



Pyruvate kinase 2 from *Synechocystis* sp. PCC 6803 increased substrate affinity via glucose-6-phosphate and ribose-5-phosphate for phosphoenolpyruvate consumption

Masahiro Karikomi¹ · Noriaki Katayama¹ · Takashi Osanai¹

Received: 8 June 2023 / Accepted: 30 November 2023 / Published online: 17 May 2024
© The Author(s) 2024

Abstract

Pyruvate kinase (Pyk, EC 2.7.1.40) is a glycolytic enzyme that generates pyruvate and adenosine triphosphate (ATP) from phosphoenolpyruvate (PEP) and adenosine diphosphate (ADP), respectively. Pyk couples pyruvate and tricarboxylic acid metabolisms. *Synechocystis* sp. PCC 6803 possesses two *pyk* genes (encoded *pyk1*, sl10587 and *pyk2*, sl11275). A previous study suggested that *pyk2* and not *pyk1* is essential for cell viability; however, its biochemical analysis is yet to be performed. Herein, we biochemically analyzed *Synechocystis* Pyk2 (hereafter, SyPyk2). The optimum pH and temperature of SyPyk2 were 7.0 and 55 °C, respectively, and the K_m values for PEP and ADP under optimal conditions were 1.5 and 0.053 mM, respectively. SyPyk2 is activated in the presence of glucose-6-phosphate (G6P) and ribose-5-phosphate (R5P); however, it remains unaltered in the presence of adenosine monophosphate (AMP) or fructose-1,6-bisphosphate. These results indicate that SyPyk2 is classified as PykA type rather than PykF, stimulated by sugar monophosphates, such as G6P and R5P, but not by AMP. SyPyk2, considering substrate affinity and effectors, can play pivotal roles in sugar catabolism under nonphotosynthetic conditions.

Key message

Glucose-6-phosphate and ribose-5-phosphate increased *Synechocystis* Pyk2 affinity for PEP, possibly contributing to PEP consumption under nonphotosynthetic conditions.

Keywords Glycolysis · Microalgae · Pyruvate kinase · *Synechocystis* sp. PCC 6803

Introduction

Cyanobacteria can utilize CO₂ via photosynthesis to synthesize value-added metabolites for a low-carbon society (Hidese et al. 2020; Angermayr et al. 2014; Hasunuma et al. 2018). *Synechocystis* sp. PCC 6803 (hereafter, *Synechocystis*) is a unicellular, non-nitrogen fixing model cyanobacterium that is utilized for bioproduction (Ruffing 2011; Wang et al. 2012; Yu et al. 2013). *Synechocystis* produces carboxylic acids, such as D-lactate, and polyhydroxy-3-butyrate (PHB), as food additives and bioplastics; these two

metabolites are derived from pyruvate (Osanai et al. 2015; Hidese et al. 2020; Ito et al. 2017; Carpine et al. 2017).

Various groups have widely studied primary carbon metabolism in *Synechocystis*, including metabolic regulation, pathway identification, and metabolic enzyme biochemistry (Fig. 1). *Synechocystis* has several glucose catabolic routes, such as the Embden–Meyerhof–Parnas (EMP) and oxidative pentose phosphate (OPP) pathways (You et al. 2014). *Synechocystis* has a unique tricarboxylic acid (TCA) cycle lacking 2-oxoglutarate dehydrogenase and possessing alternative pathways, such as a γ -butyric amino acid (GABA) shunt (Zhang and Bryant 2011; Xiong et al. 2014). The properties of the enzymes of the *Synechocystis* TCA cycle have been studied, including those of citrate synthase (CS encoded by *gltA*, sl10401) (Ito et al. 2019), aconitase (Aco encoded by *acnB*, slr0665) (Nishii et al. 2021; de Alvarenga et al. 2020), isocitrate dehydrogenase (IDH encoded

✉ Takashi Osanai
tosanai@meiji.ac.jp

¹ School of Agriculture, Meiji University, 1-1-1, Higashimita, Tama-Ku, Kawasaki, Kanagawa 214-8571, Japan

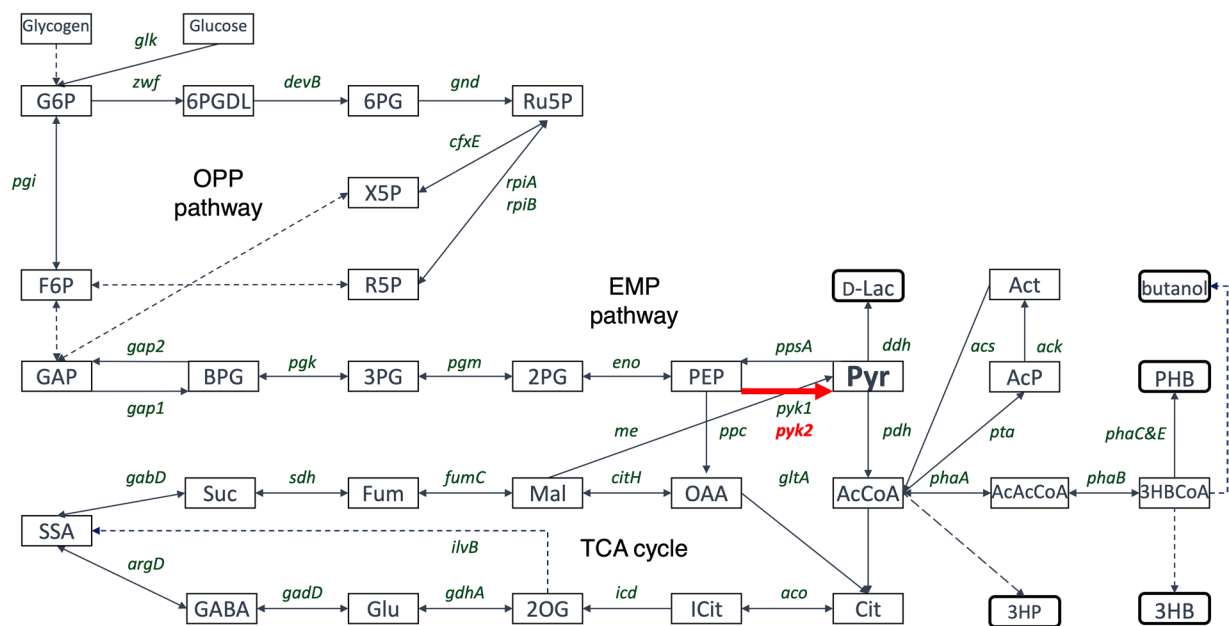


Fig. 1 Pathway map of *Synechocystis* sp. PCC 6803 (*Synechocystis*). The metabolic maps of the Embden–Meyerhof–Parnas (EMP) pathway/gluconeogenesis, oxidative pentose phosphate (OPP) pathway, pyruvate metabolism, and tricarboxylic acid (TCA) cycle. The gene

names encoding metabolic enzymes in *Synechocystis* were obtained from the Kyoto Encyclopedia of Genes and Genomes database. The rounded rectangle indicated value-added metabolites from *Synechocystis*

by *icd*, slr1289) (Muro-Pastor and Florencio 1992), malate dehydrogenase (MDH encoded by *citH*, sl10891) (Takeya et al. 2018), malic enzyme (ME encoded by *me*, sl10721) (Katayama et al. 2022), and succinate dehydrogenase (SDH encoded by *sdh*, sl10823 and sl11625) (Cooley and Vermaas 2001). Two enzymes, phosphoenolpyruvate carboxylase (PEPC) and pyruvate kinase (Pyk), catalyze specific reactions that provide carbon sources to the TCA cycle. *Synechocystis* possesses one PEPC encoded by *ppc* (sl10920) and two Pyks encoded by *pyk1* (sl10587) and *pyk2* (sl11275) (Kaneko et al. 1996). *Synechocystis* PEPC exhibits a unique allosteric regulation uninhibited by several metabolic effectors, such as malate, aspartate, and fumarate (Takeya et al. 2017; Scholl et al. 2020). Pyk enzymatic activity from *Synechocystis* cell cultures has been measured and reported to be higher under nonphotosynthetic conditions than those under photoautotrophic and mixotrophic conditions (Knowles and Plaxton 2003).

The phylogenetic analysis of the Pyks of *Synechocystis* revealed bacterial Pyk and an evolutionary distance between the two isoforms of Pyks, Pyk1 (hereafter, SyPyk1) and Pyk2, in cyanobacteria (Haghighi 2021). Bacterial Pyk is classified as PykA and PykF, and sugar monophosphates, such as AMP, G6P, and R5P, stimulate PykA. PykF is activated by sugar diphosphates, such as FBP, in *Escherichia coli* (Kornberg and Malcovati 1973; Waygood et al. 1975, 1976). SyPyk2 is classified into *pykF*, and *pyk2* knockout causes severe growth defects (Yao et al. 2020). In a previous

study, the biochemical analysis of the Pyk of another cyanobacterium, *Synechococcus* sp. PCC 6301 (hereafter, *Synechococcus* Pyk), was reported to be homologous to that of *Synechocystis pyk2*, suggesting that ATP and TCA metabolism inhibited *Synechococcus* Pyk, thus indicating its roles under dark conditions (Knowles et al. 2001). *pyk2* expression increases in the wild-type strain in the presence of glucose (Kaniya et al. 2013). *pyk2* expression patterns remain unchanged during the day/night cycle (Saha et al. 2016). These reports indicate that SyPyk2 is essential during photosynthetic and nonphotoautotrophic conditions in *Synechocystis*. This study revealed the regulatory properties of SyPyk2 via biochemical analysis and demonstrated that sugar phosphates activated SyPyk2 activity.

