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

Perrine Zeller^{1,#}, Annick Méjean^{2*}, Isabelle Biegala³, Vincent Contremoulins⁴, and Olivier Ploux^{1,2*}

¹Chimie ParisTech, 75005 Paris, France

²Laboratoire des Energies de Demain, LIED, UMR 8236 CNRS, Université Paris Diderot-Paris 7, 75013 Paris, France

³Aix-Marseille Université, CNRS/INSU, Université de Toulon, IRD, Mediterranean Institute of Oceanography (MIO) UM110, 13288 Marseille, France

⁴Institut Jacques Monod, CNRS UMR 7592, Université Paris Diderot, Sorbonne Paris Cité, 75205 Paris Cedex, France; ImagoSeine, Institut Jacques Monod, CNRS UMR 7592, Université Paris Diderot, Sorbonne Paris Cité, 75205 Paris Cedex, France.

[#]Present address: INSERM U1193, Physiopathogénèse et Traitement des Maladies du Foie, Hôpital Paul Brousse, bâtiment Lavoisier, 14 avenue Paul Vaillant Couturier, 94807 Villejuif Cedex, France

***Corresponding authors:** O.P.: Phone: +(33) 1 57 27 84 71; E-mail: olivier.ploux@chimie-paristech.fr; A.M.: Phone: +(33) 1 57 27 84 51; E-mail: annick.mejean@univ-paris-diderot.fr

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: AQPY000000000 ; *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	GGTCTTTTTCGGAAGATAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCTAGGT	120
PCC_7806_rRNA16S	GGGAATCTTCGGATTCTAGTGGCGGACGGGTGAGTAACGCGTAAGAATCTAACTTCAGGA	120
PCC_7005_rRNA16S	GGGAATCTTCGGATTCTAGTGGCGGACGGGTGAGTAACGCGTAAGAATCTAACTTCAGGA	120
	** * *****	
PCC_6912_rRNA16S	TCGGGACAACCACTTGGAAACGGTGGCTAATACCGGATGTGCCGAAGAGGTGAAAGGCTAG	180
PCC_7806_rRNA16S	CGGGGACAACAGTTGGAAACGACTGCTAATACCCGATGTGCCGCAAG-GTGAAACCTAAT	179
PCC_7005_rRNA16S	CGGGGACAACAGTTGGAAACGACTGCTAATACCCGATGTGCCGCAAG-GTGAAACCTAAT	179

PCC_6912_rRNA16S	CTGCCTAGAGATGAGCTCGCGTCTGATTAGCTAGATGGTGGGGTAAGAGCCTACCATGGC	240
PCC_7806_rRNA16S	TGGCCTGGAGAAGAGCTTGCCTCTGATTAGCTAGTGGTGGGGTAAGAGCCTACCAAGGC	239
PCC_7005_rRNA16S	TGGCCTGAAGAAGAGCTTGCCTCTGATTAGCTAGTGGTGGGGTAAGAGCCTACCAAGGC	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	CGCCGCGTGAGGGAGGAAGGCTCTTGGATTGTAAACCTCTTTTCTCAAGGAAGAAGTTCT	419
PCC_7005_rRNA16S	CGCCGCGTGAGGGAGGAAGGCTCTTGGATTGTAAACCTCTTTTCTCAAGGAAGAAGTTCT	419

PCC_6912_rRNA16S	GACGGTACCTGAGGAAGAAGCATCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAG	480
PCC_7806_rRNA16S	GACGGTACTTGAGGAATCAGCCTCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGGG	479
PCC_7005_rRNA16S	GACGGTACTTGAGGAATCAGCCTCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGGG	479

PCC_6912_rRNA16S	GATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCCGTAGGTGGTGATGCAAGTCT	540
PCC_7806_rRNA16S	GAGGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCCGAGGTGGTCAGCCAAGTCT	539
PCC_7005_rRNA16S	GAGGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCCGAGGTGGTCAGCCAAGTCT	539
	** *****	
PCC_6912_rRNA16S	ATTGTCAAAGCGTGCGGCTCAACCGCATAAAGGCAGTGGAACCTGTGTAACCTAGAGTGCA	600
PCC_7806_rRNA16S	GCCGTCAAATCAGGTTGCTTAACGACCTAAAGGCGGTGGAACTGGCAGACTAGAGAGCA	599
PCC_7005_rRNA16S	GCCGTCAAATCAGGTTGCTTAACGACCTAAAGGCGGTGGAACTGGCAGACTAGAGAGCA	599

