biodegradation potential, i.e. crude oil degradation efficiency reached up to 50% at the
94 optimum growth conditions of pH 6-9, temperature 20-30 °C and salinity 10‰-35‰.
95 The microbial consortium was cultivated in beef extract peptone medium at 30 °C
96 with shaking at 120 rpm for 24 h before used.

97 Marine microalgae (*Dicrateria sp.*, *Skeletonema costatum* and *Phaeodactylum*
98 *tricornutum*) used in toxicity assessment experiments were obtained from The First
99 Institute of Oceanography, SOA (Qingdao, Shandong, China). The microalgae were
100 cultivated at 20 ± 1 °C, with an irradiance of 3000-4000 lux cold light source and a 12
101 h light, 12 h dark photoperiod. The algae were sampled at a certain time and fixed
102 with Lugol's solution. Then algal cells were counted using a hemocytometer under a
103 light microscope.

104 2.1.3 Seawater and sand samples

105 Seawater and sand used for the simulated bioremediation experiments were
106 collected from Shilaoren beach (Qingdao, Shandong, China). Seawater with pH of 8.1
107 and salinity of 32‰, was filtrated with 0.45 µm pore-size filters before used in
108 microalgae toxicity assessment experiments.

109 2.1.4 Media

110 Nutrient (N, P and Si) solution was composed of (1 L filtered seawater) 75 g
111 NaNO_3 , 5 g $\text{NaH}_2\text{PO}_4 \cdot \text{H}_2\text{O}$ and 30 g $\text{Na}_2\text{SiO}_3 \cdot 9\text{H}_2\text{O}$. Trace elements solution was
112 composed of (1 L filtered seawater) 2.45 mg $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, 19.9 mg $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$,
113 22 mg $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$, 10 mg $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 180mg $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$, 1.3 mg H_2SeO_3 , 2.7
114 mg $\text{NiSO}_4 \cdot 6\text{H}_2\text{O}$, 1.84 mg Na_3VO_4 and 1.94 mg K_2CrO_4 . Vitamins solution was
115 composed of (1 L filtered seawater) 1.0 g VB_{12} , 0.1 g VH and 0.2 g thiamine
116 hydrochloride. Final medium for cultivating marine microalgae was composed of 1 L
117 filtered seawater to which 1 mL of nutrient, 1 mL trace elements and 0.5 mL vitamins
118 solutions were added. These media were prepared for cultivating marine microalgae.

119 Crude oil medium used for bioremediation experiments was composed of 20 g
120 NaCl , 0.7 g $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 3.0 g KH_2PO_4 , 1.5 g Na_2HPO_4 , 0.1 g anhydrous CaCl_2 , 1.0
121 g yeast extract powder and 5.0 g crude oil, the substances to make the medium were
122 added to 1 L of distilled water. Beef extract peptone medium was composed of 10 g
123 peptone, 20 g NaCl and 3.0 g beef extract. The pH of crude oil medium and beef extract
124 peptone medium were adjusted to 7.0-7.5 with either HCl or NaOH solutions, then
125 they were sterilized in an autoclave at 121 °C for 20 min.

126 **2.2 Identification of bacteria isolates**

127 2.2.1 Biochemical characterization

128 Biochemical tests such as gram staining, catalase reaction, methyl red test, V-P,
129 indole and the hydrolysis of cellulose were performed to identify the morphological,
130 physiological and biochemical characterization of the isolates, according to manual of
131 common bacterial identification.²⁴

132 2.2.2 DNA extraction, PCR amplification and sequences analysis

133 Total DNA was extracted from the bacterial strains using a TIANamp Bacteria
134 DNA extraction Kit (Tiangen Biotech Co., Ltd, Beijing, China). PCR (Polymerase
135 chain reaction) was performed on the DNA extracts of the isolates using a pair of PCR
136 universal primers 27F (5'-AGAGTTTGATCCTGGCTCAG-3') and 1492R
137 (5'-AAGGAGGTGATCCAGCCGCA-3'). The reaction mixture (50 μL) contained 10
138 \times PCR buffer (5 μL), 1.5 $\text{mmol}\cdot\text{L}^{-1}$ MgCl_2 (3 μL), 2.5 $\text{mmol}\cdot\text{L}^{-1}$ dNTP (1 μL), 0.4 U
139 of Tap DNA polymerase, 10 $\mu\text{mol}\cdot\text{L}^{-1}$ 27F (1 μL), 10 $\mu\text{mol}\cdot\text{L}^{-1}$ 1492R (1 μL) and 0.8
140 μL template DNA. Amplification program was performed with initial denaturation
141 step at 94 $^\circ\text{C}$ for 5 min; followed by 32 cycles of 1 min denaturation step at 94 $^\circ\text{C}$, 1
142 min annealing step at 55 $^\circ\text{C}$ and 90 s elongation step at 72 $^\circ\text{C}$; and a final extension
143 step at 72 $^\circ\text{C}$ for 15 min. The amplified products were purified and cloned. The DNA
144 sequences were determined with the chain-termination method on a DNA sequencer.
145 All sequences were aligned in the GenBank database using the BLASTN program and
146 subjected to a similarity search on the NCBI website (<http://www.ncbi.nlm.nih.gov>).
147 Many relevant available 16S rDNA gene sequences were selected as the references
148 from GenBank. The sequence alignment was carried out with ClusterX (version 2.0).
149 Phylogenetic trees were constructed using the neighbor-joining (NJ) method by
150 software MEGA 4.0. The scale bar indicated the average number of amino acid
151 substitutions per site.