Materials and methods

Construction of cloning vector for recombinant SyPyk2

The amino acid sequence of Pyk2 (sl11275) polypeptide was obtained from the Kyoto Encyclopedia of Genes and Genomes database (<https://www.genome.jp/kegg/>) and synthesized by Eurofins Genomics Japan (Tokyo, Japan). The synthesized fragment was inserted within the BamHI–XhoI site of the vector pGEX6P-1 (GE Healthcare Japan, Tokyo, Japan). The cloned expression vector was transformed into

competent *E. coli* BL21 cells (Takara Bio, Shiga, Japan) and cultured in 6 mL of Luria–Bertani medium at 30 °C with shaking at 150 rpm. Recombinant *E. coli* BL21 cells from 1.2-L culture were suspended in 40 mL of phosphate-buffered saline/Tween (PBST) (1.37 M NaCl, 27 mM KCl, 81 mM Na₂HPO₄·12H₂O, 14.7 mM KH₂PO₄, and 0.05% Tween 20) and sonicated (model VC-750; EYELA, Tokyo, Japan). This procedure was repeated 10 times at 20% intensity for 20 s. The lysed cells were centrifuged twice at 12,500 rpm for 15 min at 4 °C. The supernatant was transferred into a 50 mL tube, and 2 mL of Glutathione Sepharose 4 B resin (Cytiva Japan, Tokyo, Japan) was added. The tubes were shaken gently for 60 min on ice. The mixture was centrifuged at 8,000 rpm for 2 min at 4 °C to remove the supernatant. The resin was transferred to a 15 mL tube and washed using PBST. After washing, the recombinant protein was eluted five times using 650 µL of glutathione-S-transferase (GST) elution buffer (50 mM Tris–HCl, pH 9.6-, and 10-mM reduced glutathione) and incubated in Vivaspin 500 MWCO 50,000 device (Sartorius, Göttingen, Germany) for protein concentration. The protein concentrations were determined using Pierce BCA Protein Assay Kit (Thermo Fisher Scientific, Rockford, IL, USA). The solution was transferred to a 1.5 mL tube, and 40 units of PreScission Protease (equivalent to the purified recombinant protein) (Cytiva) were added and allowed to stand at 4 °C for 16 h to remove GST-tag from the recombinant proteins. Approximately 750 µL of Glutathione Sepharose 4B resin was added, rotated for 1 h at room temperature to remove the cleaved tag from the solution, at 11,000 rpm for 4 min at 4 °C, and the supernatant was collected. Sodium dodecyl sulfate–polyacrylamide gel electrophoresis was performed to confirm protein purification, and gels were stained using Quick Blue reagent (BioDynamics Inc. Tokyo, Japan).

Enzyme assay

All solutions were prepared using Milli-Q water; the SyPyk2 reaction was coupled with lactate dehydrogenase (LDH) from a pig heart (Wako Chemicals, Osaka, Japan) reaction and measured at 30 °C or 55 °C by monitoring NADH oxidation at 340 nm in a final volume of 1 mL. The experiments were performed using 1.88 pmol of the recombinant SyPyk2 proteins. We measured SyPyk2 activity at an intracellular condition of 30 °C and pH 7.8 (Inoue et al. 2001; Nakamura et al. 2021). Unless otherwise indicated, the assay conditions for SyPyk2 were 100 mM Tris–HCl (pH 7.8) or 100 mM MES–NaOH (pH 7.0), 15 mM MgCl₂ or 5 mM MnCl₂, 100 mM KCl, 0.2 mM NADH, 2 mM ADP-2Na, 15 units/mL desalted LDH from pig heart, and 5 mM PEP–Na. All measurements were performed using 15 mM Mg²⁺ except where indicated. One unit of SyPyk2 activity was defined as the oxidation of 1 µmol NADH per minute

produced. Each effector was added 0.1 mM each: glucose-6-phosphate-2Na (G6P); fructose-6-phosphate-2Na (F6P); fructose-1, 6-bisphosphate-3Na (FBP); ribose-5-phosphate-2Na (R5P); 6-phospho-D-gluconate (6PG); adenosine monophosphate-Na (AMP); adenosine diphosphate-2Na (ADP); adenosine triphosphate-2Na (ATP); citrate-3Na; 2-oxoglutarate (2OG); succinate-2Na; fumarate; malate-Na. The results were plotted as a graph of the reaction rate to substrate and coenzyme concentration. K_m and V_{max} values were calculated by curve fitting using Kaleida Graph ver. 4.5 software and k_{cat} were calculated from the V_{max} .

Statistical analyses

Paired two-tailed Student's *t*-tests were performed to calculate the *P*-values using Microsoft Excel for Windows (Redmond, WA, USA). All experiments were conducted independently in triplicate.

Results

Purification of SyPyk2 and determination of optimal temperature and pH

We expressed GST-tagged SyPyk2 proteins in *E. coli* BL21 and purified them using affinity chromatography (Fig. 2a). SyPyk2 activity for PEP was the highest in MES–NaOH buffer at pH 7.0 and temperature 55 °C (Fig. 2b and c). The experiments measured at pH 8.5 and 9.0 Tri–HCl using Mn²⁺ was precipitated (Fig. 2b). Following this, SyPyk2 activities for PEP were measured under optimal conditions (55 °C and pH 7.0) or intracellular conditions (30 °C and pH 7.8).

Dependence SyPyk2 cations for catalytic activity

Similar to the other bacterial Pyks (Waygood and Sanwal 1974; Kapoor and Venkitasubramanian 1983; Wu and Turpin 1992; Snášel and Pichová 2019), SyPyk2 activity was dependent on divalent cations such as Mg²⁺ or Mn²⁺, and the V_{max} (maximum reaction velocity) of SyPyk2 activity in the presence of Mn²⁺ was half of that in the presence of Mg²⁺ (Figs. 3, 4a, and b). The activity of SyPyk2 was higher in the presence of divalent cations than in the presence of monovalent cations, and its activation by monovalent cations was not K⁺-specific (Fig. 3). We determined the kinetic parameters of SyPyk2 with respect to its dependence on Mg²⁺ and Mn²⁺. Under optimal conditions, the K_m (half-saturation concentration) value of SyPyk2 for Mg²⁺ and Mn²⁺ dependence was 3.54 ± 0.61 and 0.296 ± 0.02 mM, respectively (Fig. 4a and b). Under intracellular conditions, the K_m value of SyPyk2 for Mg²⁺ and Mn²⁺ dependence was 6.70 ± 0.26 and 2.18 ± 0.51 mM, respectively (Fig. 4a and

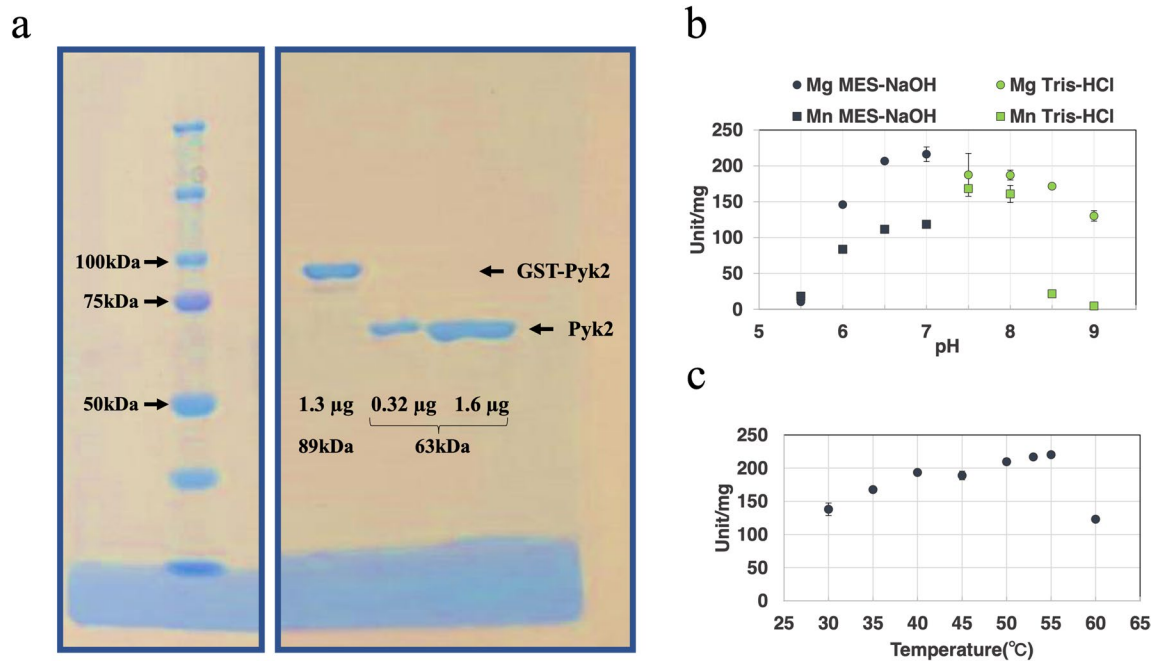


Fig. 2 Sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE) and optimal pH and temperature for *Synechocystis* pyruvate kinase 2 (SyPyk2). **a** Purified GST-tagged SyPyk2 (89 kDa) and untagged SyPyk2 (63 kDa) proteins. GST-Pyk2 indicated GST-tagged SyPyk2, and Pyk2 indicated untagged SyPyk2. The gel was prepared using 8% (w/v) acrylamide and stained with Quick Blue G250. Optimum pH and temperature for SyPyk2. **b** Effects of the pH on SyPyk2 activity. The circle and square represented Mg^{2+} and Mn^{2+} , respectively. Blue and green represented the buffer MES-NaOH and Tris-HCl, respectively. The concentrations of phospho-

enolpyruvate (PEP), adenosine diphosphate (ADP), and KCl were fixed at 5.0, 2.0, and 100 mM, respectively. The experiments of Mn^{2+} measured at pH 8.5 and 9.0 Tris-HCl was precipitated. The mean \pm SD values were calculated from three independent experiments. **c** The effects of temperature on SyPyk2 activity. This experiment was measured in MES-NaOH buffer pH 7.0, and 15 mM Mg^{2+} of the cofactor was used. PEP, ADP, and KCl concentrations were fixed at 5.0, 2.0, and 100 mM, respectively. The mean \pm SD values were calculated from three independent experiments

