Mixotrophic and photoheterotrophic metabolism in *Cyanothece* sp. ATCC 51142 under continuous light

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The unicellular diazotrophic cyanobacterium *Cyanothece* sp. ATCC 51142 (*Cyanothece* 51142) is able to grow aerobically under nitrogen-fixing conditions with alternating light–dark cycles or continuous illumination. This study investigated the effects of carbon and nitrogen sources on *Cyanothece* 51142 metabolism via 13C-assisted metabolite analysis and biochemical measurements. Under continuous light (50 μmol photons m−2 s−1) and nitrogen-fixing conditions, we found that glycerol addition promoted aerobic biomass growth (by twofold) and nitrogenase-dependent hydrogen production [up to 25 μmol H2 (mg chlorophyll)−1 h−1], but strongly reduced phototrophic CO2 utilization. Under nitrogen-sufficient conditions, *Cyanothece* 51142 was able to metabolize glycerol phototrophically, and the activity of light-dependent reactions (e.g. oxygen evolution) was not significantly reduced. In contrast, *Synechocystis* sp. PCC 6803 showed apparent mixotrophic metabolism under similar growth conditions. Isotopomer analysis also detected that *Cyanothece* 51142 was able to fix CO2 via anaplerotic pathways, and to take up glucose and pyruvate for mixotrophic biomass synthesis.

**INTRODUCTION**

Rising concerns about global warming due to the greenhouse effect have renewed research focused on the biological capture of CO2. Cyanobacteria have versatile metabolic capabilities, which allow them to grow under autotrophic, heterotrophic and mixotrophic conditions (Bottomley & Van Baalen, 1978; Eiler, 2006; Yang et al., 2002). More importantly, some cyanobacteria can capture solar energy to fix nitrogen and generate H2, thereby serving as a source of biofertilizer and biofuel, while simultaneously consuming atmospheric CO2 (Bernat et al., 2009; Dutta et al., 2005; Fay, 1992; Madamwar et al., 2000; Tamagnini et al., 2007; Tuli et al., 1996). *Cyanothece* sp. ATCC 51142 (*Cyanothece* 51142), a unicellular diazotrophic cyanobacterium, is able to grow aerobically under nitrogen-fixing conditions and has been recognized as contributing to the marine nitrogen cycle. The recent sequencing of the *Cyanothece* 51142 genome and its transcriptional analysis have uncovered the diurnally oscillatory metabolism of the bacterium in alternating light–dark cycles (photosynthesis during the day and nitrogen fixation at night) (Stöckel et al., 2008; Toepel et al., 2008; Welsh et al., 2008). In general, cyanobacteria use spatial or temporal separation of oxygen-sensitive nitrogen fixation and oxygen-evolving photosynthesis as a strategy for diazotrophic growth (Benemann & Weare, 1974; Fay, 1992). Interestingly, *Cyanothece* 51142 demonstrates simultaneous N2 fixation and O2 evolution under continuous-light conditions, though it appears to be unicellular (Colon-Lopez et al., 1997; Huang & Chow, 1986). For example, a recent study of the transcriptional and translational regulation of continuously illuminated *Cyanothece* has revealed a strong synthesis capability for nitrogenase and circadian expression of 10% of its genes (Toepel et al., 2008). Furthermore, *Cyanothece* strains usually utilize exogenous carbon substrates for mixotrophic growth under light conditions and for heterotrophic growth under dark conditions (Reddy et al., 1993). Carbon substrates are key factors controlling the efficiency of cyanobacterial aerobic growth and hydrogen production (Berman-Frank et al., 2003; Reddy et al., 1993; Tamagnini et al., 2007). Genome analysis studies have revealed that *Cyanothece* 51142 has a unique gene cluster on its linear chromosome that contains key genes involved in glucose
and pyruvate metabolism (Welsh et al., 2008). However, the ability of this strain to metabolize glucose or pyruvate remains unknown.

