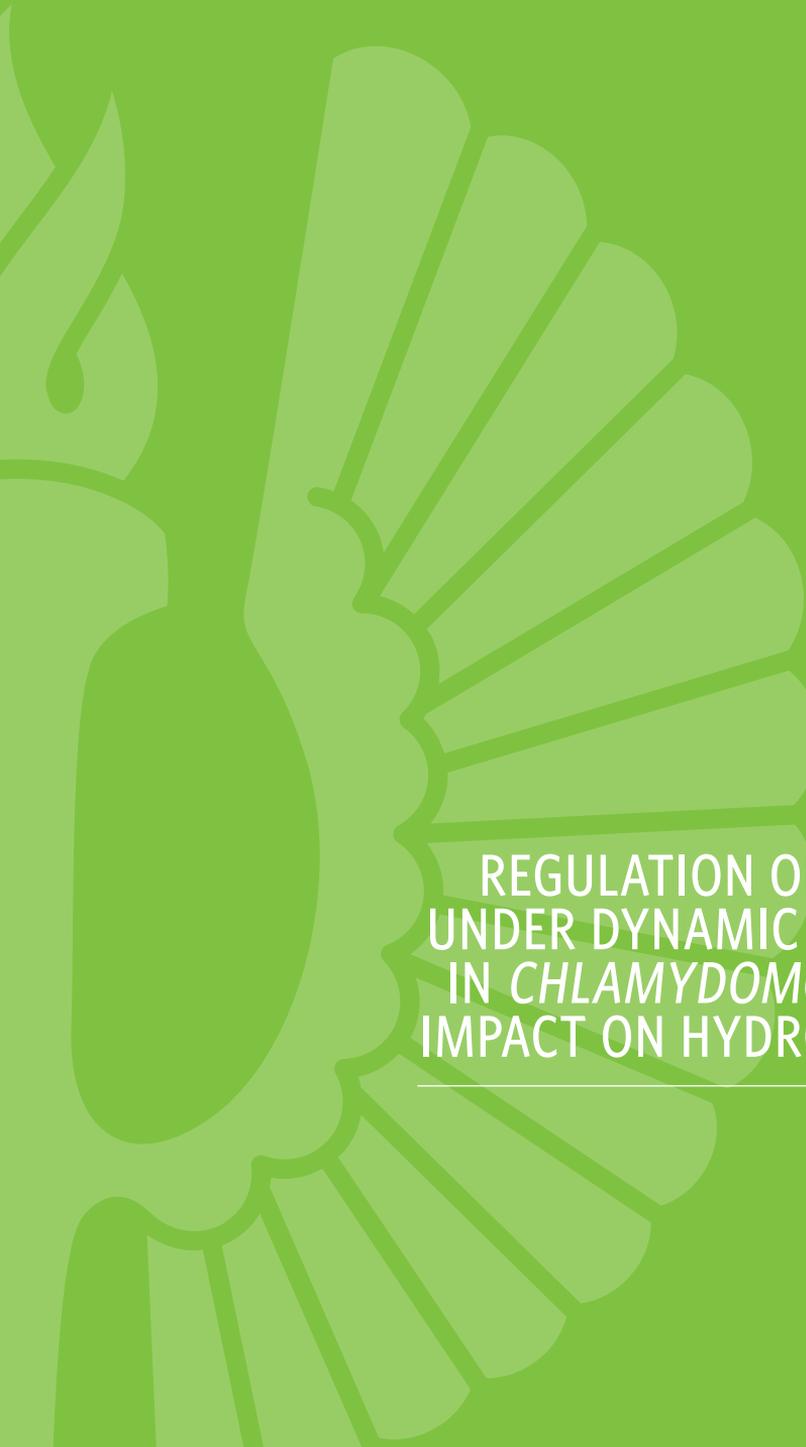




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A large, stylized green leaf graphic is positioned on the left side of the cover. It has a central vein and several smaller veins branching out, creating a fan-like shape. The leaf is rendered in a lighter shade of green than the background.

# REGULATION OF PHOTOSYNTHESIS UNDER DYNAMIC LIGHT CONDITIONS IN *CHLAMYDOMONAS REINHARDTII*: IMPACT ON HYDROGEN PRODUCTION

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Martina Jokel



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Other publications related to the topic:

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- Gerotto C, Alboresi A, Meneghesso A, Jokel M, Suorsa M, Aro EM and Morosinotto T. (2016) Flavodiiron proteins act as safety valve for electrons in *Physcomitrella patens*. *PNAS* 113, 12322-12327.

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**ABBREVIATIONS**

AA	antimycin A
AET	alternative electron transport
ATP	adenosine triphosphate
CBB	Calvin-Benson-Bassham cycle
CCM	carbon concentrating mechanism
cDNA	complementary DNA
CET	cyclic electron transport
Chl	chlorophyll <i>a</i> and <i>b</i>
CL	constant light
COX	cytochrome <i>c</i> oxidase
Cyt	cytochrome
$\Delta\text{pH}$	proton gradient
$\Delta\Psi$	electric potential
DCBQ	2,5-Dichloro-1,4-benzoquinone
DNA	deoxyribonucleic acid
ECS	electrochromatic shift
ETR	electron transport rate
$F_0$	the minimal level of fluorescence in the dark
$F_m$	the maximum fluorescence in the dark
$F_m'$	the maximum level of fluorescence under the light
$F_s$	the level of steady-state fluorescence under the light
$F_v$	variable fluorescence
FAD	flavin adenine dinucleotide
Fd (FDX1)	ferredoxin (ferredoxin 1)
FDP, FLV	flavodiiron protein
FeCy	ferricyanide
FL	fluctuating light
FMN	flavin mononucleotide
FNR	ferredoxin:NADP <sup>+</sup> oxidoreductase
FQR	ferredoxin plastoquinol reductase

