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Fluorescence in situ hybridization (FISH) of *Microcystis* strains producing microcystin using specific mRNA probes

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Supporting information

Figure S1. Alignment (Clustal Omega; <http://www.ebi.ac.uk/Tools/msa/clustalo/>) of the rRNA 16S sequences of the cyanobacterial strains used in this study. The complementary sequences of the EUB338 and MICR3 probes are highlighted in purple and green, respectively. A star indicates identity. Accessions: *Microcystis aeruginosa* PCC 7806, EMBL: AM778843–AM778958; *Microcystis aeruginosa* PCC 7005: GenBank: AQPY00000000 ; *Chlorogloeopsis fritschii* PCC 6912 GenBank: AJLN01000001–AJLN01000161.

Percent identity matrix for 1474 bases

	PCC 6912	PCC 7806	PCC 7005	
PCC 6912	100.00	89.27	89.27	
PCC 7806	89.27	100.00	99.80	
PCC 7005	89.27	99.80	100.00	
PCC_6912_rRNA16S	AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGTATGCTTAACACATGCAAGTCGAAC			60
PCC_7806_rRNA16S	AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGAAC			60
PCC_7005_rRNA16S	AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGAAC			60
***** **				
PCC_6912_rRNA16S	GGTCTTTTTTCGGAAGATAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCTAGGT			120
PCC_7806_rRNA16S	GGGAATCTTCGGATTTCTAGTGGCGGACGGGTGAGTAACGCGTAAGAATCTAACTTCAGGA			120
PCC_7005_rRNA16S	GGGAATCTTCGGATTTCTAGTGGCGGACGGGTGAGTAACGCGTAAGAATCTAACTTCAGGA			120
** * *****				
PCC_6912_rRNA16S	TCGGGACAACCACTGGAAACGGTGGCTAATACCGGATGTGCCGAAGAGGTGAAAGGCTAG			180
PCC_7806_rRNA16S	CGGGGACAACAGTTGGAAACGACTGCTAATACCGGATGTGCCGCAAG-GTGAAACCTAAT			179
PCC_7005_rRNA16S	CGGGGACAACAGTTGGAAACGACTGCTAATACCGGATGTGCCGCAAG-GTGAAACCTAAT			179
***** ***** ***** * ***** *				
PCC_6912_rRNA16S	CTGCCCTAGAGATGAGCTCGCGTCTGATTAGCTAGATGGTGGGGTAAGAGCCTACCATGGC			240
PCC_7806_rRNA16S	TGGCCTGGAGAAGAGCTTTCGCTCTGATTAGCTAGTGGTGGGGTAAGAGCCTACCAAGGC			239
PCC_7005_rRNA16S	TGGCCTGAAGAAGAGCTTTCGCTCTGATTAGCTAGTGGTGGGGTAAGAGCCTACCAAGGC			239
**** ** *****				
PCC_6912_rRNA16S	GACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCAG			300
PCC_7806_rRNA16S	GACGATCAGTAGCTGGTCTGAGAGGATGAGCAGCCACACTGGGACTGAGACACGGCCAG			299
PCC_7005_rRNA16S	GACGATCAGTAGCTGGTCTGAGAGGATGAGCAGCCACACTGGGACTGAGACACGGCCAG			299

PCC_6912_rRNA16S	ACTCCTACGGGAGGCAGCAGTGGGGAATTTCCGCAATGGGCGAAAGCCTGACGGAGCAA			360
PCC_7806_rRNA16S	ACTCCTACGGGAGGCAGCAGTGGGGAATTTCCGCAATGGGCGAAAGCCTGACGGAGCAA			359
PCC_7005_rRNA16S	ACTCCTACGGGAGGCAGCAGTGGGGAATTTCCGCAATGGGCGAAAGCCTGACGGAGCAA			359