PCC_6912_rRNA16S	TTGCGGGCAGGGGAATTCCTGGTGTAGCGGTGAAATGCGTAGAGATCAGGAAGAACACC	660
PCC_7806_rRNA16S	GTAGGGGTAGCAGGAATTCCTAGTGTAGCGGTGAAATGCGTAGAGATTGGGAAGAACATC	659
PCC_7005_rRNA16S	GTAGGGGTAGCAGGAATTCCTAGTGTAGCGGTGAAATGCGTAGAGATTGGGAAGAACATC	659
	* **** *	

PCC_6912_rRNA16S	GGTGGCGAAAGCGCCCTGCTAGGCTGCAACTGACACTGAGGGACGAAAGCTAGGGGAGCG	720
PCC_7806_rRNA16S	GGTGGCGAAAGCGTGCTACTGGGCTGTATCTGACACTCAGGGACGAAAGCTAGGGGAGCG	719
PCC_7005_rRNA16S	GGTGGCGAAAGCGTGCTACTGGGCTGTATCTGACACTCAGGGACGAAAGCTAGGGGAGCG	719
	***** ** * ***** * ***** *****	
PCC_6912_rRNA16S	AATGGGATTAGATACCCAGTAGTCTAGCTGTAAACGATGGATACTAGGCGTTGCGTGT	780
PCC_7806_rRNA16S	AAAGGGATTAGATACCCCTGTAGTCTAGCCGTAAACGATGGATACTAGGCGTGGCTTGT	779
PCC_7005_rRNA16S	AAAGGGATTAGATACCCCTGTAGTCTAGCCGTAAACGATGGATACTAGGCGTGGCTTGT	779
	** ***** ***** ***** ** **	
PCC_6912_rRNA16S	ATCGACCCACGCAGTGCCGTAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGC	840
PCC_7806_rRNA16S	ATCGACCCGAGCCGTGCCGAAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGC	839
PCC_7005_rRNA16S	ATCGACCCGAGCCGTGCCGAAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGC	839
	***** ** ***** ***** *****	
PCC_6912_rRNA16S	AAGTGTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAAGCGGTGGAGTATGTGGTTTAA	900
PCC_7806_rRNA16S	AAGTGTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAAGCGGTGGAGTATGTGGTTTAA	899
PCC_7005_rRNA16S	AAGTGTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAAGCGGTGGAGTATGTGGTTTAA	899