$g_{H^+}$	proton conductivity
GC MS	gas chromatographic mass spectrometry
GL	growth light
H <sub>2</sub> ase	hydrogenase
HC	high CO <sub>2</sub> conditions (3% CO <sub>2</sub> )
HL	high light conditions
HSM	high salt minimal medium
LC	low CO <sub>2</sub> conditions, air level CO <sub>2</sub>
LET	linear electron transfer
LED	light-emitting diode
LHC	light harvesting complex
LL	low light
MIMS	membrane inlet mass spectrometry
MS/MS	tandem mass spectrometry
NADH	nicotinamide adenine dinucleotide (reduced)
NADPH	nicotinamide adenine dinucleotide phosphate (reduced)
NADP <sup>+</sup>	nicotinamide adenine dinucleotide phosphate (oxidized)
NDA2	NAD(P)H dehydrogenase
NPQ	non-photochemical quenching
OD <sub>750</sub>	optical density at 750 nm
P <sub>m</sub>	maximum level of oxidizable P700
P <sub>m</sub> '	maximum level of oxidizable P700 under the light
P680/P680 <sup>+</sup>	red/ox primary electron donor of Photosystem II
P700/P700 <sup>+</sup>	red/ox primary electron donor of Photosystem I
PAGE	polyacrylamide gel electrophoresis
PAM	pulse amplitude modulation
PAR	photosynthetically active radiation
PC	plastocyanin
PCR	polymerase chain reaction
PET	photosynthetic electron transport
PGR5	proton gradient regulation 5
PGRL1	PGR5-like protein 1

## 8 ABBREVIATIONS

pH	negative logarithm of the proton concentration
<i>pmf</i>	proton motive force
PS	photosystem
PQH <sub>2</sub> /PQ	plastoquinol/plastoquinone
Q <sub>A</sub>	the primary electron-accepting plastoquinone of PSII
Q <sub>B</sub>	the secondary electron-accepting plastoquinone of PSII
qE	energy-dependent NPQ
qI	photoinhibition-dependent NPQ
qT	state transition-dependent NPQ
qRT PCR	quantitative real-time reverse transcription PCR
RNA	ribonucleic acid
RNAi	RNA interference
RNAseq	next-generation RNA sequencing
ROS	reactive oxygen species
RuBisCo	ribulose biphosphate carboxylase/oxygenase
RuBP	ribulose-1,5-biphosphate
SDS	sodium dodecyl sulphate
SHAM	salicylhydroxamic acid
SMR	steam methane reforming
TAP (-S/-Mg)	Tris/Acetate/Phosphate medium (without sulfur/magnesium)
wt	wild type
WWC	water-water cycle
Y(I)	effective yield of Photosystem I
Y(II)	effective yield of Photosystem II
Y(NA)	PSI acceptor-side limitation
Y(ND)	PSI donor-side limitation

## ABSTRACT

The development of renewable biofuels to ensure sustainable energy supply is one of the biggest global challenges of modern society. Hydrogen has great potential to become the fuel of the future, since it provides energy without CO<sub>2</sub> emission. The green alga *Chlamydomonas reinhardtii* possesses hydrogenase enzymes and is able to photoproduce hydrogen under specific conditions. Hydrogenases, together with flavodiiron proteins (FDPs), PROTON GRADIENT-REGULATION 5 (PGR5), and PGR5-LIKE PHOTOSYNTHETIC PHENOTYPE 1 (PGRL1), represent key players of alternative electron transport (AET) in *C. reinhardtii*. Photosynthetic organisms have evolved AET routes such as these to adjust the photosynthetic apparatus under dynamic environmental conditions, like changing carbon supply or fluctuating light (FL) intensity. The interplay of all of these AET routes was the subject of my doctoral research, which was performed in order to understand AET regulation and to identify possible bottlenecks towards commercially profitable hydrogen production by *C. reinhardtii*.

In the first part of my thesis, I demonstrated that all three proteins; FDPs, PGR5, and PGRL1, contribute to the photoprotection of *C. reinhardtii* under FL. FDPs form a rapid electron sink downstream of PSI and are absolutely crucial for survival under FL conditions. PGR5 operates on a slower time-scale than FDPs and is the next important protein to act under FL stress. A lack of PGR5 inhibits cell growth, even under mild FL conditions. It is possible that PGR5 acts as a redox-dependent regulator of photosynthesis. The importance of PGRL1 on the growth performance is only observed under severe FL conditions, despite the importance of PGRL1-mediated cyclic electron transport during high light transients.

In the second section of my thesis, I studied the role of FDPs in H<sub>2</sub>-photoproduction during the transition to anaerobiosis. Anoxic culture conditions are necessary to enable the function of oxygen-sensitive hydrogenases. Here, it is shown that FDPs may accelerate the transition of *C. reinhardtii* cells to anaerobiosis during S-deprivation. Furthermore, application of a magnesium (Mg)-deprivation protocol resulted in prolonged H<sub>2</sub> production and improved cell viability. High accumulation levels of FDPs during the H<sub>2</sub> production phase suggested a contribution of these proteins to the maintenance of anoxia when Mg-deprivation is employed to induce H<sub>2</sub> production.