To quantitatively examine the effect of carbon and nitrogen sources on *Cyanotheca* central metabolism, this study investigated the effect of three carbon sources (glucose, glycerol and pyruvate, as representatives of sugar, lipid derivatives and organic acids from central metabolic pathways, respectively) on *Cyanotheca* 51142 growth and metabolism. Two nitrogen sources other than N₂, ammonia and nitrate, were also examined. Precise readouts of metabolic state and activity were based on ¹³C-assisted metabolite analysis integrated with biochemical assays and the gene expression patterns obtained by RT-PCR (Fong et al., 2006; Pingitore et al., 2007; Tang et al., 2007c, 2009; Wu et al., 2010). Superior to the traditional ¹⁴C method (Bottomley & Van Baalen, 1978), the non-radioactive ¹³C method can provide rich information about which carbons within a metabolite are labelled, and thus enable an in-depth understanding of carbon utilization and metabolic regulation in *Cyanotheca* 51142.

**METHODS**

**Bacterial strains and growth conditions.** *Cyanotheca* 51142 was first grown in 150 ml Erlenmeyer flasks fed with ASP2 medium (Reddy et al., 1993) without nitrate. Ambient CO₂ provided the sole carbon source. For experiments examining the effects of nitrogen sources, 18 mM NaN₃ or 17 mM NH₄Cl was added to the medium. Cultures were grown aerobically under continuous light (50 µmol photons m⁻² s⁻¹) on a shaker at 150 r.p.m. and 30 °C. Cells at late mid-exponential phase were subcultured into different culture media with various nitrogen and carbon sources. Isotopically labelled carbon substrates (Cambridge Isotope Laboratories) were used for mixotrophic growth, including 54 mM glycerol (2-¹³C, >98%), 26 mM glucose (U-¹³C, >98%) and 11 mM sodium pyruvate (3-¹³C, >98%). For tracer experiments, a 3% inoculum from unlabelled stock culture was used to inoculate 50 ml of medium containing labelled carbon sources. At the mid-exponential phase of growth, a 3% inoculum from the first isotopically labelled culture was used to inoculate 50 ml of medium containing labelled carbon sources. At the mid-exponential phase of growth, a 3% inoculum from the first inoculum of unlabelled stock culture was used to inoculate 50 ml of medium containing labelled carbon sources. At the mid-exponential phase of growth, a 3% inoculum from the first inoculum was removed to collect 20 ml culture by centrifugation (8000 rpm for 10 min) for 1 min at 94 °C. Finally, a 10 min continuous light (50 µmol photons m⁻² s⁻¹). A modified protocol was used to quantify hydrogen (Rey et al., 2007). Briefly, hydrogen that accumulated in the headspace of the sealed culture vials (for 5 h) was withdrawn with a Hamilton gas-tight syringe and quantified on an Agilent 6890N gas chromatograph with a Molsieve 5A 60/80 column (inner dimensions 6’’ × 1/8’’ (1830 × 3.17 mm)) and thermal conductivity detector. Injection, oven and detector temperatures were 100, 50 and 100 °C, respectively. Argon was the carrier gas (flow rate 65 ml min⁻¹). All measurements included three biological replicates.

Photosynthesis activities were determined based on measurements of chlorophyll fluorescence and oxygen evolution. Chlorophyll fluorescence profiles of photosystem II (PSII) of *Cyanotheca* 51142 under different nutrient conditions were detected by an FL100 fluorometer (Photon Systems Instruments, Brno, Czech Republic) as described previously (Roose & Pakrasi, 2004). All samples taken for measurement were diluted to OD₇₃₀ = 0.2 using cell-free ASP2 medium. The samples were first adapted for 3 min in total darkness. During the measurement (performed at room temperature), the fluorometer emitted saturating light pulses to determine the fluorescence yield of the samples. The photosynthesis activity was derived by the maximum quantum yield (Fm/Fm') according to the formula Fm'/Fm = (Fm' - Fp)/Fm', where Fp is initial fluorescence and Fm' is maximum fluorescence at the beginning of measurement (Krause & Weis, 1991).

Oxygen evolution rates of *Cyanotheca* 51142 grown under different nutrient conditions were measured with a Hansatech oxygen electrode. Assays were performed at 30 °C on whole cells in ASP2 medium with a saturating light intensity of 8250 µmol photons m⁻² s⁻¹ for 2 min in a 2.5 ml reaction volume. For each reaction, the chlorophyll concentration of each sample was diluted to ~6 µg ml⁻¹. The oxygen evolution rates [µmol O₂ (mg chlorophyll)⁻¹ h⁻¹] were then measured and normalized based on chlorophyll concentration.