PCC_6912_rRNA16S	TACCGCGTGAGGGAGGAAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAAGAGAT			420
PCC_7806_rRNA16S	CGCCGCGTGAGGGAGGAAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAAGTTCT			419
PCC_7005_rRNA16S	CGCCGCGTGAGGGAGGAAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAAGTTCT			419
***** *****				
PCC_6912_rRNA16S	GACGGTACCTGAGGAAGAAGCATCGGCTAACTCCGTGCCAGCAGCCCGGTAATACGGAG			480
PCC_7806_rRNA16S	GACGGTACCTGAGGAATCAGCCTCGGCTAACTCCGTGCCAGCAGCCCGGTAATACGGGG			479
PCC_7005_rRNA16S	GACGGTACCTGAGGAATCAGCCTCGGCTAACTCCGTGCCAGCAGCCCGGTAATACGGGG			479
***** ***** **				
PCC_6912_rRNA16S	GATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCCGTAGGTGGTGTGCAAGTCT			540
PCC_7806_rRNA16S	GAGGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCCGTAGGTGGTGTGCAAGTCT			539
PCC_7005_rRNA16S	GAGGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCCGTAGGTGGTGTGCAAGTCT			539
** *****				
PCC_6912_rRNA16S	ATTGTCAAAGCGTGCGGCTCAACCGCATAAAGGCAGTGAAACTGTGTAACCTAGAGTGCA			600
PCC_7806_rRNA16S	GCCGTCAAATCAGGTTGCTTAACGACCTAAAGGCGGTGGAACTGGCAGACTAGAGAGCA			599
PCC_7005_rRNA16S	GCCGTCAAATCAGGTTGCTTAACGACCTAAAGGCGGTGGAACTGGCAGACTAGAGAGCA			599
***** * * ** * * * * *****				
PCC_6912_rRNA16S	TTCGGGGCAGGGGAATTCCTGGTGTAGCGGTGAAATGCGTAGAGATCAGGAAGAACACC			660
PCC_7806_rRNA16S	GTAGGGGTAGCAGGAATTCACAGTGTAGCGGTGAAATGCGTAGAGATTGGGAAGAACATC			659
PCC_7005_rRNA16S	GTAGGGGTAGCAGGAATTCACAGTGTAGCGGTGAAATGCGTAGAGATTGGGAAGAACATC			659
* **** * * *****				

PCC_6912_rRNA16S	GGTGGCGAAAGCGCCCTGCTAGGCTGCAACTGACACTGAGGGACGAAAGCTAGGGGAGCG	720
PCC_7806_rRNA16S	GGTGGCGAAAGCGTGCTACTGGGCTGTATCTGACACTCAGGGACGAAAGCTAGGGGAGCG	719
PCC_7005_rRNA16S	GGTGGCGAAAGCGTGCTACTGGGCTGTATCTGACACTCAGGGACGAAAGCTAGGGGAGCG	719
	***** ** * ***** * ***** *****	
PCC_6912_rRNA16S	AATGGGATTAGATACCCAGTAGTCTTAGCTGTAAACGATGGATACTAGGCGTTGCGTGT	780
PCC_7806_rRNA16S	AAAGGGATTAGATACCCCTGTAGTCTTAGCCGTAACGATGGATACTAGGCGTGGCTTGT	779
PCC_7005_rRNA16S	AAAGGGATTAGATACCCCTGTAGTCTTAGCCGTAACGATGGATACTAGGCGTGGCTTGT	779
	** ***** ***** ***** ***** ** **	
PCC_6912_rRNA16S	ATCGACCCAGCAGTGCCGTAGCTAACGCGTTAAGTATCCCGCTGGGGAGTACGCACGC	840
PCC_7806_rRNA16S	ATCGACCCAGCAGCGTGCCGAACTAACGCGTTAAGTATCCCGCTGGGGAGTACGCACGC	839
PCC_7005_rRNA16S	ATCGACCCAGCAGCGTGCCGAACTAACGCGTTAAGTATCCCGCTGGGGAGTACGCACGC	839
	***** ** ***** ***** ***** *****	
PCC_6912_rRNA16S	AAGTGTGAAACTCAAAGGAATTGACGGGGCGCCGACAAAGCGGTGGAGTATGTGGTTAA	900
PCC_7806_rRNA16S	AAGTGTGAAACTCAAAGGAATTGACGGGGCGCCGACAAAGCGGTGGAGTATGTGGTTAA	899
PCC_7005_rRNA16S	AAGTGTGAAACTCAAAGGAATTGACGGGGCGCCGACAAAGCGGTGGAGTATGTGGTTAA	899

