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Published in: Applied and Environmental Microbiology

DOI: 10.1128/AEM.02295-15

Citation for published version (APA):

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Strains of the Harmful Cyanobacterium *Microcystis aeruginosa* Differ in Gene Expression and Activity of Inorganic Carbon Uptake Systems at Elevated CO₂ Levels

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Cyanobacteria are generally assumed to be effective competitors at low CO₂ levels because of their efficient CO₂-concentrating mechanism (CCM), and yet how bloom-forming cyanobacteria respond to rising CO₂ concentrations is less clear. Here, we investigate changes in CCM gene expression at ambient CO₂ (400 ppm) and elevated CO₂ (1,100 ppm) in six strains of the harmful cyanobacterium *Microcystis*. All strains downregulated *cmpA* encoding the high-affinity bicarbonate uptake system BCT1, whereas both the low- and high-affinity CO₂ uptake genes were expressed constitutively. Four strains downregulated the bicarbonate uptake genes *bicA* and/or *sbtA*, whereas two strains showed constitutive expression of the *bicA-sbtA* operon. In one of the latter strains, a transposon insert in *bicA* caused low *bicA* and *sbtA* transcript levels, which made this strain solely dependent on BCT1 for bicarbonate uptake. Activity measurements of the inorganic carbon (Ci) uptake systems confirmed the CCM gene expression results. Interestingly, genes encoding the RuBisCO enzyme, structural carboxysome components, and carbonic anhydrases were not regulated. Hence, *Microcystis* mainly regulates the initial uptake of inorganic carbon, which might be an effective strategy for a species experiencing strongly fluctuating Ci concentrations. Our results show that CCM gene regulation of *Microcystis* varies among strains. The observed genetic and phenotypic variation in CCM responses may offer an important template for natural selection, leading to major changes in the genetic composition of harmful cyanobacterial blooms at elevated CO₂.
PCC 7803 (27–30), CCM gene expression patterns of the environmentally relevant cyanobacterium Microcystis have attracted only recent interest (31–33).

In this study, we compare expression of the Ci uptake genes in response to changing CO2 conditions among Microcystis strains representative of the different Ci uptake genotypes. Studies with Synechosystis PCC 6803 showed that genes for the high-affinity uptake systems for CO2 (NDH-I3) and bicarbonate (SbtA and BCT1) are induced at low CO2, whereas the expression of low-affinity Ci uptake systems (BicA and NDH-I2) remains unaltered (29, 30). It seems likely that the same expression patterns apply to Microcystis, although the presence of different Ci uptake genotypes could lead to variation in gene expression among Microcystis strains. We therefore defined two hypotheses for our study: (i) high-affinity Ci uptake genes are downregulated at elevated CO2 (1,100 ppm), whereas (ii) low-affinity Ci uptake genes are expressed constitutively in Microcystis. To investigate these hypotheses, we compared the CCM gene expression of six Microcystis strains at ambient and elevated CO2 levels. Furthermore, we measured O2 evolution of the strains exposed to different CO2 conditions to compare the activity of their Ci uptake systems. The results reveal an unexpected diversity of CO2 responses within the genus Microcystis.

MATERIALS AND METHODS

Microcystis strains. We studied six Microcystis strains with different Ci uptake systems (Fig. 1). The Ci uptake genotypes of these strains were described in a previous study (17). Strain PCC 7806 contains the bicA gene but lacks the sbtA gene and belongs to CcI uptake genotype I. Strains NIES-843 and CCAP 1450/11 contain the sbtA gene but lack a complete bicA gene and hence belong to genotype II. Strain NIVA-CYA 140 combines sbtA with a complete bicA gene that is no longer functional because of a transposon insert, and therefore this strain was also assigned to genotype II. Strains HUB 5-3 and PCC 7005 contain both the bicA and sbtA genes in the same operon and are therefore assigned to genotype III (Fig. 1). The four genes encoding the high-affinity bicarbonate transporter BCT1 (ccm-pABCD), as well as the genes encoding the high-affinity CO2 uptake system NDH-I3 (chpY, ndhD3, ndhF3, and other ndh genes) and the low-affinity CO2 uptake system NDH-I4 (chpX, ndhD4, ndhF4, and other ndh genes), were present in all six strains (17). Moreover, genome-wide microarray analysis showed that Microcystis PCC 7806 expresses all its CCM genes (32).

Experimental setup. We used the experimental phase of batch culture experiments exposed to ambient pCO2 (400 ppm) and elevated pCO2 (1100 ppm) in the gas flow to study gene expression and activity of the Ci uptake systems.