**RNA extraction and RT-PCR.** The bacteria grown under different cultural conditions were harvested at mid-exponential phase according to the corresponding growth curves. The total RNA was extracted by using a PureLinkRNA Mini kit (Invitrogen), following the manufacturer’s instructions. cDNA was synthesized from ~2 µg RNA by using a High Capacity cDNA Reverse Transcription kit (Invitrogen). The primers for RT-PCRs were designed using Primer Premier 5 software (PREMIER Biosoft) and analysed by OligoAnalyser 3.0 software (Integrated DNA Technologies). The forward primer 5’-AGCGGTCGGATGATCCTGG-3’ and reverse primer 5’-GGCTGGTTGATGAGATT-3’ were employed to amplify the 16S rRNA gene as a control. The forward primer 5’-CCGACTACACTCCGAAAG-3’ and reverse primer 5’-ACGTAAGCCCGCGTAAATGC-3’ were used to amplify the ribulose-1,5-bisphosphate carboxylase oxygenase (RuBiCO) (rbcL) gene, and the forward primer 5’-TAATCAGCAGAAGGGAG-3’ and reverse primer 5’-CACCACATCCCGTATTG-3’ to amplify the prk gene. PCRs were conducted with the following cycle conditions: 2 min of activation of the polymerase at 94 °C, followed by 30 cycles consisting of 1 min at 94 °C, 30 s at 53 °C and 2 min at 72 °C; finally, a 10 min extension was performed at 72 °C. The final PCR product was observed directly on 2% agarose gels after electrophoresis.

**Isotopic analysis.** The preparation and isotopic analysis of proteogenic amino acids were performed as previously described (Tang et al., 2007a, b). In brief, exponentially growing biomass from ~20 ml culture was collected by centrifugation (8000 g 10 min, 4 °C) and hydrolysed in 6 M HCl at 100 °C for 24 h. The amino acid mix was dried and derivatized in tetrahydrofurann (THF) and N-(tert-butyl dimethylsilyl)-N-methyl-trifluoroacetamide (Sigma-Aldrich) at 70 °C for 1 h. A gas chromatograph (Hewlett Packard model 7890A, Agilent Technologies) equipped with a DB5-MS column (J&W Scientific) and
a mass spectrometer (5975C, Agilent Technologies) were used for analysing amino acid labelling profiles. The ion \([M-57]^+\) from unfragmented amino acids was detected and mass fractions of key amino acids were calculated (Wahl et al., 2004). The substrate utilization ratio \(R\) (reflecting the degree of mixotrophic metabolism) for an amino acid \(X\) was calculated from the labelling patterns of proteogenic amino acids by the following equation:

\[
0.98 \times n \times V_{\text{sub}} + 0.01 \times V_{\text{CO}_2} = \frac{\sum_{i=1}^{C} i \times M_i}{C} \Rightarrow R = \frac{V_{\text{sub}}}{V_{\text{CO}_2}} \tag{1}
\]

where the ratio \(R\) indicates the utilization of labelled carbon substrate over unlabelled \(\text{CO}_2\) for producing an amino acid \(X\) (and its precursors), \(M_i\) is the GC-MS isotopomer fraction for amino acid \(X\) (i.e. \(M_0\) is the unlabelled fraction, \(M_1\) is the singly labelled fraction, \(M_2\) is the doubly labelled fraction, \(M_3\) is the triply labelled fraction, etc.), \(C\) is the total number of carbon atoms in the amino acid molecule, \(V_{\text{sub}}\) is the carbon flux from \(^{13}\text{C}\)-labelled substrate, \(V_{\text{CO}_2}\) is the carbon flux from \(\text{CO}_2\), 0.98 is the purity of the labelled carbon substrate, 0.01 is the natural abundance of \(^{13}\text{C}\), \(m\) is the total number of carbons in the substrate molecule and \(n\) is the total number of labelled carbons in the substrate molecule. \(R\) indicates the amount of labelled carbon that percolated through the central metabolic networks (Fig. 1).