PCC_6912_rRNA16S	TTTCGATGCAACGCGAAGAACCTTACCAGGCTTGACATGTCGGGAACCGAAGTAAAGCT	960
PCC_7806_rRNA16S	TTTCGATGCAACGCGAAGAACCTTACCAGACTTGACATGTCGGGAACCGTGGTAAAGCT	959
PCC_7005_rRNA16S	TTTCGATGCAACGCGAAGAACCTTACCAGACTTGACATGTCGGGAACCGTGGTAAAGCT	959
	***** * ***** ***** *****	
PCC_6912_rRNA16S	TCGGGTGCCCTTCGGGAGCCGGAACACAGGTGGTGATGGCTGTCGTTCAGCTCGTTCGTG	1020
PCC_7806_rRNA16S	GGGGGTGCCCTTCGGGAGCCGGAACACAGGTGGTGATGGCTGTCGTTCAGCTCGTTCGTG	1019
PCC_7005_rRNA16S	GGGGGTGCCCTTCGGGAGCCGGAACACAGGTGGTGATGGCTGTCGTTCAGCTCGTTCGTG	1019
	***** ***** ***** ***** *****	
PCC_6912_rRNA16S	AGATGTTGGGTTAAGTCCCACGAGCGCAACCCTCGTTCCTTAGTTGCCAGCATTCCG	1080
PCC_7806_rRNA16S	AGATGTTGGGTTAAGTCCCACGAGCGCAACCCTCGTTCCTTAGTTGCCAGCATTAG	1078
PCC_7005_rRNA16S	AGATGTTGGGTTAAGTCCCACGAGCGCAACCCTCGTTCCTTAGTTGCCAGCATTAG	1078
	***** * *	
PCC_6912_rRNA16S	GTGGGACTCTAAGGAGACTGCCGCTGACAAACCGAGGAAGGTGGGGATGACGTCAGT	1140
PCC_7806_rRNA16S	TTGGGGACTCTAAGGAGACTGCCGCTGACAAACCGAGGAAGGTGGGGATGACGTCAGT	1138
PCC_7005_rRNA16S	TTGGGGACTCTAAGGAGACTGCCGCTGACAAACCGAGGAAGGTGGGGATGACGTCAGT	1138
	**** *****	
PCC_6912_rRNA16S	CAGCATGCCCTTACGCTCCGGGCTACACACGTACTACAATGCTCAAGACAGAGGGCAGC	1200
PCC_7806_rRNA16S	CAGCATGCCCTTACGCTCTGGGGACACACGTACTACAATGCTCGGGACAAAGGCAGC	1198
PCC_7005_rRNA16S	CAGCATGCCCTTACGCTCTGGGGACACACGTACTACAATGCTCGGGACAAAGGCAGC	1198
	***** ***** ***** ***** *****	
PCC_6912_rRNA16S	AAGCTAGCGATAGCAAGCAAACTCT-CGTAAACTTGGGCTCAGTTCAGATCGCAGGCTGCA	1259
PCC_7806_rRNA16S	GAACTCGCGAGAGCCAGCGAATCCAGCAAAACCGGCTCAGTTCAGATTGCAGGCTGCA	1258
PCC_7005_rRNA16S	GAACTCGCGAGAGCCAGCGAATCCAGCAAAACCGGCTCAGTTCAGATTGCAGGCTGCA	1258
	* * * * * * * * * * * * * * * * * *	
PCC_6912_rRNA16S	ACTCGCCTGCGTGAAGGAGGAATCGCTAGTAATCGCAGGTGAGCTACTGCGGTGAATTC	1319
PCC_7806_rRNA16S	ACTCGCCTGCGTGAAGGAGGAATCGCTAGTAATCGCAGGTGAGCTACTGCGGTGAATTC	1318
PCC_7005_rRNA16S	ACTCGCCTGCGTGAAGGAGGAATCGCTAGTAATCGCAGGTGAGCTACTGCGGTGAATTC	1318
	***** ***** ***** ***** *****	
PCC_6912_rRNA16S	GTTCCCGGGCCTTGTACACACCGCCGTCACACCATGGAAGCTGGTCATGCCCGAAGTTCG	1379
PCC_7806_rRNA16S	GTTCCCGGGCCTTGTACACACCGCCGTCACACCATGGAAGCTGGTCACGCCCGAAGTTCG	1378
PCC_7005_rRNA16S	GTTCCCGGGCCTTGTACACACCGCCGTCACACCATGGAAGCTGGTCACGCCCGAAGTTCG	1378
	***** ***** ***** ***** *****	
PCC_6912_rRNA16S	TTACCTCAACTCTTTTGGAGGGGGATGCCGGAAGCGGGACTGGTACTGGGGTGAAGT	1439
PCC_7806_rRNA16S	TTACCTCAACCGCA---AGGAGGGGGATGCCGGAAGCGGGACTGGTACTGGGGTGAAGT	1435
PCC_7005_rRNA16S	TTACCTCAACCGTA---AGGAGGGGGATGCCGGAAGCGGGACTGGTACTGGGGTGAAGT	1435
	**** * * ***** * * * *****	
PCC_6912_rRNA16S	CGTAACAAGGTAGCCGTACCGGAAGGTGGTGGCTGGATCA	1478
PCC_7806_rRNA16S	CGTAACAAGGTAGCCGTACCGGAAGGTGGTGGCTGGATCA	1474
PCC_7005_rRNA16S	CGTAACAAGGTAGCCGTACCGGAAGGTGGTGGCTGGATCA	1474