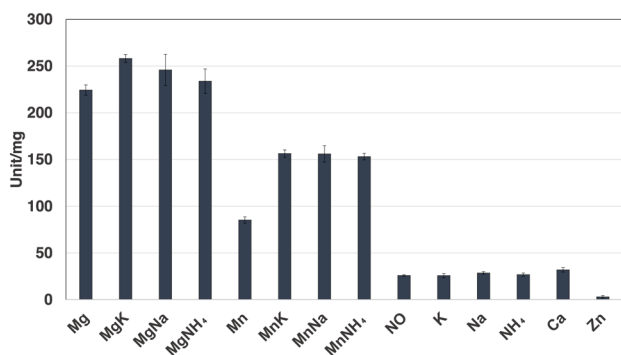


Fig. 3 Effects of cofactor monovalent and divalent cations for *Synechocystis* pyruvate kinase 2 (SyPyk2) activity. The monovalent and divalent cations were fixed at 100 and 5 mM, respectively, except for $MgCl_2$ and $ZnCl_2$ fixed at 15 and 0.5 mM. The experiment was performed using 100 mM MES-NaOH buffer (pH 7.0) at 55 °C. The concentrations of PEP and ADP were fixed at 5.0 and 2.0 mM, respectively. The mean \pm SD values were calculated from three independent experiments. K, KCl; Na, NaCl₂; NH₄, NH₄Cl; Mg, $MgCl_2 \cdot 6H_2O$; Mn, $MnCl_2 \cdot 4H_2O$; Ca, CaCl₂; Zn, $ZnSO_4 \cdot 7H_2O$

b). The K_m value of *Synechococcus* Pyk and *Synechocystis* PEPC for Mg^{2+} dependence were 2.9 and 4.27 ± 0.46 mM, respectively (Knowles et al. 2001; Scholl et al. 2020). Thus, we defined that the optimum conditions for SyPyk2 were 15 mM $MgCl_2$ and 5 mM $MnCl_2$.

Determination of kinetic parameters of SyPyk2

We measured the kinetic parameters of SyPyk2 for PEP and ADP under optimal conditions. The saturation curves of SyPyk2 for PEP displayed a sigmoidal curve with V_{max} and K_m of 241 ± 10.5 unit/mg and 1.53 ± 0.07 mM, respectively, and a Hill coefficient of 3.10 ± 0.11 , indicating positive homotropic cooperativity (Fig. 5a and Table 1). The saturation curves of SyPyk2 for ADP followed a hyperbolic (Michaelis–Menten) curve with V_{max} and K_m of 239 ± 6 unit/mg and 0.0527 ± 0.0075 mM, respectively (Fig. 5b and Table 1). The saturation curves of SyPyk2 for PEP and ADP under intracellular conditions were determined. The saturation curves of SyPyk2 for PEP showed a sigmoidal curve with V_{max} and K_m of 119 ± 7 unit/mg and 2.54 ± 0.12 mM, respectively, and a Hill coefficient of 2.60 ± 0.18 ,

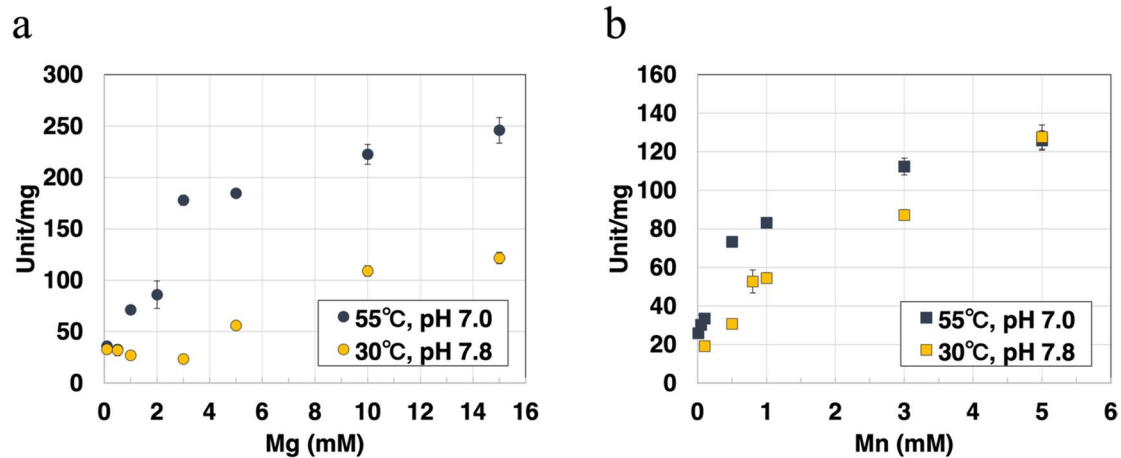


Fig. 4 *Synechocystis* pyruvate kinase 2 (SyPyk2) activity at different concentrations of $MgCl_2$ (a) and $MnCl_2$ (b). These experiments were performed under optimum conditions at 55 °C and pH 7.0 in MES-NaOH buffer (blue) or intracellular conditions at 30 °C and pH 7.8

in Tris–HCl buffer (yellow). These experiments fixed the phosphoenolpyruvate (PEP), adenosine diphosphate (ADP), and KCl concentrations at 5.0, 2.0, and 100 mM, respectively. The mean \pm SD values were calculated from three independent experiments

suggesting positive homotropic cooperativity (Fig. 5a and Table 1). The saturation curves of SyPyk2 for ADP exhibited a hyperbolic curve with V_{max} and K_m of 80.3 ± 5.3 Unit/mg and 0.0602 ± 0.0081 mM, respectively (Fig. 5b and Table 1). Similar to *Synechococcus* Pyk and other bacterial Pyks, the saturation curves of SyPyk2 for PEP showed sigmoidal curves (Knowles et al. 2001; Jetten et al. 1994; Abdelhamid et al. 2019; 2021), and for ADP, hyperbolic curves (Abdelhamid et al. 2019; 2021). Additionally, we measured the activity of SyPyk2 at 30 °C and pH 7.0; the conditions were optimal for *Synechocystis* PEPC (Takeya et al. 2017) and competed with SyPyk2 for PEP consumption. The saturation

curves of SyPyk2 for PEP displayed a sigmoidal curve with V_{max} and K_m of 132 ± 5 unit/mg and 2.36 ± 0.2 mM, respectively, and a Hill coefficient of 2.61 ± 0.18 , indicating positive homotropic cooperativity and intracellular conditions (Supplemental Fig. 1a and Table 2). The saturation curves of ADP followed a hyperbolic curve with V_{max} and K_m of 123 ± 9 unit/mg and 0.111 ± 0.017 mM, respectively (Supplemental Fig. 1b and Table 2). In these conditions, the K_m value of SyPyk2 for PEP was approximately 30-, 40-, or 20-fold higher than that of SyPyk2 for ADP under optimum, intracellular, and optimum for *Synechocystis* PEPC conditions, respectively (Tables 1 and 2). The K_m value of SyPyk2

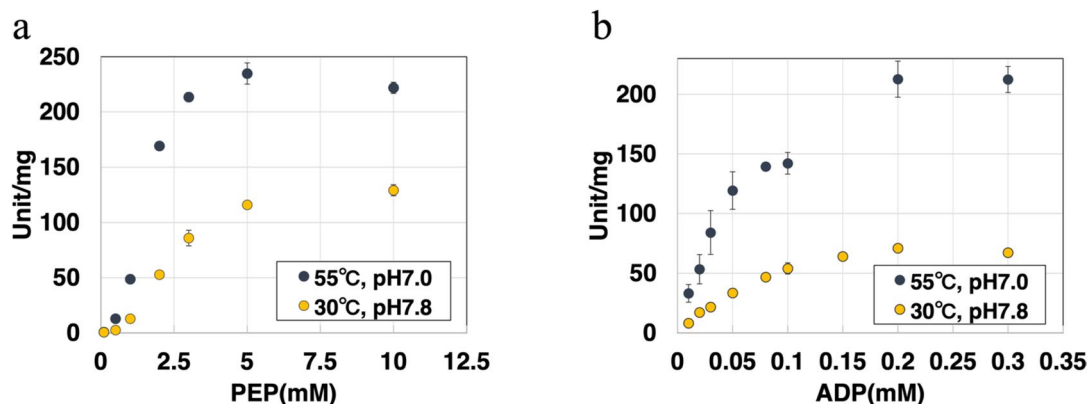


Fig. 5 Saturation curves of *Synechocystis* pyruvate kinase 2 (SyPyk2) for phosphoenolpyruvate (PEP) and adenosine diphosphate (ADP). a The saturation curves of SyPyk2 for PEP. These measurements were performed in an optimum condition at 55 °C and pH 7.0 in MES-NaOH buffer (blue) or an intracellular condition of 30 °C and pH 7.8 in Tris–HCl (yellow). The ADP concentration was 2.0 mM. The mean \pm SD values were calculated from three independent experi-

ments. b The saturation curves of SyPyk2 for ADP. These measurements were performed in an optimum condition at 55 °C and pH 7.0 in MES-NaOH buffer (blue) or an intracellular condition of 30 °C and pH 7.8 in Tris–HCl (yellow). The PEP concentration was 5 mM. The concentrations of KCl and $MgCl_2$ were 100 and 15 mM, respectively. The mean \pm SD values were calculated from three independent experiments

Table 1 Kinetic parameters of pyruvate kinase 2 under optimal and intracellular conditions