**RESULTS**

**Cell growth with different carbon and nitrogen sources**

Fig. 2 and Supplementary Fig. S1 show the effects of carbon and nitrogen substrates on the growth of *Cyanothece* 51142 under continuous light. Biomass growth was significantly enhanced by the addition of glycerol to ASP2 medium. For example, glycerol addition doubled the specific growth rate from 0.28 to 0.63 day\(^{-1}\) under \(\text{N}_2\)-fixing conditions. These results are consistent with an earlier report on two *Cyanothece* strains (Reddy et al., 1993). On the other hand, *Cyanothece* growth was apparently not enhanced by either glucose or pyruvate (Supplementary Fig. S1), and a high concentration of pyruvate (64 mM) inhibited *Cyanothece* growth. Compared with nitrogen-fixing cultures, the presence of nitrate salts in the growth media increased *Cyanothece* autotrophic growth rates from 0.28 day\(^{-1}\) (\(\text{N}_2\)-fixation condition) to 0.37 day\(^{-1}\) (nitrate-sufficient condition). Similarly, the presence of glycerol enhanced the growth rate by approximately twofold (from 0.60 to 1.02 day\(^{-1}\)). As expected, high concentrations of

![Fig. 1. Central metabolic pathways of *Cyanothece* 51142 with glucose, glycerol and pyruvate as carbon substrates. The dashed lines show the metabolic pathway with glycerol as carbon substrate; the heavy solid line indicates glucose; the solid line shows the common pathway for all carbon conditions. Abbreviations: ACCOA, acetyl-CoA; E4P, erythrose 4-phosphate; F6P, fructose 6-phosphate; G6P, glucose 6-phosphate; GAP, glyceraldehyde 3-phosphate; GLY, glycerol; GLU, glucose; ICIT, citrate/isocitrate; MAL, malate; OAA, oxaloacetate; OXO, 2-oxoglutarate; PEP, phosphoenolpyruvate; 3PG, 3-phosphoglycerate; PYR, pyruvate; R5P, ribose 5-phosphate; R15P, ribulose 1,5-bisphosphate; S7P, sedoheptulose 7-phosphate; Xu5P, xylulose 5-phosphate.](image-url)
ammonium salts (17 mM) fully inhibited growth (data not shown) because of their well-known deleterious effect on the photosystems of cyanobacteria (Drath et al., 2008; Dai et al., 2008).

Isotopic analysis of amino acids

$^{13}$C-enrichment patterns in key metabolites were used to estimate the relative utilization of labelled carbon substrates (i.e. glucose, pyruvate and glycerol) and CO$_2$ for metabolite synthesis under mixotrophic growth. Fig. 1 shows the central metabolic pathways in Cyanothecae 51142 (http://www.genome.jp/kegg/). The labelling of five amino acids was analysed: histidine (precursors: ribose 5-phosphate and 5,10-methyl-THF), synthesized from the Calvin cycle and pentose phosphate pathway; serine (precursor: 3-phosphoglycerate, a product from the Calvin cycle); alanine (precursor: pyruvate, originating from carbon substrates or CO$_2$ fixation); and aspartate and glutamate (precursors: oxaloacetate and 2-oxoglutarate, respectively; synthesized from the citric acid cycle). Under nitrate-sufficient conditions, glycerol could be used as the sole carbon source for the synthesis of alanine, serine and histidine (as indicated by R values approaching infinity). This indicates that the cell was undergoing completely heterotrophic metabolism. R values of some key amino acids in glucose and pyruvate cultures were positive, and thus these two carbon sources were actually utilized for biomass synthesis (Table 1). However, their measured R values were between 0 and 0.3, which indicated that CO$_2$ was the main carbon source for metabolite synthesis. This result was consistent with the fact that glucose and pyruvate did not apparently improve the biomass growth. Compared with nitrogen-sufficient conditions, nitrogen-fixing conditions further limited glucose and glycerol utilization, as shown by the decreased labelling fractions of three key amino acids (i.e. alanine, serine and histidine) (Table 1).