Figure S2. Alignment (Clustal Omega) of the *rpoB* gene sequences of the *M. aeruginosa* strains used in this study. The complementary sequence of the RPOB probe is highlighted in red. The sequences show 97.10% identity (indicated by a star) for 3312 bases. Accessions: *Microcystis aeruginosa* PCC 7806, EMBL: AM778843–AM778958; *Microcystis aeruginosa* PCC 7005; GenBank: AQPY00000000.

PCC7806rpoB	ATGAACAATCTTACCTTTAATCTCTTACCCGACCTGATCGAAATCCAACACTCCAGTTTT	60
PCC7005RpoB	ATGAACAATCTTACCTTTAACCTCTTACCCGACCTCATCGAAATCCAACACTCCAGTTTT	60

PCC7806rpoB	CGGTGGTTTTTTGGAAGAAGGACTCATCGAGGAACGAATAGCTTTTCCCCCATCAGCGAC	120
PCC7005RpoB	CGGTGGTTTTTTGGAAGAAGGACTAATCGAGGAACGAACAGCTTTTCCCCCATCAGCGAC	120

PCC7806rpoB	TATACAGGTAAATTAGAATACATTTCCCTCGGCCAGGACTACAGACTCAAAGAACCGAAA	180
PCC7005RpoB	TATACAGGTAAATTAGAATACATTTCCCTCGGCCAGGACTACAGACTCAAAGAACCGAAA	180

PCC7806rpoB	TACAACGTCGATGAAGCCAACGACGCGATAGCAGCTATTCTGTTTCAGATGTACGTTCCC	240
PCC7005RpoB	TACAACGTCGATGAAGCCAACGACGCTGATAGCACCTATTCCGTTTCAGATGTACGTTCCCT	240

PCC7806rpoB	ACCCGTCTAATCAACAAAGAAACGGGAGAAAACATCGAACAGGAAGTTTTATCGGCGAT	300
PCC7005RpoB	ACCCGTCTAATCAACAAAGAAACGGGAGAAAACATCGAACAGGAAGTTTTATCGGCGAT	300

PCC7806rpoB	TTACCCCTGATGACCGAACGGGAACTTTATCATTAACGGGGCTGAACGAGTCAATCGTC	360
PCC7005RpoB	TTACCCCTGATGACCGAACGGGAACTTTATCATTAACGGGGCTGAACGAGTCAATCGTC	360

PCC7806rpoB	AATCAGATCGTCCGTTCCCGGTTTACTACAAAGCCGAAATCGACAAAAACGGTCCG	420
PCC7005RpoB	AATCAGATCGTCCGTTCCCGGTTTACTACAAAGCCGAAATCGACAAAAACGGTCCG	420

PCC7806rpoB	CGCACCTACTCCGTTCCCTGATTTCCCAACCGAGGAGCTTGGTTAAAATTTGAAACCGAC	480
PCC7005RpoB	CGTACCTACTCCGTTCCCTGATTTCCCAACCGAGGAGCTTGGTTAAAATTTGAAACCGAC	480
	** *****	
PCC7806rpoB	AAAAACGGCTTAGTTTGGGTCAGAATCGACAAAACCCGTAATATCCGCCAAGTTCTC	540
PCC7005RpoB	AAAAACGGCTTAGTTTGGGTCAGAATCGACAAAACCCGTAATATCCGCCAAGTTCTC	540

PCC7806rpoB	CTGAAAGCGATCGGATTGAGCGATAACGAAATCTTTGACTCCCTACGCCATCCCGAATTT	600
PCC7005RpoB	CTGAAAGCGATCGGATTGAGCGATAACGAAATCTTTGACTCCCTACGCCATCCCGAATTT	600

PCC7806rpoB	TACCAAAAAACCCTCGACAAAGAAGGCAATCCACGGAAGAAGAGGCCCTGCTCGACCTG	660
PCC7005RpoB	TACCAAAAAACCCTCGACAAAGAAGGCAATCCACCGGAAGAAGAGGCACCTCTCGACCTG	660