First, the six Microcystis strains were precultured in 1-liter Erlenmeyer flasks in modified BG11 medium (34; with 10 mmol liter−1 NaNO3 and no added Na2CO3/NaHCO3) for 1 week. The precultures were incubated at 25°C with 400 ppm of pCO2 and at 120 rpm in an orbital shaker incubator (Gallenkamp, Leicester, United Kingdom), with light provided by TL-D 30W/33-640 white fluorescent tubes (Philips, Eindhoven, The Netherlands) at 20 μmol photons m−2 s−1. Microscopy checks did not reveal any contaminations.

Subsequently, new 1-liter Erlenmeyer flasks with 400 ml of modified BG11 medium were inoculated with the exponentially growing precultures at an optical density at 750 nm (OD750) of ~0.080. Four biological replicates were used for each strain. The Erlenmeyer flasks were topped with foam stoppers to allow gas exchange and placed in an Infors HT Multitron Pro incubator (Infors Benelux, Doetinchem, The Netherlands) at 25°C with 400 ppm of pCO2 and at 120 rpm in an orbital shaker incubator (Gallenkamp, Leicester, United Kingdom), with light provided by TL-D 30W/33-640 white fluorescent tubes (Philips, Eindhoven, The Netherlands) at 20 μmol photons m−2 s−1. Microscopy checks did not reveal any contaminations.

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μmol photons m⁻² s⁻¹ during the batch culture experiments to minimize possible effects of microcysts on carbon fixation. After 2 days at 400 ppm, the pCO₂ in the incubator was increased to 1,100 ppm. The pCO₂ concentration in the gas mixture was checked regularly with an environmental gas monitor for CO₂ (EGM-4; PP Systems, Amesbury, MA). The flasks were sampled on a daily basis, and after 4 days the experiment was ended.

**pH, dissolved inorganic carbon (DIC), and cell counts.** The pH was measured immediately after sampling with a Lab 860 pH meter in combination with a BlueLine 28 Gel pH electrode (Schott Instruments GmbH, Mainz, Germany). To determine the concentrations of DIC, culture samples were immediately pelleted (5 min at 4,000 × g and 20°C). Supernatant was filtered over 0.45-μm-pore-size 47-mm polyethersulfone membranes (Sartorius AG, Goettingen, Germany). The filtrate was transferred to sterile plastic urine analysis tubes (VF-109SURI; Terumo Europe N.V., Leuven, Belgium), which were filled completely (using a needle to leave all air out), and stored at 4°C until analysis. A TOC-VCPH TOC analyzer (Shimadzu, Kyoto, Japan) was used to determine the DIC (measured 3- to 5-fold per sample). DIC concentrations were converted to CO₂ (aq), bicarbonate, and carbonate concentrations using the measured pH of the samples (36). Cell numbers and biovolumes of samples from the different cultures were determined in triplicate using a Casy 1 TTC cell counter with a 60-μm-capillary (Säureförm System GmbH, Reutlingen, Germany). Because the strains differed in cell size, we report the cyanobacterial abundances as biovolumes.

**RNA extraction.** Just before and 20 h after increasing pCO₂ from 400 to 1,100 ppm, 40-ml samples were taken for reverse transcription-quantitative PCR (RT-qPCR) analysis, immediately cooled on ice, and centrifuged for 5 min at 4,000 × g and 4°C in a precooled centrifuge. The pellets were immediately resuspended in 1 ml of TRIzol (Life Technologies, Grand Island, NY), frozen in liquid nitrogen, and stored at −80°C. Subsequent RNA extraction and purification was performed as described previously (32). RNA concentrations were quantified by using a NanoDrop 1000 spectrophotometer (Thermo Scientific, San Jose, CA), and all RNA samples had A₂₆₀/A₂₃₀ and A₂₆₀/A₃₃₀ values above 1.8.

**RT-qPCR analysis.** We investigated the expression of CCM genes using primers designed in this and previous studies (17, 32) (see also Table S1 in the supplemental material). The transcripts of the following CCM genes were targeted: ccmA (encoding a subunit of the high-affinity bicarbonate transporter BCT1), bicA and sbtA (the two sodium-dependent bicarbonate transporters), chpX (degradation subunit of the low-affinity CO₂ uptake system NDH₁), chpY (degradation subunit of the high-affinity CO₂ uptake system NDH₁), ccmR and ccmR2 (two CCM transcriptional regulators), rbcX (chaperone for Rubisco), ccmM (structural component of the carboxysomes), ccaA1 and ccaA2 (two carboxysomal carbonic anhydrases), and ecaA (periplasmic carbonic anhydrase). In addition, we targeted transcripts of the 16S rRNA gene and the mcyB gene (microcystin synthetase).