152 2.3 Simulated bioremediation experiments on oil spill-polluted marine shoal

153 The simulated bioremediation experiments on oil spill-polluted marine intertidal

154 zone were conducted in five custom-designed tanks with 0.6 m (*L*) × 0.3 m (*W*) ×
155 0.4 m (*H*). Each tank was filled with 41 kg sand, 205 g crude oil and 20 L seawater to
156 simulate oil-spill marine shoal. Enhanced bioremediation technology influenced by
157 microbes, surfactant and nutrient was employed. To test the impact of nitrogen
158 (N)-source, phosphorus (P)-source, surfactant and microbes on components of crude
159 oil biodegradation, different experimental designs were applied whose details are
160 shown in Table 1. The tanks were named from 1# to 5#. Tank 1#, 3#, 4# and 5# were
161 supplemented with 20 g yeast powder and 60 g KH₂PO₄. Tween-80 (15mL) was
162 added into tank 4# and 5#. Tank 3# and 5# were spiked with 5% (v/v) of the microbial
163 consortium. All tanks were put in dry and ventilated places at ambient temperature (25
164 °C) for 21 d. The seawater was added in the tank following the sand covered on the
165 bottom of the tank. Marked the seawater level on each tank after the water claming.
166 The seawater was drained after heated oil (approximately 50 °C) spread evenly on it
167 with a slow flow to make the oil attaching on the sand naturally after the oil
168 stabilizing on the water surface. After standing 12 h, the seawater was added to the
169 calibration recorded. Moreover, the aeration equipment was employed to cycle the
170 oxygen in the seawate.

171 **2.4 Petroleum hydrocarbons analysis**

172 Analyses for *n*-alkanes, PAHs and biomarker compounds were performed on a
173 Shimadzu (Kyoto, Japan) GC-MS-QP2010. A DB-5MS capillary column (30 m×0.25
174 mm I.D.) was used for GC-MS. Helium was employed as a carrier gas. System
175 control and data acquisition were achieved with a GC-MS solution software. Detailed

176 chromatographic conditions and quality control were described in the papers of
177 Wang²⁵ and Sun.²⁶

178 **2.5 Toxicity effect of biotreated seawater on microalgae**

179 The acute toxicity effects of dissolved crude oil, microbial consortium, surfactant
180 (Tween-80) and biotreated seawater on three microalgae were assessed in three batch
181 experiments. In the first experiment, dissolved crude oil adjusted to 0, 10, 20, 40, 60
182 and 80 mg•L⁻¹ in f/2 medium was used. In the second experiment, the effects of f/2
183 media spiked with 5% (v/v) of the microbial consortium and/or 0.075% (v/v) of
184 surfactant were evaluated. In the third experiment, biotreated seawater was collected
185 from tanks 1# to 5# after 21 d of the simulated bioremediation. This water was
186 inoculated with three microalgae and then incubated in photochemical incubator.

187 Toxicity effect on algae in all three experiments was assessed by measuring cell
188 densities at different time points during 96 hours.

189 **3 Results and discussion**

190 **3.1 Characterization and identification of the isolates**

191 Three bacterial strains composing the utilized microbial consortium were named
192 as S-1, S-2 and S-3. Their morphological, physiological and biochemical
193 characteristics were shown in Table 2. The colonies of S-1, S-2 and S-3 were
194 milky-white, white and orange colors, respectively. All bacteria were gram-positive
195 and found to be baculine by electron microscope. They were oxidized form in the
196 glucose oxidation test. Strains S-1 and S-3 had spores, while S-2 did not have spores.

197 Based on GenBank database, the 16S rDNA gene sequences of the three bacterial
198 strains were aligned and checked their similar strains manually. The 16S rDNA
199 sequences of strains S-1, S-2 and S-3 had 97%, 98% and 99% similarity to *Bacillus*
200 *cereus* (GenBank ID: GU369810.1), *Lysinibacillus fusiformis* (GenBank ID:
201 JQ900546.1) and *Rhodococcus* sp. (GenBank ID: KC200263.1) are respectively
202 shown. The three genera were isolated from petroleum-contaminated environment and
203 employed in bioremediation processes.²⁷⁻³⁰ The phylogenetic trees of the three strains
204 were respectively shown in Fig. 1 a-c. Sequence analysis of the 16S rDNA gene,
205 BLAST sequence comparison and phylogenetic analysis confirmed that the bacteria
206 S-1, S-2 and S-3 (GenBank IDs) were respectively affiliated with *Bacillus cereus*
207 (KF033125), *Lysinibacillus* sp. (KF033126) and *Rhodococcus rubber* (KF033127).

208 **3.2 Biodegradation of crude oil**

209 To investigate the biodegradation efficiency of crude oil with different enhanced
210 bioremediation agents on oil spill-contaminated marine shoal, the degradation process
211 in oil-amended mesocosm with the microbial consortium, *N*-source, *P*-source and
212 Tween-80 was assessed by studying the changes in the chemical composition of crude
213 oil using pristane and phytane as internal conservative markers. During the
214 remediation process, crude oil in tanks with the microbial consortium and/or
215 Tween-80 were emulsified and gradually turned into small pellets or patches in
216 different degrees, which has consistent results with the reports of Zahed et al.³¹ The
217 seawater became more turbid due to the cell growth and dissolved crude oil than the
218 corresponding control.

