PGR5 is needed for redox-dependent regulation of ATP synthase both in chloroplasts and in cyanobacteria

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SUMMARY

• Control of the proton motive force (*pmf*) via regulation of ATP synthase constitutes a key
mechanism for photosynthetic organisms to maintain redox balance and induce
photoprotective mechanisms under light fluctuations.

• Using time-resolved electrochromic shift measurements in various photosynthetic organisms,
we found that ATP synthase is dynamically regulated during light fluctuations. While light-
induced reduction of the $CF_1\gamma$ subunit is known to activate chloroplast ATP synthase, it did
not account for the regulation in fluctuating light in *Arabidopsis thaliana*, suggesting
alternative mechanisms.

• The PROTON GRADIENT REGULATION 5 (PGR5) protein is important for
photoprotection in algal and plant chloroplasts. PGR5 has been proposed to facilitate cyclic
electron transport around PSI (CET), but it also affects ATP synthase activity. The
physiological role of cyanobacterial Pgr5 has remained elusive.

• We characterised a Δ*pgr5* mutant of *Synechocystis* sp. PCC 6803 and investigated *pmf*
dynamics in *pgr5* mutants of *Chlamydomonas reinhardtii*, *Arabidopsis*, and the C_4 grass
Setaria viridis. While PGR5 was not required for CET in *Synechocystis*, it was needed for
downregulating ATP synthase under high irradiance in all tested organisms via a thiol redox
state dependent mechanism.

• As AtPGR5 interacted with $AtCF_1\gamma$, PGR5 may have a conserved function as an inhibitor of
ATP synthase.

KEYWORDS: Photosynthesis, ATP synthase, proton motive force, chloroplast, cyanobacteria,
Arabidopsis, electrochromic shift

INTRODUCTION

Oxygenic photosynthesis by plants, algae, and cyanobacteria uses light energy to drive oxidation of water to produce ATP and NADPH for CO_2 fixation and other cellular processes. In their natural habitats, oxygenic photosynthetic organisms undergo constant fluctuation of irradiance. Mechanisms to adjust the redox homeostasis in chloroplasts and cyanobacterial cells have evolved to prevent energy-consuming futile reactions and damage to the photosynthetic machinery and other biomolecules via generation of reactive oxygen species (ROS) by the photosynthetic apparatus. ROS can be generated as a result of excitation imbalance between the photosystems, or when electron transport rate exceeds the sink capacity of the reactions downstream of the photosynthetic electron transport chain (PETC). Resulting accumulation of reduced electron carriers in the PETC triggers charge recombination reactions within the photosystems and direct reduction of O_2, generating highly reactive ROS such as superoxide ($O_2^{\bullet-}$) and hydrogen peroxide (H_2O_2) at PSI and singlet oxygen ($^1O_2$) primarily at PSII (Foyer & Hanke, 2022). PSI and its iron sulphur clusters are particularly vulnerable to over-reduction-induced damage, and plants, algae, and cyanobacteria invest heavily in their protection (Tiwari et al., 2016, 2024). These protective mechanisms involve cyclic electron transport around PSI (CET), redistribution of excitation energy between the photosystems via state transitions, non-photochemical quenching (NPQ), and inhibition of PQH_2 oxidation at the cytochrome b_6f complex, known as photosynthetic control (Degen & Johnson, 2024; Eckardt et al., 2024; Nikkanen et al., 2021; Shimakawa et al., 2016; Tikkanen & Aro, 2014). Additionally, in photosynthetic organisms apart from angiosperms, flavodiiron proteins provide a photoprotective electron sink on the acceptor side of PSI by catalysing controlled reduction of O_2 to water (the Mehler-like reaction) (Allahverdiyeva et al., 2013; Ilik et al., 2017).

As photosynthetic control and NPQ (in plants and algae) are induced by acidic pH of the thylakoid lumen, an important mechanism to maintain photosynthetic redox balance involves control of the proton motive force *(pmf)* via regulation of the thylakoid ATP synthase (Kanazawa et al., 2017; Takagi et al., 2017). The pH-dependent component of *pmf* (ΔpH), is generated by translocation of protons from the stroma (or the cytosol in cyanobacteria) to the lumenal side of the thylakoid membrane by linear and cyclic electron transport as well as consumption of protons on the stromal side. The proton gradient is released mainly via efflux through the ATP synthase, providing the driving force for ATP synthesis. Proton-conductivity of the ATP synthase is therefore an important regulatory factor for adjusting the magnitude of the *pmf*.

In addition to ΔpH, the *pmf* comprises an electric field component ($\Delta\Psi$). $\Delta\Psi$ derives from charge separation within the photosystems, the positive charge of protons, and pumping of cations (e.g. K^+, Ca^{2+} and Mg^{2+}) in and anions (e.g. Cl^-) out of the lumen by ion transporters in the thylakoid membrane (Armbruster et al., 2017). ΔpH and $\Delta\psi$ are thermodynamically equivalent and both drive

ATP synthesis (Hangarter & Good, 1982). However, build-up of sufficient ΔpH over the thylakoid

membrane is required for induction of photoprotective mechanisms upon sudden increases in light

intensity, namely dissipation of excessive excitation energy as heat in NPQ (Krishnan-Schmieden et

al., 2021; Niyogi & Truong, 2013) and photosynthetic control (Degen & Johnson, 2024; Tikhonov et

al., 1981). These mechanisms prevent over-reduction of the electron transport chain and photodamage

to PSI. Conversely, it is also important to down-regulate ΔpH (and consequently, NPQ and

photosynthetic control) upon sudden decreases in irradiance in order to maintain sufficient supply of

electrons on the acceptor side of the electron transfer chain for carbon fixation in the Calvin–Benson

cycle (CBC).

ATP synthase is regulated via several mechanisms. The $F_1\varepsilon$ (epsilon) subunits of the chloroplast

(CF_0CF_1) ATP synthase (Feniouk et al., 2006) and the cyanobacterial ATP synthase (Imashimizu et

al., 2011; Murakami et al., 2018) have inhibitory roles preventing ATP hydrolysis. $F_1\varepsilon$ undergoes

conformational changes triggered by *pmf* generation and changes in ATP/ADP ratio, allowing

inhibition of ATP hydrolysis (Feniouk et al., 2006; Richter & McCarty, 1987). Moreover, upon dark-

to-light transitions, the chloroplast ATP synthase is activated by thioredoxin (TRX)-mediated

reduction of a disulphide in the γ subunit ($CF_1\gamma$) (Akiyama et al., 2023; McKinney et al., 1978; Nalin &

McCarty, 1984). $CF_1\gamma$ is kept in an inactive oxidised state in darkness to avoid hydrolysis of ATP by

reverse activity or loss of the proton gradient (Hahn et al., 2018; Hisabori et al., 2013; Kohzuma et al.,

2017). Maintenance of adequate dark-*pmf* via ATP synthase dark-light regulation is also needed for

powering the insertion of new proteins into the thylakoid membrane via the Tat- and Sec-pathways to

maintain the integrity of the photosynthetic apparatus (Kohzuma et al., 2017). $CF_1\gamma$ is reduced in

seconds upon illumination, which lowers the threshold *pmf* for activation of the ATP synthase

(Buchert et al., 2021; Kohzuma et al., 2017; Konno et al., 2012; Kramer et al., 1990; Nikkanen et al.,

2018). In turn, as ΔpH also facilitates reduction of the $CF_1\gamma$ disulphide bond (Sekiguchi et al., 2024),

while dissipation of ΔpH promotes oxidation of $CF_1\gamma$ (Sekiguchi et al., 2022). F- and m-type

chloroplast TRX isoforms have been understood to be mainly responsible for light-dependent

reduction of $CF_1\gamma$ (Schwarz et al., 1997; Sekiguchi et al., 2020), and chloroplast TRX-like proteins

catalyse the oxidation of the subunit in the dark (Sekiguchi et al., 2022). Additionally, *in vivo* studies

have revealed the involvement of the NADPH-dependent TRX system (NTRC) in $CF_1\gamma$ reduction in

low light conditions (Carrillo et al., 2016; Nikkanen et al., 2016), while the atypical TRX CDSP32

was recently suggested to play a role in reduction of $CF_1\gamma$ in potato (Rey et al., 2024).

Reduction of $CF_1\gamma$ constitutes an on/off switch controlling the activation of the ATP synthase upon

the onset of illumination in chloroplasts of plants and algae, and does not occur in mitochondria or in

cyanobacteria (Hisabori et al., 2013). The cyanobacterial γ subunit still has a role in preventing ATP

hydrolysis however, via an ADP-dependent mechanism (Sunamura et al., 2010). Moreover, the small

AtpΘ protein (Song et al., 2022) has been reported to function as an inhibitor of the cyanobacterial

ATP synthase in the dark and in low *pmf* conditions, preventing ATP hydrolysis and collapse of the

proton gradient. Interestingly, the $F_1\alpha$ (AtpA) and $F_1\beta$ (AtpB) subunits of the ATP synthase also

contain conserved Cys residues, and $F_1\alpha$ has been identified as a prospective TRX target in

cyanobacteria (Guo et al., 2014; Lindahl & Florencio, 2003), and $F_1\beta$ in plants (Balmer et al., 2006).

Moreover, the mitochondrial ATP synthase in *Xenopus laeviis* oocytes is regulated by reversible

oxidation of thiols in the $F_1\alpha$ subunit (Cobley et al., 2020).

There are also other regulatory mechanisms that adjust the activation state of the ATP synthase

according to the metabolic state of the stroma or cytosol, such as substrate (ADP and P_i) availability

(Avenson et al., 2005; Kanazawa & Kramer, 2002; Takagi et al., 2017). High CO_2 supply results in

increase of chloroplast ATP synthase activity by a mechanism that is independent of $CF_1\gamma$ redox state

(Kiirats et al., 2009; Kohzuma et al., 2013). Another potential regulatory mechanism involves

phosphorylation of the β subunit (del Riego et al., 2006).