Reverse transcription reactions were done as described previously (32), using Superscript III (Life Technologies, Grand Island, NY). Subsequently, the qPCR Maxima SYBR green master mix (2X; Thermo Fisher Scientific, Pittsburgh, PA) was applied with our primers to the obtained cDNA samples as described previously (32) to analyze PCR amplification in a ABI 7500 real-time PCR device (Applied Biosystems, Foster City, CA). The two-step cycling protocol was used, with a denaturation temperature of 95°C (15 s) and a combined annealing/extension temperature of 60°C (60 s) during 40 cycles. Melting-curve analysis was performed on all measured samples to rule out nonspecific PCR products. ROX solution (passive reference dye) was used to correct for any well-to-well variation.

We calculated relative changes in gene expression after 20 h of elevated pCO₂ using the 16S rRNA gene as a reference gene. The LinRegPCR software tool version 2012.3 (37, 38) was used for baseline correction, calculation of quantification cycle (Cq) values and calculation of the amplification efficiency (E) of each individual run using linear regression (see Table S1 in the supplemental material). Amplification efficiencies of individual samples were between 1.8 and 2.0. The relative changes in gene expression were calculated with the comparative cycle threshold (Ct) method (39).

One-tailed t tests were applied to identify significant changes in gene expression (n = 4 biological replicates), using the false discovery rate (FDR) to correct for multihypothesis testing (55). FDR-adjusted P values of <0.05 combined with log₂ expression changes of <−0.8 or >0.8 were considered significant.

**O₂ evolution experiments.** We studied the activity of different C₄ uptake systems of *Microcystis* strains aclimated to low or high CO₂ levels using O₂ measurements with an Oxy-4 mini O₂ optode (PreSens GmbH, Regensburg, Germany). In mineral medium without nitrate, the initial O₂ evolution rate reflects the C₄ uptake rate of cyanobacteria (32, 40). Cells aclimated to low CO₂ levels were obtained from batch cultures exposed to 400 ppm pCO₂ for 4 days. As a result, the C₄ availability of the mineral medium was low, CO₂(aq) was depleted to 0.0018 ± 0.0004 μmol liter⁻¹ and the bicarbonate concentration was 76 ± 10 μmol liter⁻¹ (see Fig. S1 in the supplemental material). Cells aclimated to high CO₂ levels were obtained from batch cultures exposed to 400 ppm pCO₂ for 2 days and subsequently to 1,100 ppm of pCO₂ for 2 days. The C₄ availability in these cultures was high, the CO₂(aq) value was 4.2 ± 1.3 μmol liter⁻¹, and the bicarbonate concentration was 1.062 ± 43 μmol liter⁻¹ (see Fig. S1 in the supplemental material).

Samples from these batch cultures were pelleted (4,000 × g for 5 min at 20°C), washed once, and then resuspended in C₄-deplete and N-deplete modified BG11 medium (no added NaCO₃/NH₄HCO₃ and NaNO₃, but with added 0.1 mmol liter⁻¹ NaCl and 10 mmol liter⁻¹ CAPSO-KOH [pH 9.8]). The medium was aerated with N₂ gas before usage. The response of the cells was studied at pH 9.8 to mimic dense blooms in which bicarbonate is the dominant C₄ species. The OD₇₅₀ of strains PCC 7806 and PCC 7005 were saturated at 400 and 400 μmol photons m⁻² s⁻¹, respectively. Cells were added to block bicarbonate uptake. In total, we applied six different treatments, which each activated or suppressed one or more different C₄ uptake systems. Sodium ions were added to stimulate the sodium-dependent bicarbonate transporters BicA and SbtA, whereas lithium ions were added to block bicarbonate uptake. In total, we applied six different treatments, which each activated or suppressed one more different C₄ uptake systems (Table 1). The different bicarbonate concentrations stimulate different C₄ uptake systems. Sodium ions were added to stimulate the sodium-dependent bicarbonate transporters BicA and SbtA, whereas lithium ions were added to block bicarbonate uptake. In total, we applied six different treatments, which each activated or suppressed one or more different C₄ uptake systems (Table 1). The units were converted to μmol O₂ · g⁻¹ · h⁻¹ using data from chlorophyll a [chl a] of strains PCC 7806 and PCC 7005 were saturated at −400 μmol photons m⁻² s⁻¹ and did not decrease up to 1,000 μmol photons m⁻² s⁻¹. Therefore, we used an incident light intensity (Iₐ) of 500 μmol photons m⁻² s⁻¹ for the O₂ evolution experiments.