PCC_6912_rRNA16S	TTTCGATGCAACGCGAAGAACCTTACCAGGGCTTGACATGTCGGAACCGAAGTGAAAGCT	960
PCC_7806_rRNA16S	TTTCGATGCAACGCGAAGAACCTTACCAAGACTTGACATGTCGCGAACCCTGGTGAAAGCT	959
PCC_7005_rRNA16S	TTTCGATGCAACGCGAAGAACCTTACCAAGACTTGACATGTCGCGAACCCTGGTGAAAGCT	959
	***** * ***** *****	
PCC_6912_rRNA16S	TCGGGTGCCCTTCGGGAGCCGGAACACAGGTGGTGCATGGCTGTCGTCAGCTCGTGTCTGTG	1020
PCC_7806_rRNA16S	GGGGGTGCCCTTCGGGAGCCGGAACACAGGTGGTGCATGGCTGTCGTCAGCTCGTGTCTGTG	1019
PCC_7005_rRNA16S	GGGGGTGCCCTTCGGGAGCCGGAACACAGGTGGTGCATGGCTGTCGTCAGCTCGTGTCTGTG	1019
	***** *****	
PCC_6912_rRNA16S	AGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCCAGCACTTCGG	1080
PCC_7806_rRNA16S	AGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCCAGCATTA-AG	1078
PCC_7005_rRNA16S	AGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCCAGCATTA-AG	1078
	***** * *	
PCC_6912_rRNA16S	GTGGGCACCTCTAAGGAGACTGCCGGTGACAAACCGAGGAGGTGGGGATGACGTCAAGT	1140
PCC_7806_rRNA16S	TTGGGGACTCTAAGGAGACTGCCGGTGACAAACCGAGGAGGTGGGGATGACGTCAAGT	1138
PCC_7005_rRNA16S	TTGGGGACTCTAAGGAGACTGCCGGTGACAAACCGAGGAGGTGGGGATGACGTCAAGT	1138
	**** *****	
PCC_6912_rRNA16S	CAGCATGCCCTTACGTCCTGGGCTACACACGTACTACAATGCTCAAGACAGAGGGCAGC	1200
PCC_7806_rRNA16S	CAGCATGCCCTTACGTCCTGGGCGACACACGTACTACAATGGTCGGGACAAAGGGCAGC	1198
PCC_7005_rRNA16S	CAGCATGCCCTTACGTCCTGGGCGACACACGTACTACAATGGTCGGGACAAAGGGCAGC	1198
	***** ***** ** *****	
PCC_6912_rRNA16S	AAGCTAGCGATAGCAAGCAAACTCT-CGTAAACTTGGGCTCAGTTCAGATCGCAGGCTGCA	1259
PCC_7806_rRNA16S	GAAGTCGCGAGAGCCAGCGAATCCAGCAAAACCCGGCCTCAGTTCAGATTGCAGGCTGCA	1258
PCC_7005_rRNA16S	GAAGTCGCGAGAGCCAGCGAATCCAGCAAAACCCGGCCTCAGTTCAGATTGCAGGCTGCA	1258
	* * * * * * * * * * * * * * * *	
PCC_6912_rRNA16S	ACTCGCCTGCGTGAAGGAGGAATCGCTAGTAATCGCAGGTCAGCATACTGCGGTGAATTC	1319
PCC_7806_rRNA16S	ACTCGCCTGCGTGAAGGAGGAATCGCTAGTAATCGCCGGTCAGCATACTGCGGTGAATTC	1318
PCC_7005_rRNA16S	ACTCGCCTGCGTGAAGGAGGAATCGCTAGTAATCGCCGGTCAGCATACTGCGGTGAATTC	1318
	***** *****	
PCC_6912_rRNA16S	GTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGAAGCTGGTCATGCCCCGAAGTCG	1379
PCC_7806_rRNA16S	GTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGAAGCTGGTCACGCCCCGAAGTCA	1378
PCC_7005_rRNA16S	GTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGAAGCTGGTCACGCCCCGAAGTCA	1378
	***** *****	
PCC_6912_rRNA16S	TTACCCTAACTCTTTTGTAGAGGGGGATGCCGAAGGCGGGACTGGTGACTGGGGTGAAGT	1439
PCC_7806_rRNA16S	TTACCTCAACCGCA---AGGAGGGGGATGCCTAAGGCAGGGCTAGTGACTGGGGTGAAGT	1435
PCC_7005_rRNA16S	TTACCTCAACCGTA---AGGAGGGGGATGCCTAAGGCAGGGCTAGTGACTGGGGTGAAGT	1435
	***** ** ***** * * *	
PCC_6912_rRNA16S	CGTAACAAGGTAGCCGTACCGGAAGGTGTGGCTGGATCA	1478
PCC_7806_rRNA16S	CGTAACAAGGTAGCCGTACCGGAAGGTGTGGCTGGATCA	1474
PCC_7005_rRNA16S	CGTAACAAGGTAGCCGTACCGGAAGGTGTGGCTGGATCA	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: AQPY000000000.