**Nitrogenase-dependent hydrogen production, photosynthesis and Calvin cycle activity**

Hydrogen production under continuous light with different carbon substrates (N$_2$ as the sole nitrogen source) was measured by the slope of the CO$_2$ evolution rate. Hydrogen production rates were as follows: glycerol, $25 \pm 6 \mu$mol H$_2$ (mg chlorophyll)$^{-1}$ h$^{-1}$; glucose, $13 \pm 9 \mu$mol H$_2$ (mg chlorophyll)$^{-1}$ h$^{-1}$; pyruvate, $4 \pm 2 \mu$mol H$_2$ (mg chlorophyll)$^{-1}$ h$^{-1}$; and under photoautotrophic conditions, $5 \pm 1 \mu$mol H$_2$ (mg chlorophyll)$^{-1}$ h$^{-1}$. Under all conditions, ammonium chloride inhibited hydrogen production. The measurement of photosynthetic parameters (Fig. 3) suggested that, compared with photoautotrophic conditions, addition of an exogenous carbon source (glucose, pyruvate or glycerol) did not strongly suppress the maximal quantum yield of PSII (F$_{v}$/F$_{m}$) or the oxygen evolution rate. Nitrate-sufficient conditions enhanced the oxygen evolution rates by two- to threefold compared with nitrogen-fixing conditions, while the changes of the quantum yields of PSII were much less significant (10–30%). Gene expression in the carbon fixation pathway was also determined (Fig. 4). RT-PCR results indicated that two key enzymes in the Calvin cycle [RuBisCO (rbcL) and phosphoribulokinase (prk)] were functional under conditions of growth with glycerol or glucose. The above measurements confirmed that the light-dependent reactions were active under all culture conditions, even though carbon substrates reduced the relative contribution of CO$_2$ fixation to biomass synthesis.

**DISCUSSION**

**Carbon substrate utilization and regulation**

In continuous light, Cyanothecae 51142 can efficiently utilize glycerol for aerobic growth. Based on the measurement of carbon substrates in the culture medium during the exponential growth phase, the uptake rates for glycerol were $0.22 \pm 0.05 \text{ g (g dry biomass)$^{-1}$ day}^{-1}$ under nitrogen-fixing and $0.35 \pm 0.06 \text{ g (g dry biomass)$^{-1}$ day}^{-1}$ under nitrate-sufficient conditions. Glycerol promoted Cyanothecae 51142 growth because it provided carbon and energy sources. Under nitrate-sufficient conditions, the high values of R for the serine, alanine and histidine labelling data indicated that the 3-phosphoglycerate,
reduce energy costs related to CO2 fixation (fixation of one carbon atom requires two ATPs and one NADPH). The contribution of CO2 photofixation to amino acid synthesis (Table 1) was minimal. In contrast, glycerol, while the contribution of CO2 photofixation to glyceraldehyde synthesis (Table 1) was negligible. As a comparison, the measured R values (Table 1) for serine (0.92), alanine (0.98), and histidine (1.73) indicated that the labelled glucose had percolated through all the central metabolic pathways, thereby confirming the ability of Synechocystis 6803 to metabolize glucose. The R values of all key amino acids were below 0.05 for both nitrogen-fixation and nitrate-sufficient conditions, suggesting that a large fraction of the carbon in the biomass had originated from CO2 fixation. In contrast, glucose is the most favourable carbon source for Synechocystis species (Yang et al., 2002), and the R values (Table 1) for key amino acids were ~0.4–1.7. While both Synechocystis 6803 and Synechocystis 51142 have completely annotated central pathways for glucose metabolism, Synechocystis 6803 contains a glucose transporter (gene code Sll0771) that shares a sequence relationship with mammalian glucose transporters (Bottomley & Van Dover, 1993). This study shows that rapidly growing Cyanothece 51142 cells can shift their metabolic strategy from mixotrophic or autotrophic growth to photoheterotrophic growth, possibly because maximal utilization of an energy-rich carbon substrate (glycerol) can reduce energy costs related to CO2 fixation (fixation of one CO2 requires two ATPs and one NADPH) and building-block synthesis, so that maximal biomass growth can be achieved.