At the start of the experiments, cells were allowed to take up all remaining C₄ in the incubation chambers, which was monitored by a gradual decrease of the O₂ evolution. Subsequently, the rate of O₂ evolution (mg liter⁻¹ min⁻¹) was measured during 15-min intervals in a control treatment without additions and after adding 20, 300, or 10,000 μmol liter⁻¹ of KHCO₃ in the presence of different concentrations of NaCl and LiCl (Table 1). The different bicarbonate concentrations stimulate different C₄ uptake systems. Sodium ions were added to stimulate the sodium-dependent bicarbonate transporters BicA and SbtA, whereas lithium ions were added to block bicarbonate uptake. In total, we applied six different treatments, which each activated or suppressed one more different C₄ uptake systems (Table 1). The units were converted to μmol O₂ · mg⁻¹ · chl a · min⁻¹ using data from chlorophyll a measurements that were acquired with HPLC as described previously (32). For each strain aclimated at low or high pCO₂ levels, we tested whether O₂ evolution rates were different between the treatments using one-way analysis of variance with post hoc comparison of the means based on Tukey’s HSD test (α = 0.05; n = 4 per treatment).
RESULTS

Changes in DIC and pH at elevated CO2. Six *Microcystis* strains (PCC 7806, NIES-843, CCAP 1450/10, NIVA-CYA 140, HUB 5-3, and PCC 7005) with different C\textsubscript{i} uptake systems were grown under atmospheric pCO\textsubscript{2} conditions of 400 ppm (Fig. 2). Assuming equilibrium with this atmospheric pressure, one would expect a CO\textsubscript{2}(aq) concentration of 13.5 \text{mol liter}^{-1}, and the pH of the mineral medium without cells would be \(~7\). However, owing to the photosynthetic activity of the *Microcystis* population, the CO\textsubscript{2}(aq) concentration was depleted to \(~0.1\) \text{mol liter}^{-1}, the bicarbonate concentration was \(~330\) \text{mol liter}^{-1}, and the pH increased to 10 to 11 depending on the strain (Fig. 2 and 3). After 2 days, we raised the pCO\textsubscript{2} in the gas flow to 1,100 ppm. As a consequence, the CO\textsubscript{2}(aq) concentration increased to 1 to 12 \text{mol liter}^{-1} depending on the strain, the bicarbonate concentration increased to 800 to 1,500 \text{mol liter}^{-1}, and the pH dropped 1 to 2 U (Fig. 2 and 3).

Changes in gene expression at elevated CO2. The expression of selected CCM genes was monitored before and 20 h after increasing the pCO\textsubscript{2} in the gas flow (Fig. 4 and Table S2 in the

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Dissolved inorganic carbon</th>
</tr>
</thead>
<tbody>
<tr>
<td>KHCO\textsubscript{3} (\text{µmol liter}^{-1})</td>
<td>NaCl (mmol liter\textsuperscript{-1})</td>
</tr>
<tr>
<td>0</td>
<td>0.1</td>
</tr>
<tr>
<td>20</td>
<td>0.1</td>
</tr>
<tr>
<td>20</td>
<td>25</td>
</tr>
<tr>
<td>300</td>
<td>25</td>
</tr>
<tr>
<td>300</td>
<td>25</td>
</tr>
<tr>
<td>10,000</td>
<td>25</td>
</tr>
</tbody>
</table>

\textsuperscript{a}Different concentrations of KHCO\textsubscript{3}, NaCl, and LiCl were added to induce or block the activity of specific C\textsubscript{i} uptake systems. The resulting CO\textsubscript{2}(aq) and HCO\textsubscript{3} concentrations expected at pH 9.8 and 20.3\textdegreeC are shown. The last column indicates which C\textsubscript{i} uptake systems are mostly active at the applied conditions.
supplemental material). At an elevated pCO2, all strains showed significant downregulation of cmpA, although four strains (PCC 7806, CCAP 1450/10, NIVA-CYA 140, and PCC 7005) showed a stronger downregulation than two others (NIES-843 and HUB 5-3). The sbtA gene encoding the high-affinity bicarbonate transporter SbtA was significantly downregulated in strains NIES-843, CCAP 1450/10, and HUB 5-3 but was constitutively expressed in strains NIVA-CYA 140 and PCC 7005. The bicA gene encoding the low-affinity bicarbonate transporter BicA was downregulated in strains PCC 7806 and HUB 5-3 but was also constitutively expressed in strains NIVA-CYA 140 and PCC 7005. None of the six strains showed significant changes in gene expression of the CO2 uptake genes chpX and chpY (Fig. 4).

