

A comparison of bacterial community structure, activity and microcystins associated with formation and breakdown of a cyanobacterial scum

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Table S1: Primer sequences used in this study.

Amplification of 400 bp region of 16S rRNA gene for high-throughput sequencing

Forward	IllumF-Bakt_341F	5'-TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCTACGGNGGCWGCAG-3'
Reverse	IllumR-Bakt_805R	5'-GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGACTACHVGGTATCTAATCC-3'
Reference	(Herlemann et al. 2011, Klindworth et al. 2012), modified to include Illumina™ adapters	

Amplification of spacer region 2 of the rRNA gene operon of *Oncorhynchus keta* salmon sperm for inhibition test

Forward	SketaF2	5'-GGTTCCGCAGCTGGG-3'
Reverse	SketaR3	5'-CCGAGCCGTCCTGGTCTA-3'
Primer probe	SketaP2	5'-6FAM-AGTCGCAGGCCACCCT-TAMRA-3'
Reference	(Haugland et al. 2005)	

Amplification of *mcyE* open reading frame of the microcystin synthase gene for determination of *mcyE* gene copy number

Forward	<i>mcyE</i> -F2	5'-GAAATTGTGTAGAAGGTGC-3'
Reverse	MicmcyE-R8	5'-CAATGGGAGCATAACGAG-3'
Primer probe	<i>mcyE</i> -probe	5'-(6-FAM)-ATCAAGTTAAGGTCAATGG-(BHQ1)-3'
Reference	(Vaitomaa et al. 2003, Rueckert & Cary 2009)	

Amplification of HEP PCR fragment for detection of microcystin-producing cyanobacteria

Forward	HEP-F	5'-TTGGGGTTAACCTTTGGCATAGTC-3'
Reverse	HEP-R	5'-AATTCTGAGGCTGTAATCGGGTTT-3'
Reference	(Jungblut & Neilan 2006)	

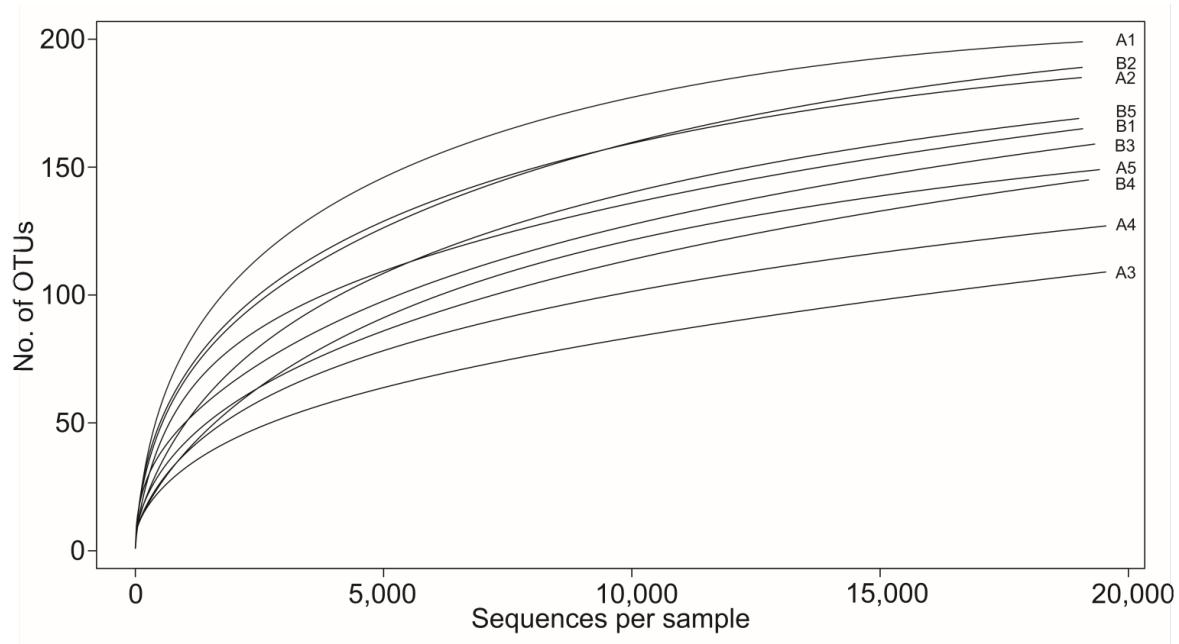


Figure S1. Rarefaction curves for samples (Bay A-Site 1-5 and Bay B-Site 1-5). See Figure 1B and C for location of sites within the bays.