Additionally, thylakoid conductivity and the *pmf* can be adjusted through the activities of ion channels

and transporters in the thylakoid membrane (Spetea et al., 2017). A lack of the K^+/H^+ exchanger

KEA3, the two-pore K^+ channel TPK3, or the Cl^- channels CLCe and VCCN1 has been shown to

affect the *pmf* and/or induction and relaxation of NPQ in plants (Armbruster et al., 2014; Carraretto

et al., 2013; Herdean, Nziengui, et al., 2016; Herdean, Teardo, et al., 2016; von Bismarck et al., 2023;

Wang & Shikanai, 2019). Similarly, lack of the cyanobacterial K^+ channel SynK resulted in decreased

ΔpH generation and impairment of photosynthetic control in the model cyanobacterium *Synechocystis*

sp. PCC 6803 (*Synechocystis*) (Checchetto et al., 2012). Controlling the ionic environment of the

thylakoid membrane is particularly important to avoid drastic increases in ΔΨ, which result in

production of damaging $^1O_2$ via recombination reactions in PSII (Davis et al., 2016).

Plants deficient in the PROTON GRADIENT REGULATION 5 (PGR5) protein suffer from impaired

pmf generation (Munekage et al., 2002). In plant chloroplasts, PGR5 forms redox-dependent

heterodimers with PGRL1 (PGR5-LIKE 1), which have been proposed to mediate or regulate cyclic

electron transport (CET) from ferredoxin to the plastoquinone pool (DalCorso et al., 2008; Hertle et

al., 2013; Yamamoto & Shikanai, 2019), contributing to *pmf* formation (Wang et al., 2015). More

recently, a functional PGRL1-analogue was identified also in cyanobacteria (Dann & Leister, 2019).

The *pgr5* knockout plants are unable to induce photosynthetic control and NPQ during transitions

from low to high light (HL) (Munekage et al., 2002; Suorsa et al., 2012; Yamamoto & Shikanai,

2019). Consequently, exposure of *pgr5* mutant plants to HL results in over-reduction of the electron

transport chain and photodamage to the iron sulphur clusters of PSI (Tiwari et al., 2016, 2024).

Accordingly, the lack of PGR5 is lethal in fluctuating light conditions in *Arabidopsis thaliana*

(Arabidopsis) (Suorsa et al., 2012; Tikkanen et al., 2010) and severely inhibits growth of the model C_4 plant *Setaria viridis* (Woodford et al., 2024) as well as of the model green alga *Chlamydomonas reinhardtii (Chlamydomonas)* (Jokel et al., 2018). *Synechocystis* cells deficient in a PGR5-orthologue (SynPgr5) suffer from slightly increased HL-sensitivity (Yeremenko et al., 2005), but no growth impairment was observed in fluctuating light conditions (Allahverdiyeva et al., 2013). Interestingly, however, there is strong selection pressure against overexpression of SynPgr5 (Margulis et al., 2020).

The physiological functions of PGR5 and PGRL1 remain controversial, with some reports linking the proteins to regulation of linear instead of cyclic electron transport from PSI (Johnson et al., 2014; Joliot & Johnson, 2011; Maekawa et al., 2024; Nandha et al., 2007; Rantala et al., 2020; Takagi & Miyake, 2018; Tikkanen et al., 2015), or regulation of the Q-cycle at the cytochrome b_6f complex (Buchert et al., 2020). Impaired *pmf* generation and induction of photoprotection in the *pgr5* mutant could also derive from the inability of the mutant plants to limit the conductivity of the thylakoid membrane under HL (Avenson et al., 2005; Degen et al., 2023; Nikkanen et al., 2018). Interestingly, elevated thylakoid (ATP synthase) conductivity upon HL exposure was not observed in isolated and ruptured *pgr5* mutant chloroplasts (Wang et al., 2018). This suggests that a stromal component that is lost in ruptured chloroplasts plays a role in the effect of PGR5 on thylakoid conductivity.

In the current study, we elucidated the dynamics of *pmf* regulation under light in a variety of photosynthetic organisms focusing on the potential role of PGR5. We performed *in vivo* characterisation of photosynthetic electron transport and *pmf* formation in *Synechocystis, Chlamydonomas*, *Arabidopsis,* and *S. viridis.* Our results reveal that in *Arabidopsis*, dynamic regulation of ATP synthase conductivity during fluctuations in light intensity is independent of the thiol redox state of the $CF_1\gamma$ subunit. We show that downregulation of the ATP synthase activity upon transitions to HL depends on PGR5 as well as the thiol redox state of the stroma or cytosol in both chloroplasts and cyanobacteria. PGR5 is only essential for oxidation of the PETC in plants though, and not in cyanobacteria. Moreover, we demonstrate that cyanobacterial SynPgr5 is not needed for CET, and suggest that the observed effect of plant PGR5 on cyclic electron transport may be an indirect consequence of misregulation of ATP synthase and increased photoinhibition of PSI.

RESULTS

Dynamic changes in thylakoid conductivity are independent of the thiol redox state of $CF_1\gamma$ in plants

In plants and algae, measurement of dark-interval relaxation kinetics (DIRK) of the electrochromic shift (ECS) signal has been widely used for *in vivo* determination of the magnitude of the *pmf*,

partitioning of the *pmf* between ΔpH and $\Delta\Psi$, as well as the conductivity of the thylakoid membrane, which is mainly determined by the activity of ATP synthase (Bailleul et al., 2010; Cruz et al., 2001, 2005; Sacksteder & Kramer, 2000; Schreiber & Klughammer, 2008). Recently, a reliable method to measure ECS has also been developed for cyanobacteria (Nikkanen et al., 2020; Santana-Sánchez et al., 2023; Viola et al., 2019).

Time-resolved ECS analysis in wild type (WT) *Arabidopsis* revealed that upon the onset of illumination of dark-adapted leaves, the conductivity of the ATP synthase (g_H+) initially decreased for c.a. 30 s (Fig. 1a), as observed previously (Guinea Diaz et al., 2020; Nikkanen et al., 2018). This initial decrease in g_H+ allowed transient build-up of *pmf* (Fig. 1b) and induction of photoprotective mechanisms (Fig. 1c–d) in order to avoid over-reduction of the electron transport chain when redox-regulated CBC enzymes such as Fructose-1,6-bisphosphatase (FBPase) are not yet activated (i.e. reduced). After the initial decrease, at c.a. 30 s of illumination, g_H+ started to increase gradually, resulting in decrease of *pmf* to a steady-state level (Fig. 1a–b). Importantly, these changes in g_H+ did not correlate with the thiol redox state of $CF_1\gamma$. $CF_1\gamma$ was rapidly reduced at the onset of illumination, becoming almost fully reduced after 20 s, and remained reduced thereafter (Fig. 1e). In contrast, FBPase remained mostly oxidised (inactive) for a full minute in low light, and only became partially reduced when leaves were exposed to HL (Fig. 1f). These results demonstrate that the initial downregulation of ATP synthase activity during dark-to-light transitions is independent of $CF_1\gamma$ redox state and must occur via another mechanism.

When WT *Arabidopsis* leaves were exposed to a light regime where light intensity alternates between periods of low light (LL) and HL, mimicking natural fluctuations, intricate regulatory dynamics of the *pmf* and g_H+ could be observed. During LL phases, g_H+ increased substantially, which contributed to a rapid decline in *pmf* (Fig. 1a–b). This upregulation of g_H+ allowed relaxation of photosynthetic control (measured as donor-side limitation of PSI) and NPQ (Fig. 1c–d), allowing sufficient supply of electrons to stromal reactions. Similarly to downregulation of g_H+ during dark-to-light transitions, the upregulation of g_H+ during LL happened independently of the thiol redox state of $CF_1\gamma$, which remained fully reduced throughout the change in light intensity (Fig. 1e).

In contrast to LL phases, g_H+ was rapidly downregulated in WT leaves during HL phases (Fig. 1a), enabling sufficient *pmf* build-up (Fig. 1b) for induction of photosynthetic control and NPQ (Fig. 1c–d). Again, the decrease in g_H+ did not coincide with oxidation of $CF_1\gamma$, which remained fully reduced (Fig. 1e).

Thylakoid conductivity is dynamically regulated under fluctuating light also in cyanobacteria and unicellular algae

When WT *Synechocystis* cells were subjected to sudden fluctuations between moderate light (ML)

and HL, time-resolved ECS-DIRK measurements revealed downregulation of g_H+ during HL phases

(Fig. 2a), resembling that observed in *Arabidopsis*. As in plants, this downregulation likely occurs to

maintain an adequate *pmf* (Fig. 2b) for induction of photosynthetic control. Accordingly, strong donor

side limitation of PSI (Y(ND)) was measured during HL phases (Fig. 2d) indicative of limitation of

electron transport from Cyt b_6f. In contrast to *Arabidopsis*, g_H+ remained low during the ML phases of

the experiment (Fig. 2a).

We also probed the *pmf* and g_H+ dynamics under fluctuating light in the unicellular green alga

Chlamydomonas. While *pmf* underwent similar changes as in plants and in cyanobacteria (Fig. 3a), no

clear downregulation of g_H+ was observed during HL, and during the LL phases g_H+ remained low

(Fig. 3b).