PCC7806rpoB	TACCGCAAACCTACGCCCGGGGAACCTCCACCGTCACTGGCGGACAACAACCTACTCGAA	720
PCC7005RpoB	TACCGCAAACCTACGCCCGGGGAACCTCCACCGTCACTGGCGGACAACAACCTACTCGAA	720

PCC7806rpoB	TCGCGCTTTTTTGACAATAAACGCTACGATCTCGGGCGCGTTGGTTCGTTATAAACTCAAC	780
PCC7005RpoB	TCGCGCTTTTTTGACAATAAACGCTACGATCTCGGGCGCGTTGGTTCGTTATAAACTCAAC	780

PCC7806rpoB	AAAAAACTACGCCCTCAACGTCCCCGATAACCAGCGCGTTCTCACCACCACCGACATTTTA	840
PCC7005RpoB	AAAAAACTACGCCCTCAACGTCCCCGATAACCAGCGCGTTCTCACCACCACCGACATTTTA	840

PCC7806rpoB	TCGGCGATCGACTACCTAATTAACCTCGAATTCGACATCGGTAACACCGACGACATCGAC	900
PCC7005RpoB	TCGGCGATCGACTACCTAATTAACCTCGAATTTGACATCGGCAACACCGACGACATCGAC	900

PCC7806rpoB	CACCTCGGCAACCGTCGCGTCCGTTCCGTTGGGTGAAGTGTCCAAAACCAAGTGCAGTA	960
PCC7005RpoB	CACCTCGGCAACCGTCGCGTCCGTTCCGTTGGGTGAAGTGTCCAAAACCAAGTGCAGTA	960

PCC7806rpoB	GGTTTAAACCGCTTAGAAAGAATCATTCGGGAACGGATGACCGTCAGCGAATCCCAAAAC	1020
PCC7005RpoB	GGTTTAAACCGCTTAGAAAGAATCATTCGGGAACGGATGACCGTCAGCGAATCCCAAAAC	1020