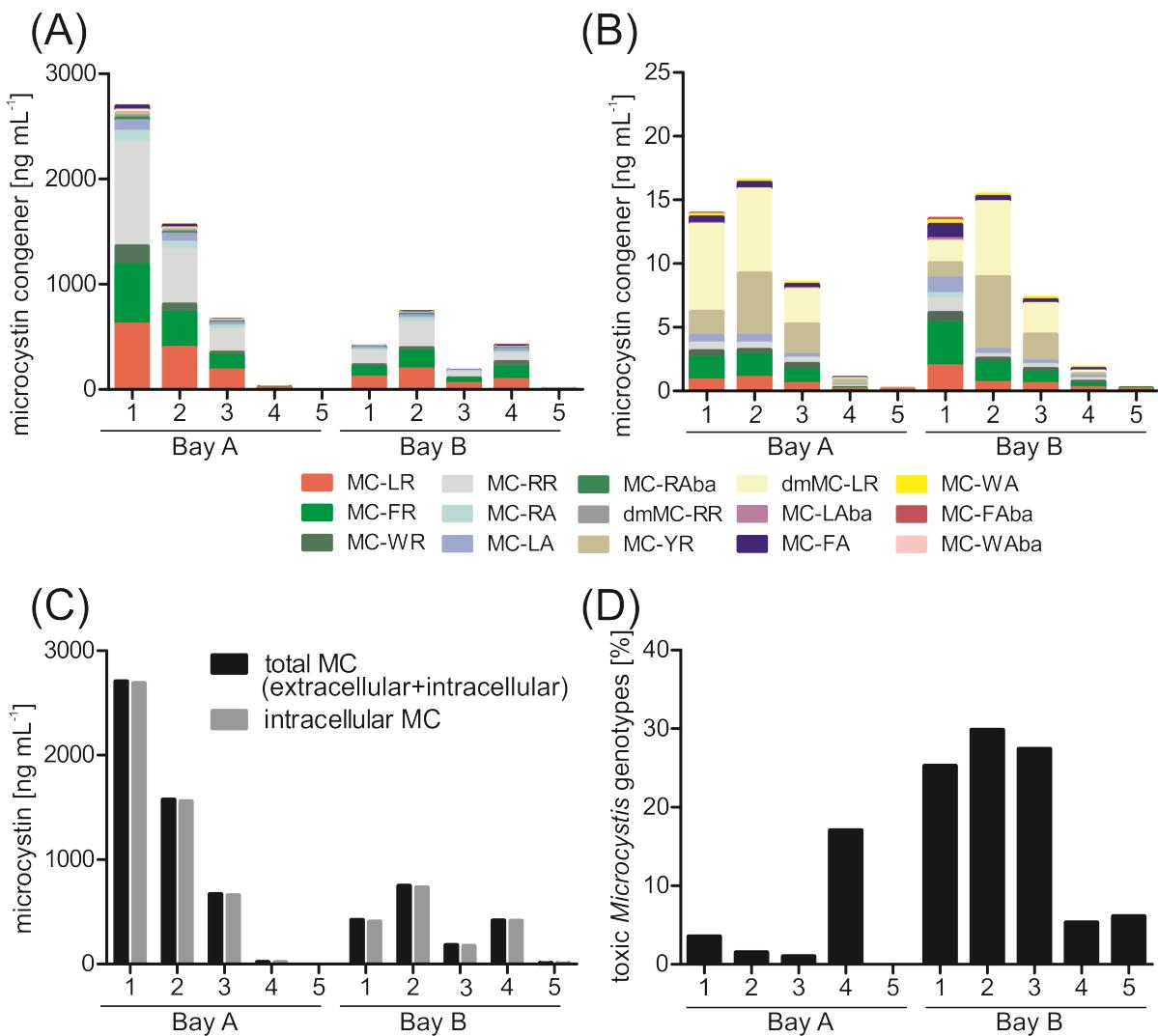


Figure S2. Concentration of: (A) intracellular microcystin (MC) congeners and (B) extracellular microcystin congeners. Letters L,R, F, W, A and Y stand for L-Aminoacids Leusine, Arginine, Phenylalanine, Tryptophan, Alanine and Tyrosine respectively. Demethyl (DM), Aminoisobutyric acid (Aba). (C) Total microcystin concentration and intracellular portion. (D) Toxic *Microcystis* genotypes relative to total *Microcystis* cell concentrations.

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