Figure 1. Effect of PGR5 and CF$_1\gamma$ redox state on *pmf*, thylakoid conductivity, and photoprotection in fluctuating

light in *Arabidopsis*. (a) Proton conductivity of the thylakoid membrane (g_H+ s^{-1}) and **(b)** magnitude of the *pmf* in

fluctuating light, as determined from dark-interval relaxation kinetics (DIRK) of the ECS signal. ECS was measured from

dark-adapted WT-gl1 and *pgr5* mutant *Arabidopsis* leaves under a light regime alternating between 1 min periods of low (50

μmol photons $m^{-2}s^{-1}$) and high light (825 μmol photons $m^{-2}s^{-1}$). The values in (a) are averages from 9 and in (b) 11 biological

replicates ± SEM. **(c)** Quantum yield of non-photochemical quenching (Y(NPQ)) and **(d)** fraction of oxidised P700 (donor

side limitation of PSI, Y(ND)) in a fluctuating light regime supplemented with saturating pulses at 15 s intervals. The values

in C–D are averages from 3 biological replicates ± SEM. **(e)** A mobility shift assay of the in vivo thiol redox state of the

CF$_1$γ subunit of the chloroplast ATP synthase and **(f)** the CBC enzyme FBPase in fluctuating light (1 min periods of 50

μmol photons $m^{-2}s^{-1}$, LL, and 825 μmol photons $m^{-2}s^{-1}$, HL, in WT leaves. The break between the 140 and 160 sec samples

in (e) represents division between two gels.

PGR5 is needed for downregulation of thylakoid conductivity under strong illumination across photosynthetic organisms

During dark-to-LL transitions, the *Arabidopsis pgr5* mutant plants had a lower *pmf* than WT (Fig.

1B), as shown previously and attributed to lower linear electron transport rates (Nikkanen et al.,

2018). In fluctuating light, the *pgr5* mutants were unable to decrease g_H+ during HL phases (Fig. 1a),

resulting in partial loss of *pmf* (Fig. 1b), in agreement with previous studies (Avenson et al., 2005;

Nikkanen et al., 2018). The mutant plants also exhibited impaired induction of NPQ (Fig. 1c) and

photosynthetic control, resulting in an inability to oxidise P700 (Fig. 1d). Interestingly, and in contrast

to their behaviour during HL phases, *pgr5* mutant plants showed a lower g_H+ and slightly lower *pmf*

than WT during LL phases (Fig. 1a–b).

The *Arabidopsis pgr5-1* mutant used in our experiment has been reported to also contain an additional

mutation in the At2g1724 gene, which slightly exacerbates PSI photoinhibition in the mutant (Wada

et al., 2021). Mutants where an intact At2g1724 has been re-introduced (*pgr5*^{hope1} and *pgr5-Cas*) are,

however, also unable to induce photosynthetic control to oxidise PSI (Wada et al., 2021), and have

similarly elevated g_H+ and diminished *pmf* as the *pgr5-1* mutant (Maekawa et al., 2024; Penzler et al.,

2022). While it is therefore unlikely that the At2g1724 mutation in *pgr5-1* plants would have a

significant effect on the phenotypes examined in the current study, we confirmed this by repeating the

ECS experiment (Fig. 1a–b) also with the *pgr5-Cas* mutant (Penzler et al., 2022). Results with *pgr5-*

Cas plants were similar to the ones with *pgr5-1,* apart from the decrease in *pmf* during initial dark-to-

LL transitions being less prominent in *pgr5-Cas* plants than in *pgr5-1* in comparison to WT (Fig. S1).

Moreover, while a diminished proton flux (v_H+) in LL and immediately upon shifts to HL was

measured in *pgr5-1* mutants in comparison to WT (Fig. S2a), this decrease was absent in *pgr5-Cas*

plants, which instead exhibited elevated v_H+ during the first HL phase (Fig. S1c).

We proceeded to investigate whether lack of SynPgr5 affects regulation of g_H+ in *Synechocystis*.

Elevated g_H+ was indeed detected upon exposure of Δ*pgr5* cells to HL after illumination in moderate

light (ML) in a fluctuating light regime (Fig. 2a, c), concomitant with diminished *pmf* (Fig. 2b, c). The

increased g_H+ was not due to an elevated amount of ATP synthase, as the protein level of AtpB

remained unchanged in the mutant (Fig. S3). Increased thylakoid conductivity resulted in

diminishment of pmf (Fig. 2b). Despite the elevated g_H+ and in contrast to AtPGR5-deficient

Arabidopsis, no decrease in donor-side limitation (indicative of impairment of photosynthetic control)

or increase in acceptor side limitation of PSI was detected during transitions to HL in *Synechocystis*

$\Delta pgr5$ cells (Fig. 2c–d). Interestingly, a slight, albeit statistically non-significant decrease in donor

side limitation of PSI was detected in $\Delta pgr5$ upon transitions from HL to LL (Fig. 2d). This may be

due to faster deactivation of photosynthetic control by faster dissipation of pmf (Fig. 2b).

The ability of the *Synechocystis* $\Delta pgr5$ strain to maintain sufficient PSI oxidation for unimpaired

photosynthetic activity may be due to the strong electron sink capacity of the Mehler-like reaction

catalysed by flavodiiron proteins (FDPs) under light (Allahverdiyeva et al., 2013). Therefore, we

tested the PSI oxidation capacity of a $\Delta flv3\ pgr5$ double mutant strain, which is deficient in both

SynPgr5 as well as the Flv1/3 hetero-oligomers (Fig. S3) that are mainly responsible for the strong,

rapidly induced Mehler-like reaction (Santana-Sanchez et al., 2019). We detected slightly aggravated

impairment of PSI oxidation in the double mutant in comparison to the $\Delta flv3$ mutant during initial LL-

to-HL transitions (Fig. 2c) due to slightly increased acceptor side limitation of PSI (Fig. 2d). The

additional effect of Pgr5 deficiency was minor compared to lack of Flv3, and no additional

aggravation of ferredoxin redox kinetics, CO_2 fixation, or O_2 evolution was observed in $\Delta flv3\ pgr5$ in

comparison to $\Delta flv3$ (Fig. S4). These results indicate that SynPgr5 may affect PSI oxidation also in

cyanobacteria, but its importance is minor compared to plants, while flavodiiron proteins have a

crucial role. This was also reflected in the growth phenotypes of the strains. In agreement with

previous results (Allahverdiyeva et al., 2013), no difference in growth was detected between WT and

$\Delta pgr5$ under fluctuating light, while additional deficiency of Flv3 in $\Delta pgr5\ flv3$ prevented growth

entirely (Fig. 2f), similarly to $\Delta flv3$ (Allahverdiyeva et al., 2013).

The $\Delta flv3$ mutant showed a decreased g_H+ in the HL phases of fluctuating light (Fig. 2a), which

allowed it to compensate for diminished v_H+ (Fig. S2b) and maintain WT-level pmf (Fig. 2b). The

$\Delta pgr5\ flv3$ double mutant, however, exhibited WT-like g_H+, v_H+, and pmf (Fig. 2b, Fig. S2b),

indicating that the downregulation of g_H+ observed in $\Delta flv3$ is also at least partly dependent on

SynPgr5.

To clarify whether SynPgr5 is involved in CET in *Synechocystis* as previously concluded (Dann &

Leister, 2019; Yeremenko et al., 2005), we quantified the rates of CET and linear electron transport

(LET) in WT and $\Delta pgr5$ cells using DIRK analysis of near-infrared absorbance difference signals, as

described by (Theune et al., 2021). Our results showed that the CET rate was not decreased in the

deletion mutant (Fig. 4a), indicating that SynPgr5 is not involved in CET, at least at steady state

conditions. It has been previously reported that a *Synechocystis* $\Delta pgr5$ mutant has a slowed-down rate

of P700 oxidation under far-red light as measured (Dann & Leister, 2019), which can be an indication

of decreased CET, although results from such assays should be interpreted with caution (Fan et al.,

2007). In contrast to the previous report, we detected no difference between WT and Δ*pgr5* in far-red-

induced P700 oxidation rate when measured as the deconvoluted P700 signal using the Dual-KLAS-

NIR instrument (Fig. S5).

Figure 2. ***Pmf* dynamics, PSI oxidation, and growth under fluctuating light in *Synechocystis*.** Thylakoid conductivity
(g_{H+}) **(a)**, and *pmf* **(b)** were determined by the ECS DIRK method from WT and Δ*pgr5* cells. The values in A-B are averages
from 3–6 (depending on the quality of the first-order DIRK fit) biological replicates ± SEM. **(c)** Representative ECS decay
kinetics in WT and Δ*pgr5* cells during the second-to-last 600 ms dark interval in the experiment. First order exponential fits
are shown in magenta and yellow. **(d)** Donor (Y(ND)) and **(e)** acceptor side limitation (Y(NA)) of PSI in WT, Δ*pgr5*, Δ*pgr5
flv3*, and Δ*flv3* strains of *Synechocystis* during transitions from low light (25 uE, LL) to high light (525 uE, HL). Y(NA) and
Y(ND) were determined from P700 redox kinetics using the saturating pulse method on a DUAL-PAM 100
spectrophotometer. Traces are averages of 3–4 biological replicates ± SEM (ribbons). **(f)** Growth curves (OD 750 nm) of
WT, Δ*pgr5* and Δ*pgr5 flv3* cells under fluctuating light (5 min at 20 μmol photons $m^{-2}s^{-1}$ to 30 sec at 500 μmol photons $m^{-2}s^{-1}$). The values are averages from 3 biological replicates ± SEM.

Near-infrared spectroscopy revealed no significant differences in the deconvoluted redox signals for

ferredoxin (Fed), plastocyanin (PC) or P700 between WT and Δ*pgr5* cells upon onset of strong

illumination (Fig. 4b). Moreover, analysis of *in vivo* O_2 and CO_2 gas exchange by membrane inlet

mass spectrometry (MIMS) showed that oxygen evolution (Fig. 4c), dark respiration rate (Fig. 4d),

light-induced O_2 uptake rate indicative of FDP activity (Fig. 4c, e), as well as CO_2 fixation (Fig. 4f)

were all unchanged in Δ*pgr5* in comparison to WT cells. When cells were grown under fluctuating

light and O_2 gas exchange was measured under similar conditions, however, a slightly elevated light-

induced O_2 uptake rate was observed in Δ*pgr5*, although the difference was statistically significant

only during the first HL phase (Fig. 5).