## TIIVISTELMÄ

Yksi nyky-yhteiskunnan suurimmista maailmanlaajuisista haasteista on uusiutuvien biopolttoaineiden kehitys kestäväen energialähteen turvaamiseksi. Vedyllä on suunnattomat mahdollisuudet tulla tulevaisuuden polttoaineeksi, koska se tarjoaa energiaa ilman hiilidioksidipäästöjä. *Chlamydomonas reinhardtii* viherlevällä on hydrogenaasi entsyymejä, ja tietyissä olosuhteissa se kykenee tuottamaan vetyä valoenergian avulla. Yhdessä FDP-proteiinien (Flavodiiron proteins), PGR5:n (PROTON GRADIENT-REGULATION 5) ja PGRL1:n (PGR5-LIKE PHOTOSYNTHETIC PHENOTYPE 1) kanssa hydrogenaasit ovat vaihtoehtoisten elektroninsiirtoreittien kannalta keskeisiä proteiineja. Yhteyttävät eliöt ovat kehittäneet tämän kaltaisia vaihtoehtoisia elektroninsiirtoreittejä säätääkseen yhteyttämiskoneistoaan muuttuvissa ympäristöolosuhteissa kuten käytettävissä olevan hiilen määrän tai valointensiteetin vaihdellessa. Väitöskirjatutkimukseni aiheena oli kaikkien näiden vaihtoehtoisten elektroninsiirtoreittien välinen vuoropuhelu. Tutkimus suoritettiin vaihtoehtoisten elektroninsiirtoreittien säätelyn ymmärtämiseksi ja *C. reinhardtii* kaupallisen vedyntuotannon mahdollisten pullonkaulojen tunnistamiseksi.

Väitöskirjani ensimmäisessä osassa osoitin, että kaikki kolme proteiinia, FDP:t, PGR5 ja PGRL1, osallistuvat *C. reinhardtii* valoreaktioiden suojeluun vaihtelevissa valo-olosuhteissa. FDP:t muodostavat nopean elektroninielun valoreaktio I:ltä alavirtaan ja ovat elintärkeitä vaihtelevassa valossa selviytymiselle. PGR5 toimii hitaammalla aikaskaalalla kuin FDP:t ja on seuraava tärkeä proteiini, joka toimii vaihtelevan valon stressissä. PGR5:n puuttuminen rajoittaa solujen kasvua jopa vain lievästi vaihtelevassa valossa. On mahdollista, että PGR5 toimii yhteyttämisen hapetus-pelkistys säätelijänä. PGRL1:n merkitys solujen kasvun kannalta tuli ilmeiseksi ainoastaan rajusti vaihtelevissa valo-olosuhteissa, vaikka PGRL1-välitteinen syklinen elektroninsiirto on tärkeä siirryttäessä korkeaan valoon.

Väitöskirjani toisessa osassa tutkin FDP:iden roolia vedyntuotannossa anaerobisiin oloihin siirryttäessä. Hapettomat kasvatusolosuhteet ovat välttämättömiä happiherkkien hydrogenaasien toiminnan mahdollistamiseksi. Tässä työssä näytetään, että FDP:t voivat nopeuttaa *C. reinhardtii* solujen siirtymistä anaerobioosiin rikkipuutoksen aikana. Magnesium-puutoksen käyttö taas johti pidentyneeseen vedyn tuotantoon ja solujen parempaan elinvoimaisuuteen. Kun magnesiumin puutosta sovellettiin vedyntuotannon käynnistämiseen, FDP:iden havaittiin kertyvän korkealle tasolle, mikä viittasi näiden proteiinien osallistuvan hapettomien olosuhteiden ylläpitoon vedyntuotannon aikana.

*Es ist schon so: Die Fragen sind es,  
aus denen das, was bleibt, entsteht.*

*- Erich Kästner -*

## 1. INTRODUCTION

### 1.1. Green algae - *Chlamydomonas reinhardtii* as a model organism

Green algae comprise a large group of photosynthetic eukaryotic organisms including streptophytes, such as Charales and Zygnematales, which are close relatives of the last common ancestor of land plants (Wodniok et al., 2011). Green algae diverged over a billion years ago from stramenopiles (Yoon et al., 2004), thus linking them closely to several other microalgae, including diatoms. The relatively low position of green algae on the evolutionary tree makes them an interesting target for developmental comparisons. Unicellular green algae can occupy both aquatic and terrestrial habitats and can live under photoautotrophic, heterotrophic or mixotrophic conditions when provided with the right carbon source, which in laboratory conditions is commonly acetate. Moreover, green algae possess great variation in cellular architecture and metabolic capacity, making them useful as model organisms for the study of different lifestyles (Harris, 2001).

Green algae own unique features as model systems in research and for commercial purposes (Brennan & Owende, 2013; Scaife et al., 2015). Specifically, the use of green algae for low value, high volume biofuels provides a potential solution to many environmental problems that come with crop-based production (Chisti, 2007). However, to make this economically feasible, a biorefinery approach is required whereby bio-remediation of waste water and/or the production of other economically interesting high value / low volume biomolecules would offset the cost of cell harvest and conversion processes (Sambusiti et al., 2015; Yen et al., 2013). Microalgae are capable of producing valuable compounds like carbohydrates, lipids, proteins, starch, cellulose, polyunsaturated fattyacids, antioxidants, pigments, pharmaceuticals, natural colorants, fertilizer, and after oil extraction, remaining biomass can be utilized as animal feed (Mata et al., 2010; Yen et al., 2013; Trivedi et al., 2015).