219 3.2.1 *n*-alkanes

220 The crude oil samples in different tanks showed similar changes for the
221 *n*-alkanes in the C₉ to C₃₀ range. The degradation depletion was calculated by the
222 different value divided by the initial value, while the different value was between the
223 amount of crude oil before and after the experiments. The degradation of *n*-alkanes
224 decreased as the carbon number increased. It appeared that the *n*-alkanes (from C₉ to
225 C₃₀) were removed in different degrees(Fig. 2 a). *n*-alkanes ranging from C₉ to C₂₄
226 were highly degraded compared with *n*-alkanes ranging from C₂₅ to C₃₀ in tank 3# and
227 5#, while in tank 2# and 4# *n*-alkanes ranging from C₉ to C₁₅ were fluctuated
228 degraded. Most of the short chain *n*-alkanes (i.e., C₁₁-C₂₄) were degraded by day 21.
229 However, the content of the long chain *n*-alkanes (C₂₅-C₃₀) in tank 1#, 2#, 4# and 5#
230 and the short chain *n*-alkanes (C₉ and C₁₀) in tank 1# and 2# were increased after day
231 21. This resulted in the bacteria consumed the short chain *n*-alkanes (C₁₁-C₂₄) first to
232 much shorter *n*-alkanes (C₉ and C₁₀), the longer chain *n*-alkanes (C₂₅-C₃₀) have not
233 been consumed by the bacteria, however the total *n*-alkane is reduced, compared to
234 the beginning of the control group, the percentage is relatively negative. Comparing
235 tank (3# and 5#) with tank (1#, 2# and 4#), the *n*-alkanes (from C₉ to C₂₄) were
236 significantly removed, which may be caused by the biodegradation of the microbial
237 consortium. The enhanced bioremediation efficiency of *n*-alkanes was the most
238 significant in tank 5# due to the addition of the N-, P-source and Tween-80. Rahman³²
239 et al had reported significant positive effects on the bioremediation of *n*-alkane in
240 petroleum sludge by adding bacterial consortium, rhamnolipid biosurfactant and

241 nitrogen, phosphorus and potassium solution. In tank 5#, the shorter chain *n*-alkanes of
242 C₉-C₁₂ were completely degraded, the *n*-alkanes of C₁₃-C₂₄ were degraded by
243 60%-70%. However, the longer ones of C₂₆-C₃₀ were resistant to degradation. The
244 degradation ratio of total *n*-alkanes in tank 5# was higher than 58% on average.
245 Dastgheib et al.³³ have isolated a halotolerant *Alcanivorax* sp. Strain Qtet3 which
246 degrades a wide range of *n*-alkanes (from C₁₀ to C₃₄) with considerable growth on C₁₄
247 and C₁₆ with the highest hydrocarbon degradation of 26.1% observed at 2.5% NaCl.
248 Two strains growing on crude oil from hypersaline sabkhas in Kuwait also utilized
249 Tween 80 and a wide range of individual aliphatic hydrocarbons (C₉-C₄₀) and the oil
250 biodegradation *M. sedimentalis* and *M. flavimaris* was 76 - 90 and 71 % respectively
251 ³⁴. The oil degradation in this paper is just between the results of the two studies
252 above, therefore further research should be conducted to rise the degradation.

253 3.2.2 PAHs

254 Five targeted alkylated PAH homologues (naphthalene, phenanthrene,
255 diphenylazoethiophene, fluorene and chrysene) were selected to represent aromatic
256 hydrocarbon compounds. The degradation depletion on the distribution of 2-4 ringed
257 aromatics were shown in Fig. 2 b. The alkylated PAHs were almost removed above
258 32% in all tanks, however the weathering effect on degradation was weak. The total
259 biodegradation depletion of phenanthrene, chrysene and their alkyl derivatives in tank
260 5# were greatly higher than those in tank 1#-4#, reached 30% and 60% respectively.
261 The total removal efficiency of all targeted alkylated PAH homologues by
262 biodegradation was higher than 41% on average in tank 5#. These biodegradation

263 removal are significantly higher than the reported results of a recent study on the
264 degradation of the *Prestige* fuel oil by a highly specialized PAH-degrading microbial
265 consortium that showed a 22-30% degradation of alkyl fluoranthenes/pyrenes and a
266 22-25% degradation of alkyl chrysenes.³⁵ Acevedo et al³⁶ isolated a white-rot fungus
267 *Anthracophyllum discolor* which had a high removal capability for
268 phenanthrene(62%), anthracene(73%), fluoranthene (54%), pyrene (60%) and
269 benzo(a)pyrene (75%). These biodegradation percentages are substantially higher than
270 our research, so suitable conditions must be found to promote the biodegradation
271 percentage of the PAHs. Vila et al³⁷ isolated a marine microbial consortium proved
272 highly efficient in removing three to five-ring polycyclic aromatic hydrocarbons
273 [PAHs; including anthracene, fluoranthene, pyrene, benzo(a)anthracene, chrysene, and
274 benzo(a)pyrene] (30-100%), and shown to considerably degrade their alkyl
275 derivatives. The biodegradation of *n*-alkanes and PAHs could be possibly explained
276 that the surfactant stimulated crude oil dissolved in formation and microbial
277 consortium promoted the biodegradation of petroleum. Campo³⁸ et al reported oil
278 biodegradation in the Gulf of Mexico was not inhibited by dispersants and that
279 Corexit EC9500A can increase the extent of oil degradation under some
280 circumstances for some hydrocarbon classes.