Figure 3. *Pmf* dynamics in *Chlamydomonas reinhardtii* under fluctuating light. (a) Thylakoid conductivity (g_{H^+}). **(b)**
pmf ($\Delta ECS/ECS_{ST}$). **(c)** Proton flux (v_{H^+}). The ECS signal was measured from WT137c, *pgr5* knockout mutant, and PGR5
complementation line (PGR5C) cells using the same protocol as described in the Figure 1 legend. Values are mean ± SEM
from three biological replicates.

Figure 4. Photosynthetic phenotype of the *Synechocystis Δpgr5* strain. (a) Quantification of LET and CET rates in
Synechocystis WT and *Δpgr5*. Chlorophyll was adjusted to 20 μg/ml in BG-11 pH 7.5. Using a Dual KLAS-NIR
spectrophotometer, cells were illuminated for 2 min under 500 μmol photons m^{-2}s^{-1} before administering 100x 40 ms dark
intervals 10 s apart to monitor the relaxation kinetics of the P700 and PC signals. The measurement was then repeated in the
presence of 10μM DCMU to inhibit LET. **(b)** *In vivo* redox kinetics of P700, PC, and Fed in WT and *Δpgr5* strains of
Synechocystis as monitored with the DUAL-KLAS/NIR spectrophotometer. Dark-adapted cells were illuminated for 3 s with
3000 μmol photons m^{-2}s^{-1}. The traces are averages of 7 biological replicates ± SD. **(c)** *In vivo* O_2 gas exchange in WT and
Δpgr5 cells, as analysed by membrane inlet mass spectrometry (MIMS). Cells were adjusted to 10 μg Chl/ml, and $^{18}O_2$
added in equilibrium with $^{16}O_2$ in order to distinguish O_2 uptake from O_2 evolution. Cells were dark-adapted for 10 min,
after which gas exchange was monitored for 5 min in dark, 5 min under 500 μmol photons m^{-2}s^{-1} illumination, and 5 min in
post-illumination dark. **(d)** Dark respiration rates as averages of O_2 uptake during the first two minutes of darkness in (e) ±
SD. **(e)** Maximum light-induced O_2 uptake rates as averages of O_2 uptake peaks around 30 s of illumination - dark

respiration rate ± SD. **(f)** CO₂ fixation rates as averages of CO₂ uptake rates during the final minute in light in (e) +

respiration rate during the first two minutes of darkness.

Figure 5. O₂ gas fluxes in fluctuating light in WT and *Δpgr5 Synechocystis* cells. Cells were grown in fluctuating light (1

min 25 μmol photons m⁻²s⁻¹ / 1 min 500 μmol photons m⁻²s⁻¹), and real-time gas fluxes were measured by MIMS mimicking

the same light conditions, with a 5 min dark period on either side of 3 LL-HL cycles. The values are averages of 4 biological

replicates ± SD. The bar chart shows the maximum O₂ uptake rates + SD during the first HL phase of the experiment (dotted

arrow). * indicates statistically significant difference to WT according to a two-sample Student's t-test (P<0.05).

There is no PGR5 orthologue identified in the genome of another cyanobacterial model species,

Synechococcus elongatus sp. PCC 7942 (*Synechococcus*) (Shimakawa et al., 2016). We therefore

proceeded to investigate whether the regulation of g_H+ in response to fluctuating light conditions in

Synechococcus differs from *Synechocystis*. Interestingly, no major difference was observed in

comparison to the g_H+ kinetics in *Synechocystis*, with down-regulation of g_H+ occurring during the

HL phases after an initial increase (Fig. S6). This suggests that the downregulation of g_H+ in HL is

achieved via a different mechanism in *Synechococcus*.

Elevated g_H+ under HL was also observed in the *Chlamydomonas pgr5* mutant, in comparison to WT

or a CrPGR5 complementation strain (Fig. 4a). Interestingly, this did not result in lower *pmf* under HL

due to elevated proton flux (v_H+) (Fig. 4b, c). Finally, the increase in g_H+ during the HL phases of a

fluctuating light regime was also detected in a *pgr5* mutant of the model C₄ grass *S. viridis* (Fig. S7),

highlighting a conserved function of PGR5 in regulation of the proton conductivity of ATP synthase

from cyanobacteria to chloroplasts in algae, C₃, and C₄ plants.

Elucidating the mechanism of redox-dependent inhibition of thylakoid conductivity

We have previously shown that increasing the reducing capacity of the chloroplast thiol redox

regulation systems through overexpression of NTRC in *Arabidopsis* intensifies the downregulation of

g_H+ upon increases in light intensity (Nikkanen et al., 2018). We therefore proceeded to investigate

potential thiol regulation of thylakoid conductivity or ATP synthase activity, as well as the role of

PGR5 in it.

Addition of methyl viologen (MV) results in lowered conductivity of the thylakoid membrane, which

has been interpreted as prevention of TRX-mediated reduction of the $CF_1\gamma$ disulphide (Kramer &

Crofts, 1989). MV facilitates electron transfer from PSI or reduced ferredoxin to O_2 (the Mehler

reaction), resulting in generation of ROS (Fujii et al., 1990; Sétif, 2015; Shapiguzov et al., 2019,

2020). However, MV is also able to donate electrons to redox-regulated enzymes such as nitrite

reductase in spinach (Hirasawa & Tamura, 1980) and glutathione reductase in yeast (Llobell et al.,

1986). To further elucidate the relationship between stromal/cytosolic thiol redox state and PGR5-

dependent downregulation of thylakoid conductivity, we investigated the effects of MV on

chloroplastic thiol-regulated enzymes and *pmf* in *Arabidopsis.* We first determined the *in vivo* thiol

Although electron supply to the TRX systems from PSI is limited by MV, addition of MV caused

strong reduction of the 2-cysteine peroxiredoxin (2-CysPrx), FBPase, and $CF_1\gamma$ pools even in

darkness (Fig. 6a). NTRC, whose redox state is mostly unaffected by light conditions, thereby acting

as a buffer system for plastidial redox state (Nikkanen et al., 2018; Zimmer et al., 2021), also became

strongly reduced after 90 min of illumination when treated with MV (Fig. 6a).

Next, we investigated the effect of MV on regulation of *pmf* and g_H+ in WT *Arabidopsis* leaves. Upon

illumination of dark-adapted leaves, g_H+ was initially significantly higher in MV-treated WT leaves

than in control leaves (Fig. 6b), most likely due to dark-reduction of $AtCF_1\gamma$ by MV (Fig. 6a). As

illumination continued, g_H+ diminished in MV-treated leaves and remained at a very low level

throughout the rest of the experiment, even during HL (Fig. 6c). This results in very high *pmf* (Fig.

6d) and NPQ (Shapiguzov et al., 2020). In contrast, MV-treatment of *pgr5* mutant leaves caused only

a minor decrease in g_H+ and increase in *pmf* during illumination, and in HL g_H+ was in fact higher in

MV-treated *pgr5* mutant than in WT control leaves (Fig. 6c–d), suggesting that the MV-mediated g_H+

decrease is dependent on AtPGR5.

Figure 6. Effect of methyl viologen (MV) on thiol redox states of chloroplast enzymes and on regulation of *pmf* in *Arabidopsis*. (a) Mobility shift assays of AtCF$_1$y, 2-CysPrxs, NTRC, and FBPase thiol redox state in vivo. WT Arabidopsis leaves were incubated in H$_2$O with (+) or without (-) 1 μM MV in dark and then illuminated in GL conditions for 180 min, with samples taken from darkness (0) and after 30, 90, and 180 min of illumination. Total protein extracts were labelled with MALPEG as described in Materials and Methods, separated by SDS-PAGE and probed with appropriate antibodies. MALPEG-labelled (in vivo oxidised) forms migrate more slowly than unlabelled forms (in vivo reduced). –DTT indicates control sample where no alkylation of thiols by MALPEG should occur, and * indicates dimeric 2CysPrx. **(b)** Conductivity of the thylakoid membrane (g$_H$+) after 1 s of illumination in growth light (GL, 95 μmol photons m^{-2}s^{-1}) in dark-adapted WT and *pgr5* mutant leaves incubated in H$_2$O with or without 1 μM MV. The values are mean + SD from 4–7 biological replicates. Statistical significance of differences was tested by one-way ANOVA and Tukey's tests (p<0.05). **(c)** Thylakoid conductivity and **(d)** *pmf* in dark-adapted WT and *pgr5* mutant leaves incubated in H$_2$O with or without 1 μM MV during 5 min illumination in GL (95 μmol photons m^{-2}s^{-1}) and consequent increase in light intensity to 825 μmol photons m^{-2}s^{-1} (HL), as determined from dark-interval relaxation kinetics of the ECS signal. The values in C-D are averages from 4–7 biological replicates ± SEM (ribbon).

We also investigated the effect of perturbing the thiol redox state of the cell on thylakoid conductivity in *Synechocystis*. As moderate concentrations of MV have only minor effects on cyanobacterial electron transport (Sétif, 2015), with no significant impact on g$_H$+ observed after addition of 0.5 mM MV (Fig. S8), we opted to test the effect of supplementation with the thiol-alkylating agent N-ethylmaleimide (NEM). Addition of 0.1 mM NEM to WT *Synechocystis* cultures resulted in a significant increase in g$_H$+ after 5 seconds of illumination (Fig. 7a), similarly to results recently reported for another maleimide compound 2-methylmaleimide (Hubáček et al., 2024). In Δ*pgr5* cells,

only a slight, statistically non-significant NEM-induced increase in g_H+ was observed. In
Synechococcus, which does not have PGR5, NEM did not have a significant effect on g_H+ (Fig. 7b).
Finally, we also tested the effect of NEM on g_H+ in *Arabidopsis* WT and *pgr5* mutant leaves,
repeating the fluctuating light experiment from Figure 1. NEM decreased g_H+ throughout the
experiment in WT (Fig. 7c), albeit not as dramatically as MV treatment. In contrast, *pgr5* mutant
leaves did not respond to NEM treatment during the first LL-HL cycle (Fig. 7c). During subsequent
cycles g_H+ in NEM-treated *pgr5* mutant leaves decreased slightly in comparison to untreated *pgr5*
mutant leaves, while still remaining higher than untreated WT leaves.