On the other hand, glucose was apparently not consumed by Synechocystis 6803 (nitrate medium) below 1 mM in all experiments). In the Synechocystis 51142 (the consumed concentrations were below 0.02, technical replicates, n=2) experiments (Table 1), all five amino acids contained labelled carbons, which indicated that the labelled glucose had percolated through all the central metabolic pathways, thereby confirming the ability of Cyanothece 51142 to metabolize glucose. The R values of all key amino acids were below 0.05 for both nitrogen-fixation and nitrate-sufficient conditions, suggesting that a large fraction of the carbon in the biomass had originated from CO2 fixation. In contrast, glucose is the most favourable carbon source for Synechocystis species (Yang et al., 2002), and the R values (Table 1) for key amino acids were ~0.4–1.7. While both Synechocystis 6803 and Synechocystis 51142 have completely annotated central pathways for glucose metabolism, Synechocystis 6803 contains a glucose transporter (gene code Sll0771) that shares a sequence relationship with mammalian glucose transporters (Bottomley & Van Dover, 1993).

Table 1. Isotopic analysis of the labelling profiles of amino acids in Cyanothece 51142 and Synechocystis 6803 under different growth conditions (the standard error for GC-MS measurement was below 0.02, technical replicates, n=2)

<table>
<thead>
<tr>
<th>Amino acid</th>
<th>[M-57]+</th>
<th>N2</th>
<th>NaNO3</th>
<th>Synechocystis 6803 (nitrate medium)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Glucose</td>
<td>R*</td>
<td>Pyruvate</td>
<td>Glycerol</td>
</tr>
<tr>
<td>Ala</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>M0</td>
<td>0.67</td>
<td>0.032</td>
<td>0.41</td>
<td>0.597</td>
</tr>
<tr>
<td>M1</td>
<td>0.19</td>
<td>0.55</td>
<td>0.71</td>
<td></td>
</tr>
<tr>
<td>M2</td>
<td>0.11</td>
<td>0.03</td>
<td>0.10</td>
<td></td>
</tr>
<tr>
<td>Ser</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>M0</td>
<td>0.65</td>
<td>0.033</td>
<td>0.98</td>
<td>0.20</td>
</tr>
<tr>
<td>M1</td>
<td>0.22</td>
<td>0.02</td>
<td>0.72</td>
<td></td>
</tr>
<tr>
<td>M2</td>
<td>0.10</td>
<td>0.09</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asp</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>M0</td>
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<td>0.030</td>
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<td>0.01</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Glu†</td>
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<td></td>
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<tr>
<td>M0</td>
<td>0.43</td>
<td>0.041</td>
<td>0.15</td>
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<tr>
<td>M1</td>
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<td>0.44</td>
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<tr>
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<td>0.37</td>
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</tr>
<tr>
<td>M3</td>
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<td>0.04</td>
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</tr>
<tr>
<td>M4</td>
<td>0.02</td>
<td>0.001</td>
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</tr>
<tr>
<td>His</td>
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<td></td>
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</tr>
<tr>
<td>M0</td>
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<td>0.032</td>
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<tr>
<td>M5</td>
<td>0.001</td>
<td>0.01</td>
<td></td>
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*Values in bold type are the carbon substrate (glycerol, pyruvate or glucose) utilization ratios (substrate/CO2 fixation) for amino acid synthesis, calculated according to equation (1).†The glutamate synthesis pathway involves the loss of two carbons from pyruvate to α-ketoglutarate. Such a microbial process changes the labelling enrichment, and the negative values indicate the net loss of unlabelled CO2.
Baalen, 1978; Flores & Schmetterer, 1986; Schmetterer, 1990). So far, the presence of a glucose transporter in Cyanothece 51142 has not been rigorously verified. From the genome database (DOE Joint Genome Institute, http://www.jgi.doe.gov/), a gene (ccc_3842) has been identified as a glucose transport protein that shared weak (25%) amino acid identity with the Sll0771 protein of Synechocystis PCC6803. Based on the glucose-dependent growth data, we conclude that the enzymes involved in glucose transport or utilization in Cyanothece 51142 may not be as efficient as those of Synechocystis PCC6803.