Expression of the CCM transcriptional regulator ccmR was reduced significantly at elevated CO2 levels in all strains, except for strain HUB 5-3. In contrast, expression of the additional transcriptional regulator ccmR2 located upstream of the bicA-sbtA operon of Microcystis did not change significantly in any of the strains. The expression of several other CCM genes (rbcX, ccmM, ccaA1, ccaA2, and ccaA) was also not affected by elevated CO2 in any of the strains. The expression of mcyB was unaltered in PCC 7806 and NIES-843 and increased slightly but significantly in NIVA-CYA 140.

C1 uptake activity of low- and high-CO2 acclimated cells. We studied O2 evolution of the Microcystis strains to compare the activity of their C1 uptake systems when the strains were acclimated to low- or high-CO2 conditions (Fig. 5). We applied six different treatments to activate different C1 uptake systems, as explained in Table 1. For the interpretation of these results, we note that the response of the O2 evolution rates to the treatments can be compared within each strain at a given pCO2 level (i.e., within the panels of Fig. 5) but cannot be compared quantitatively among the strains or among the two different pCO2 levels (i.e., among the panels of Fig. 5). The reason is that other factors also influence the O2 evolution rates, for example, the pigment concentrations and amounts of PSI and PSII may differ between strains and can also change with elevated CO2 (32). The results can be compared among strains in a relative sense, for example, two different strains can show a significant increase in O2 evolution after addition of 20 μmol liter−1 KHCO3 while a third strain does not. The O2 evolution rates of strain NIES-843 were highly variable among the biological replicates and declined strongly after 2 h. Repetition of the O2 evolution experiments with this strain did not improve the results, indicating that NIES-843 could not withstand the incubation conditions. Therefore, we only report the results for the other five Microcystis strains.

For cells acclimated to low-CO2 conditions, the addition of 20 μmol liter−1 KHCO3 in the presence of only 0.1 mmol liter−1 NaCl induced significantly more O2 production than the control for all strains, except for strain HUB 5-3 which showed a nonsignificant response (Fig. 5A to E). This result indicates that BCT1 was active in all strains, although its activity was low in strain HUB 5-3. Application of 20 μmol liter−1 KHCO3 and 25 mmol liter−1 NaCl led to a significantly higher O2 production than at 20 μmol liter−1 KHCO3 and 0.1 mmol liter−1 NaCl for strains PCC 7806, CCAP 1450/10, and HUB 5-3. This result indicates that in response to the added sodium ions, these three strains activated their sodium-dependent bicarbonate transporter SbtA. However, strain PCC 7806 does not have SbtA, and its response might indicate activation of the other sodium-dependent bicarbonate transporter BicA. The O2 production at 300 μmol liter−1 KHCO3 and 25 mmol liter−1 NaCl was not significantly higher than at 20 μmol
O2 evolution. The strains were acclimated to either low CO2 levels (A to E) or specific Ci uptake systems, as indicated in Table 1. Error bars indicate standard deviations (n = 4 biological replicates per treatment). Different letters above the bars indicate significant differences between the treatments, as tested by one-way analysis of variance with post hoc comparison of the means based on Tukey’s HSD test (α = 0.05).

FIG 5 Activity of Ci uptake systems of five Microcystis strains, inferred from O2 evolution. The strains were acclimated to either low CO2 levels (A to E) or high CO2 levels (F to J). O2 evolution was measured after addition of different concentrations of KHCO3, NaCl, and LiCl to induce or block the activity of specific Ci uptake systems, as indicated in Table 1. Error bars indicate standard deviations (n = 4 biological replicates per treatment). Different letters above the bars indicate significant differences between the treatments, as tested by one-way analysis of variance with post hoc comparison of the means based on Tukey’s HSD test (α = 0.05).