PCC7806rpoB	ATGAACAATCTTACCTTTAATCTCTTACCCGACCTGATCGAAATCCAACACTCCAGTTTT	60
PCC7005RpoB	ATGAACAATCTTACCTTTAATCTCTTACCCGACCTCATCGAAATCCAACACTCCAGTTTT	60

PCC7806rpoB	CGGTGGTTTTTTGGAAGAAGGACTCATCGAGGAACGAATAGCTTTTCCCCCATCAGCGAC	120
PCC7005RpoB	CGGTGGTTTTTTGGAAGAAGGACTAATCGAGGAACGAACAGCTTTTCCCCCATCAGCGAC	120

PCC7806rpoB	TATACAGGTAAATTAGAACTACATTTCTCGGCCAGGACTACAGACTCAAAGAACCGAAA	180
PCC7005RpoB	TATACAGGTAAATTAGAACTACATTTCTCGGCCAGGACTACAGACTCAAAGAACCGAAA	180

PCC7806rpoB	TACAACGTCGATGAAGCCAAACGACGCGATAGCAGCTATTCTGTTCAGATGTACGTTCCC	240
PCC7005RpoB	TACAACGTCGATGAAGCCAAACGACGCTGATAGCACCTATTCCGTTTCAGATGTACGTTCCCT	240

PCC7806rpoB	ACCCGTCTAATCAACAAAGAAACGGGAGAAAACATCGAACAGGAAGTTTTTATCGGCGAT	300
PCC7005RpoB	ACCCGTCTAATCAACAAAGAAACGGGAGAAAACATCGAACAGGAAGTTTATCGGCGAT	300

PCC7806rpoB	TTACCCCTGATGACCGAACGGGGAACCTTTATCATTACGGGGCTGAACGAGTCATCGTC	360
PCC7005RpoB	TTACCCCTGATGACCGAACGGGGAACCTTTATCATTACGGGGCGAACGAGTCATCGTC	360

PCC7806rpoB	AATCAGATCGTCCGTTCCCCCGGTGTTTACTACAAAGCCGAAATCGACAAAAACGGTCGC	420
PCC7005RpoB	AATCAGATCGTCCGTTCCCCCGGTGTTTACTACAAAGCCGAAATCGACAAAAACGGTCGC	420

PCC7806rpoB	CGCACCTACTCCGCTTCCCTGATTCCCAACCGAGGAGCTTGGTTAAAATTTGAAACCGAC	480
PCC7005RpoB	CGTACCTACTCCGCTTCCCTGATTCCCAACCGAGGAGCTTGGTTAAAATTTGAAACCGAC	480
	** *****	
PCC7806rpoB	AAAAACGGCTTAGTTTGGGTCAGAATCGACAAAACCCGTAAATTATCCGCCCAAGTTCTC	540
PCC7005RpoB	AAAAACGGCTTAGTTTGGGTCAGAATCGACAAAACCCGTAAATTATCCGCCCAAGTTCTC	540

PCC7806rpoB	CTGAAAGCGATCGGATTGAGCGATAACGAAATCTTTGACTCCCTACGCCATCCCGAATTT	600
PCC7005RpoB	CTGAAAGCGATCGGATTGAGCGATAACGAAATCTTTGACTCCCTACGCCATCCCGAATTC	600

PCC7806rpoB	TACCAAAAAACCCTCGACAAAGAAGGCAATCCACGCAAGAAGAGGCCCTGCTCGACCTG	660
PCC7005RpoB	TACCAAAAAACCCTCGACAAAGAAGGCAATCCACCGCAAGAAGAGGCATCCTCGACCTG	660

PCC7806rpoB	TACCGCAAACCTACGCCCGGGGAACCTCCACCGTCACTGGCGGACAACAACCTACTCGAA	720
PCC7005RpoB	TACCGCAAACCTACGCCCGGGGAACCCCCACCGTCAACGGCGGACAACAACCTACTCGAA	720

PCC7806rpoB	TCGCGCTTTTTTGACAATAAACGCTACGATCTCGGGCGCGTTGGTCGTTATAAACTCAAC	780
PCC7005RpoB	TCGCGCTTTTTTGACAATAAACGCTACGATCTCGGGCGCGTTGGTCGTTATAAACTCAAC	780

PCC7806rpoB	AAAAAACTACGCCCTCAACGTCCCCGATAACCAGCGCGTTCTCACCACCACCGACATTTTA	840
PCC7005RpoB	AAAAAACTACGCCCTCAACGTCCCCGATAACCAGCGCGTTCTCACCACCACCGACATCTTA	840