	V_{\max} (Unit/mg)	K_m (mM)	k_{cat} (s^{-1})	k_{cat}/K_m ($\text{s}^{-1} \text{mM}^{-1}$)	n_H
PEP (55 °C, pH 7.0)	241 ± 10.5	1.53 ± 0.07	253 ± 11	166 ± 3	3.10 ± 0.11
ADP (55 °C, pH 7.0)	238 ± 5	0.0527 ± 0.0076	251 ± 6	4837 ± 733	1.25 ± 0.11
PEP	119 ± 7	2.54 ± 0.118	126 ± 8	49.4 ± 1.2	2.64 ± 0.18
ADP	80.3 ± 5.3	0.0602 ± 0.0081	84.5 ± 5.6	1411 ± 100	1.37 ± 0.24
PEP + ATP	107 ± 5	2.74 ± 0.09	114 ± 5	41.2 ± 0.4	3.06 ± 0.65
PEP + G6P	122 ± 5	0.607 ± 0.009	128 ± 5	212 ± 9	2.00 ± 0.10
PEP + G6P & ATP	130 ± 30	0.62 ± 0.22	137 ± 31	227 ± 25	1.77 ± 0.36
PEP + R5P	125 ± 18	0.548 ± 0.132	131 ± 19	243 ± 29	1.41 ± 0.15
PEP + R5P & ATP	83.0 ± 7.2	0.613 ± 0.100	91.9 ± 7.6	151 ± 10	1.66 ± 0.22

The kinetic parameters of the activity of *Synechocystis* pyruvate kinase 2 (SyPyk2) in the presence of activators (glucose-6-phosphate, G6P and ribose-5-phosphate, R5P) or inhibitor (adenosine triphosphate, ATP) and coexisting metabolites. All experiments were performed under intracellular conditions of 30 °C and pH 7.8 in Tris–HCl buffer, except for those marked as 55 °C and pH 7.0 in MES–NaOH buffer. Each kinetic parameter is explained as follows: V_{\max} (maximum reaction velocity); K_m , half-saturation concentration; k_{cat} , turnover number; k_{cat}/K_m , catalytic efficiency; n_H , Hill coefficient. Mean ± SD values were calculated from three independent experiments

Table 2 Kinetic parameters of *Synechocystis* pyruvate kinase 2 and PEPC under optimal conditions for *Synechocystis* PEPC

	V_{\max} (Unit/mg)	K_m (mM)	k_{cat} (s^{-1})	k_{cat}/K_m ($\text{s}^{-1} \text{mM}^{-1}$)	n_H
PEP (30 °C, pH 7.0)	132 ± 5	2.36 ± 0.20	139 ± 5	59.1 ± 3.1	2.61 ± 0.17
ADP (30 °C, pH 7.0)	123 ± 9	0.111 ± 0.017	130 ± 9	1179 ± 90	0.76 ± 0.04
<i>Synechocystis</i> PEPC (Takeya et al. 2017) (30 °C, pH 7.0)	1.74	0.34	na	na	na
<i>Synechocystis</i> PEPC (Scholl et al. 2020) (28 °C, pH 8.0)	24.2 ± 2.30	0.88 ± 0.15	48.71 ± 4.63	na	na

This table shows the kinetic parameters of the activity of *Synechocystis* pyruvate kinase 2 (SyPyk2) under optimal conditions for *Synechocystis* phosphoenolpyruvate carboxylase (PEPC) at 30 °C and pH 7.0 (Takeya et al. 2017). The experiments SyPyk2 were performed at 30 °C and pH 7.0 in MES–NaOH buffer. Each kinetic parameter is explained as follows: V_{\max} (maximum reaction velocity); K_m , half-saturation concentration; k_{cat} , turnover number; k_{cat}/K_m , catalytic efficiency; n_H , Hill coefficient; na, data not available. The mean ± SD values were calculated from three independent experiments

for ADP was half of that of *Synechococcus* Pyk, and the K_m value of SyPyk2 for PEP was 5-fold higher than that of *Synechococcus* Pyk (Knowles et al. 2001). Compared with the K_m value of *Synechocystis* PEPC (0.34 mM: Takeya et al. 2017, 0.88 mM: Scholl et al. 2020) for PEP, SyPyk2 required more than 2-fold PEP (Tables 1 and 2).

Activation and inhibition of SyPyk2 by sugar phosphates and organic acids

We measured the relative catalytic activity of SyPyk2 for PEP in the presence of sugar phosphates from the EMP/gluconeogenesis and OPP pathways at 1 mM, and PEP and ADP was fixed at K_m (2.5 mM) and 2 mM respectively, under intracellular conditions. The effectors did not affect LDH (coupled enzyme) used in the experiment. Additionally, several effector metabolites known to inhibit Pyk from the TCA cycle, such as citrate and 2OG, were added at 1 mM

under optimum conditions (Wu and Turpin 1992; Knowles et al. 2001). Under optimal conditions, SyPyk2 was activated by 1 mM G6P and R5P up to 200 and 150%, respectively, and inhibited down to 75% by ATP (Fig. 6). Under intracellular conditions, SyPyk2 was activated in the presence of 1 mM G6P and R5P by 150 and 125%, respectively, and inhibited in the presence of ATP by up to 75% (Fig. 6). Unlike *Synechococcus* Pyk and green alga, *Chlamydomonas reinhardtii* Pyk, SyPyk2 was not activated by AMP or F6P and not inhibited by the TCA cycle metabolites, such as citrate, 2OG, and malate (Fig. 6; Wu and Turpin 1992; Knowles et al. 2001).

Furthermore, we calculated the kinetic parameters of SyPyk2 for PEP in the presence of activators or inhibitors under intracellular conditions. The saturation curves of SyPyk2 for PEP in the presence of G6P revealed a hyperbolic curve with V_{\max} and K_m of 122 ± 5 unit/mg and 0.607 ± 0.01 mM, respectively, and a Hill coefficient

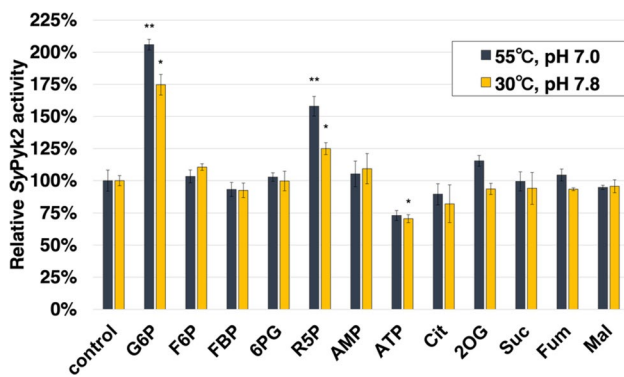


Fig. 6 Effects of effectors for *Synechocystis* pyruvate kinase 2 (SyPyk2) activity. The effects of various metabolites on the activity SyPyk2. These experiments measured optimum conditions at 55 °C and pH 7.0 in MES-NaOH buffer (left blue bar) and intracellular conditions at 30 °C and pH 7.8 in Tris-HCl buffer (right yellow bar). The mean \pm SD values were calculated from three independent experiments. The concentration of PEP and ADP were fixed at K_m (2.5 mM) and 2.0 mM, respectively. In the measurements of the saturation curves of SyPyk2, the concentrations of KCl and MgCl₂ were 100 and 15 mM, respectively. The concentration of several effectors was 1.0 mM. G6P, glucose-6-phosphate-2Na; F6P, fructose-6-phosphate-2Na; FBP, fructose-1, 6-bisphosphate-3Na; R5P, ribose-5-phosphate-2Na; 6PG, 6-phospho-D-gluconate; AMP, adenosine monophosphate-Na; ADP, adenosine diphosphate-2Na; ATP, adenosine triphosphate-2Na; Cit, citrate-3Na; 2OG, 2-oxoglutarate; Suc, succinate-2Na; Fum: fumarate, Mal: malate-Na. The asterisks indicated significant differences between the absence and presence of the salt (Student's *t*-test; * $P < 0.01$, ** $P < 0.005$)

of 2.0 ± 0.1 , indicating G6P converting SyPyk2 from sigmoidal to hyperbolic kinetics (Fig. 7a and Table 1). The enzymatic activities of SyPyk2 for PEP in the presence of R5P displayed a hyperbolic curve with V_{max} and K_m of 125 ± 18 unit/mg and 0.548 ± 0.132 mM, respectively, and a Hill coefficient of 1.4 ± 0.2 , indicating R5P altering SyPyk2 from sigmoidal to hyperbolic kinetics (Fig. 7a and Table 1). Similar to *Synechococcus* Pyk, G6P and R5P decreased the K_m value of SyPyk2 for PEP to one-fifth of its value (Knowles et al. 2001 and Table 1). Moreover, the K_m value of SyPyk2 was increased by ATP from 2.54 to 2.73 mM (Fig. 7b and Table 1). To demonstrate the effects of ATP for SyPyk2, we calculated the kinetic parameters of SyPyk2 for PEP in the presence of ATP and either G6P or R5P under intracellular conditions (Fig. 7a and b). G6P, R5P, and ATP concentrations were fixed at 1 mM. The saturation curves of SyPyk2 for PEP in the presence of ATP and G6P revealed a hyperbolic curve with V_{max} and K_m of 130 ± 29.5 unit/mg and 0.619 ± 0.022 mM, respectively, and a Hill coefficient of 1.73 ± 0.36 (Fig. 7a and b, and Table 1). The enzymatic activities of SyPyk2 for PEP in the presence of ATP and R5P displayed a hyperbolic curve with V_{max} and K_m of 84.0 ± 7.08 unit/mg and 0.572 ± 0.111 mM, respectively, and a Hill coefficient of 1.89 ± 0.41 (Fig. 7a and b and Table 1). G6P and R5P relieved the effects of ATP (Fig. 7b). Additionally, the IC_{50} (median inhibition concentration) of ATP for SyPyk2 was 4.1 mM (Supplemental Fig. 2), which was approximately 3-fold higher than that of *Synechococcus* Pyk (1.5 mM, Knowles et al. 2001). G6P and R5P increased the