281 **3.3 Acute toxicity effect on marine microalgae**

282 3.3.1 Acute toxicity effect of crude oil on marine microalgae

283 The acute toxicity effects of dissolved crude oil with different concentrations on
284 the growth of three microalgae are depicted in Fig. 3. The cell densities of *Dicrateria*

285 sp. and *Skeletonema costatum* were higher than the individual control on 24 h when
286 the concentration of dissolved crude oil was lower than $20 \text{ mg}\cdot\text{L}^{-1}$, but their growth
287 was inhibited with increasing exposition time and remained unchanged at $80 \text{ mg}\cdot\text{L}^{-1}$
288 of crude oil concentration. From these results, it is possible to infer that lower
289 concentration of dissolved crude oil could stimulate the growth of the two microalgae
290 in a shorter time, while inhibited the growth in a longer time. The growth of
291 *Phaeodactylum tricornerutum* increased with the increasing concentration of the
292 dissolved oil ($0\text{-}80 \text{ mg}\cdot\text{L}^{-1}$.) These results demonstrated that *Dicrateria* sp. and
293 *Skeletonema costatum* were sensitive to dissolved crude oil, while *Phaeodactylum*
294 *tricornerutum* had a certain resistance to crude oil. Physiological acclimatization was
295 considered as a plausible explanation for the microalgae diversity in different
296 concentration gradients of crude oil and crude oil inhibited the photosynthesis of
297 microalgae which led to the decrease of algae density.³⁹Fabregas et al. indicated that
298 toxicity for marine microalga *Tetraselmis suecica* was increased with higher
299 concentrations, and longer extension of the lag phase and lower cellular density in the
300 stationary phase occurred.⁴⁰Hing et al. designed a continuous culture conditions to
301 model the effect of diesel on the growth behaviour of natural phytoplankton
302 communities in the oceans in the event of an oil spill and the results showed the effect
303 of diesel on steady state growth differed among species and the number of cells
304 affected was largely dependent on the cell concentration at steady state. The higher
305 the cell concentration at steady state, the lower the effect of diesel on the
306 phytoplankton.⁴¹ Chao et al. verified the acute toxicity of four fuel oils including F120,

307 F180, F380 and No.-20 to the marine microalgae *Chlorella spp.* (Chlorophyta) and
308 *Skeletonema costatum* (Bacillariophyta) and showed that F180 was the most toxic to
309 both microalgae, and the 96 h EC₅₀ value for *Skeletonema costatum* and *Chlorella spp.*
310 was 9.41 and 13.63 mg/L expressed in concentration of total petroleum hydrocarbons,
311 respectively. These studies are focused on the toxicity of crude oil, oil spill and fuel for
312 marine microalgae, not considering the remediation effects of microorganism on the
313 contaminated environment, while in this paper this effect was concerned.

314 3.3.2 Acute toxicity effect of microbes and surfactant on marine microalgae

315 Fig. 4 shows the effect of the microbial consortium and/or surfactant Tween-80
316 treated seawater on the growth of the three microalgae. The impact of different
317 substrates on three microalgae followed a decreasing order: the microbial consortium
318 plus Tween-80 > the microbial consortium > Tween-80. The effect of the microbial
319 consortium plus surfactant Tween-80 on the three microalgae was the most significant
320 and became prominent along the time, which probably resulted because of the
321 biological competition for the nutrients between the microbial consortium and
322 microalgae and the toxicity of Tween-80 to the microalgae. Tween-80 is a non-ionic
323 surfactant and may be adsorbed into the cell membrane to affect the growth of
324 microalgae. Previous studies reported that adsorbed surfactant LAS could exert
325 toxicity on cells through the denaturation and the binding of proteins in the cell wall
326 and consequently the alteration of membrane permeability to nutrients and
327 chemicals.⁴² Rial et al⁴³ assessed the effects of four cleaning agents on microalgal
328 growth kinetics and conducted that spill-treating agents had different toxicity,

329 especially Agma OSD 569. The results from above suggested Tween-80 might
330 produce toxicity effect on microalgae in a similar way as surfactant LAS and Agma
331 OSD 569 did.

332 3.3.3 Acute toxicity effect of biotreated seawater on marine microalgae

333 To assess the ecological response to the enhanced bioremediation of marine oil
334 spill, the toxicity effect on microalgae in the bioremediation process was evaluated in
335 many reports^{44,45}. Fig. 5 showed the acute toxicity effect of the repaired seawater on
336 the cell densities of the three microalgae. The three microalgae in tank 1# grew more
337 vigorously than those in tank 2#, which indicated that nutrients could stimulate the
338 growth of microalgae even in the toxic environment. Comparing tank (1#, 2# and 4#)
339 with tank (3# and 5#), the cell densities of three microalgae with the microbial
340 consortium were lower than those without the microbes, which was similar to the
341 result described in **section 3.3.2**. In addition, the holistic impact of nutrients,
342 surfactant and microbes on three microalgae in tank 5# was the most obvious. These
343 results were mainly due to the changes of phytoplankton magnitude, the group
344 involved in food web and the physical characteristics of the water, such as
345 concentrations of dissolved organic compounds and nutrient loading affected the
346 growth of marine microalgae and further impacted the marine ecosystems.⁴⁶ However,
347 these three microalgae were dead in the seawater. During 96 h, the cell densities of
348 *Dicrateria* sp., *Skeletonema costatum* and *Phaeodactylum tricornutum* in the
349 biotreated seawater by 21-day-bioremediation were boosted along the time, which
350 were increased from 4.0×10^5 , 1.0×10^5 and 2.5×10^5 cells·mL⁻¹ to 1.7×10^6 , 8.5×10^5 and

351 2.5×10^6 cells·mL⁻¹ respectively. Moreover, the petroleum-resistant mutants were
352 undeveloped in a short time.¹⁶ These results suggested that the seawater contaminated
353 by oil spill was significantly improved during the bioremediation process.