PCC7806rpoB	TCGGCGATCGACTACCTAATTAACCTCGAATTCGACATCGGTAACACCGACGACATCGAC	900
PCC7005RpoB	TCGGCGATCGACTACCTAATTAACCTCGAATTTGACATCGGCAACACCGACGACATCGAC	900

PCC7806rpoB	CACCTCGGCAACCGTCGCGTCCGTTCCGTTGGGTGAAGTGTCCAAAACCAAGTGCAGTA	960
PCC7005RpoB	CACCTCGGCAACCGTCGCGTCCGTTCCGTTGGGTGAAGTGTCCAAAACCAAGTGCAGTA	960

PCC7806rpoB	GGTTTAAACCGCTTAGAAAGAATCATTCGGGAACGGATGACCGTCAGCGAATCCCAAAAC	1020
PCC7005RpoB	GGTTTAAACCGCTTAGAAAGAATCATTCGGGAACGGATGACCGTCAGCGAATCCCAAAAC	1020

PCC7806rpoB	CTCACCCCGCTTCCCTAGTCAACCCGAAACCCCTAGTAGCGGCGATTAAAGAATTCTTT	1080
PCC7005RpoB	CTCACCCCGCTTCCCTAGTCAACCCGAAACCCCTAGTAGCGGCGATTAAAGAATTCTTT	1080

PCC7806rpoB	GGTTCCTCGCAACTCTCCAGTTTATGGATCAAACCAACCCCTAGCGGAATTGACCCAT	1140
PCC7005RpoB	GGTTCCTCGCAACTCTCCAGTTTATGGATCAAACCAACCCCTAGCGGAATTGACCCAT	1140

PCC7806rpoB	AAACGCGGTATTTCCGCCCTTGGACCCGGCGGTCTCACCCGGGAACGGGCCGGTTTGCC	1200
PCC7005RpoB	AAACGCGCATTTTCCGCCCTTGGACCTGGCGGTCTGACCCGGGAACGGGCCGGTTTGCC	1200

PCC7806rpoB	GTGCGCGACATTCACCCCTCCACACCGTTCGATTTGTCCGGTGAAACCCAGAAAGGT	1260
PCC7005RpoB	GTGCGCGACATTCACCCCTCCACACCGTTCGATTTGTCCGGTGAAACCCAGAAAGGT	1260

PCC7806rpoB	CCCAACGCTGGTTTAAATCGGTTCCCTAGCCACCTACGCCCGGTCAACGACTACGGTTTT	1320
PCC7005RpoB	CCCAACGCGGTTTAAATCGGTTCCCTAGCCACCTACGCTCGGTCAACGACTACGGTTTT	1320

PCC7806rpoB	ATTGAAACCCCTGTTATGGGGTGAAAAATGGCCGAGTTCGCTACGATCTCCCCGTCAA	1380
PCC7005RpoB	ATTGAAACCCCTGTTATGGGGTGAAAAATGGCCGAGTTCGCTATGATCTCCCCGTAAA	1380

PCC7806rpoB	TACCTCACGCGGACGAAGAAGACGATCTCAGAGTCGCCCCGGGAGACGTGGCCACCGAT	1440
PCC7005RpoB	TACCTCACGCGGACGAAGAAGACGATCTCAGAGTCGCCCCGGGAGACGTGGCCACCGAT	1440

PCC7806rpoB	GAAATGGTTATATCCTCGGCGAAACTATCCCCGTGCGCTATCGGCAGGAATTCTCCACC	1500
PCC7005RpoB	GAAATGGTTATATCCTCGGCGAAACTATCCCCGTGCGCTATCGGCAGGAATTCTCCACC	1500