Analysis of labelled pyruvate-grown Cyanothece cells showed that serine (precursor 3-phosphoglycerate) and histidine (precursor ribose 5-phosphate) were completely unlabelled (R = 0). Such a labelling profile suggests that CO2 was used as the sole carbon source for synthesis of metabolites in glycolysis and the pentose phosphate pathway (i.e. there was no gluconeogenesis activity). Pyruvate was used only to synthesize alanine (R = 0.3–0.6) and metabolites in the tricarboxylic acid cycle (pyruvate→oxaloacetate→Asp) (pyruvate→acetyl-CoA→citrate→2-oxoglutarate→glutamate), as reflected by the labelled carbon present in glutamate and aspartic acid. Interestingly, the R values for alanine (0.60) and glutamate (1.25) were higher under nitrogen-fixing conditions than under nitrate-sufficient conditions, indicating that relatively more labelled pyruvate was used for glutamate synthesis under these conditions. The nitrogen fixation was via nitrogenase: N2 + 6H++ 6e−→2NH3, and the nitrogenase-generated ammonium was assimilated into amino acids through the glutamine synthetase/glutamate synthase pathway (Postgate, 1998). Utilization of supplemented pyruvate for glutamate synthesis could facilitate the nitrogen-fixation process.

The enzyme RuBisCO is known to be the rate-limiting factor in the Calvin cycle for capturing CO2 to synthesize three-carbon sugars (glycerate 3-phosphate) (Atsumi et al.,
We examined RuBisCO (rbcL) and phosphoribulokinase (prk) gene expression to reveal the metabolic regulation in the Calvin cycle at the transcriptional level. Under photoautotrophic, mixotrophic and heterotrophic growth conditions, expression of the two genes was clearly observed. Although the Calvin cycle genes were expressed, *Cyanothece* 51142 still grew heterotrophically in the presence of glycerol and nitrate, based on the isotopomer data (no apparent incorporation of CO2 from the Calvin cycle). These inconsistencies indicate that 13C-assisted metabolite analysis provides a direct readout of actual metabolic status, while gene expression results alone cannot be relied upon, as there are many points of possible post-transcriptional regulation.

Furthermore, *Cyanothece* 51142 can fix CO2 via anaplerotic pathways (i.e. C4 carbon fixation) (Slack & Hatch, 1967). In the presence of glycerol and under nitrate-sufficient conditions (Table 1), the R ratio for aspartate synthesis was 1.53, much smaller than the R ratios (R = ∞) for Ala, Ser and His. This indicates that, even though phototrophic CO2 fixation was significantly inhibited, CO2 was utilized for the synthesis of C4 metabolites in the tricarboxylic acid cycle via anaplerotic pathways: (1) PEP + CO2 → oxaloacetate (catalysed by phosphoenolpyruvate carboxylase or phosphoenolpyruvate carboxykinase) or (2) pyruvate + CO2 → malate (catalysed by malic oxidoreductase). Such anaplerotic pathways synthesize key TCA cycle metabolites such as oxaloacetate and succinate (precursors of chlorophyll).

Meanwhile, CO2 was generated by two reactions (i.e. pyruvate → acetylCoA + CO2; isocitrate → 2-oxoglutarate + CO2), which are essential steps for glutamate synthesis. These catabolic processes cause the loss of unlabelled carbon when the second-position labelled glycerol is used as the main carbon source. Therefore, the coefficients VCO2 (CO2 utilization flux) and R (carbon utilization ratio) were both negative for glutamate synthesis (equation 1) in glycerol-supplemented cultures (under both nitrogen-fixation and nitrate-sufficient conditions) (Table 1).

**Photosynthesis activity**

Photosynthesis activity was estimated by the Fv/Fm parameter (maximum quantum efficiency of PSII) (Pirintsos *et al.*, 2009). When glycerol or glucose was utilized, the maximum quantum yield Fv/Fm (i.e. efficiency of PSII) in *Cyanothece* 51142 was not significantly affected (changes were within ~30%, Fig. 3a). Although chlorophyll fluorescence estimation is not an accurate method for the determination of absolute PSII activity (Schreiber *et al.*, 1995; Ting & Owens, 1992), we have used it in our study as a tool only to confirm active photon capture in the light-harvesting antenna complexes of PSII under both heterotrophic and mixotrophic conditions.