The most widely used research model organism among green algae is the unicellular flagellate *Chlamydomonas reinhardtii* (Harris, 2001; Merchant et al., 2007). *C. reinhardtii* is an ~10 µm long, wet soil dwelling green alga with several mitochondria, two flagella for motility and sexual reproduction, and a large cup-shaped chloroplast that contains the photosynthetic apparatus (Dent et al., 2001, Fig. 1). In 1945, Gilbert Smith isolated the first laboratory strain of *C. reinhardtii* in soil samples from Amherst, Massachusetts, USA (Harris, 2001).

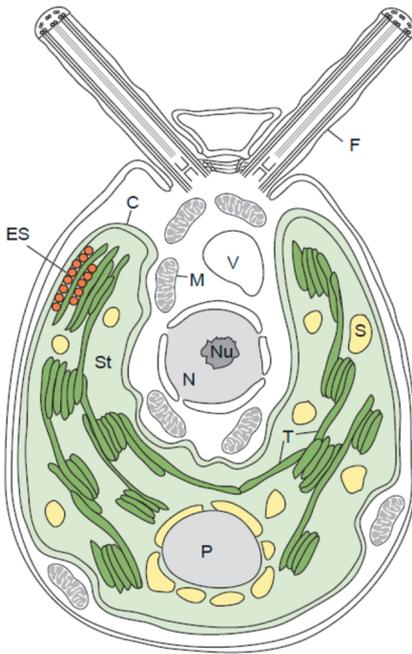


Fig. 1: The morphology of *Chlamydomonas reinhardtii*. The scheme shows the nucleus (N) with the nucleolus (Nu) in the center. It is surrounded by the large cup-shaped chloroplast (C) with the thylakoid membranes (T), stroma (St), starch grains (S) and the pyrenoid (P) inside. The pyrenoid inside the chloroplast houses large amounts of RuBisCo and is the place of CO<sub>2</sub> assimilation into starch. The eye-spot (ES) is located beside the inner envelope membrane of the chloroplast. Two flagella (F) branch from the apical region where is also the contractile vacuole (V) located. In the cytoplasm several mitochondria (M) are situated (adapted from Dent et al., 2001).

*C. reinhardtii* persists in its haploid stage as one of the two mating types ( $mt^+$  or  $mt^-$ ) during the vegetative phase (Harris, 2001). The nuclear, mitochondrial and chloroplast genomes are sequenced (Merchant et al., 2007) and the roughly 17 000 genes identified are ~93% correctly annotated, following complementary expression analysis (Blaby et al., 2014). Comparative genomic analyses have revealed that many genes, especially those connected to photosynthesis and plastid metabolism, can be traced back to a common green algae and plant ancestor. However, *C. reinhardtii* also carries many genes related to the animal kingdom that are lost in angiosperms (Merchant et al., 2007).

*C. reinhardtii* possesses several practical advantages as a model organism. It is easy to cultivate, to make genetic crosses, and there are relatively simple protocols available for genetic manipulation (Graham, 1996). The chloroplast genome can be specifically manipulated by homologous recombination (Day & Goldschmidt-Clermont, 2011). However, the nuclear genome is transformed by random integration and followed by extensive screening of multiple transformants (Debuchy et al., 1989). The generation of a knock-out library, currently consisting of more than 37 000 mutant lines, has thus become an invaluable tool for genetic approaches to photosynthesis research (Li et al., 2016).

## 1.2. Photosynthetic light reactions

Through oxygenic photosynthesis, cyanobacteria, green algae and higher plants harvest and convert solar energy into chemical energy of carbon compounds via the simultaneous splitting of water into protons, electrons and O<sub>2</sub>. Therefore, photosynthesis not only maintains atmospheric O<sub>2</sub> levels but also supplies Earth with energy in form of organic molecules (Blankenship, 2013). In eukaryotic organisms, photosynthesis takes place in chloroplasts, with the synthesis of ATP and NADPH occurring in the light reactions via the major photosynthetic protein complexes located in the thylakoid membrane. The photosynthetic apparatus of photosynthetic organisms is fairly similar, particularly among eukaryotic photosynthetic organisms. However, *C. reinhardtii* has some unique features, which differ from higher plants like *Arabidopsis thaliana*. It also has some features preserved from cyanobacterial ancestors, which have disappeared from *A. thaliana* (Hohmann-Marriott & Blankenship, 2011).

In the stroma, the Calvin-Benson-Bassham (CBB) cycle uses ATP and NADPH to convert inorganic carbon into starch, referred to as the dark reaction (Raines, 2003).

### 1.2.1. Linear electron transport

Specialized light-harvesting pigment-protein complexes, LHCII and LHCI, harvest sunlight and transfer excitation energy to the reaction centers, Photosystem II (PSII) and Photosystem I (PSI), where the photochemical reactions take place (Blankenship, 2013). In PSII, the energy of the harvested photons is used to excite P680 and to shuttle an electron via pheophytin and a plastoquinone (PQ), Q<sub>A</sub>, to another PQ molecule, Q<sub>B</sub> (Takahashi et al., 1987; Minagawa & Takahashi, 2004). When Q<sub>B</sub> is doubly reduced, it binds two protons from the stroma, is converted to plastoquinol (PQH<sub>2</sub>) and is released into the PQ-pool. Simultaneously, water splitting occurs at the Mn<sub>4</sub>CaO<sub>5</sub> cluster on the donor side of PSII (Umena et al., 2011). The protons originating from this reaction are released into the lumen and the electrons reduce oxidized P680.