Figure 7. Effect of NEM on thylakoid conductivity under illumination. (a) The effect of 0.1 mM NEM on g_H+ in
Synechocystis WT and $\Delta pgr5$ cells. ECS DIRK were measured 5 seconds after the onset of illumination at 500 µmol photons
$m^{-2} s^{-1}$. The values are averages of 7–11 biological replicates + SD. Statistical significance of differences was tested by one-
way ANOVA and Tukey's tests for comparison of means (P<0.05**). (b)** The effect of 0.1 mM NEM on g_H+ in
Synechococcus elongatus sp. PCC 7942 WT cells. ECS DIRK were measured as averaged decay kinetics from 5 dark
intervals spaced 5 seconds apart, with the first DIRK being administered 5 seconds after the onset of illumination at 500
µmol photons $m^{-2} s^{-1}$. The values are averages of 3 biological replicates + SD. n.s. = statistically non-significant difference
according to a paired *t*-test (P=0.20). **(c)** g_H+ was measured in *Arabidopsis* WT-gl1 and *pgr5* mutant leaves incubated on
water or water + 0.1 mM NEM. The water samples are the same as in Figure 1, while the +NEM values are averages of 4
biological replicates ± SEM.

These results provided evidence that PGR5 is involved in a redox-dependent regulatory mechanism of
ATP synthase activity that is distinct from $F_1\gamma$ redox state. Interestingly, it has been reported that
PGR5 from cucumber (*Cucumis sativus L.*) can interact with the AtpB subunit of the chloroplast ATP
synthase in yeast-two-hybrid tests (Wu et al., 2021)**.** To investigate the ability of PGR5 to directly
interact with ATP synthase *in planta*, we performed bimolecular fluorescence complementation
(BiFC) tests between AtPGR5 and AtCF$_1\gamma$. Indeed, strong YFP fluorescence co-localising with
chlorophyll autofluorescence was detected, indicating interaction between the two proteins in
chloroplast thylakoid membranes (Fig. 8a). As negative controls we performed BiFC tests between

AtPGR5 and the NdhS subunit of the chloroplast NAD(P)H dehydrogenase-like complex, another

major thylakoid protein complex, as well as $AtCF_1\gamma$ and Thioredoxin x, a chloroplast protein similar

in size to AtPGR5 (Fig. S9). Moreover, an Alphafold2 Multimer model predicts that SynPgr5 can

bind to the $F_1\gamma$ subunit of the *Synechocystis* ATP synthase (Fig. 8b). As the $F_1\varepsilon$-subunit likely remains

bound to $F_1\gamma$ even in its non-inhibitory conformation (Kato et al., 1997), we also included $F_1\varepsilon$ in our

model.

Figure 8. Protein–protein interaction between ATP synthase and PGR5. **(a)** Bimolecular fluorescence complementation

(BiFC) test for protein-protein interaction between Arabidopsis $CF_1\gamma$ fused to an N-terminal fragment of yellow fluorescent

protein ($AtCF_1\gamma$:YFP-N) and Arabidopsis PGR5 fused to a C-terminal YFP fragment (AtPGR5:YFP-C) in tobacco leaves.

The left panel shows Chlorophyll *a* autofluorescence in purple, the middle panel YFP fluorescence in yellow, and the right

panel a merged image of YFP and chlorophyll images. The scale bar is 10 µm. **(b)** An Alphafold2 Multimer prediction of an

interaction complex between *Synechocystis* ATP synthase γ subunit (*sll1327*, green), ATP synthase ε subunit (*slr1330,*

yellow*)*, and *Synechocystis* Pgr5 (*ssr2016*, magenta). The top-ranked model with a pTM score of 0.797 and an ipTM score of

0.702 is shown. Structure of a full Spinach chloroplast ATP synthase ($SoCF_0CF_1$) (Hahn et al., 2018) is shown for reference,

with the $CF_1\gamma$ and $CF_1\varepsilon$ subunits highlighted in green and yellow, respectively.

DISCUSSION

Substantial adjustments of thylakoid conductivity take place during sudden changes in light intensity
in both chloroplasts and cyanobacteria, in order to control induction of the photoprotective
mechanisms. Results shown herein indicate that this regulation is independent of the thiol redox state
of $CF_1\gamma$ (Fig. 1), but dependent on another redox-based mechanism that involves the PGR5 protein
(Fig. 6, Fig. 7) in a manner that has been conserved in evolution from free-living cyanobacteria to
green algae and C_3 plants, as well as C_4 plants.

PGR5 has an evolutionarily conserved role in regulation of thylakoid conductivity

The PGR5 protein has been previously understood to either directly catalyse or facilitate CET around
PSI in plants (Munekage et al., 2002) and cyanobacteria (Yeremenko et al., 2005). Lack of PGR5
caused a distinct inability to oxidise PSI in chloroplasts, which was interpreted as being caused by
failure to induce photosynthetic control and NPQ due to insufficient acidification of the thylakoid
lumen in the absence of PGR5-mediated CET (Yamamoto & Shikanai, 2019). However, contrasting
evidence was already provided early on showing that ferredoxin-dependent CET does function in the
absence of PGR5 (Nandha et al., 2007), suggesting that the phenotype of the *pgr5* mutant may be
caused by another mechanism.

We showed previously that in *pgr5 Arabidopsis* plants overexpressing the chloroplast NADPH-
dependent thioredoxin reductase (OE-NTRC *pgr5*), *pmf* was restored to a WT-level during LL-to-HL
transitions (Nikkanen et al., 2018). This was insufficient however, to induce photosynthetic control,
resulting in the OE-NTRC *pgr5* plants suffering from almost as severe over-reduction of the electron
transport chain as *pgr5* plants. Concurring results were more recently reported from *Arabidopsis*
plants expressing Plastid terminal oxidase 2 from *Chlamydomonas reinhardtii* (CrPTOX2) in the *pgr5*
mutant background: The introduction of CrPTOX2 resulted in restoration of WT-like (ΔpH-
dependent) NPQ, but oxidation of PSI was still as impaired as in *pgr5* mutants (Zhou et al., 2023).
These results suggest that the inability of *pgr5* mutants to induce photosynthetic control in HL is not
simply caused by loss of ΔpH, but the AtPGR5 protein is directly required. Similarly to *pgr5*, OE-
NTRC *pgr5* plants still showed elevated g_H+ during transitions to HL (Nikkanen et al., 2018). These
findings argue for a complex role of AtPGR5 in regulation of thylakoid proton conductivity and
electron transport.

The *Synechocystis* Δ*pgr5* mutant showed no impairment of CET (Fig. 3a). Our data is in line with a
study by Miller et al. showing that the antimycin a-sensitive pathway (=PGR5-dependent) does not
contribute to *pmf* formation during dark/light transitions in *Synechocystis*. Instead, the CET-dependent
fraction of *pmf* generation was entirely attributable to the NDH-1 complex (Miller et al., 2021). As the
extra ATP produced by CET is understood to enable more efficient operation of the CBC by adjusting

the ATP:NADPH ratio, the fact that no impairment of CO_2 fixation rate was observed in $\Delta pgr5$ (Fig. 4f) further indicates that SynPgr5 is not needed for CET in *Synechocystis.*

Our ECS results both with the *Chlamydomonas pgr5* mutant (Fig. 3c) as well as the *pgr5-Cas Arabidopsis* mutant (Fig. S1C) showed elevated proton flux (v_H+) in HL, which is also incompatible with a significant role for PGR5 in CET, and may rather indicate enhancement of the CET rate. Accordingly, CrPGR5 was not detected in CET supercomplexes (Iwai et al., 2010). It was also recently reported, based on simultaneous near-infrared and chlorophyll fluorescence spectroscopy, that the absence of AtPGR5 enhanced CET activity in *Arabidopsis* (Maekawa et al., 2024). A lower v_H+ in LL that cannot be fully explained by a lower linear electron transport rate has, however, been reported in *Arabidopsis* (Degen et al., 2023) and *S. viridis* (Fig. S7) (Woodford et al., 2024) *pgr5* mutants. Interestingly though, the *Arabidopsis pgr5-Cas* mutant showed WT-like v_H+ in LL (Fig. S1c), suggesting that the low v_H+ in the *pgr5-1* mutant (Fig. S2a) may be affected by the additional mutation of the At2g1724 gene (Wada et al., 2021).

If PGR5 was directly involved in ferredoxin-dependent CET, one would expect *pgr5* mutants to suffer from a bottleneck of electron transfer at ferredoxin. It was recently shown that the Arabidopsis *pgr5* mutant accumulates PSI centres with damaged FeS clusters, which results in an inability to reduce Fed (Tiwari et al., 2024), meaning that the bottleneck likely forms already at P700. The accumulation of damaged PSI centres makes it appear as if the mechanism of ferredoxin-dependent CET itself is impaired. These results suggest that the phenotype of *pgr5* mutants may not be caused by direct impairment of CET.