PCC7806rpoB	CTCACCCCGCTTCCCTAGTCAACCCGAAACCCCTAGTAGCGGCGATTAAAGAATCTTTT	1080
PCC7005RpoB	CTCACCCCGCTTCCCTAGTCAACCCGAAACCCCTAGTAGCGGCGATTAAAGAATCTTTT *****	1080
PCC7806rpoB	GGTTCCTCGCAACTCTCCAGTTTATGGATCAAACCAACCCCTAGCGGAATTGACCCAT	1140
PCC7005RpoB	GGTTCCTCGCAACTCTCCAGTTTATGGATCAAACCAACCCCTAGCGGAATTGACCCAT *****	1140
PCC7806rpoB	AAACGCCGATTTCCGCCCTTGGACCCGGCGGTCTCACCCGGGAACGGGCCGTTTGGCC	1200
PCC7005RpoB	AAACGCCGATTTCCGCCCTTGGACTGGCGGTCTCACCCGGGAACGGGCCGTTTGGCC *****	1200
PCC7806rpoB	GTGCGGACATTCACCCCTCCACACCGTTCGATTTGTCCGGTGGAAACCCAGAAAGGT	1260
PCC7005RpoB	GTGCGGACATTCACCCCTCCACACCGTTCGATTTGTCCGGTGGAAACCCAGAAAGGT *****	1260
PCC7806rpoB	CCCAACGCTGGTTTAAATCGGTTCCCTAGCCACCTACGCCCGGTCAACGACTACGGTTTT	1320
PCC7005RpoB	CCCAACGCGGTTTAAATCGGTTCCCTAGCCACCTACGCCCGGTCAACGACTACGGTTTT *****	1320
PCC7806rpoB	ATTGAAACCCCTGTTATGGGGTGGAAAAATGGCCGAGTTCGCTACGATCTCCCGTCAA	1380
PCC7005RpoB	ATTGAAACCCCTGTTATGGGGTGGAAAAATGGCCGAGTTCGCTACGATCTCCCGTCAA *****	1380
PCC7806rpoB	TACCTCACCGCCGACGAAGAAGACGATCTCAGAGTCGCCCGGGAGACGTGGCCACCGAT	1440
PCC7005RpoB	TACCTCACCGCCGACGAAGAAGACGATCTCAGAGTCGCCCGGGAGACGTGGCCACCGAT *****	1440
PCC7806rpoB	GAAATGGTTATATCCTCGGCGAAACTATCCCGTGCCTATCGGCAGGAATTCTCCACC	1500
PCC7005RpoB	GAAATGGTTATATCCTCGGCGAAACTATCCCGTGCCTATCGGCAGGAATTCTCCACC *****	1500
PCC7806rpoB	ACCTCCCCGAACAAGTGGACTACGTTTGTGTTTCCCCGTGCAAATTGTCTCGGTGGCC	1560
PCC7005RpoB	ACTTCCCCGAACAAGTGGACTACGTTTGTGTTTCCCCGTGCAAATTGTCTCGGTGGCC ** *****	1560
PCC7806rpoB	ACTTCCCTGATTCCCTTCCCTCGAACACGACGACGCTAACCGCGCCCTCATGGGTCCAAT	1620
PCC7005RpoB	ACTTCCCTGATTCCCTTCCCTCGAACACGACGACGCTAACCGCGCCCTCATGGGTCCAAT *****	1620
PCC7806rpoB	ATGCAGCGACAAGCGGTTCCCTGCTGCGTCCCGAACGTCCCTTGTGGGAACGGGATTG	1680
PCC7005RpoB	ATGCAGCGACAAGCGGTTCCCTGCTGCGTCCCGAACGTCCCTTGTGGGACTGGATTG *****	1680
PCC7806rpoB	GAAGCACAGGCCGCTCGCGACTCCGGCATGGTTCATCGTTTCCCGTACCAATGGAGTAGTT	1740
PCC7005RpoB	GAAGCACAGGCCGCTCGCGACTCCGGCATGGTTCATCGTTTCCCGTACCAATGGGTCGTT *****	1740
PCC7806rpoB	TCCACGTCGATGCTAACCGGATTCGCATCAAAGTGGCGGATCAAGACAAAGAGATTTTC	1800
PCC7005RpoB	TCCACGTCGATGCTAACCGGATTCGCATCAAAGTGGCGGATCAAGACAAAGAGATTTTC *** *****	1800
PCC7806rpoB	GGCAAGAGCGAGATCGAGTACGAAATTCAGAAATATCAACGCTCTAACCAAGATACCTGC	1860
PCC7005RpoB	GGCAAGAGCGAGATCGAGTACGAAATTCAGAAATATCAACGCTCTAACCAAGATACCTGC *****	1860
PCC7806rpoB	CTAAATCAGCGTCTTTGGTCTATCAAGGGGAACAAGTTGTGCCGGGCGAGATCCTCGCC	1920
PCC7005RpoB	CTAAATCAGCGTCTTTGGTCTATCAAGGGGAACAAGTTGTGCCGGGCGAGATCCTCGCC *****	1920
PCC7806rpoB	GATGGTTCCGCCACCGAAGGAGGAGAAATCGCCCTCGGCCAGAATATTCTCGTCGCCTAT	1980
PCC7005RpoB	GATGGTTCCGCCACCGAAGGAGGAGAAATCGCCCTCGGCCAGAATATTCTCGTCGCCTAT *****	1980
PCC7806rpoB	ATGCCCTGGGAAGGCTATAACTACGAAGACGCGATTTTAATCAGTGAAAGACTGGTGGCA	2040
PCC7005RpoB	ATGCCCTGGGAAGGCTATAACTACGAAGATGCGATTTTAATCAGTGAAAGACTGGTGGCA *****	2040
PCC7806rpoB	CAAGATGTCTATACCAGTATCCACATTGAAAAATACGAAATCGAAGCCCGTCAAACATAA	2100
PCC7005RpoB	CAAGACCTACACCAGTATCCACATTGAAAAATACGAAATCGAAGCCCGTCAAACATAA *****	2100
PCC7806rpoB	CTCGGACCAGAGGAAATCACCAGGAAATTCCCAACGTCGGTGAAGATGCCCTGCGAAAC	2160
PCC7005RpoB	CTAGGACCAGAGGAAATCACCAGGAAATTCCCAACGTCGGTGAAGATGCCCTGCGAAAC ** *****	2160
PCC7806rpoB	CTCGATGAACGCGGATTATTTCGATCGGAGCTTGGGTAGAAGCCAGCGATATCCTTGTG	2220
PCC7005RpoB	CTCGATGAACGCGGATTATTTCGATCGGAGCTTGGGTAGAAGCCAGCGATATCCTTGTG *****	2220

PCC7806rpoB	GGGAAAGTCACCCAAAAGGCGAATCAGACCAACCCCCGAAGAAAACTACTGCGGGCA	2280
PCC7005RpoB	GGGAAAGTCACCCGAAAGGCGAATCAGACCAACCCCCGAAGAAAACTACTGCGGGCA	2280