The PQH<sub>2</sub> molecule is a mobile carrier that moves inside the thylakoid membrane to the Cytochrome (Cyt) *b<sub>6</sub>f* complex where it is oxidized. Cyt *b<sub>6</sub>f* mediates electron transfer between the two photosystems and is a dimeric protein complex. Each monomer consists of eight subunits; the large subunits cytochrome *f*, cytochrome *b<sub>6</sub>*, Rieske iron-sulfur protein and subunit IV, and the small subunits

PetG, PetL, PetM, and PetN (Takahashi et al., 1996; Baniulis et al., 2008). A PQH<sub>2</sub> binds to the Q<sub>0</sub> pocket in Cyt *b*<sub>6</sub>*f* and transfers one electron onto the Rieske subunit and Cyt *f* and one electron onto Cyt *b*<sub>6</sub>. Because the next electron carrier, plastocyanin (Pc), can accept only one electron, the so-called Q-cycle in the Cyt *b*<sub>6</sub>*f* complex regulates this process (Mitchell, 1975). The Q-cycle consists of several consecutive redox reactions and results in one electron being redirected back to the PQ-pool. During the Q-cycle, protons are translocated from the stroma to the lumen. At PSI, photons excite P700, the primary donor of PSI. P700\* transfers an electron onto Chl A<sub>0</sub>, this is then shuttled via several intermediate acceptors (phylloquinone A<sub>1</sub>, the Fe<sub>4</sub>-S<sub>4</sub> clusters F<sub>A</sub>, F<sub>B</sub>, and F<sub>X</sub>) onto ferredoxin (Fd) in the stroma (Ben-Shem et al., 2003). Pc in turn, is necessary to reduce P700<sup>+</sup>. Ultimately, electrons are transferred to nicotinamide adenine dinucleotide phosphate (NADP<sup>+</sup>) and form NADPH. This reaction is catalyzed by ferredoxin:NADP<sup>+</sup> reductase (FNR). This whole electron transport chain from PSII to NADPH is called linear electron transfer (LET) and is depicted in Fig. 2 by black arrows (Haehnel, 1984).

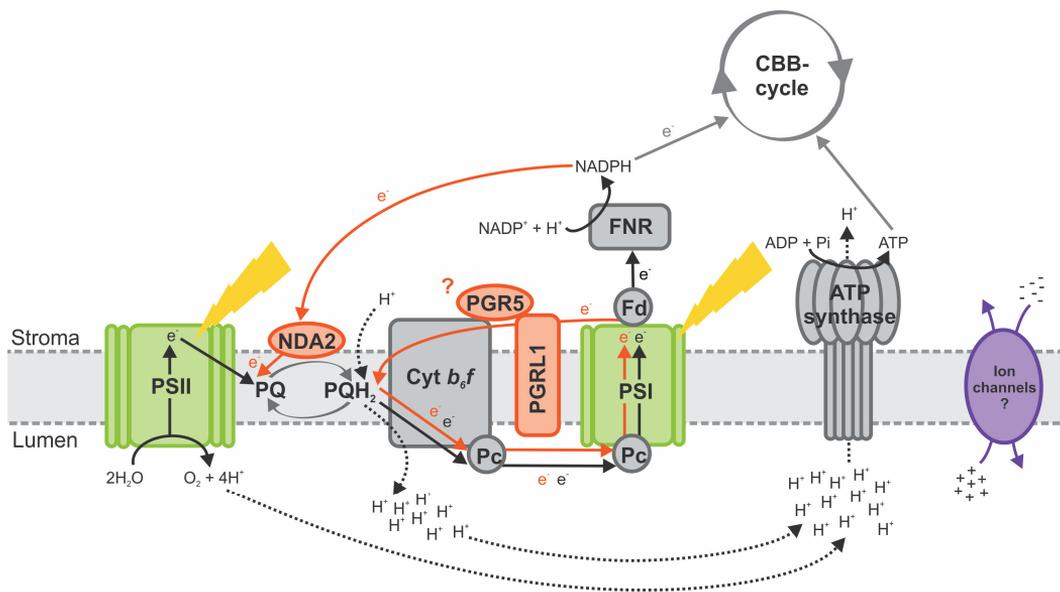


Fig. 2: Simplified scheme of the photosynthetic linear and cyclic electron transfer routes in *C. reinhardtii* thylakoid membranes. LET is marked by black and CET by red arrows. Black dashed arrows illustrate the proton fluxes over the thylakoid membrane. The counter ion fluxes are illustrated in purple. Carbon fixation by the CBB-cycle is marked in grey.

As a result of water splitting at PSII and proton pumping from the stroma via the Q-cycle at Cyt *b<sub>6</sub>f*, the lumen becomes acidified (Sacksteder et al., 2000). This proton gradient,  $\Delta\text{pH}$ , is used to synthesize ATP via the chloroplast  $F_0F_1$ -ATP synthase by adding an inorganic phosphate (Pi) to ADP in the stroma (Fig. 2, black dashed arrows). Thus, the final products of the photosynthetic light reactions are NADPH and ATP (Mitchell & Moyle, 1967) that then are used to fuel the carbon fixation by the CBB-cycle (Fig. 2 grey arrows).