DISCUSSION

Evaluation of hypotheses. Our results enable evaluation of the hypotheses that (i) high-affinity Ci uptake genes of Microcystis are downregulated at elevated CO2 (1,100 ppm), whereas (ii) low-affinity but high-flux Ci uptake genes are constitutively expressed. Consistent with the first hypothesis, our results show that the cmpA gene encoding the bicarbonate-binding subunit of the high-affinity bicarbonate transporter BCT1 was downregulated in all strains. Downregulation of BCT1 at elevated CO2 could potentially be cost-effective for the cells, because bicarbonate uptake by BCT1 is expected to require 1 ATP molecule per molecule of bicarbonate. Strain PCC 7005, indicating that these strains activated their sodium-dependent bicarbonate transporter SbtA. Strain PCC 7006 does not have SbtA, and its response might indicate activation of the other sodium-dependent bicarbonate transporter BicA. The O2 production at 300 μmol liter−1 KHCO3 and 25 mmol liter−1 NaCl was significantly higher than at 0.1 mmol liter−1 NaCl for strains PCC 7806, HUB 5-3, and PCC 7005, indicating that these strains activated their sodium-dependent bicarbonate transporter SbtA. Subsequent addition of 25 mmol liter−1 LiCl blocked bicarbonate uptake and, as a consequence, the O2 production of all strains was reduced to levels similar to that for the control treatment. Finally, the addition of 10,000 μmol liter−1 KHCO3 in the presence of 25 mmol liter−1 LiCl and 25 mmol liter−1 NaCl strongly increased the CO2(aq) concentration in the medium (see Table S1 in the supplemental material) and restored O2 production in all strains (Fig. 5A to E). Since lithium still blocked bicarbonate uptake, this result indicates that CO2 uptake was active in all strains.

For cells acclimated to high-Ci conditions, the addition of 20 μmol liter−1 KHCO3 in the presence of only 0.1 mmol liter−1 NaCl induced significantly more O2 production than the control only for strain PCC 7005 (Fig. 5F to J). This result indicates that the high-affinity bicarbonate transporter BCT1 was hardly active in any of the strains acclimated to high-Ci conditions, except for strain PCC 7005. Application of 20 μmol liter−1 KHCO3 and 25 mmol liter−1 NaCl led to a significantly higher O2 production than at 0.1 mmol liter−1 NaCl for strains PCC 7806, HUB 5-3, and PCC 7005, indicating that these strains activated their sodium-dependent bicarbonate transporter SbtA. For cells acclimated to high-Ci conditions, the addition of 20 μmol liter−1 KHCO3 in the presence of 25 mmol liter−1 NaCl strongly increased the CO2(aq) concentration in the medium (see Table S1 in the supplemental material) and restored O2 production in all strains (Fig. 5A to E). Since lithium still blocked bicarbonate uptake, this result indicates that CO2 uptake was active in all strains.

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TABLE 2 Gene expression of the five different C4 uptake systems in Microcystis and three model cyanobacterial strains

<table>
<thead>
<tr>
<th>C4 uptake system (genes involved)</th>
<th>Energy cost (21, 51, 52)</th>
<th>Gene expressionb</th>
<th>Synechocystis PCC 6803 (29, 30)</th>
<th>Synechococcus PCC 7002 (50)</th>
<th>Synechococcus PCC 7942 (45, 46)</th>
</tr>
</thead>
<tbody>
<tr>
<td>BCT1 (cmpABCD)</td>
<td>1 ATP per HCO3−</td>
<td>Inducible under low pCO2</td>
<td>Inducible under low pCO2</td>
<td>–</td>
<td>Inducible under low pCO2</td>
</tr>
<tr>
<td>SbtA (sbtA)</td>
<td>0.5 ATP per HCO3−</td>
<td>Constitutively expressed/inducible under low pCO2</td>
<td>Inducible under low pCO2</td>
<td>Inducible under low pCO2</td>
<td>–</td>
</tr>
<tr>
<td>BicA (bicA)</td>
<td>0.25 ATP per HCO3−</td>
<td>Constitutively expressed/inducible under low pCO2−</td>
<td>Constitutively expressed</td>
<td>Inducible under low pCO2</td>
<td>–</td>
</tr>
<tr>
<td>NDH-I4 (chpY and others)</td>
<td>1 NADPH per CO2-to-HCO3− conversion</td>
<td>Constitutively expressed</td>
<td>Inducible under low pCO2</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>NDH-I4 (chpX and others)</td>
<td>1 NADPH per CO2-to-HCO3− conversion</td>
<td>Constitutively expressed</td>
<td>Constitutively expressed</td>
<td>Constitutively expressed</td>
<td>Constitutively expressed</td>
</tr>
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</table>

* The estimated energy costs of the different C4 uptake systems are indicated in terms of molecules of ATP or NADPH per molecule CO2 or HCO3−. The source or reference(s) are indicated in parentheses in the headings for each column of data. A dash (−) indicates that the C4 uptake system is absent.