Oxygen evolution was measured as one molecule of the pigment chlorophyll absorbs one photon and uses its energy to generate NADPH, ATP and O2 via the light-dependent reactions (Kaftan *et al.*, 1999). The oxygen evolution rates in *Cyanothece* 51142 rose by two- to threefold under all nitrate-sufficient conditions compared with corresponding nitrogen-fixation conditions (Fig. 3b). The significantly higher rates of oxygen evolution indicated that the photosynthetic process of water splitting was more active and provided more energy (ATP and NADPH) to support biomass growth under nitrate-sufficient conditions.

Finally, precise determination of the photosynthetic activity of *Cyanothece* 51142 is difficult, as its metabolic behaviour fluctuates under continuous light due to its circadian rhythm (Colon-Lopez *et al.*, 1997; Toepel *et al.*, 2008). The photoreaction activity data in Fig. 3 represent only qualitative (not quantitative) evidence to support the presence of active light-dependent reactions under all culture conditions.

**Nitrogen utilization and nitrogenase-dependent hydrogen production**

Under anaerobic conditions (using argon gas to flush the culture), hydrogen production rates of *Cyanothece* 51142 were as high as 100 μmol (mg chlorophyll) −1 h −1 (data not shown). Under aerobic conditions, the hydrogen production enzyme (nitrogenase) is completely inactivated by oxygen (Tamagnini *et al.*, 2007). *Cyanothece* 51142 uses nitrogenase for both nitrogen fixation and hydrogen production. Nitrate, ammonium and some amino acids inhibit nitrogenase activity and thus fully prohibit aerobic hydrogen production by cyanobacteria (Rawson, 1985). Furthermore, NH4+ is a direct nitrogen source (nitrate is reduced to NH4+) that can be incorporated into biomass via glutamine/glutamate synthase (Muro-Pastor *et al.*, 2005). *Cyanothece* 51142, however, only grows at low concentrations of NH4+ (below 1 mM) because of an inhibition effect (Galmozzi *et al.*, 2007; Rawson, 1985). Nitrogen fixation is an energy-demanding process:

\[ \text{N}_2 + 8\text{H}^+ + 8\text{e}^- + 16\text{ATP} \rightarrow 2\text{NH}_3 + \text{H}_2 + 16\text{ADP} + 16\text{P}_i \]

The addition of glycerol reduces CO2 fixation via the Calvin cycle, so more energy (ATP and NADH) can be directed to nitrogen fixation, thus promoting hydrogen production four- to fivefold (Dutta *et al.*, 2005; Madamwar *et al.*, 2007). Glucose and pyruvate cannot significantly promote hydrogen production because their utilization is very low and their effect on the energy economy limited. Hydrogen production rates dropped for all mixotrophic cultures of *Cyanothece* 51142 after 9 days, suggesting that inhibitory metabolites that reduced nitrogenase activity accumulated during cultivation (Atsumi *et al.*, 2009; Nyström, 2004). Finally, the coexistence of oxygen-evolving photosynthesis and oxygen-sensitive nitrogen fixation (indicated by hydrogen evolution) is an attractive characteristic in some cyanobacteria (Benemann & Weare, 1974; Huang & Chow, 1986). Unlike filamentous cyano-
bacterial species, in which nitrogen fixation and oxygenic photosynthesis are spatially segregated (Berman-Frank et al., 2001), *Cyanothece* 51142 is able to maintain activities for N$_2$ fixation, respiration and photosynthesis within the same cell under continuous light. The strain not only has a strong ability to scavenge intracellular oxygen and synthesize nitrogenase (Colon-Lopez et al., 1997; Fay, 1992), but also develops a highly circadian mechanism for nitrogen fixation (Elvitigala et al., 2009).

This study improves our understanding of *Cyanothece* 51142 physiology with different carbon and nitrogen sources as well as its potential application for hydrogen production. In general, exogenous carbon substrates may improve cellular growth but have strong negative effects on CO$_2$ fixation. Continuously illuminated *Cyanothece* 51142 shows simultaneous oxygen evolution and nitrogenase-dependent hydrogen production, while hydrogen production can be significantly enhanced by the addition of glycerol. A comparison of metabolic status under autotrophic, mixotrophic and heterotrophic growth conditions indicated that *Cyanothece* 51142 has an inherent metabolic strategy for maximal biomass production at low energy cost. Finally, this study has further confirmed that $^{13}$C-assisted metabolite analysis is a high-throughput method which can provide new and precise information to understand a biological system.

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