Two components comprise the proton motive force (*pmf*):  $\Delta\text{pH}$  and the electric potential at the thylakoid membrane ( $\Delta\Psi$ ). They are thermodynamically equal and both contribute to ATP synthesis (Cruz et al., 2001). However, only the  $\Delta\text{pH}$  component induces regulative mechanisms like non-photochemical quenching (NPQ) or photosynthetic control via acidification of the lumen. Recently, it was shown that elevated  $\Delta\Psi$  can also induce alterations in photosynthetic regulation and PSII photodamage (Davis et al., 2016). At low light intensities, the contribution of  $\Delta\text{pH}$  and  $\Delta\Psi$  to *pmf* is equal, but  $\Delta\text{pH}$  increases upon transition to high light and induces photosynthetic regulative mechanisms (Yamamoto et al., 2016). To balance *pmf* it is necessary to regulate the  $\Delta\Psi$  component. Therefore, an efflux of counter cations, like  $\text{K}^+$  and  $\text{Mg}^{2+}$  or influx of anions like  $\text{Cl}^-$  to the lumen (Fig. 2, purple arrows) is needed to store *pmf* dominantly as  $\Delta\text{pH}$  (Kramer et al., 2003; Shikanai & Yamamoto, 2017).

Most thylakoid ion channels and transporters are characterized in *A. thaliana*, with predicted homologs found in many green algae and cyanobacteria (Spetea et al., 2017). Examples of such channels include: the potassium channel TPK3, which releases  $\text{K}^+$  from the thylakoid lumen and thus decreases  $\Delta\Psi$  (Carraretto et al., 2016); the voltage-dependent  $\text{Cl}^-$  channels VCCN1, VCCN2 (Herdean et al., 2016a) and the CLCe  $\text{Cl}^-$  channel/transporter (Herdean et al., 2016b), which effects both *pmf* and the  $\text{H}^+$  conductivity,  $g_{\text{H}^+}$ , of the ATP synthase; and the KEA3  $\text{K}^+/\text{H}^+$  antiporter, which increases the contribution of  $\Delta\Psi$  to total *pmf* (Armbruster et al., 2014). This KEA3  $\text{K}^+/\text{H}^+$  channel is redox-regulated and increases the efficiency of photosynthesis by accelerating the relaxation of NPQ upon a high to low light transition.

### **1.2.2. Cyclic electron transport**

Differences between eukaryotic photosynthetic organisms are evident in the mechanisms that mediate cyclic electron transport (CET) in the thylakoid membrane. Assimilation of one  $\text{CO}_2$  in the CBB-cycle requires 3 ATP and 2 NADPH

molecules. The concept of CET around PSI was initially suggested to compensate for the scarcity of ATP produced in LET alone (Allen, 2002).

When four quanta of photons are absorbed by PSII and PSI each, two water molecules are split and four protons and molecular O<sub>2</sub> are released into the thylakoid lumen. The four resulting electrons are transferred onto the intersystem PQ pool. Via LET, these four electrons reduce two NADP<sup>+</sup> and translocate eight protons into the thylakoid lumen (Sacksteder et al., 2000). In total 12 protons resulting from LET (Fig. 2, dashed black arrows) can bind to the proton-binding c-subunits that form a ring structure at the CF<sub>0</sub> sub-complex of the ATP synthase. However, there are actually 14 c-subunits, therefore the protons from LET do not completely rotate the CF<sub>0</sub> sub-complex and only produce 2.57 ATP molecules (Vollmar et al., 2009). To achieve the full count of three ATP, one electron needs to be recycled from PSI to Cyt *b<sub>6</sub>f* (Fig. 2, red arrows) where two additional protons are pumped into the lumen. In this way, CET acidifies the chloroplast lumen without creating NADPH (Allen, 2002; Munekage et al., 2004). However, there have been observations of LET yielding three ATP and two NADPH (Steigmiller et al., 2008), questioning the relevance of CET. Nevertheless, ATP and NADPH are also consumed in many other cellular reactions, requiring frequent adjustment between LET and CET. Additionally, CET is needed to increase the  $\Delta$ pH component of *pmf* to activate NPQ (Shikanai & Yamamoto, 2017).

There are two different CET pathways that have been proposed in *A. thaliana*: the Fd-dependent and the type-I NAD(P)H dehydrogenase (NDH)-dependent CET (Peng et al., 2008). NDH is a huge multisubunit protein complex, which pumps protons into the lumen, similar to complex I in mitochondria. In the past, NAD(P)H has been considered to be the electron donor. However, it was recently demonstrated that Fd in fact donates electrons to NDH, rendering it a ferredoxin-plastoquinone reductase (Munekage et al., 2004; Yamamoto et al., 2011; Peltier et al., 2016). NDH is able to form a supercomplex with PSI via the two antenna proteins LHCA5 and LHCA6 (Peng et al., 2008; Yadav et al., 2017). Higher plant NDH has evolved from a structurally simpler cyanobacterial NDH-1 complex, which can have different subunit composition depending on its metabolic function (Battchikova et al., 2011). Cyanobacterial NDH-1 is also involved in CET and additionally in respiration and the carbon concentrating mechanism (CCM) (Ogawa, 1991). The functions of type-2 NAD(P)H:PQ oxidoreductases (NDH-2) in higher plants and cyanobacteria are not well known, however they do not pump protons and seem to be involved in the  $\alpha$ -tocopherol redox cycle and/or vitamin K1 synthesis

in plants (Fatihi et al., 2015) and in even more diverse systems in cyanobacteria (Peltier et al., 2016).