PCC7806rpoB	ACCTCCCCCGAACAAGTGGACTACGTTTGTGTTTCCCCCGTGCAAATTGTCTCGGTGGCC	1560
PCC7005RpoB	ACTTCCCCCGAACAAGTGGACTACGTTTGTGTTTCCCCCGTGCAAATTGTCTCGGTGGCC	1560
** *****		
PCC7806rpoB	ACTTCCCTGATTCCCTTCCTCGAACACGACGACGCTAACCGCGCCCTCATGGGGTCCAAT	1620
PCC7005RpoB	ACTTCCCTGATTCCCTTCCTCGAACACGACGACGCTAACCGCGCCCTCATGGGGTCTAAT	1620

PCC7806rpoB	ATGCAGCGACAAGCGGTTCCCTGCTGCGTCCCGAACGTCCCCTTGTGGGAACGGGATTG	1680
PCC7005RpoB	ATGCAACGACAAGCGGTTCCCTGCTGCGTCCCGAACGTCCCCTGGTGGGTACTGGATTG	1680

PCC7806rpoB	GAAGCACAGGCCGCTCGCGACTCCGGCATGGTCATCGTTTCCCGTACCAATGGAGTAGTT	1740
PCC7005RpoB	GAAGCACAGGCCGCTCGCGACTTCGGTATGGTCATCGTTTTCGCGTACCAATGGGGTCGTT	1740

PCC7806rpoB	TCCCACGTCGATGCTAACCGGATTTCGCATCAAAGTGGCGGATCAAGACAAAGAGATTTTC	1800
PCC7005RpoB	TCCTAGCTCGATGCTAACCGGATTTCGCATCAAAGTGGCGGATGAAGACAAAGAGATTTT	1800
*** *****		
PCC7806rpoB	GGCAAGAGCGAGATCGAGTACGAAATTCAGAAATATCAACGCTCTAACCAAGATACCTGC	1860
PCC7005RpoB	GGCAAGAGCGAGATCGAGTACGAAATTCAGAAATATCAACGCTCTAACCAAGATACCTGC	1860

PCC7806rpoB	CTAAATCAGCGTCCTTTGGTCTATCAAGGGGAACAAGTTGTGCCGGGCGAGATCCTCGCC	1920
PCC7005RpoB	CTAAATCAGCGTCCTTTAGTCTATCAAGGTGAACAGGTTGTGCCAGGGCGAGATCCTCGCC	1920

PCC7806rpoB	GATGGTTCCGCCACCGAAGGAGAGAAATCGCCCTCGGCCAGAATATTCTCGTCGCCTAT	1980
PCC7005RpoB	GATGGTTCCGCCACCGAAGGAGAGAAATCGCCCTCGGCACAGAATATCCTCGTCGCCTAT	1980

PCC7806rpoB	ATGCCCTGGGAAGGCTATAACTACGAAGACGCGATTTTAAATCAGTGAAAGACTGGTGGCA	2040
PCC7005RpoB	ATGCCCTGGGAAGGCTATAACTACGAAGATGCGATTTTAAATCAGTGAAAGACTGGTGGCA	2040

PCC7806rpoB	CAAGATGTCTATACCAGTATCCACATTGAAAAATACGAAATCGAAGCCCGTCAAACATAA	2100
PCC7005RpoB	CAAGACACCTACACCAGTATCCACATTGAAAAATACGAAATCGAAGCCCGTCAAACATAA	2100

PCC7806rpoB	CTCGGACCAGAGGAAATCACCAGGAAATTCCCAACGTCGCTGAAGATGCCCTGCGAAAC	2160
PCC7005RpoB	CTAGGACCAGAGGAAATCACCAGGAAATTCCCAACGTCGCTGAAGATGCCCTGCGAAAC	2160
** *****		
PCC7806rpoB	CTCGATGAACGCGCATATTTCGCATCGGAGCTTGGGTAGAAGCCAGCGATATCCTTGTA	2220
PCC7005RpoB	CTCGATGAACGCGCATATTTCGCATCGGTGCTGGGTAGAAGCCAGCGATATCCTTGTA	2220

PCC7806rpoB	GGGAAAGTCACCCCAAAGGCGAATCAGACCAACCCCCGAAGAAAACTACTGCGGGCA	2280
PCC7005RpoB	GGGAAAGTCACCCCAAAGGCGAATCAGACCAACCCCCGAAGAAAACTACTGCGGGCA	2280