PCC7806rpoB	ATTTTCGGCGAAAAGGCCGGGATGTACGGGATAACTCCCTGCGCGTCCCCAACGGCGAA	2340
PCC7005RpoB	ATTTTCGGCGAAAAGGCCGGGATGTACGGGATAACTCCCTGCGCGTCCCCAACGGCGAA	2340

PCC7806rpoB	AAAGGCCGGGTAGTGGATGTACGGGTATTTACCCGCGAACAGGGGACGAATTACCCCC	2400
PCC7005RpoB	AAAGGCCGGGTAGTGGATGTGCGCGTATTTACCCGCGAACAGGGAGATGAATTACCCCCT	2400

PCC7806rpoB	GGGGCTAATATGGTAGTGCGGGTTTACGTTGCCCAAAAACGCAAAATCCAAGTGGGCGAT	2460
PCC7005RpoB	GGGGCCAATATGGTGGTAAGGGTTTACGTTGCCCAAAAACGCAAAATCCAAGTGGGCGAT	2460

PCC7806rpoB	AAAAATGGCGGGTCTGCACGGCAATAAAGGGATTATTTCTCGGATTTGCCCTAGAAGAT	2520
PCC7005RpoB	AAAAATGGCGGGTCTGCACGGCAATAAAGGGATTATTTCTCGGATTTGCCCTGGAAGAT	2520

PCC7806rpoB	ATGCCCTACCTCCCCGATGGTTCGTCGCCGATATCGTTCTCAATCCCCTAGGGGTCCC	2580
PCC7005RpoB	ATGCCCTACCTCCCCGATGGTTCGTCGCCGATATCGTTCTTAATCCCCTAGGGGTCCC	2580

PCC7806rpoB	AGTCGCATGAACGTCGGTCAGGTGTTTGAATGTTTACTGGGTGGGCTGGCGAAAATCTG	2640
PCC7005RpoB	AGTCGCATGAACGTCGGTCAGGTGTTTGAATGTTTACTGGGTGGGCGCGAAAATCTG	2640

PCC7806rpoB	GGCGTGCCTTTAAGATTACTCCCTTTGATGAAATGTATGGGGAAGAAGCCAGCCGTTT	2700
PCC7005RpoB	GGCGTGCCTTTAAGATTACTCCCTTTGATGAAATGTATGGGGAAGAAGCCAGCCGTTT	2700

PCC7806rpoB	ACCGTCCACGGATTGCTAGAAAATGCCTCGAAAAACCCCAATCGTGATTGGGTGTTCAAG	2760
PCC7005RpoB	ACCGTTCACGGATTGCTAGAAAATGCCTCGAAAAACCCCAATCGCGATTGGGTGTTCAAG	2760

PCC7806rpoB	GAAGAACACGCGGGCAAAGTCACCGTTTACGATGGTCGCACCGCGGAACCCCTTGACCGT	2820
PCC7005RpoB	GAAGAACACGCGGGCAAAGTCACCGTTTACGATGGTCGCACCGCGGAACCCCTTGACCGT	2820

PCC7806rpoB	CCCGTTACCGTTCGGTATGGCTATATGTTAAAACGGTTACCTGGTTGATGATAAAATT	2880
PCC7005RpoB	CCCGTTACCGTTCGGTATGGCTATATGTTAAAACGGTTACCTGGTTGATGATAAAATT	2880

PCC7806rpoB	CACGCCCGTCTACCGGTCCCTACTCCTTGGTTACTCAGCAACCCCTGGGCGGTAAAGCT	2940
PCC7005RpoB	CACGCCCGTCTACCGGTCCCTACTCCTTGGTTACTCAGCAACCCCTGGGCGGTAAAGCT	2940

PCC7806rpoB	CAACAGGGGGCCAGCGCTTCGGAGAAATGGAAGTCTGGGCCCTGGAGGCCTACGGGGCG	3000
PCC7005RpoB	CAACAGGGAGGCCAGCGCTTCGGAGAAATGGAAGTCTGGGCCCTAGAAGCCTACGGGGCG	3000

PCC7806rpoB	GCCTATACCTTGCAGGAATTGCTAACGGTGAATCCGATGATATGCAAGGACGGAATGAG	3060
PCC7005RpoB	GCCTATACCTTGCAGGAATTGCTAACGGTGAATCCGATGATATGCAAGGACGGAATGAG	3060