Intriguingly, the NDH-1 complex is missing in *C. reinhardtii* (Maul et al., 2002) and instead NDH-2 (NDA2) reduces PQ and mediates CET without pumping additional protons (Desplats et al., 2009; Jans et al., 2008). NDA2 is thus less effective in establishing  $\Delta\text{pH}$  than the NDH-1 complex. However, its fairly simple structure, comprising only one polypeptide, may be easier to maintain by the cell metabolism.

Two proteins, called PROTON GRADIENT REGULATION 5 (PGR5) and PGR5-LIKE PHOTOSYNTHETIC PHENOTYPE 1 (PGRL1) have been proposed to function in antimycin A (AA)-sensitive CET in *A. thaliana* (DalCorso et al., 2008; Munekage et al., 2002). PGRL1 is an integral thylakoid protein that has two transmembrane domains with both the N- and C-terminus exposed to the stroma (DalCorso et al., 2008). It has been demonstrated that PGRL1 interacts with PGR5 *in vitro* and is able to accept electrons from Fd to reduce PQ. This model suggests that PGRL1 and PGR5 form the elusive ferredoxin-plastoquinone reductase, FQR (Hertle et al., 2013). PGR5 is predicted to be a small extrinsic thylakoid protein without an explicit sequence motif which could predict its function. The regulation of (AA)-sensitive Fd-dependent CET and an interaction of PGR5 with the stromal side of PGRL1 *in vivo* in *A. thaliana* was suggested by DalCorso et al., (2008). Later, it was proposed that the main role of PGR5 is the regulation of LET via photosynthetic control at Cyt *b<sub>6</sub>f* to prevent photodamage of PSI under fluctuating light conditions in *A. thaliana* (Suorsa et al., 2012). In *C. reinhardtii*, PGRL1 has been shown to mediate CET under anoxic and oxic conditions (Terashima et al., 2012; Tolleter et al., 2011), while the involvement of PGR5 in CET has been exclusively demonstrated only under anoxic conditions (Alric, 2014; Johnson et al., 2014). Additionally, in *C. reinhardtii* Fd-mediated CET is not AA-sensitive, probably due to a mutation in the amino acid sequence of PGR5 (Sugimoto et al., 2013).

In *C. reinhardtii*, the molecular machinery for Fd-CET was identified by Iwai et al., (2010) as a supercomplex consisting of PSI-LHCI, LHCII, Cyt *b<sub>6</sub>f*, PETC, PetD, PETO, FNR and PGRL1. In a later study, the  $\text{Ca}^{2+}$  sensor protein (CAS) and ANAEROBIC RESPONSE 1 (ANR1) were identified as further components of this CET supercomplex, possibly regulating CET efficiency in response to calcium signaling (Terashima et al., 2012). The absence of PGR5 in the functional CET supercomplex suggests that it is not an essential component of CET, but is possibly involved in ensuring efficient CET under certain environmental conditions. Indeed, it has only been possible to isolate the CET supercomplex from anaerobic conditions when the

stromal carriers are over-reduced and the switch from LET to CET is enhanced (Takahashi et al., 2013; Johnson et al., 2014). The formation of a CET supercomplex brings all necessary components for efficient CET in close proximity and thus, possibly eliminates the competition of CET and LET for commonly shared components like PQ, Cyt *b<sub>6</sub>f*, Pc, PSI, Fd and FNR (Johnson, 2011). However, such a CET supercomplex has never been identified in higher plants. Instead, in *A. thaliana* complexes of PSI with NDH or PSI with Cyt *b<sub>6</sub>f* have been identified (Peng et al., 2008; Yadav et al., 2017).

### 1.3. Alternative electron sinks of photosynthesis

While the recycling of electrons via CET regulates photosynthesis for the metabolic needs of the cell for ATP and NADPH, it does not represent a true sink for excess electrons. In situations where the electron pressure in the PET chain suddenly increases, it is necessary to release these electrons in a safe way to avoid harm to the photosynthetic protein complexes and the production of dangerous reactive oxygen species (ROS) (Asada, 1999). Photosynthetic organisms have developed several alternative electron sinks to fine-tune PET under changing environments. These alternative electron sinks differ between cyanobacteria, green algae and higher plants. Excess ROS production is prevented by O<sub>2</sub> photoreduction processes in the chloroplast. These processes use O<sub>2</sub> as final electron acceptor, reducing it to H<sub>2</sub>O (Fig. 3, blue arrows). *C. reinhardtii* mostly relies on O<sub>2</sub> photoreduction via flavodiiron proteins (FDPs), the Water-Water-Cycle (WWC), and the plastoquinone terminal oxidase (PTOX) as alternative electron sinks (Peltier et al., 2010). However, when facing anoxic conditions, *C. reinhardtii* is able to use protons as a final electron acceptor, creating H<sub>2</sub> instead of H<sub>2</sub>O (Ghysels et al., 2013; Fig. 3, orange arrows). This H<sub>2</sub>ase reaction is described in more detail in section 1.5.1.