PCC7806rpoB	ATTTTCGGCGAAAAGGCCGGGATGTACGGGATAACTCCCTGCGCGTCCCCAACGGCGAA	2340
PCC7005RpoB	ATTTTCGGCGAAAAGGCCGGGATGTACGGGATAACTCCCTGCGCGTCCCCAACGGCGAA	2340

PCC7806rpoB	AAAGGCCGGGTAGTGGATGTACGGGTATTTACCCGCGAACAGGGGACGAATTACCCCC	2400
PCC7005RpoB	AAAGGCCGGGTAGTGGATGTGCGCGTATTTACCCGCGAACAGGGAGATGAATTACCCCCT	2400
***** **		
PCC7806rpoB	GGGGCTAATATGGTAGTGC GG GTTACGTTGCCCAAAAACGCAAAATCCAAGTGGGCGAT	2460
PCC7005RpoB	GGGGCCAATATGGTGGTAAGGGTTTACGTTGCCCAAAAACGCAAAATCCAAGTGGGCGAT	2460

PCC7806rpoB	AAAAATGGCGGGTCGTCACGGCAATAAAGGGATTATTTCTCGGATTCTGCCCTAGAAGAT	2520
PCC7005RpoB	AAAAATGGCGGGTCGTCACGGCAATAAAGGGATTATTTCTCGGATTCTGCCCTGGAAGAT	2520

PCC7806rpoB	ATGCCCTACCTCCCCGATGGTCGTCGCCGTCGATATCGTTCTCAATCCCCTAGGGGTTCCT	2580
PCC7005RpoB	ATGCCCTACCTCCCCGATGGTCGCCCCGTCGATATCGTTCTTAATCCCCTAGGGGTTCCT	2580

PCC7806rpoB	AGTCGCATGAACGTCGGTCAGGTGTTTGAATGTTTACTGGGTGGGCTGGCGAAAAATCTG	2640
PCC7005RpoB	AGTCGCATGAACGTCGGTCAGGTGTTTGAATGTTTACTGGGTGGGCGCGCGAAAAATCTG	2640

PCC7806rpoB	GGCGTGCCTTTAAGATTACTCCCTTTGATGAAATGTATGGGGAAGAAGCCAGCCGTTTG	2700
PCC7005RpoB	GGCGTGCCTTTAAGATTACTCCTTTTGACGAAATGTATGGGGAAGAAGCCAGCCGTTTA	2700

PCC7806rpoB	ACCGTCCACGGATTGCTAGAAAATGCCTCGAAAAACCCCAATCGTGATTGGGTGTTCAAG	2760
PCC7005RpoB	ACCGTTCACGGATTGCTAGAAAATGCCTCGAAAAACCCCAATCGCGATTGGGTGTTCAAG	2760

PCC7806rpoB	GAAGAACACGCGGGCAAAGTCACCGTTTACGATGGTCGCACCGCGGAACCCCTTGACCGT	2820
PCC7005RpoB	GAAGAACACGCGGGCAAAGTCACCGTTTACGATGGTCGCACCGCGGAACCCCTTGACCGT	2820

PCC7806rpoB	CCCGTTACCGTCGGTATGGCCTATATGTTAAACTGGTTCACCTGGTTGATGATAAAATT	2880
PCC7005RpoB	CCCGTTACCGTCGGTATGGCCTATATGTTAAACTGGTTCACCTGGTTGATGATAAAATT	2880

PCC7806rpoB	CACGCCCGCTCTACCGGTCCCTACTCCTTGGTTACTCAGCAACCCCTGGGCGGTAAAGCT	2940
PCC7005RpoB	CACGCCCGCTCTACCGGTCCCTACTCCTTGGTTACTCAGCAACCCCTGGGCGGTAAAGCT	2940

PCC7806rpoB	CAACAGGGGGGCCAGCGCTTCGGAGAAATGGAAGTCTGGGCCCTGGAGGCCTACGGGGCG	3000
PCC7005RpoB	CAACAGGGAGGCCAGCGCTTCGGAGAAATGGAAGTCTGGGCCCTAGAAGCCTACGGGGCG	3000
***** **		
PCC7806rpoB	GCCTATACCTTGCAAGGAATTGCTAACGGTGAAATCCGATGATATGCAAGGACGGAATGAG	3060
PCC7005RpoB	GCCTATACCTTGCAAGGAATTGCTAACGGTGAAATCCGATGATATGCAAGGACGGAATGAG	3060