354 4 Conclusions

355 Simulated bioremediation experiments on oil spill-polluted marine intertidal
356 zone were conducted in open custom-designed devices using a microbial consortium
357 of *Bacillus cereus* S-1, *Lysinibacillus* sp. S-2 and *Rhodococcus ruber* S-3. This
358 microbial consortium exhibited exceptional ability of degrading crude oil. GC-MS
359 analysis showed that removal efficiencies of *n*-alkanes and PAH homologues in crude
360 oil were higher than 58% and 41% using enhanced bioremediation. Moreover, the
361 acute toxicity effects of different substrates on three microalgae were estimated.
362 During 96 h, the cell densities of *Dicrateria* sp., *Skeletonema costatum* and
363 *Phaeodactylum tricorutum* in the biotreated seawater showed a significant growth
364 trend, suggesting the oil spill-polluted seawater quality was obviously improved by
365 the bioremediation. The simulation and assessment of the ecological response to
366 enhanced bioremediation with bacteria used in this study can facilitate the better
367 management of future oil spill pollution.

368

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533

Table 1 The Details of Enhanced Bioremediation Condition

Tank Number	Crude oil	Hydrocarbon degradation bacteria	Nutrients	Surfactant (Tween-80)
1#	+	-	+	-
2#	+	-	-	-
3#	+	+	+	-
4#	+	-	+	+
5#	+	+	+	+

“+”represents that the substrates exist in the tank, while “-” represents that the substrates do not exist in the tank.

Table 2 Morphological, Physiological and Biochemical Identification of the Three

Bacterial Isolates			
Item	S-1^a	S-2^a	S-3^a
Colony color	Milky-white	white	Orange
Colony surface	Wet smooth	Wet smooth	Wet smooth
Sharpe of cells	Rod	Short rod	Short rod
Gram staining	+	+	+
Spore staining	+	-	+
Catalase reaction	+	+	+
Methyl red test	-	-	+
V-P test	+	-	-
Gelatin liquefaction	+	+	-
Amylolysis test	-	-	-
Hydrate cellulose	-	-	-
Glucose oxidation	Oxidized form	Oxidized form	Oxidized form

^a Results of substrate-utilizing test were interpreted after 24 h incubation at 36 °C in bacteriological incubator.