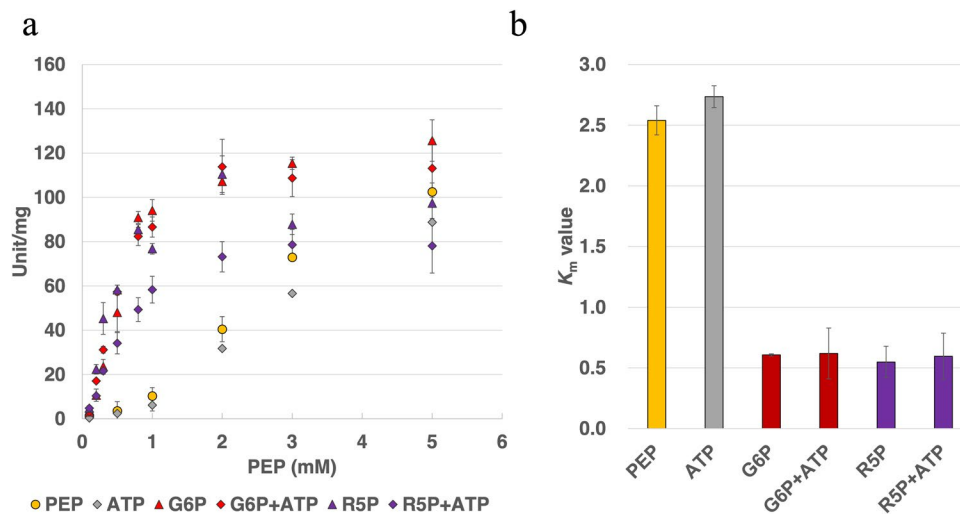


Fig. 7 a Influence of several effectors for *Synechocystis* pyruvate kinase 2 (SyPyk2) activity. Circles (blue) indicated the phosphoenolpyruvate (PEP) saturation curve, squares (red and purple) indicated 1.0 mM of glucose-6-phosphate (G6P) and ribose-5-phosphate (R5P), diamonds (gray) indicated 1.0 mM of adenosine triphosphate (ATP) added, and red or purple diamonds indicated the presence of

G6P and R5P with ATP added respectively. The mean \pm SD values were calculated from three independent experiments. **b** This figure shows the K_m value of SyPyk2 for PEP in the presence of G6P, R5P, and ATP, coexisting intracellular conditions of 30 °C and pH 7.8 in Tris-HCl buffer. The mean \pm SD values were calculated from three independent experiments

affinity of SyPyk2 for PEP and remained unaltered in the presence of AMP, F6P, or FBP (Figs. 6, 7a, and b, Table 1).

Discussion

This study demonstrated the properties of SyPyk2 via biochemical analysis, with G6P and R5P increasing the affinity of SyPyk2 for PEP *in vitro*. The optimum pH and temperature of Pyks were discovered in bacteria (Chai et al. 2016; Kapoor and Venkatasubramanian 1983; Abbe and Yamada 1982). The optimum pH of Pyks displayed a wide peak range, from acidic to alkaline (Chai et al. 2016; Abbe and Yamada 1982). For *Synechococcus* Pyk, the optimal pH ranged from 6.0 to 7.8, and it was active in the dark (Knowles et al. 2001). The intracellular pH of *Synechocystis* under the photoautotrophic condition was 7.8 (Nakamura et al. 2021), and light to dark transition decreases the intracellular pH of other cyanobacteria from alkaline to neutral (Falkner et al. 1976; Mangan et al. 2016). Thus, the broad pH range of SyPyk2 indicated that SyPyk2 could act on PEP consumption under any cultivation conditions. The optimum temperature of SyPyk2 was 55 °C (Fig. 2c). *Synechocystis* grows at ~30 °C (Inoue et al. 2001), and the optimum temperature of SyPyk2 is higher than that of the cultivation conditions (Fig. 2c). Although for a short time 5 min, *Synechocystis* is viable up to 54 °C (Inoue et al. 2001). Under heat shock conditions, ATP plays a crucial role in protein maintenance through chaperones (Soini et al. 2005). The gene expression of *pyk2* increases during heat shocks (Slabas et al. 2006), and hence, SyPyk2 may contribute to ATP production by increasing its enzymatic activity.

Pyks have been studied for their properties and primary sequences (Hunsley and Suelter 1969; Cottam et al. 1969; Abdelhamid et al. 2019; 2021). All Pyks require divalent cations, such as Mg²⁺ or Mn²⁺, and numerous Pyks require K⁺ for activity (Baek and Nowak 1982; Kachmar and Boyer 1953). SyPyk2 showed Mg²⁺- and Mn²⁺-dependent activity and other bacterial Pyks, and its activity was stimulated by monovalent cations, such as K⁺, Na⁺, or NH₄⁺ (Fig. 3). Bacterial Pyks are classified into two types: PykA, which is stimulated by sugar monophosphates, such as AMP, G6P, and R5P, and PykF, activated by sugar diphosphates, such as FBP in *E. coli* (Kornberg and Malcovati 1973; Waygood et al. 1975, 1976). Moreover, SyPyk2 is classified as PykF (Kaneko et al. 1996). *In silico* analysis suggests that two isozymes, Pyk1 and Pyk2 have the same allosteric sites for G6P, R5P, FBP, AMP, and ATP (Haghighi 2021). Pyks containing Pyk1 and Pyk2 from *Synechocystis* cells are activated by G6P, F6P, R5P, and AMP but not by FBP (Knowles and Plaxton 2003). Based on these findings, we demonstrated the regulation

of SyPyk2 by adding various metabolites from the OPP pathway, EMP/gluconeogenesis pathway, and TCA cycle (Fig. 7a). Our findings reveal a decrease in the K_m value of SyPyk2 with K-type characteristics, indicative of altered substrate affinity and allosteric activation by G6P and R5P (Fig. 7b and Table 1). Our results suggest that G6P and R5P may also activate SyPyk1. Therefore, SyPyk2 is dependent on divalent cations, such as Mg²⁺ and Mn²⁺, and is classified as PykA type rather than PykF, stimulated by sugar monophosphates, such as G6P and R5P, but not by AMP.

The K_m values of SyPyk2 for PEP were 40-fold higher than ADP, indicating a higher requirement for PEP in its enzymatic reaction than ADP under intracellular conditions (Table 1). The K_m value of *Synechococcus* Pyk for PEP is higher than that for ADP (Knowles et al. 2001). The K_m value of SyPyk2 for PEP is higher than *Synechococcus* Pyk 5-fold (Table 1 and Knowles et al. 2001). Additionally, the absolute concentration of ADP in *Synechocystis* cells is three times higher than that of PEP (Dempo et al. 2014). These data indicate that these two Pyk enzymes, *Synechocystis* and *Synechococcus*, are limited by PEP concentration in their reactions under photosynthetic conditions. However, its mechanism is different. *Synechococcus* Pyk has high PEP affinity and allosteric inhibition by citrate and ATP (Knowles et al. 2001). *Synechocystis* has a low affinity and not inhibited by either citrate or ATP (Table 1 and Fig. 6). Thus, these findings suggested that the availability of PEP limited the enzymatic activity of SyPyk2 for the flux of PEP to pyruvate via SyPyk2 under photosynthetic conditions.

Rapid glycogen catabolism induces glucan polymer such as G6P and signaling metabolites such as 2OG occur during nitrogen depletion (Joseph et al. 2014), indicating that G6P may activate SyPyk2. Although *Synechococcus* Pyk is repressed by 2OG, SyPyk2 is not (Fig. 6). However, a previous study reveals that *pyk1* expression is induced 3.5-fold, and *pyk2* expression is reduced by half during nitrogen-deficient conditions (Osanai et al. 2006). Hence, these findings indicate that to provide a carbon source to the TCA cycle for 2OG production, SyPyk2 may act during the initial stages of nitrogen depletion through G6P and R5P activation and then be replaced with SyPyk1. Furthermore, *pyk1* is regulated by several nitrogen-related regulators such as SigE, Rre37 thorough with NtcA (Giner-Lamia et al. 2017; Iijima et al. 2014; Osanai et al. 2005). Therefore, in *Synechocystis*, we consider SyPyk1 and SyPyk2 to mainly function as pyruvate kinase during the late and initial nitrogen depletion stages, respectively.

In comparison to the K_m value of PEP for *Synechocystis* PEPC (0.34 mM: Takeya et al. 2017; 0.88 mM: Scholl et al. 2020 and Table 2), SyPyk2 (2.54 mM, Table 1) required more than 2-fold higher concentration of PEP (Tables 1 and 2). The K_m value of SyPyk2 for PEP was decreased from

2.54 to 0.607 or 0.548 mM by G6P or R5P, respectively (Fig. 7a and b and Table 1). The higher PEP requirement and the enhanced affinity of SyPyk2 for PEP by G6P and R5P, suggesting a role for SyPyk2 in *Synechocystis* cells. In a previous study, Pyk from *Synechocystis* demonstrated a higher Pyk activity under heterotrophic conditions than under photoautotrophic and mixotrophic conditions (Knowles and Plaxton 2003). Recently, ME, which generates pyruvate from malate by the ME-dependent TCA cycle, was reportedly active under photoautotrophic conditions (Katayama et al. 2022), indicating that pyruvate is synthesized by ME and not by Pyk (Bricker et al. 2004; Qian et al. 2018). The pathway involving PEPC, MDH, and ME constitutes an alternate route for pyruvate formation in *Synechocystis* cells under photosynthetic conditions (You et al. 2014; Bricker et al. 2004). ATP functions as an inhibitor of *Synechococcus* Pyk, which is the homolog of SyPyk2 (Knowles et al. 2001). This observation suggests that the lack of Pyk flux under photosynthetic conditions can be attributed to ATP inhibition (Bricker et al. 2004). In *E. coli*, the intracellular concentration of ATP is suggested to be 0.6 mM (Boecker et al. 2019) and not much different from *Synechocystis* (Wan et al. 2017). G6P and ATP exhibit comparable concentrations, approximately 1.84×10^0 and 2.14×10^0 $\mu\text{mol/g-dry cell weight}$, respectively (Dempo et al. 2014). R5P is one-tenth of the concentration of ATP, amounting to 1.95×10^{-1} $\mu\text{mol/g-dry cell}$ (Dempo et al. 2014). Hence, to demonstrate the in vivo effects of metabolites, we maintained uniform effector concentrations at 1 mM. Inhibition by 1 mM ATP decreased the V_{max} and increased the K_m value of SyPyk2 activity (Table 1 and Fig. 7b). The V_{max} of SyPyk2 for PEP decreased from 119 ± 7 to 107 ± 5 , and the K_m value of SyPyk2 for PEP increased from 2.54 to 2.74 mM (1.07-fold) (Fig. 7b and Table 1). In comparison, the K_m value of *Synechococcus* Pyk increased from 0.54 to 0.75 mM (1.37-fold) by 0.5 mM ATP (Knowles et al. 2001). Furthermore, compared to the IC_{50} of *Synechococcus* Pyk for ATP (1.5 mM: Knowles et al. 2001), SyPyk2 (4.1 mM: Supplemental Fig. 2) was approximately 3-fold higher, indicating that SyPyk2 is less affected by ATP than *Synechococcus* Pyk. Additionally, the presence of G6P and R5P alleviated the inhibitory effects of ATP, reducing the K_m value of the substrate concentration to approximately one-fifth (Fig. 7a and b). Our results showed that the effects of ATP on SyPyk2 are less potent than those of G6P and R5P. Considering the IC_{50} and the slight increase in the K_m value by ATP, it suggests that SyPyk2 is less influenced by ATP. Therefore, we conclude that the low flux of PEP to pyruvate via Pyk is due to its extremely low affinity for PEP (Tables 1 and 2; Knowles et al. 2001) and the absence of activators such as G6P and R5P under photosynthetic conditions.