PCC7806rpoB	GCTTTAAATGCGATCGTAAAAGGCAAGCCGATTCCCCGCCGGGTACGCCAGAATCCTTT	3120
PCC7005RpoB	GCTTTAAATGCGATCGTAAAAGGCAAGCCGATTCCCCGCCGGGTACGCCAGAATCCTTT	3120

PCC7806rpoB	AAGGTTTGTATGCGAGAATTGCAATCCCTCGGCCTCGATATCGCCGTTTACAAGGTGGAA	3180
PCC7005RpoB	AAGGTTTGTATGCGAGAATTGCAATCCCTCGGCCTCGATATCGCCGTTTACAAGGTGGAA	3180

PCC7806rpoB	AATGCCCCGATGGTACTTCCCGCATGTGGAGGTGGATCTGATGGTCGATGTCGGTCTG	3240
PCC7005RpoB	AATGCCCCGATGGTACTTCCCGCATGTGGAGGTGGATCTGATGGTCGATGTCGGTCTG	3240

PCC7806rpoB	CGCGCCCCCTCTCGCCCCACTACGAATCCTTAACCACAGAAGACCTTGAGGAAGAAGAA	3300
PCC7005RpoB	CGCGCCCCCTCTCGCCCCACTACGAATCCTTAACCACAGAAGACCTTGAGGAAGAAGAA	3300

PCC7806rpoB	TCGGAAGTGTA 3312	
PCC7005RpoB	TCGGAAGTGTA 3312	

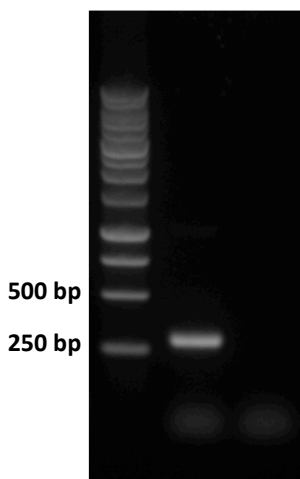
Figure S3. Nucleotide sequence of the *mcyA* gene from *M. aeruginosa* PCC 7806 Accessions: EMBL: AM778843–AM778958. The sequence of the PCR product obtained in this study is in red, and the complementary sequence of the MCYA probe is highlighted in blue. The gel of the corresponding PCR is shown.

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>mcyA PCC 7806
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Ladder
 PCC 7806
 PCC 7005

Figure S4. Epifluorescence micrographs (FITC filter set; $\times 40$ magnification; 100 ms exposure; scale bar 30 μm) of *Microcystis aeruginosa* PCC 7806 (A), of *Microcystis aeruginosa* PCC 7005 (B) and of *Chlorogloeopsis fritschii* PCC 6912 (C) with the EUB338-HRP probe.

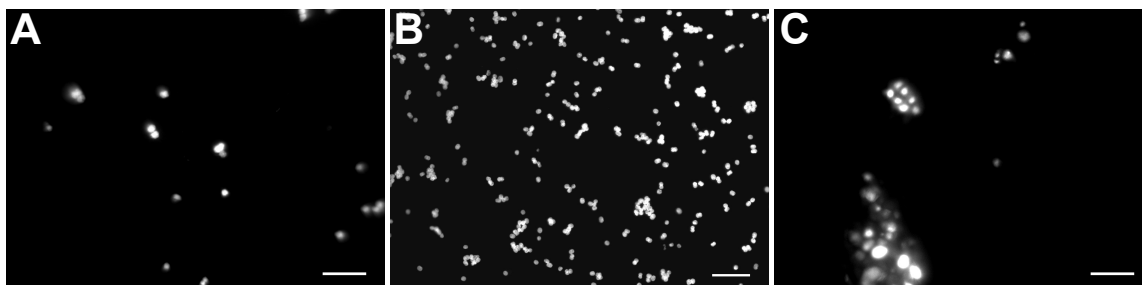


Figure S5. Epifluorescence micrographs (superposition of two images, one obtained with the Cy3 filter set, in red, and the other one obtained with the FITC filter set, in green; $\times 63$ magnification; 500 ms exposure; scale bar 30 μm) of *Microcystis aeruginosa* PCC 7806 (A) unlabeled, (B) labeled with probe MCYA-HRP and (C) labeled with probe RPOB-HRP, and of *Microcystis aeruginosa* PCC 7005 (D) unlabeled, (E) labeled with probe MCYA-HRP and (F) labeled with probe RPOB-HRP.

