Supporting Information (SI) for

Evaluating adsorption and biodegradation mechanisms during the removal of microcystin-RR by periphyton

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1. The equations of sorption energy (E) and Gibbs free energy (ΔG°)

The mean sorption energy E (kJ/mol) can be calculated using the following equation (1, 2).

$$E = \frac{1}{\sqrt{2\beta}} \quad (1S)$$

The Gibbs free energy (ΔG°) was calculated from equilibrium constant value (K_L) following the equation:

$$\Delta G^\circ = -RT \ln(K_L) \quad (2S)$$

2. The method for characterizing the diversity of bacteria with flaA gene

5.0 g of dried periphyton (86% moisture content) was placed into a centrifuge tube and centrifuged for 10 min. DNA was extracted from periphyton by the method provided by Di Giovanni *et al.* (3). PCR amplification of the flaA gene was performed using the forward oligonucleotide primer (5'-AGCTCTTAGCTCCATGAGTT3') and the reverse primer (5'-ACATTGTAGCTAAGGCGACT 3') (4, 5). For ERIC-PCR, the forward primer (5'-ATGTAAGCTCCTGGGGA-TTCAC-3') and the reverse primer (5'-AAGTAAGTGACTGGGG-TGAGCG) were used (6). Reactions were performed in a 50 μ L volume in a Perkin Elmer thermocycler (Gene Amp PCR System 2,400). Reaction mixtures contained 1 μ M of each primer, 50 to 100 ng of genomic DNA, 1.5 mM $MgCl_2$, each deoxynucleoside triphosphate (dATP, dTTP, dCTP, dGTP; Promega, USA) at a concentration of 0.2 mM, and 1 U of Taq DNA polymerase (Promega, USA). For flaA amplification, cycle conditions of 1 cycle at 94 °C for 2 min; 35 cycles of 94 °C for 1 min, 65 °C for 30 s, and 72 °C for 30 s; and 1 cycle at 72 °C for 10 min were used. For ERIC-PCR, the amplification was

accomplished by running 30 cycles of denaturing at 90 °C for 30 s, annealing at 50 °C for 30 s and extending at 50 °C for 30 s, and the initial denaturing at 95 °C for 5 min, initial extending at 72 °C for 8 min. All amplification products were electrophoresized in agarose gels, stained with ethidium bromide, detected under a short-wavelength UV light source, and photographed with a Polaroid 667 camera. The 100 bp DNA Ladder (Promega) was used as a molecular size marker. The Shannon-Weaver diversity index (7) of bacteria carrying *flaA* gene in periphyton was calculated based on the relative area of ERIC-PCR fingerprint peak.

3. The method for analyzing MCRR in water and periphyton

A high-performance liquid chromatograph with a UV detector was used for MCRR analysis. The system consisted of a Waters 600 pump, a 600E controller and a 2487 dual 1 UV-Vis detector. Separation was accomplished under a reversed-phase isocratic condition with a Delta-pak C₁₈ column (150×3.9 mm, Waters) and a mobile phase of methanol (0.01% TFA (trifluoroacetic acid): water=55:45). The flow rate was 1 mL min⁻¹. The concentration of MCRR was determined by comparing the peak area at 238 nm with that of the MCRR standard. Standards of MCRR were purchased from Sigma Co. (Japan). All solvents and chemicals used in this study were HPLC or analytical grade. Double-distilled water was used throughout, and its conductivity at room temperature was ranged from 0.20 μS cm⁻¹ to 0.60 μS cm⁻¹. The MCRR in periphyton was extracted using 75% methanol, according to the method described by Fastner *et al.* (8).

4. Figure 1S

(a)

(b)

Figure 1. (a) The SEM image of periphyton using for removing MCRR; and (b) ERIC-PCR fingerprint of bacteria of flaA gene. The reference bands are on the right (M) and the sample bands are on the left (1).

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