The flux through the OPP pathway increases under nonphotosynthetic conditions (Wan et al. 2017) relative

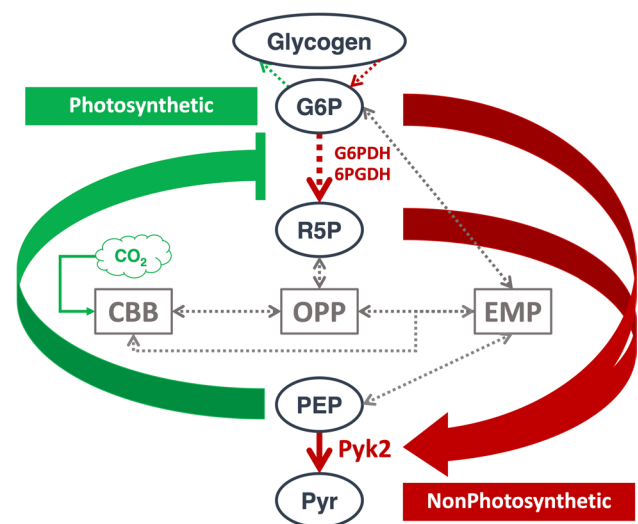


Fig. 8 Model of glucose-6-phosphate (G6P), ribose-5-phosphate (R5P) and phosphoenolpyruvate (PEP) regulation of carbon flow under photosynthetic or nonphotosynthetic conditions in *Synechocystis* sp. PCC 6803. EMP, Embden–Meyerhof–Parnas pathway; OPP, oxidative pentose phosphate pathway; CBB, Calvin Benson Bassham cycle; Pyr, pyruvate; G6PDH, glucose-6-phosphate dehydrogenase; 6PGDH, 6-phosphogluconate dehydrogenase; Pyk2, pyruvate kinase 2

to photosynthetic conditions (Young et al. 2011), indicating a significant elevation in the levels of G6P and R5P under nonphotosynthetic conditions. Moreover, PEP increases and decreases under photosynthetic and nonphotosynthetic conditions, respectively (Werner et al. 2019). Consequently, the accumulation of G6P and R5P under nonphotosynthetic conditions upregulates the SyPyk2 reaction. Following SyPyk2 activation in the presence of G6P and R5P, PEP is consumed by SyPyk2, alleviating glucose-6-phosphate dehydrogenase (G6PDH encoded by *zwf*, *slr1843*) inhibition, a rate-limiting enzyme of the OPP pathway (Ito and Osanai 2020). Furthermore, PEP consumption via SyPyk2 activating relieving the inhibition of 6-phosphogluconate dehydrogenase (6PGDH encoded by *gnd*, *slr10329*) (Ito and Osanai, 2018), an enzyme involved in the third reaction of the OPP pathway (Fig. 8). In this feedforward regulation, SyPyk2 primarily acts as relieving the sugar catabolic repression under nonphotosynthetic conditions.

This study offers valuable insights into the biosynthesis and fermentation of metabolites associated with pyruvate metabolism, particularly PEP consumption in *Synechocystis*.

This study demonstrated that the regulation of SyPyk2 is dependent on PEP accumulation, the presence of G6P, R5P, and divalent cations, such as Mg^{2+} and Mn^{2+} , rather than pH and ATP. Therefore, our experiments indicated that SyPyk2 contributed less to PEP consumption under

photosynthetic conditions and that it plays a pivotal role in sugar catabolism under nonphotosynthetic conditions in response to sugar phosphate accumulation.

Supplementary Information The online version contains supplementary material available at <https://doi.org/10.1007/s11103-023-01401-0>.

Author contributions MK designed the study, performed the experiments, analyzed the data, and wrote the manuscript. NK analyzed the data. TO analyzed the data and wrote the manuscript.

Funding Open Access funding provided by Meiji University. This work was supported by the following grants to TO: JSPS KAKENHI Grant-in-Aid for Scientific Research (B) (Grant Number 20H02905) and JST-ALCA of the Japan Science and Technology Agency (Grant Number JPMJAL1306).

Data availability Not applicable.

Declarations

Competing interest The authors declare no competing interests.

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>.

References

- Abbe K, Yamada T (1982) Purification and properties of pyruvate kinase from *Streptococcus mutans*. *J Bacteriol* 149:299–305. <https://doi.org/10.1128/jb.149.1.299-305.1982>
- Abdelhamid Y, Brear P, Greenhalgh J, Chee X, Rahman T, Welch M (2019) Evolutionary plasticity in the allosteric regulator-binding site of pyruvate kinase isoform PykA from *Pseudomonas aeruginosa*. *J Biol Chem* 294:15505–15516. <https://doi.org/10.1074/jbc.RA119.009156>
- Abdelhamid Y, Wang M, Parkhill SL, Brear P, Chee X, Rahman T, Welch M (2021) Structure, function and regulation of a second pyruvate kinase isozyme in *Pseudomonas aeruginosa*. *Front Microbiol* 12:790742. <https://doi.org/10.3389/fmicb.2021.790742>
- Abernathy MH, Yu J, Ma F, Liberton M, Ungerer J, Hollinshead WD, Gopalakrishnan S, He L, Maranas CD, Pakrasi HB, Allen DK, Tang YJ (2017) Deciphering cyanobacterial phenotypes for fast photoautotrophic growth via isotopically nonstationary metabolic flux analysis. *Biotechnol Biofuels* 10:273. <https://doi.org/10.1186/s13068-017-0958-y>
- Allison W, Corey DB, Ashok P, Christie AMP (2019) A comprehensive time-course metabolite profiling of the model cyanobacterium *Synechocystis* sp. PCC 6803 under diurnal light:dark cycles
- Angermayr SA, van der Woude AD, Correddu D, Vreugdenhil A, Verzone V, Hellingwerf KJ (2014) Exploring metabolic engineering design principles for the photosynthetic production of lactic acid by *Synechocystis* sp. PCC6803. *Biotechnol Biofuels* 7:99. <https://doi.org/10.1186/1754-6834-7-99>
- Baek YH, Nowak T (1982) Kinetic evidence for a dual cation role for muscle pyruvate kinase. *Arch Biochem Biophys* 217:491–497. [https://doi.org/10.1016/0003-9861\(82\)90529-x](https://doi.org/10.1016/0003-9861(82)90529-x)
- Boecker S, Zahoor A, Schramm T, Link H, Klant S (2019) Broadening the scope of enforced ATP wasting as a tool for metabolic engineering in *Escherichia coli*. *Biotechnol J* 14:1800438. <https://doi.org/10.1002/biot.201800438>
- Bricker TM, Zhang S, Laborde SM, Mayer PR 3rd, Frankel LK, Moroney JV (2004) The malic enzyme is required for optimal photoautotrophic growth of *Synechocystis* sp. strain PCC 6803 under continuous light but not under a diurnal light regimen. *J Bacteriol* 186:8144–8148. <https://doi.org/10.1128/JB.186.23.8144-8148>
- Carpine R, Du W, Olivieri G, Pollio A, Hellingwerf KJ, Marzocchella A, dos Santos FB (2017) Genetic engineering of *Synechocystis* sp. PCC6803 for poly- β -hydroxybutyrate overproduction. *Algal Res* 25:117–127. <https://doi.org/10.1016/j.algal.2017.05.013>
- Chai X, Shang X, Zhang Y, Liu S, Liang Y, Zhang Y, Wen T (2016) A novel pyruvate kinase and its application in lactic acid production under oxygen deprivation in *Corynebacterium glutamicum*. *BMC Biotechnol* 16:79. <https://doi.org/10.1186/s12896-016-0313-6>
- Cooley JW, Vermaas WF (2001) Succinate dehydrogenase and other respiratory pathways in thylakoid membranes of *Synechocystis* sp. strain PCC 6803: capacity comparisons and physiological function. *J Bacteriol* 183:4251–4258. <https://doi.org/10.1128/JB.183.14.4251-4258.2001>
- Cottam GL, Hollenberg PF, Coon MJ (1969) Subunit structure of rabbit muscle pyruvate kinase. *J Biol Chem* 244:1481–1486. [https://doi.org/10.1016/S0021-9258\(18\)91785-0](https://doi.org/10.1016/S0021-9258(18)91785-0)
- de Alvarenga LV, Hess WR, Hagemann M (2020) AcnSP—a novel small protein regulator of aconitase activity in the cyanobacterium *Synechocystis* sp. PCC 6803. *Front Microbiol* 11:1445. <https://doi.org/10.3389/fmicb.2020.01445>
- Dempo Y, Ohta E, Nakayama Y, Bamba T, Fukusaki E (2014) Molar-based targeted metabolic profiling of cyanobacterial strains with potential for biological production. *Metabolites* 4:499–516. <https://doi.org/10.3390/metabo4020499>
- Falkner G, Horner F, Werdan K, Heldt H (1976) Concomitant changes in phosphate uptake and photophosphorylation in the blue-green *Alga Anacystis nidulans* during adaptation to phosphate deficiency. *Plant Physiol* 58:717–718. [https://doi.org/10.1016/S0176-1617\(11\)80928-4](https://doi.org/10.1016/S0176-1617(11)80928-4)
- Giner-Lamia J, Robles-Rengel R, Hernández-Prieto MA, Muro-Pastor MI, Florencio FJ, Futschik ME (2017) Identification of the direct regulon of NtcA during early acclimation to nitrogen starvation in the cyanobacterium *Synechocystis* sp. PCC 6803. *Nucleic Acids Res* 45:11800–11820. <https://doi.org/10.1093/nar/gkx860>
- Guerrero-Mendiola C, García-Trejo JJ, Encalada R, Saavedra E, Ramírez-Silva L (2017) The contribution of two isozymes to the pyruvate kinase activity of *Vibrio cholerae*: one K⁺-dependent constitutively active and another K⁺-independent with essential allosteric activation. *PLoS ONE* 12:e0178673. <https://doi.org/10.1371/journal.pone.0178673>
- Haghighi O (2021) In silico study of the structure and ligand preference of pyruvate kinases from cyanobacterium *Synechocystis* sp. PCC 6803. *Appl Biochem Biotechnol* 193:3651–3671. <https://doi.org/10.1007/s12010-021-03630-9>
- Hasunuma T, Matsuda M, Kondo A (2016) Improved sugar-free succinate production by *Synechocystis* sp. PCC 6803 following identification of the limiting steps in glycogen catabolism. *Metab Eng Commun* 3:130–141. <https://doi.org/10.1016/j.meteno.2016.04.003>