PCC7806rpoB	GCTTTAAATGCGATCGTAAAAGGCAAGCCGATTCGCCGCCGGGTACGCCAGAATCCTTT	3120
PCC7005RpoB	GCTTTAAATGCGATCGTAAAAGGCAAGCCGATTCGCCGCCGGGTACGCCAGAATCCTTT	3120

PCC7806rpoB	AAGGTTTTGATGCGAGAATTGCAATCCCTCGGCCTCGATATCGCCGTTTACAAGGTGGAA	3180
PCC7005RpoB	AAGGTTTTGATGCGAGAATTGCAATCCCTCGGCCTCGATATCGCCGTTTACAAGGTGGAA	3180

PCC7806rpoB	AATGCCCCGATGGTACTTCCCGCGATGTGGAGGTGGATCTGATGGTCGATGTCGGTCGT	3240
PCC7005RpoB	AATGCCCCGATGGTACTTCCCGCGATGTGGAGGTGGATCTGATGGTCGATGTCGGTCGT	3240

PCC7806rpoB	CGCGCCCCCTCTCGCCCCACCTACGAATCCTTAACACAGAAGACCTTGAGGAAGAAGAA	3300
PCC7005RpoB	CGCGCCCCCTCTCGCCCCACCTACGAATCCTTAACACAGAAGACCTTGAGGAAGAAGAA	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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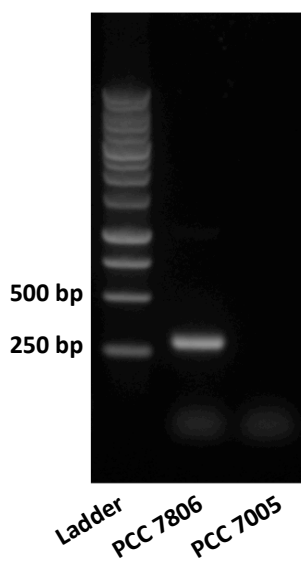


Figure S4. Epifluorescence micrographs (FITC filter set; $\times 40$ magnification; 100 ms exposure; scale bar 30 μm) of *Microcystis aeruginosa* PCC 7806 (A), of *Microcystis aeruginosa* PCC 7005 (B) and of *Chlorogloeopsis fritschii* PCC 6912 (C) with the EUB338-HRP probe.

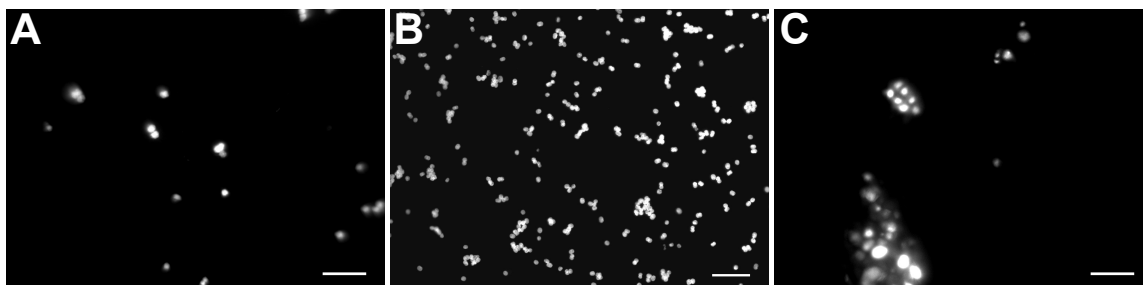


Figure S5. Epifluorescence micrographs (superposition of two images, one obtained with the Cy3 filter set, in red, and the other one obtained with the FITC filter set, in green; $\times 63$ magnification; 500 ms exposure; scale bar 30 μm) of *Microcystis aeruginosa* PCC 7806 (A) unlabeled, (B) labeled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