PGR5-mediated downregulation of ATP synthase depends on thiol redox conditions

The elevated g_H+ of PGR5-deficient *Synechocystis*, *Chlamydomonas*, *Arabidopsis,* and *S. viridis* during high-light phases of fluctuating light (Fig. 1, Fig. 2, Fig. 4, Fig. S7) is consistent with PGR5 functioning as a direct or indirect down-regulator of ATP synthase activity (Kanazawa et al., 2017; Nikkanen et al., 2018; Tikkanen et al., 2015). *In planta* interaction of AtPGR5 with AtCF$_1\gamma$ in BiFC tests (Fig. 7a) and *in silico* modelling of SynPgr5-SynF$_1\gamma$- SynF$_1\varepsilon$ interaction complex (Fig. 8b) suggest that PGR5 may inhibit ATP synthase by directly binding to the F$_1\gamma$ subunit. F$_1\varepsilon$-inhibition likely prevents ATP hydrolysis in dark and LL conditions, when *pmf* is low, while PGR5 would limit ATP synthase activity in HL, possibly allowed by the non-inhibitory "down" conformation of F$_1\varepsilon$ (Feniouk et al., 2010), to allow build-up of sufficient ΔpH for induction of photoprotection.

Moreover, this mechanism may be regulated by the thiol redox state of the chloroplast stroma or cell. PGR5 contains a conserved cysteine residue (Munekage et al., 2002; Yeremenko et al., 2005), and

which could be target for regulatory thiol modifications. In line with this hypothesis, AtPGR5 was

found able to interact with AtNTRC in an *in planta* BiFC test, and overexpression of AtNTRC

resulted in intensified downregulation of thylakoid proton conductivity during transitions to HL, but

only in the presence of AtPGR5 (Nikkanen et al., 2018). Moreover, using a *pgr5 ntrc* double mutant

of *Arabidopsis*, Naranjo et al. showed that the high NPQ observed in *ntrc* mutant plants is dependent

on the presence of AtPGR5 (Naranjo et al., 2021). *Ntrc* mutant plants have a diminished AtPGR5

protein level (Nikkanen et al., 2018), most likely to compensate for the impaired activation of ATP

synthase via reduction of the $AtCF_1\gamma$ disulphide (Carrillo et al., 2016; Nikkanen et al., 2016).

It has been suggested that a disulphide bridge between AtPGR5 and AtPGRL1 is required for

PGR5/PGRL1-dependent CET in *Arabidopsis* (Hertle et al., 2013). However, a CrPGR5 with the

conserved cysteine residue mutated to a serine was able to complement the impairment of CET in the

Chlamydomonas pgr5 mutant (Buchert et al., 2020), suggesting that the conserved cysteine residue in

PGR5 may be involved in a non-CET related regulatory mechanism.

Transient reduction of AtPGRL1 occurs upon onset of illumination, coinciding with increase in *pmf*,

PSI oxidation, and induction of NPQ (Chaturvedi et al., 2024; Hertle et al., 2013; Nikkanen et al.,

2018; Wolf et al., 2020). TRXm4 forms a disulphide bridge with AtPGRL1, and cleavage of that

disulphide (most likely by another thioredoxin isoform) and transient release of TRXm4 also occur at

dark-to-light transitions (Okegawa & Motohashi, 2020). This has been suggested to indicate activation

of CET (Chaturvedi et al., 2024; Hertle et al., 2013; Okegawa & Motohashi, 2020; Wolf et al., 2020),

but the same results could also be interpreted as reduction of AtPGRL1 affecting the association of

AtPGR5 with AtPGRL1, releasing AtPGR5 to interact with ATP synthase and to downregulate its

activity. This would limit H^+ efflux from the lumen and cause build-up of *pmf,* and consequently,

induction of NPQ and photosynthetic control. We therefore suggest that the phenotypes of *pgr5*

mutants may have been misinterpreted as being caused by directly impaired CET. For example, it was

recently shown that point mutations of disulphide-forming cysteine residues in AtPGRL1a results in

elevated *pmf*, NPQ, and donor-side limitation of PSI (Chaturvedi et al., 2024). While the authors did

not show data on g_H+, it is possible that this phenotype was caused not by increased CET, but by

constitutive inhibition of ATP synthase activity by AtPGR5. Similarly, it has been reported that

AtPGR5 can enhance CET if both AtPGRL1 and AtPGRL2, a protein causing degradation of AtPGR5

in the absence of AtPGRL1, are missing (Rühle et al., 2021). This conclusion was based on higher

pmf and NPQ in the *pgrl1a pgrl1b pgrl2* triple mutant compared to *pgrl1* or *pgr5* single mutants. We

suggest, however, that the increased *pmf* was, again, probably mediated or at least contributed to by

lowered ATP synthase conductivity.

In the current study, we explored the effects of perturbing the chloroplast or cellular redox state agents

on the conductivity of ATP synthase. Interestingly, we found that addition of methyl viologen (MV)

results in strong reduction of chloroplast enzymes in *Arabidopsis*, including AtCF$_1\gamma$ (Fig. 6a).

Accordingly, $g_{H}+$ was elevated in dark-adapted MV-treated leaves (Fig. 6b). However, strong

downregulation of $g_{H}+$ during illumination was measured in MV-leaves, but only in the presence of

AtPGR5 (Fig. 6c). Thiol-alkylating agent N-ethylmaleimide (NEM) had a similar albeit less dramatic

effect (Fig. 7c). Interestingly, lack of AtPGR5 made the plants immune to NEM-induced $g_{H}+$ decrease

under HL, but did not prevent the decrease observed under LL phases of the fluctuating light

experiment. These results provide further evidence that AtPGR5 is required for redox-dependent

downregulation of $g_{H}+$ under high irradiance. We hypothesise that in WT *Arabidopsis*, addition of

MV likely causes strong reduction of either AtPGR5/AtPGRL1/AtTRXm4 directly or some

associated factor that would, without an MV treatment, function as an inhibitor of the ATP synthase

during sudden increases in light intensity. Importantly, this inhibitory effect overrides the activating

effect of a fully reduced AtCF$_1\gamma$. In the absence of AtPGR5, the inhibitory mechanism does not

function even in presence of MV.

We cannot fully exclude the possibility of the apparent reduction of chloroplast enzymes in presence

of MV being caused by overoxidation of thiols to sulphenic acids (Huang et al., 2019), especially in

the case of 2CysPRXs (Cerveau et al., 2016; Puerto-Galan et al., 2013). S-sulphenylated proteins

cannot form disulphides and thus cannot be labelled by the alkylating agent in our protocol, migrating

similarly to fully reduced proteins in mobility shift assays. Apart from 2CysPrxs, where the thiols are

required for the catalytic activity of the enzyme, overoxidation may in fact result in in a conformation

that is functionally similar to the reduced state of the protein. However, the elevation of $g_{H}+$ at the

onset of illumination in MV-treated leaves (Fig. 6b) suggests otherwise, at least in the case of CF$_1\gamma$ in

darkness. Moreover, overoxidation would inactivate 2-CysPRXs, preventing their oxidising effect on

other thiol proteins in the chloroplast, including AtCF$_1\gamma$ (Pérez-Ruiz et al., 2017; Vaseghi et al.,

2018). Similar results obtained with addition of NEM also make this scenario unlikely.

In *Synechocystis*, addition of NEM caused an opposite phenotype to *Arabidopsis*, with $g_{H}+$ being

elevated rather than diminished (Fig. 7a). The NEM-induced $g_{H}+$ increase was diminished in

Synechocystis Δpgr5 and absent in WT *Synechococcus*, a species that does not have a PGR5

orthologue (Shimakawa et al., 2016). Untreated *Synechococcus* did, however, exhibit similar

downregulation of $g_{H}+$ under strong illumination as *Synechocystis* or *Arabidopsis* (Fig. S6). These

results suggest that the regulatory mechanisms involved in this response may differ between

organisms in terms of directionality of redox-regulation and involvement of PGR5, with

Synechococcus possibly using an unrelated, convergently evolved analogous mechanism. The

molecular details of these differing responses remain to be elucidated in future studies.

Interestingly, it has been reported that alkylation of cysteine 89 in the (*Spinacia oleracea*) SoCF$_1\gamma$ by

NEM or crosslinking Cys89 with Cys322 inhibits photophosphorylation and induces loss of the

proton gradient (Evron & Pick, 1997; McCarty & Fagan, 1973; Soteropoulos et al., 1994). This effect

was not observed in the dark, suggesting Cys89 only becomes accessible to modifications in light

upon generation of ΔpH (McCarty & Fagan, 1973). It is therefore possible that Cys89 is responsible

for the middle band in the AtCF$_1\gamma$ mobility shift assays that is also present in the control sample (Fig.

1e), where all thiols accessible in the dark are alkylated with NEM before addition of MAL-PEG.

MAL-PEG likely gains access to Cys89 after the subsequent DTT treatment, resulting in the observed

mobility shift. The F$_1\gamma$ Cys89 residue is conserved in the green lineage, including cyanobacteria

(Hisabori et al., 2013), suggesting a functional role. Our Alphafold2 model of a SynF$_1\gamma$-SynPGR5

interaction complex predicts, however, that neither the conserved Cys30 in SynPgr5 or Cys90 in

SynF1γ are involved in mediating the protein-protein interaction. This is also consistent with the lack

of changes in AtCF$_1\gamma$ redox state in fluctuating light (Fig. 1e), suggesting that thiol/disulphide

exchanges of F$_1\gamma$ are not involved in the mechanism of adjusting g$_H$+ in fluctuating light. The

predicted binding of SynPgr5 to SynF$_1\gamma$ in our model somewhat resembles the binding of the

inhibitory IF$_1$ protein to mitochondrial ATP synthase, which slots between the F$_1\gamma$, F$_1\alpha$, and F$_1\beta$

subunits (García-Bermúdez & Cuezva, 2016). This could also explain the observed interaction between

cucumber PGR5 and F$_1\beta$ (Wu et al., 2021).