- Hasunuma T, Matsuda M, Kato Y, Vavricka CJ, Kondo A (2018) Temperature enhanced succinate production concurrent with increased central metabolism turnover in the cyanobacterium *Synechocystis* sp. PCC 6803. *Metab Eng* 48:109–120. <https://doi.org/10.1016/j.ymben.2018.05.013>
- Hauf W, Schlebusch M, Hüge J, Kopka J, Hagemann M, Forchhammer K (2013) Metabolic changes in *Synechocystis* PCC6803 upon nitrogen-starvation: excess NADPH sustains polyhydroxybutyrate accumulation. *Metabolites* 3:101–118. <https://doi.org/10.3390/metabo3010101>
- Hidese R, Matsuda M, Osanai T, Hasunuma T, Kondo A (2020) Malic enzyme facilitates D-lactate production through increased pyruvate supply during anoxic dark fermentation in *Synechocystis* sp. PCC 6803. *ACS Synth Biol* 9:260–268. <https://doi.org/10.1021/acssynbio.9b00281>
- Hunsley JR, Suelter CH (1969) Yeast pyruvate kinase. I: purification and some chemical properties. *J Biol Chem* 244:4815–4818. [https://doi.org/10.1016/S0021-9258\(18\)94276-6](https://doi.org/10.1016/S0021-9258(18)94276-6)
- Iijima H, Watanabe A, Takanobu J, Hirai MY, Osanai T (2014) rre37 overexpression alters gene expression related to the tricarboxylic acid cycle and pyruvate metabolism in *Synechocystis* sp. PCC 6803. *Sci World J* 2014:921–976. <https://doi.org/10.1155/2014/921976>
- Inoue N, Taira Y, Emi T, Yamane Y, Kashino Y, Koike H, Satoh K (2001) Acclimation to the growth temperature and the high-temperature effects on photosystem II and plasma membranes in a mesophilic cyanobacterium, *Synechocystis* sp. PCC6803. *Plant Cell Physiol* 42:1140–1148. <https://doi.org/10.1093/pcp/pce147>
- Ito S, Osanai T (2018) Single amino acid change in 6-phosphogluconate dehydrogenase from *Synechocystis* conveys higher affinity for NADP⁺ and altered mode of inhibition by NADPH. *Plant Cell Physiol* 59:2452–2461. <https://doi.org/10.1093/pcp/pcy165>
- Ito S, Osanai T (2020) Unconventional biochemical regulation of the oxidative pentose phosphate pathway in the model cyanobacterium *Synechocystis* sp. PCC 6803. *Biochem J* 477(1309–1321): <https://doi.org/10.1042/BCJ20200038>
- Ito S, Takeya M, Osanai T (2017) Substrate specificity and allosteric regulation of a D-Lactate dehydrogenase from a unicellular cyanobacterium are altered by an amino acid substitution. *Sci Rep* 7:15052. <https://doi.org/10.1038/s41598-017-15341-5>
- Ito S, Koyama N, Osanai T (2019) Citrate synthase from *Synechocystis* is a distinct class of bacterial citrate synthase. *Sci Rep* 9:6038. <https://doi.org/10.1038/s41598-019-42659-z>
- Jazmin LJ, Xu Y, Cheah YE, Adebisi AO, Johnson CH, Young JD (2017) Isotopically nonstationary ¹³C flux analysis of cyanobacterial isobutyraldehyde production. *Metab Eng* 42:9–18. <https://doi.org/10.1016/j.ymben.2017.05.001>
- Jetten MS, Gubler ME, Lee SH, Sinskey AJ (1994) Structural and functional analysis of pyruvate kinase from *Corynebacterium glutamicum*. *Appl Environ Microbiol* 60:2501–2507. <https://doi.org/10.1128/aem.60.7.2501-2507.1994>
- Joseph A, Aikawa S, Sasaki K, Teramura H, Hasunuma T, Matsuda F, Osanai T, Hirai MY, Kondo A (2014) Rre37 stimulates accumulation of 2-oxoglutarate and glycogen under nitrogen starvation in *Synechocystis* sp. PCC 6803. *FEBS Lett* 588:466–471. <https://doi.org/10.1016/j.febslet.2013.12.008>
- Kachmar JF, Boyer PD (1953) Kinetic analysis of enzyme reactions, II: the potassium activation and calcium inhibition of pyruvic phosphoferase. *J Biol Chem* 200:669–682. [https://doi.org/10.1016/S0021-9258\(18\)71413-0](https://doi.org/10.1016/S0021-9258(18)71413-0)
- Kaneko T, Sato S, Kotani H, Tanaka A, Asamizu E, Nakamura Y, Miyajima N, Hirosawa M, Sugiura M, Sasamoto S, Kimura T, Hosouchi T, Matsuno A, Akiko M, Nakazaki N, Naruo K, Okumura S, Shimpo S, Takeuchi C, Wada T, Watanabe A, Yamada M, Yasuda M, Tabata S (1996) Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. Strain PCC6803. ii. Sequence determination of the entire genome and assignment of potential protein-coding regions (supplement). *DNA Res* 3:185–209. <https://doi.org/10.1093/dnares/3.3.185>
- Kaniya Y, Kizawa A, Miyagi A, Kawai-Yamada M, Uchimiya H, Kaneko Y, Nishiyama Y, Hihara Y (2013) Deletion of the transcriptional regulator cyAbrB2 deregulates primary carbon metabolism in *Synechocystis* sp. PCC 6803. *Plant Physiol* 162:1153–1163. <https://doi.org/10.1104/pp.113.218784>
- Kapoor R, Venkatasubramanian TA (1983) Purification and properties of pyruvate kinase from *Mycobacterium smegmatis*. *Arch Biochem Biophys* 225:320–330. [https://doi.org/10.1016/0003-9861\(83\)90036-X](https://doi.org/10.1016/0003-9861(83)90036-X)
- Katayama N, Iwazumi K, Suzuki H, Osanai T, Ito S (2022) Malic enzyme, not malate dehydrogenase, mainly oxidizes malate that originates from the tricarboxylic acid cycle in cyanobacteria. *Mbio* 13:e0218722. <https://doi.org/10.1128/mbio.02187-22>
- Kayne FJ (1973) 11 pyruvate kinase. *Enzymes* 8:353–382. [https://doi.org/10.1016/S1874-6047\(08\)60071-2](https://doi.org/10.1016/S1874-6047(08)60071-2)
- Knoop H, Zilliges Y, Lockau W, Steuer R (2010) The metabolic network of *Synechocystis* sp. PCC 6803: systemic properties of autotrophic growth. *Plant Physiol* 154:410–422. <https://doi.org/10.1104/pp.110.157198>
- Knowles VL, Plaxton WC (2003) From genome to enzyme: analysis of key glycolytic and oxidative pentose-phosphate pathway enzymes in the cyanobacterium *Synechocystis* sp. PCC 6803. *Plant Cell Physiol* 44:758–763. <https://doi.org/10.1093/pcp/pcg086>
- Knowles VL, Smith CS, Smith CR, Plaxton WC (2001) Structural and regulatory properties of pyruvate kinase from the cyanobacterium *Synechococcus* PCC 6301. *J Biol Chem* 276:20966–20972. <https://doi.org/10.1074/jbc.M008878200>
- Kornberg HL, Malcovati M (1973) Control in situ of the pyruvate kinase activity of *Escherichia coli*. *FEBS Lett* 32:257–259. [https://doi.org/10.1016/0014-5793\(73\)80846-4](https://doi.org/10.1016/0014-5793(73)80846-4)
- Mangan NM, Flamholz A, Hood RD, Milo R, Savage DF (2016) pH determines the energetic efficiency of the cyanobacterial CO₂ concentrating mechanism. *Proc Natl Acad Sci USA* 113:E5354–E5362. <https://doi.org/10.1073/pnas.1525145113>
- Muro-Pastor MI, Florencio FJ (1992) Purification and properties of NADP-isocitrate dehydrogenase from the unicellular cyanobacterium *Synechocystis* sp. PCC 6803. *Eur J Biochem* 203:99–105. <https://doi.org/10.1111/j.1432-1033.1992.tb19833.x>
- Nakajima T, Kajihata S, Yoshikawa K, Matsuda F, Furusawa C, Hirasawa T, Shimizu H (2014) Integrated metabolic flux and omics analysis of *Synechocystis* sp. PCC 6803 under mixotrophic and photoheterotrophic conditions. *Plant Cell Physiol* 55:1605–1612. <https://doi.org/10.1093/pcp/pcu091>
- Nakamura S, Fu N, Kondo K, Wakabayashi K, Hisabori T, Sugiura K (2021) A luminescent Nanoluc-GFP fusion protein enables readout of cellular pH in photosynthetic organisms. *J Biol Chem* 296:100134. <https://doi.org/10.1074/jbc.RA120.016847>
- Nishii M, Ito S, Katayama N, Osanai T (2021) Biochemical elucidation of citrate accumulation in *Synechocystis* sp. PCC 6803 via kinetic analysis of aconitase. *Sci Rep* 11:17131. <https://doi.org/10.1038/s41598-021-96432-2>
- Osanai T, Kanesaki Y, Nakano T, Takahashi H, Asayama M, Shirai M, Kanehisa M, Suzuki I, Murata N, Tanaka K (2005) Positive regulation of sugar catabolic pathways in the cyanobacterium *Synechocystis* sp. PCC 6803 by the group 2 σ factor SigE. *J Biol Chem* 280:30653–30659. <https://doi.org/10.1074/jbc.M505043200>
- Osanai T, Imamura S, Asayama M, Shirai M, Suzuki I, Murata N, Tanaka K (2006) Nitrogen induction of sugar catabolic gene expression in *Synechocystis* sp. PCC 6803. *DNA Res* 13:185–195. <https://doi.org/10.1093/dnares/dsl010>
- Osanai T, Oikawa A, Shirai T, Kuwahara A, Iijima H, Tanaka K, Ikeuchi M, Kondo A, Saito K, Hirai MY (2013) Capillary electrophoresis–mass spectrometry reveals the distribution of carbon