† The Microcystis strains, Synechocystis PCC 6803, and Synechococcus PCC 7942 were from freshwater (brackish water for Microcystis PCC 7806); Synechococcus PCC 7002 has a marine origin.

Consistent with the second hypothesis, the gene chpX encoding the dehydration subunit of the low-affinity CO2 uptake system NDH-I4 was constitutively expressed in all strains. However, the low-affinity bicarbonate uptake gene, bicA, was constitutively expressed only in strains NIVA-CYA 140 (where it is not functional because of a transposon insert; Fig. 1) and PCC 7005 but was downregulated at elevated CO2 in strains PCC 7806 and HUB 5-3. Hence, the second hypothesis is supported by chpX (NDH-I4), whereas the low-affinity bicarbonate uptake gene bicA shows a more variable response.

**General observations.** Given that both hypotheses received only partial support, what general observations can still be obtained from the gene expression patterns of the Microcystis strains? First, it is noteworthy that several C4 uptake systems and one of their transcriptional regulators were regulated in response to elevated CO2, whereas other important C4M genes encoding the enzyme RuBisCO, structural components of the carboxysome, and carbonic anhydrases were not regulated at all (Fig. 4). Furthermore, a recent transcriptome study of Microcystis PCC 7806 found that expression of the ppc gene, encoding phosphoenolpyruvate carboxylase involved in an alternative C4 assimilation pathway, also remained constant under elevated-CO2 conditions (see Table S4 in the supplemental material in reference 32). These results indicate that the C4M genes of Microcystis respond to elevated CO2 mainly at the very first steps of the carbon fixation process by regulating the initial acquisition of inorganic carbon. Microcystis is a buoyant cyanobacterium that can develop dense blooms in eutrophic lakes, where it will be exposed to large fluctuations in CO2 availability at both daily and seasonal time scales (41). A highly specific response that mainly adjusts the initial C4 uptake systems, without large changes in expression of the carboxysome genes and genes of the downstream carbon assimilation pathways, could preserve energy and offer a robust strategy for a species that often experiences strongly fluctuating C4 conditions (32).

Second, all of the C4 uptake genes investigated in the present study were either downregulated or remained unchanged at elevated CO2; none of them were upregulated. Hence, all C4 uptake systems that a strain was capable to produce were available for the cells at low CO2 levels, including the low-affinity C4 uptake systems. Third, the genes chpX and chpY of both C4 uptake systems were expressed constitutively, which might again be an adaptation to fluctuating CO2 conditions. Constitutive expression of the high-affinity CO2 uptake system NDH-I4 might also be an adaptation to intercept low intracellular concentrations of CO2 leaking from the carboxysomes.

**Methodological aspects.** Previously, the cellular response of strain PCC 7806 to elevated CO2 was investigated in highly controlled chemostats using whole-genome microarrays (32). In the present study, we simplified the experimental setup to batch cultures and limited our analysis to a smaller set of genes using RT-qPCR, which enabled investigation of a larger number of strains. We included strain PCC 7806 in our present study to check the consistency of the results.

Strain PCC 7806 downregulated expression of cmpA and bicA at elevated CO2 in both the previous and the present study (Fig. 4). Furthermore, both studies showed constitutive expression of the CO2 uptake, carboxysomal and RuBisCO genes, and downregulation of the transcriptional regulator gene ccmR2, although ccmR2 was only downregulated in the previous study (32). Moreover, the O2 evolution data of PCC 7806 show that BCT1 and BicA were both active under low-pCO2 conditions (Fig. 5A), whereas BicA but not BCT1 was active under high-pCO2 conditions (Fig. 5F), in agreement with the findings of the previous study (32). Hence, the results of both studies are in good agreement, which gives confidence in the applied methods.

In our O2 evolution experiments, the cells were exposed to different salt treatments (Table 1). This could potentially bias the results because Microcystis strains differ in their salt tolerance and potassium ion sensitivity (42). In particular, strain PCC 7005 is very sensitive to elevated potassium ion concentrations and lacks several salt tolerance genes, whereas strain PCC 7806 is much more tolerant to potassium ions and can withstand 170 mmol liter−1 NaCl (42, 43). We therefore tried to minimize salt stress by exposing the cells to the different treatments for only 15 min. The results show that even the salt- and potassium-sensitive strain...
both belong to genotype III (similar genotypes, such as strains HUB 5-3 and PCC 7005 that express patterns for their bicarbonate uptake genes (Fig. 4).