An alternative or additional mechanism for the regulation of g$_H$+ in fluctuating light in plants could

function through changes in intercellular inorganic carbon concentration (C$_i$). C$_i$ increases upon HL to

LL transitions as carbon fixation rate suddenly drops (Vialet-Chabrand et al., 2017), and increase in C$_i$

is known to increase g$_H$+ via an unknown regulatory pathway (Kohzuma et al., 2013). It is unlikely,

however, that the inability of *pgr5* to down-regulate g$_H$+ in HL would be caused by an elevated

concentration of C$_i$, because WT-like levels of C$_i$ were measured under HL in PGR5-deficient rice

plants (Nishikawa et al., 2012). The carbon fixation capacity of *pgr5* plants only goes down as a

consequence of prolonged HL exposure and ensuing PSI photoinhibition (Gollan et al., 2017; Lima-

Melo et al., 2018). Similarly, we detected no impairment of CO$_2$ fixation in the *Synechocystis* Δ*pgr5*

mutant (Fig. 3F). Interestingly, expression of FlvA and FlvB from the moss *Physcomitrium patens* in

the *Arabidopsis pgr5* mutant background alleviated the elevated g$_H$+ phenotype (Yamamoto &

Shikanai, 2020), highlighting the complex relationship between oxidation of PSI and regulation of

ATP synthase.

Physiological significance of PGR5-mediated downregulation of ATP synthase in *Synechocystis*

Lack of SynPgr5 caused no impairment of PSI oxidation or growth despite lowered *pmf* in

Synechocystis under fluctuating light (Fig. 2, Fig. 3b). This may be due to prevalence of FDPs as a

protective electron sink on the acceptor side of PSI in cyanobacteria (Allahverdiyeva et al., 2013;

Santana-Sanchez et al., 2019). Even in the absence of Flv1/3-mediated O_2 photoreduction in the

$\Delta pgr5\ flv3$ double mutant, however, no significant additional impairment of PSI oxidation in

comparison to $\Delta flv3$ single mutant was observed (Fig. 2d–E). Slightly elevated FDP activity was

however measured in fluctuating light grown $\Delta pgr5$ under fluctuating light (Fig. 5), which may allow

the mutant to maintain sufficient PSI oxidation in HL despite diminished *pmf* and to grow similarly to

WT in fluctuating light (Fig. 2F). We have recently proposed that dissipation of *pmf* (lower cytosolic

pH) causes FDP hetero-oligomers to associate more strongly with the thylakoid membrane, increasing

photoprotective O_2 photoreduction activity (Eckardt et al., 2024; Nikkanen et al., 2023). In $\Delta pgr5$, the

decreased *pmf* due to elevated g_{H^+} in HL (Fig. 2a) may therefore cause the slightly increased FDP

activity during the HL phases of fluctuating light conditions (Fig. 5), at least partly compensating for

the loss of photoprotective capacity via ΔpH-induced photosynthetic control.

Interestingly, there appears to be a regulatory link between FDPs, ATP synthase, and SynPgr5 in

cyanobacteria. During transitions to HL, lack of Flv1/3 results in a loss up to 75% of the proton flux

during the first minute of illumination in *Synechocystis* (Nikkanen et al., 2020) (Fig. S2b) as well as in

the filamentous model cyanobacterium *Anabaena* sp. PCC 7120 (Santana-Sánchez et al., 2023).

However, cyanobacterial cells compensate for this by downregulating g_{H^+} (Fig. 2a), achieving WT-

like *pmf* levels after the initial stages of HL transitions (Fig. 2b). In in the absence of both Flv1/3 and

SynPgr5 in the $\Delta pgr5\ flv3$ double mutant, however, this downregulation of g_{H^+} did not occur,

indicating that SynPgr5-mediated inhibition of ATP-synthase is required for the compensatory

mechanism. Interestingly, proton flux also recovered to WT-levels in $\Delta pgr5\ flv3$ (Fig. S2b),

suggesting e.g. increased CET via NDH-1.

It remains to be investigated what the environmental conditions are where SynPgr5 has a

physiologically significant role. Future studies should focus for example on mixotrophic conditions,

where overexpression of SynPgr5 has been shown to inhibit growth (Margulis et al., 2020) and

diurnal rhythms, which present additional challenges for coordination of the bioenergetic pathways

and metabolism in cyanobacteria (Ortega-Martínez et al., 2024; Solymosi et al., 2020).

Conclusion

The activity of chloroplast or cyanobacterial ATP synthase is dynamically regulated during

fluctuations in light intensity. These adjustments are not dependent on the thiol redox state of the $F_1\gamma$

subunit, but instead depend on the PGR5 protein as well as the thiol redox state of the stroma or

cytosol. This mechanism has been conserved in evolution from free-living cyanobacteria to

chloroplasts in algae, C_3 plants as well as C_4 plants. The inability to downregulate ATP synthase

activity under strong illumination is the only phenotype of PGR5-deficient knockout mutants that can

be observed in all representatives of the groups of photosynthetic organisms studied here; cyanobacterium *Synechocystis* sp. PCC 6803, green alga *Chlamydomonas reinhardtii*, C_3 plant *Arabidopsis thaliana*, and C_4 plant *Setaria viridiis*. The role of PGR5 is vital for oxidation of PSI in plants and algae, but not in cyanobacteria. We also demonstrated that the cyanobacterial Pgr5 is not needed for cyclic electron transport. We suggest that PGR5 directly binds to ATP synthase and functions an inhibitory factor in a manner that is dependent on the thiol redox state of the cell or chloroplast. The observed effect of plant PGR5 on CET is likely an indirect consequence of misregulation of ATP synthase and, as shown by (Tiwari et al., 2024), increased photoinhibition of PSI, although a role for PGR5 in regulating CET via Cyt b_6f cannot be excluded (Buchert et al., 2020). Our study lays important groundwork for understanding the regulatory mechanisms of the *pmf* and their evolution, possibly enabling biotechnologies to modulate *pmf* regulation for enhancement of photosynthetic efficiency in crop plants or microbial bioproduction platforms.

MATERIALS AND METHODS

Strains, plant lines and growth conditions

Arabidopsis thaliana WT-gl1 or WT-Col-0, *pgr5-1* (At2g05620 knockout) (Munekage et al., 2002), and *pgr5-Cas* (At2g05620 CRISPR-Cas9 mutant line) (Penzler et al., 2022) plants were grown for 4 weeks under 200 µmol photons in a 12/12h photoperiod before collecting individual leaves for experiments.

For the BiFC experiments, WT *Nicotiana benthamiana* plants were grown under 130 µmol photons $m^{-2} s^{-1}$ at 23°C in a 16/8 hr light/dark photoperiod.

Chlamydomonas reinhardtii WT 137c, *pgr5* knockout and PGR5C complementation strains (Johnson et al., 2014; Jokel et al., 2018) were grown under continuous 30 µmol photons $m^{-2} s^{-1}$ at 25 °C and 120 rpm in TAP medium.

Setaria viridis cv MEO V34-1 *pgr5* knock-out mutant was generated using CRISPR-Cas9 gene-editing as described in detail in (Ermakova et al., 2024). WT plants and plants with *pgr5-3* null alleles described in (Woodford et al., 2024) were analysed. Plants were grown in a controlled environment room with a 16 h : 8 h, light : dark photoperiod, 28°C day and 22°C night, 60% humidity and ambient CO_2 at a light intensity of 300 µmol $m^{-2} s^{-1}$ supplied by 1000 W red sunrise 3200K lamps (Sunmaster Growlamps, Solon, OH, USA). Youngest fully expanded leaves of 3–4-week-old plants were used in analysis.

WT, Δpgr5, Δflv3 (Helman et al., 2003) and *Δpgr5 flv3 Synechocystis* sp. PCC 6803 strains as well as

WT *Synechococcus elongatus* sp. PCC 7942 cells were grown under continuous 50 µmol photons m^{-2}

s^{-1} at 30 °C and air-level [CO_2] in pH 7.5 BG-11 medium. Unless stated otherwise, cultures were

grown for 4 days in 30 ml flasks, then pelleted and resuspended in fresh BG-11 at an appropriate

chlorophyll concentration for each experiment. For the growth curves under fluctuating light, WT,

Δpgr5 and *Δpgr5 flv3* cells were grown for 7 days in conditions where light intensity was held at 20

µmol photons m^{-2}s^{-1} and increased to 500 µmol photons m^{-2}s^{-1} for 30 sec every 5 min. Samples were

taken and OD$_{750\,nm}$ measured with a spectrophotometer every 24h. For Fig. 5, cells were grown in a

regime in which light intensity fluctuated between 1 min periods of 25 and 500 µmol photons m^{-2}s^{-1}.

Construction of Δ*pgr5* and Δ*pgr5 flv3* knockout mutants

The upstream and downstream flanking sequences of the *pgr5* (*ssr2016*) gene and the *aphI* (Km^R)

gene replacing the *ssr2016* open reading frame were amplified from genomic DNA of *Δpgr5* mutant

generated earlier in a different *Synechocystis* WT background as described in (Allahverdiyeva et al.,

2013). After transformation into *Synechocystis* sp. PCC 6803 WT strain and the *Δflv3* strain (Helman

et al., 2003), the transformants were selected on BG-11 plates with 50 µg/ml kanamycin. Complete

segregation of the mutation was confirmed by PCR with specific forward primer 5′-

AGCCAAACCGCATCTAACG-3′ and reverse primer 5′-TTCATAACGCCTCCGGTC-3′. The

expected PCR fragment length was 0.7 kb for the WT and 1.7 kb for the mutant (Fig. S10). The

mutation in the *flv3* open reading frame was confirmed by using forward primer 5′-

GTACGGCATGTTCACTACC-3′ and reverse primer 5′- GATCAGCGTTAGCCTGTAA-3′, and the

expected PCR fragment length was 1.0 kb for the WT and 2.6 kb for the mutant (Fig. S10). Two

separate clones of *Δpgr5* were used interchangeably for the experiments, as no difference was

detected in their phenotypes.