- metabolites during nitrogen starvation in *Synechocystis* sp. PCC 6803. *Environ Biol* 16:512–524. <https://doi.org/10.1111/1462-2920.12170>
- Osanai T, Shirai T, Iijima H, Nakaya Y, Okamoto M, Kondo A, Hirai MY (2015) Genetic manipulation of a metabolic enzyme and a transcriptional regulator increasing succinate excretion from unicellular cyanobacterium. *Front Microbiol* 6:1064. <https://doi.org/10.3389/fmicb.2015.01064>
- Qian X, Zhang Y, Lun DS, Dismukes GC (2018) Rerouting of metabolism into desired cellular products by nutrient stress: fluxes reveal the selected pathways in cyanobacterial photosynthesis. *ACS Synth Biol* 7:1465–1476. <https://doi.org/10.1021/acssynbio.8b00116>
- Ruffing AM (2011) Engineered cyanobacteria: teaching an old bug new tricks. *Bioeng Bugs* 2:136–149. <https://doi.org/10.4161/bbug.2.3.15285>
- Saha R, Liu D, Hoynes-O'Connor A, Liberton M, Yu J, Bhattacharyya-Pakrasi M, Balassy A, Zhang F, Moon TS, Maranas CD, Pakrasi HB (2016) Diurnal regulation of cellular processes in the cyanobacterium *Synechocystis* sp. strain PCC 6803: insights from transcriptomic, fluxomic, and physiological analyses. *Mbio*. <https://doi.org/10.1128/mBio.00464-16>
- Sakai H, Suzuki K, Imahori K (1986) Purification and properties of pyruvate kinase from *Bacillus stearothermophilus*. *J Biochem* 99:1157–1167. <https://doi.org/10.1093/oxfordjournals.jbchem.a135579>
- Scholl J, Dengler L, Bader L, Forchhammer K (2020) Phosphoenolpyruvate carboxylase from the cyanobacterium *Synechocystis* sp. PCC 6803 is under global metabolic control by PII signaling. *Mol Microbiol* 114:292–307. <https://doi.org/10.1111/mmi.14512>
- Slabas AR, Suzuki I, Murata N, Simon WJ, Hall JJ (2006) Proteomic analysis of the heat shock response in *Synechocystis* PCC6803 and a thermally tolerant knockout strain lacking the histidine kinase 34 gene. *Proteomics* 6:845–864. <https://doi.org/10.1002/pmic.200500196>
- Snášel J, Pichová I (2019) Allosteric regulation of pyruvate kinase from *Mycobacterium tuberculosis* by metabolites. *Biochim Biophys Acta Proteins Proteom* 1867:125–139. <https://doi.org/10.1016/j.bbapap.2018.11.002>
- Soini J, Falschlehner C, Mayer C, Böhm D, Weinel S, Panula J, Vasala A, Neubauer P (2005) Transient increase of ATP as a response to temperature up-shift in *Escherichia coli*. *Microb Cell Factories* 4:9. <https://doi.org/10.1186/1475-2859-4-9>
- Takahashi H, Uchimiyama H, Hihara Y (2008) Difference in metabolite levels between photoautotrophic and photomixotrophic cultures of *Synechocystis* sp. PCC 6803 examined by capillary electrophoresis electrospray ionization mass spectrometry. *J Exp Bot* 59:3009–3018. <https://doi.org/10.1093/jxb/ern157>
- Takeya M, Hirai MY, Osanai T (2017) Allosteric inhibition of phosphoenolpyruvate carboxylases is determined by a single amino acid residue in cyanobacteria. *Sci Rep* 7:41080. <https://doi.org/10.1038/srep41080>
- Takeya M, Ito S, Sukigara H, Osanai T (2018) Purification and characterisation of malate dehydrogenase from *Synechocystis* sp. PCC 6803: biochemical barrier of the oxidative tricarboxylic acid cycle. *Front Plant Sci* 9:947. <https://doi.org/10.3389/fpls.2018.00947>
- Tanaka K, Shirai T, Vavricka CJ, Matsuda M, Kondo A, Hasunuma T (2023) Dark accumulation of downstream glycolytic intermediates initiates robust photosynthesis in cyanobacteria. *Plant Physiol* 191:2400–2413. <https://doi.org/10.1093/plphys/kiac602>
- Wan N, DeLorenzo DM, He L, You L, Immethun CM, Wang G, Baidoo EEK, Hollinshead W, Keasling JD, Moon TS, Tang YJ (2017) Cyanobacterial carbon metabolism: fluxome plasticity and oxygen dependence. *Biotechnol Bioeng* 114:1593–1602. <https://doi.org/10.1002/bit.26287>
- Wang B, Wang J, Zhang W, Meldrum DR (2012) Application of synthetic biology in cyanobacteria and algae. *Front Microbiol*. <https://doi.org/10.3389/fmicb.2012.00344>
- Waygood EB, Sanwal BD (1974) The control of pyruvate kinases of *Escherichia coli*. I: physicochemical and regulatory properties of the enzyme activated by fructose 1,6-diphosphate. *J Biol Chem* 249:265–274. [https://doi.org/10.1016/S0021-9258\(19\)43120-7](https://doi.org/10.1016/S0021-9258(19)43120-7)
- Waygood EB, Rayman MK, Sanwal BD (1975) The control of pyruvate kinases of *Escherichia coli*. II: effectors and regulatory properties of the enzyme activated by ribose 5-phosphate. *Can J Biochem* 53:444–454. <https://doi.org/10.1139/o75-061>
- Waygood EB, Mort JS, Sanwal BD (1976) The control of pyruvate kinase of *Escherichia coli*: binding of substrate and allosteric effectors to the enzyme activated by fructose 1,6-bisphosphate. *Biochem* 15:277–282. <https://doi.org/10.1021/bi00647a006>
- Werner A, Broeckling CD, Prasad A, Peebles CAM (2019) A comprehensive time-course metabolite profiling of the model cyanobacterium *Synechocystis* sp. PCC 6803 under diurnal light: dark cycles. *Plant J* 99:379–388. <https://doi.org/10.1111/tbj.14320>
- Wu HB, Turpin DH (1992) Purification and characterization of pyruvate kinase from the green alga *Chlamydomonas reinhardtii*. *J Phycol* 28:472–481. <https://doi.org/10.1111/j.0022-3646.1992.00472.x>
- Xiong W, Brune D, Vermaas WF (2014) The γ -aminobutyric acid shunt contributes to closing the tricarboxylic acid cycle in *Synechocystis* sp. PCC 6803. *Mol Microbiol* 93:786–796. <https://doi.org/10.1111/mmi.12699>
- Yao L, Shabestary K, Björk SM, Asplund-Samuelsson J, Joensson HN, Jahn M, Hudson EP (2020) Pooled CRISPRi screening of the cyanobacterium *Synechocystis* sp PCC 6803 for enhanced industrial phenotypes. *Nat Commun* 11:1666. <https://doi.org/10.1038/s41467-020-15491-7>
- You L, Berla B, He L, Pakrasi HB, Tang YJ (2014) ^{13}C -MFA delineates the photomixotrophic metabolism of *Synechocystis* sp. PCC 6803 under light- and carbon-sufficient conditions. *Biotechnol J* 9:684–692. <https://doi.org/10.1002/biot.201300477>
- Young JD, Shastri AA, Stephanopoulos G, Morgan JA (2011) Mapping photoautotrophic metabolism with isotopically nonstationary ^{13}C flux analysis. *Metab Eng* 13:656–665. <https://doi.org/10.1016/j.ymben.2011.08.002>
- Yu Y, You L, Liu D, Hollinshead W, Tang YJ, Zhang F (2013) Development of *Synechocystis* sp. PCC 6803 as a phototrophic cell factory. *Mar Drugs* 11:2894–2916. <https://doi.org/10.3390/md11082894>
- Zavřel T, Sinetova MA, Búzová D, Literáková P, Červený J (2015) Characterization of a model cyanobacterium *Synechocystis* sp. PCC 6803 autotrophic growth in a flat-panel photobioreactor. *Eng Life Sci* 15:122–132. <https://doi.org/10.1002/elsc.201300165>
- Zhang S, Bryant DA (2011) The tricarboxylic acid cycle in cyanobacteria. *Science* 334:1551–1553. <https://doi.org/10.1126/science.1210858>

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.