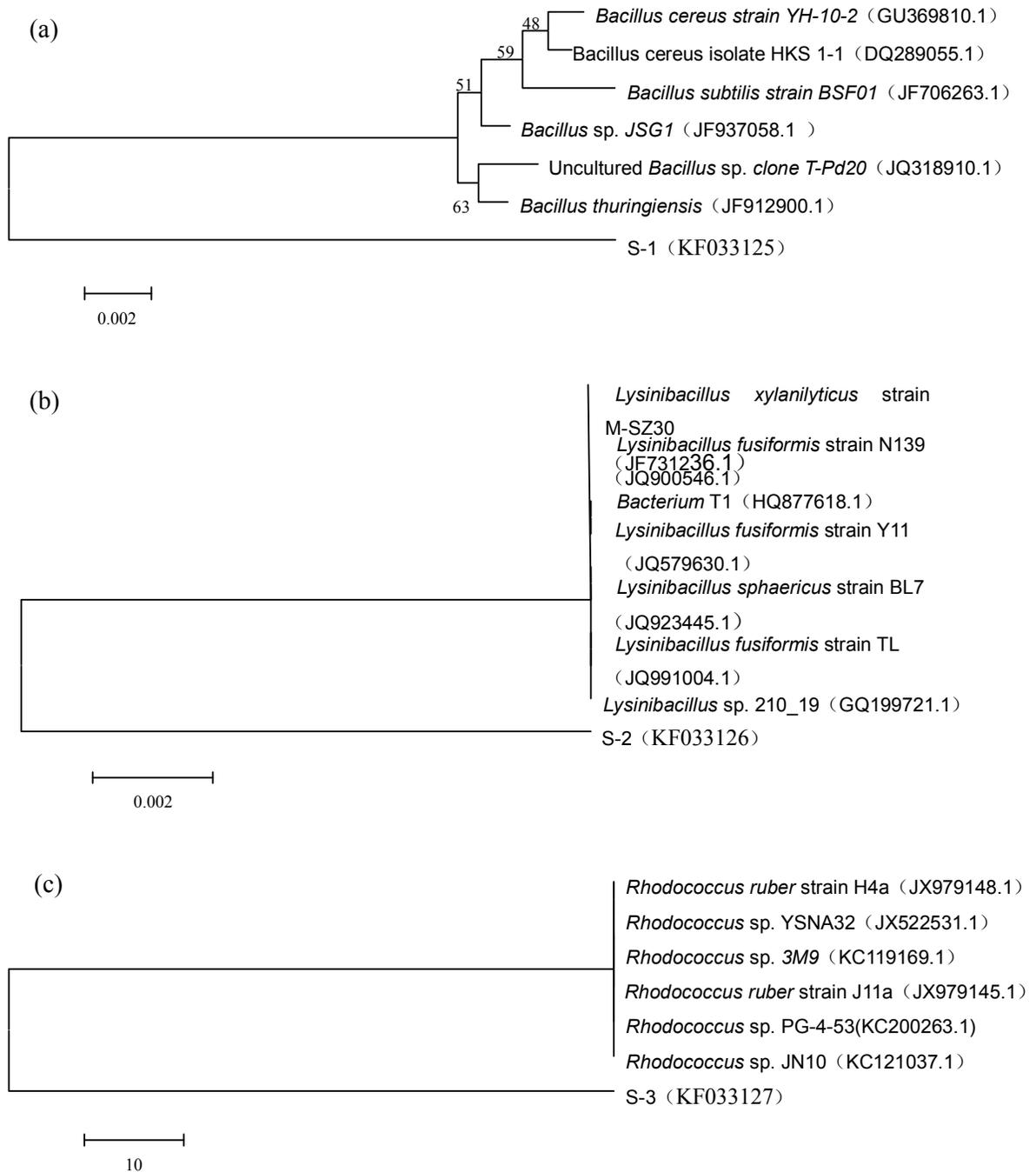


Fig. 1 Phylogenetic trees of the three strains.(a) S-1; (b) S-2; (c) S-3.

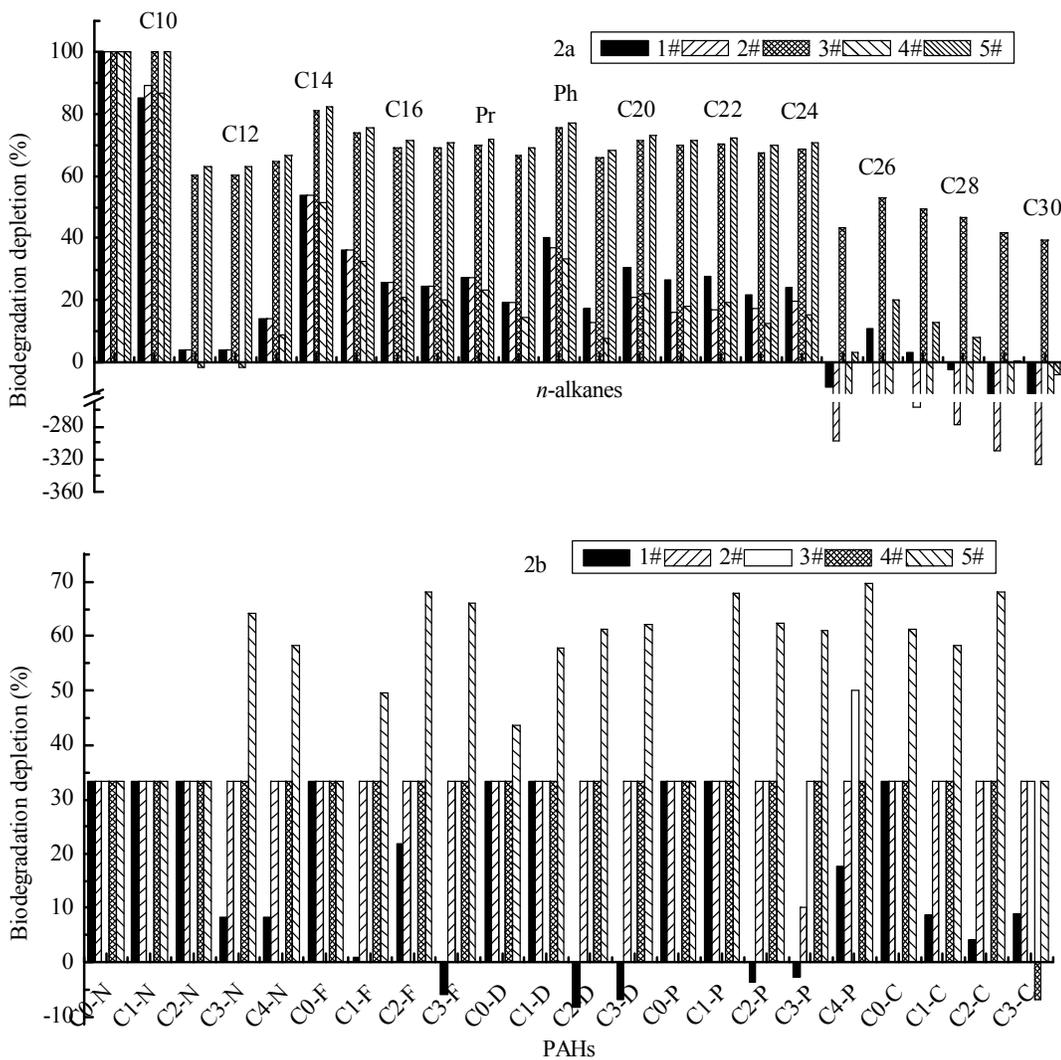


Fig. 2 Biodegradation rate of petroleum hydrocarbons. (a) n-Alkane (Including Pristane and Phytane); (b) PAHs