ATP-dependent high-affinity bicarbonate transporter BCT1, since downregulation of bicA and sbtA (possibly the high-affinity CO₂ uptake operon) would be most effective by downregulation of the bicA-sbtA operon for HUB 5-3 and by downregulation of BCT1 in PCC 7005, a finding in line with the observed changes in the expression of these two uptake systems. The constitutive expression of genes encoding the high-affinity CO₂ uptake system NDH-I₃ in all Microcystis strains and the high-affinity bicarbonate transporter SbtA in some Microcystis strains deviates from the induction of these genes in the other three cyanobacteria. The presence and expression of bicA appears to be quite variable, not only in Microcystis but also in other cyanobacteria.

The CCM transcriptional regulators also differ among the cyanobacteria (Table 3). CcmR can regulate transcription of several C₄ uptake genes. In Synechocystis PCC 6803, CcmR appeared to be a repressor of sbtA and the high-affinity CO₂ uptake operon but not of bicA (29, 47). In contrast, in Synechococcus PCC 7002, CcmR appeared to be a repressor of bicA and sbtA and possibly the low-affinity CO₂ uptake operon (48, 50). In Microcystis, CcmR probably regulates expression of the cmpABCD operon (encoding BCT1), since downregulation of ctnR at elevated pCO₂ coincided with downregulation of the cmpA gene (Fig. 4). Synechocystis PCC 6803 and Synechococcus PCC 7942 use another transcriptional regulator, CmpR, for the cmpABCD operon (27, 47), which is absent from Microcystis. CcmR2 is the most likely transcriptional regulator for the bicA and sbtA genes in Microcystis, given the location of ctnR upstream of the bicA-sbtA operon (17).

Ecological implications. In conclusion, our results reveal an unexpected diversity in CO₂ responses of cyanobacteria. It was already known that Microcystis strains differ in their C₄ uptake genes, which promotes variation in their CO₂ response (17). Our results show that, on top of this genotypic diversity, there is also considerable phenotypic variation because strains with the same C₄ uptake genes can show contrasting expression patterns and may differ widely in the activity of their C₄ uptake systems. In other

Comparison of CCM gene regulation of Microcystis with other cyanobacteria. Previously, the CCM genes of the model cyanobacteria Synechocystis PCC 6803, Synechococcus PCC 7002, and Synechococcus 7942 were studied in detail (15, 19, 27–30, 44–48). Comparison of the CCM genes of our Microcystis strains with these model cyanobacteria reveals several similarities and differences (Tables 2 and 3).

In all cyanobacteria investigated thus far, genes encoding the ATP-dependent high-affinity bicarbonate transporter BCT1 are induced under low-Ci conditions, whereas genes encoding the low-affinity CO₂ uptake system NDH-I₃ are constitutively expressed (Table 2). Hence, our two hypotheses do apply to the genes of these two uptake systems. The constitutive expression of genes encoding the high-affinity CO₂ uptake system NDH-I₃ in all Microcystis strains and the high-affinity bicarbonate transporter SbtA in some Microcystis strains deviates from the induction of these genes in the other three cyanobacteria. The presence and expression of bicA appears to be quite variable, not only in Microcystis but also in other cyanobacteria.

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words, cyanobacterial strains differ in their adaptation to changing CO₂ conditions not only because of variation in genetic composition but also because of further variation at the transcriptional and physiological level.

It is often argued that cyanobacteria generally have a very effective CCM and are therefore particularly strong competitors at low CO₂ levels in comparison to eukaryotic phytoplankton (9). However, we know now that there is major variation in the CCM tactics among cyanobacteria and even among different strains within the same genus. Some *Microcystis* strains perform well at low CO₂, whereas other strains are much better competitors under high-CO₂ conditions (17, 49). This genetic and phenotypic variation in C₄ uptake systems provides cyanobacterial communities with the potential for rapid adaptation and acclimation to changing CO₂ conditions. These differential responses also indicate that the ongoing rise in atmospheric CO₂ concentrations is likely to be more beneficial for some cyanobacterial strains than for others, which may lead to major changes in the genetic composition of harmful cyanobacterial blooms.

ACKNOWLEDGMENTS

We are grateful to the reviewers for their helpful comments.

This research was supported by the Division of Earth and Life Sciences (ALW) of the Netherlands Organization for Scientific Research (NWO).

We declare that we have no conflict of interest related to the manuscript.

REFERENCES