Electrochromic shift (ECS) measurements

Individual *Arabidopsis* leaves were measured with the Dual-PAM 100 spectrophotometer (Walz) and

its P515/535 accessory module (Schreiber & Klughammer, 2008) as described earlier (Guinea Diaz et

al., 2020; Nikkanen et al., 2018). For the experiment in Figure 1, dark-adapted (30 min) leaves were

exposed to a light regime fluctuating between 1 min periods of 50 and 825 µmol photons m^{-2} s^{-1}, with

250 ms dark intervals administered every 5 seconds for the first 30 seconds and every 10 seconds

thereafter. For the methyl viologen (MV) experiment, detached leaves were dark-incubated overnight

on water with 0.05% Tween-20 $\pm$ 1 μM MV. In the ECS measurement, dark intervals of 450 ms were administered every 4 s until 28 s during 95 μmol photons m^{-2}s^{-1} of actinic illumination, every 10 s between 28 and 58 s, every 30 s between 58 and 298 s, every 4 s after transition to 825 μmol photons m^{-2}s^{-1} between 298 and 318 s, and every 30 s thereafter. 2,000 Hz pulse frequency of the measuring light was used. ΔECS_T values were normalised to the ΔECS measured upon a single-turnover saturating flash on dark-adapted leaves (ΔECS_{ST}) (Mathiot & Alric, 2021). For the NEM experiment, detached leaves were incubated in dark on water with 0.05% Tween-20 $\pm$0.1 mM NEM for 2 hours before the experiment.

Chlamydomonas cultures were measured using the same protocol as *Arabidopsis*, with chlorophyll concentration set to 20 μg/ml. Dark-adapted *S. viridis* leaves were subjected first to 15 min at 400 μmol photons m^{-2} s^{-1} and then to 10 min cycles at irradiance alternating between 2000 and 400 μmol photons m^{-2} s^{-1}. The actinic light was switched off for 30 s at 2 min since the beginning of illumination and then at 5 min intervals.

ECS changes were measured from *Synechocystis and Synechococcus* cells by monitoring the 500-480 nm absorbance difference signal (Viola et al., 2019) using a JTS-10 spectrophotometer (BioLogic) as described in (Nikkanen et al., 2020). Cells were pelleted and resuspended in fresh BG-11 at 7.5 μg Chl ml^{-1}. When appropriate, 0.1 mM NEM was added to the samples before a 5 min dark-adaption prior to the measurement. Each measurement was also conducted with the cells illuminated only by the measuring light flashes, and the ECS changes recorded were then subtracted from the measurements under green actinic light, in order to control for any actinic effects of the measuring light. A moderate (60 μmol photons m^{-2} s^{-1}, relative to growth light of 50 μmol) rather than a low actinic light intensity was used in fluctuating light to allow a sufficient signal-to-noise ratio for DIRK analysis. The cyanobacterial ECS signals were not normalised to ECS$_{ST}$ due to a low signal-to-noise ratio of single turnover traces. Instead, a constant chlorophyll concentration was used.

The *pmf* and g$_H$+ parameters were determined as the difference between magnitude of the ECS signal in light – y0 value of a first-order fit to the decay kinetics of the signal during a dark interval, and the inverse of the time constant of the fit, respectively, while v$_H$+ was derived as *pmf* x g$_H$+ (Cruz et al., 2005). Fitting and data processing was done with the OriginPro 2024b (OriginLab) software.

Saturating pulse analysis of chlorophyll fluorescence and P700$^+$

The extents of the donor side and acceptor side limitations of PSI, Y(ND) and Y(NA), respectively, were determined under fluctuating light conditions by a saturating pulse analysis of the P700$^+$ signal using the Dual-PAM 100 (Klughammer & Schreiber, 2008). Chlorophyll autofluorescence was

788 simultaneously recorded to determine the Y(NPQ) parameter (in *Arabidopsis*) as described by

789 (Schreiber et al., 2008). Saturating pulses (8000 μmol photons m^{-2} s^{-1} for *Arabidopsis* and 3000 for

790 *Synechocystis*) were administered every 15 seconds during illumination.

Deconvoluted P700, plastocyanin, and ferredoxin redox changes

The deconvoluted plastocyanin (PC), P700, and ferredoxin redox changes were determined by NIR

absorbance difference spectroscopy using the DUAL-KLAS-NIR spectrophotometer (Walz)

(Klughammer & Schreiber, 2016). CET and LET at PSI in *Synechocystis* were quantified using

analysis of dark-interval relaxation kinetics (DIRK) according to (Theune et al., 2021) with

modifications. *Synechocystis* cells were pelleted and adjusted to 15 μg Chl ml^{-1} with fresh BG-11.

Cells were pre-illuminated for 2 min with 500μE, followed by administration of 100 dark intervals of

20 ms. The 100 decay traces were averaged and initial slopes of the PC and P700 decay curves were

used to calculate J_{PSI}. J_{PSI}-CET was determined by repeating the same experiment in the presence of

10μM DCMU to block electron transport from PSII. The NIRMAX script (Klughammer & Schreiber,

2016) modified for cyanobacteria was used to determine the maximal oxidation of PC and P700 and

maximal reduction of Fed. The model spectra for the deconvolution of PC, P700, and Fed redox

changes in *Synechocystis* were measured as described in (Nikkanen et al., 2020). Arabidopsis

NIRMAX measurements of dark-adapted leaves were conducted as described in (Nikkanen et al.,

2019). Reduction kinetics of Fed under far red light were measured after running the NIRMAX script,

illuminating detached leaves for 1 second with intensity 20 far-red light.

Protein thiol alkylation and SDS-PAGE

4-week-old *Arabidopsis* WT-Col-0 plants were dark-adapted, exposed to a light regime fluctuating

between 1-minute periods of 50 and 800 μmol photons. Samples (individual leaves) were taken every

20 seconds and quickly placed in 10% % TCA solution to freeze the thiol redox state of proteins.

TCA precipitation, alkylation of thiols with MALPEG-5000, and SDS-PAGE was then performed as

described in Nikkanen et al., (2016). Briefly, free thiol groups were first alkylated with NEM.

Following alkylation, disulphide bonds in proteins were reduced with dithiothreitol (DTT), and the

resulting thiols were then alkylated using methoxypolyethylene glycol maleimide Mn 5000 (MAL-

PEG, Sigma-Aldrich). This treatment makes the in-vivo oxidised forms of proteins migrate more

slowly than reduced ones in SDS-PAGE. For MV-treated samples, detached leaves were dark-

incubated overnight on water with 0.05% Tween-20 or water 0.05% Tween + 1 μM MV. Leaves were

then illuminated in growth conditions for 0, 30, 90, or 180 min before sample collection and

placement in 10% TCA.

Total protein extractions from *Synechocystis* cells were done as described in (Zhang et al., 2009), and

protein concentration was determined by the DC Protein Assay Kit (Bio-Rad, based on the Lowry

assay). Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and immunoblotting

were performed as previously described (Nikkanen et al., 2016). 4–15% Mini-PROTEAN TGX

precast gels (Bio-Rad) were used for electrophoresis except for Figure 5, for which 12%

polyacrylamide gels with 6M urea were cast. PVDF membranes were probed with antibodies raised

against $CF_1\gamma$ (Agrisera, AS08 312), FBPase (courtesy of Dr M. Sahrawy), AtpB (Agrisera, AS), Flv3

(Genscript), NTRC (Lepistö et al., 2009), or 2-CysPrx (courtesy of Prof. F. J. Cejudo).

Membrane Inlet Mass Spectrometry (MIMS)

Synechocystis in vivo O_2 and CO_2 gas fluxes were monitored in real-time by membrane inlet mass

spectrometry (MIMS) as described earlier (Mustila et al., 2016), with O_2 uptake distinguished from O_2

evolution by enrichment of the $^{18}O_2$ isotope in the medium. Chlorophyll concentration was set to 10

µg/ml, 1.5 mM $NaHCO_3$ was added, and cells were dark-adapted for 15 min prior to the

measurements. Gas exchange was monitored under 500 µmol photons $m^{-2}s^{-1}$ illumination for 5 min.

See legend for Fig. 3 for experimental details.

Bimolecular Fluorescence Complementation (BiFC) tests

In planta protein–protein interaction tests by bimolecular fluorescence complementation (BiFC) were

conducted as described earlier (Nikkanen et al., 2016, 2018). *Nicotiana benthamiana* plants were used

for transient expression of fusion constructs via *Agrobacterium tumefaciens* strain GV3101

infiltration. Imaging was done 3 days after infiltration using a Zeiss LSM780 confocal microscope.

Construction of the AtPGR5:YFP-C and AtNdhS:YFP-N expression vectors for YFP-fusion proteins

is described in (Nikkanen et al., 2018) and construction of the $AtCF_1\gamma$:YFP-N and AtTRXx:YFP-C

vectors in (Nikkanen et al., 2016).

In silico modelling

848   The amino acid sequences for *Synechocystis* genes *sll1327, slr1330* and *ssr2016* were retrieved from

849   the Uniprot database (entries P17253, P26533, and P73358, respectively). AlphaFold2 Multimer

850   Google Colab notebook (Mirdita et al., 2022) was used to model the interaction complex using 6

851   recycles and pdb100 template mode, with Amber relaxation of the best model. The model with the

best pTM score was selected for visualisation using the Mol* 3D viewer (Sehnal et al., 2021). The *Spinacia oleracea* chloroplast ATP synthase structure (Hahn et al., 2018) was retrieved from the RCSB PDB database (entry 6FKF) and visualised by Mol* 3D viewer.

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Author Contributions

L.N. conceived the research idea, devised the experimental plan, performed most of the experiments, analysed the data, and wrote the first draft of the article. L.T.W. performed part of the cyanobacterial ECS and DKN measurements and analysed the data. R.W. and M.E. performed the ECS measurements in *S. viridis* and analysed the data. H.M. created the *Synechocystis* Δ*pgr5* and Δ*pgr5 flv3* mutants. E.R. and Y.A. supervised research and provided resources. All authors participated in editing the article.

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