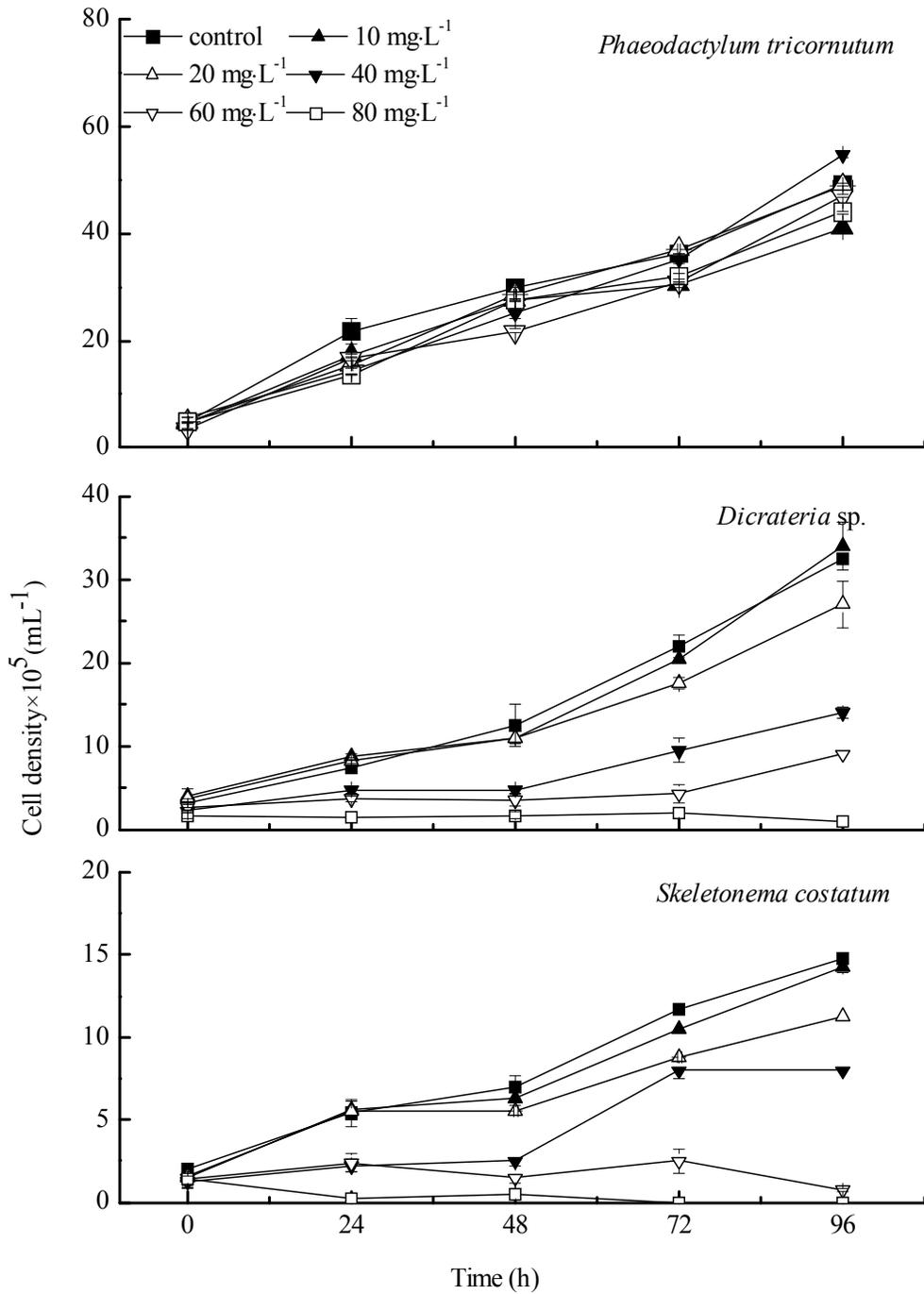


Fig. 3 Acute toxicity effect of soluble crude oil on microalgae.

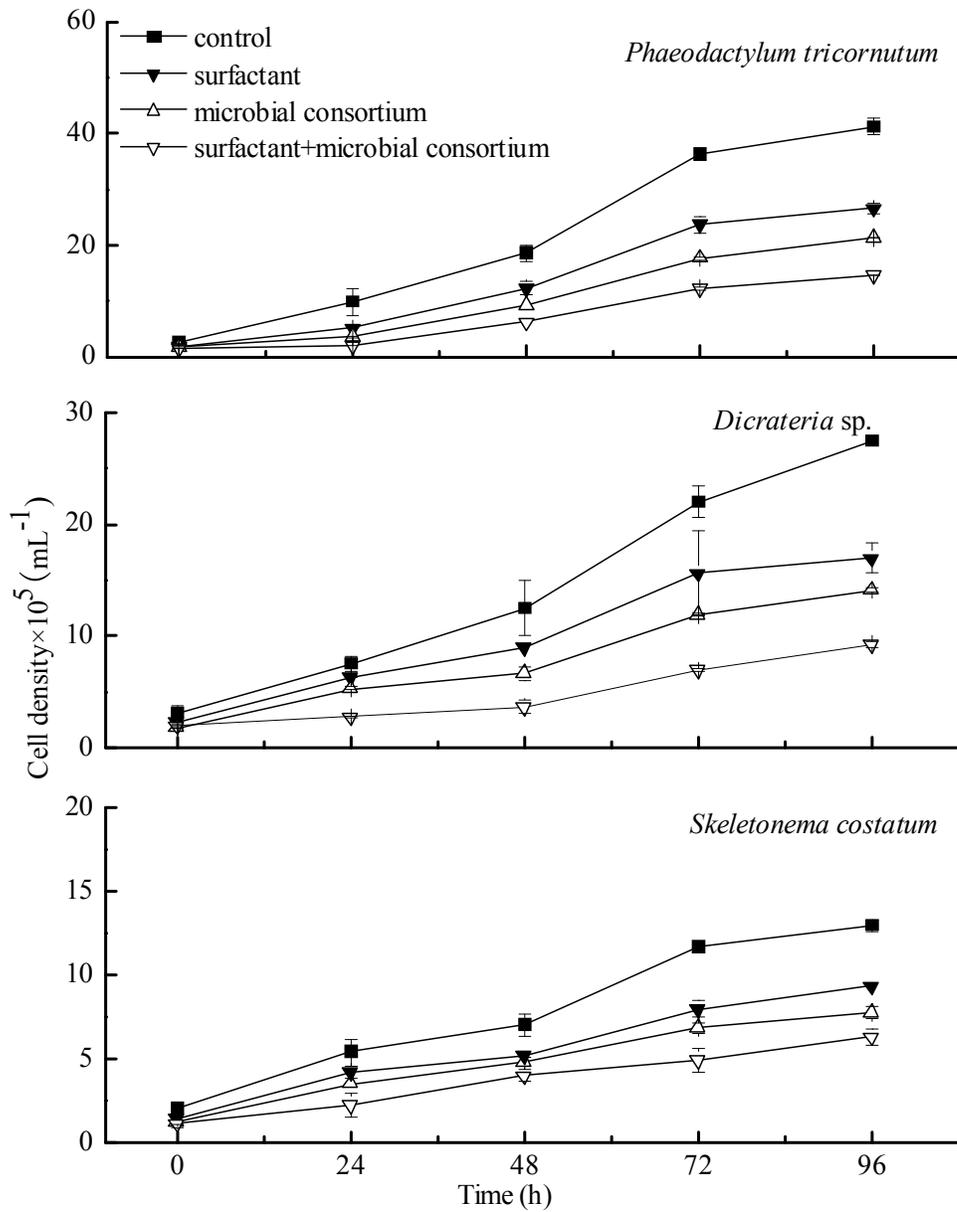


Fig. 4 Effect of microbial consortium and surfactant on microalgae.

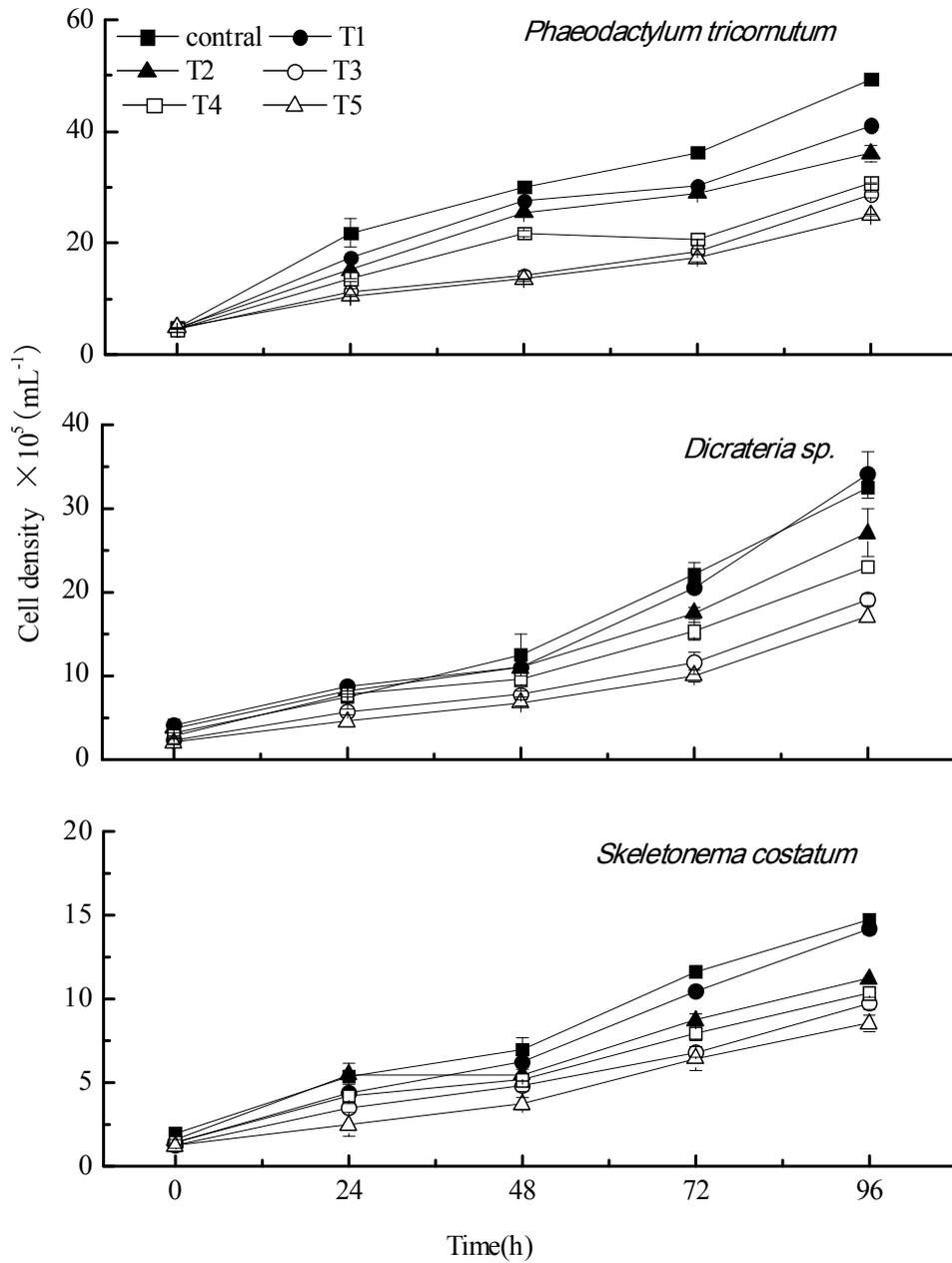


Fig. 5 Effect of biotreated seawater on microalgae.