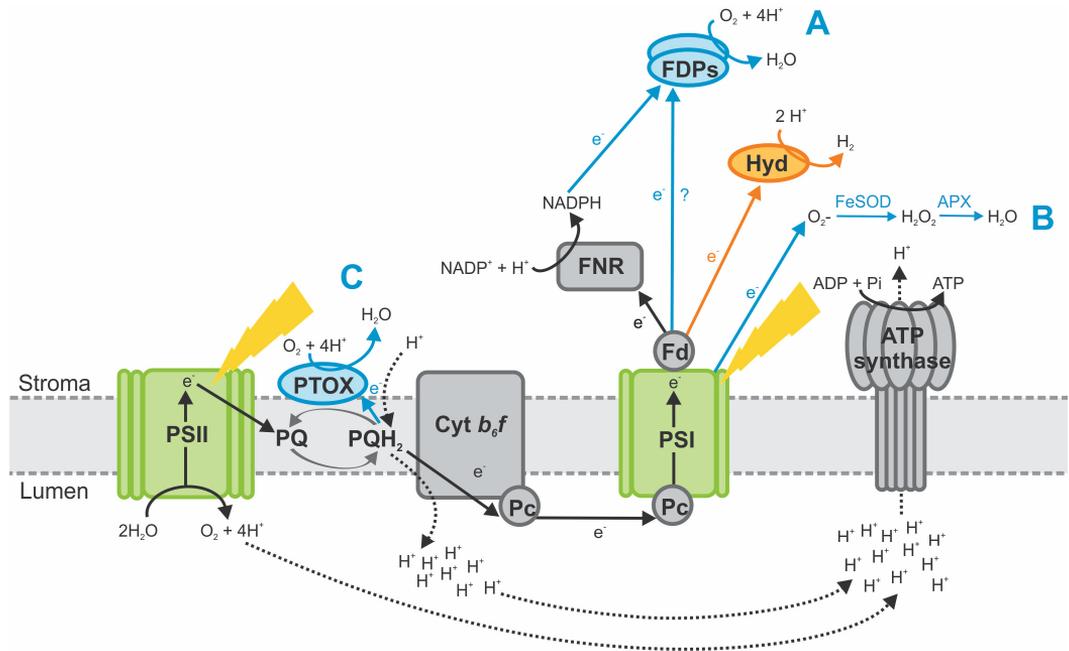


Fig. 3: Alternative electron sinks in *C. reinhardtii* photosynthesis.  $O_2$  photoreduction pathways are marked with blue arrows: FDPs (A), WWC (B) including the superoxide dismutase (FeSOD) and the ascorbate-specific peroxidase (APX), and PTOX (C). Orange arrows illustrate  $H_2$  production used as electron sink under anoxic conditions. Proton fluxes are depicted by black dashed arrows.

### 1.3.1. Flavodiiron protein-mediated $O_2$ photoreduction

The most recently elucidated route for  $O_2$  photoreduction in *C. reinhardtii* employs flavodiiron proteins (FDPs) as an electron sink downstream of PSI (Peltier et al., 2010; Allahverdiyeva et al., 2015a). FDPs are a conserved protein family present in prokaryotes (Wasserfallen et al., 1998) and some eukaryotes, including anaerobic protozoa, green algae and lower plants (Zhang et al., 2009; Peltier et al., 2010; Allahverdiyeva et al., 2015b). FDPs are enzymes with nitric oxide (NO) and/or  $O_2$  reductase activity. Thus, they are important in sustaining anoxic conditions in facultative anaerobic organisms and in detoxifying nitrosative stress (Rodrigues et al., 2006; Vicente et al., 2008a; 2008b). It is possible that some FDPs reduce both substrates,  $O_2$  and NO, but usually the substrate selection is exclusive (Seedorf et al., 2007; Vicente et al., 2007).

FDPs have a modular structure with two core domains comprising of metallo- $\beta$ -lactamase-like (FeFe)-domain at the N-terminus and a C-terminal flavodoxin-like (FMN) domain (Vicente et al., 2002; Fig.4 A).

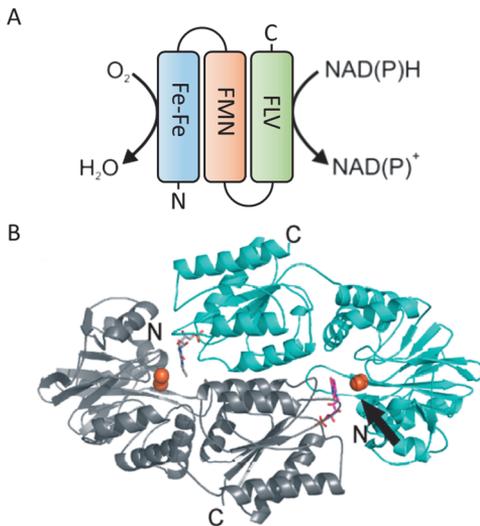


Fig. 4: Function and molecular structure of FDPs. Organization of functional domains in FDPs present in photosynthetic organisms (A). Fe-Fe,  $\beta$ -lactamase domain; FMN, flavodoxin domain; and FLV, flavin-reductase domain. The 'head-to-tail' structure of *Synechocystis* Flv2/Flv4-heterodimer (B). The arrow shows the reactive centre with FMN (magenta) of Flv2 (gray) and the diiron (orange) of Flv4 (cyan). Figures modified from Zhang et al., (2012) and Allahverdiyeva et al., (2015b).

These two core domains are part of the most elementary group of FDPs, class A (Vicente et al., 2008a; Allahverdiyeva et al., 2015b). The metallo- $\beta$ -lactamase unit engulfs a non-heme diiron center and forms the active site where NO/O<sub>2</sub> are reduced (Silaghi-Dumitrescu et al., 2003). The flavodoxin-like domain binds FMN as cofactor and functions as the electron donor for the FeFe-domain. However, the FDP monomers are not able to carry out electron transfer by themselves because the FeFe and FMN domains are fairly isolated from each other (Vicente et al., 2008a). Thus, FDPs build a 'head-to-tail' dimer structure that brings the redox centres in close proximity and enables efficient electron transfer (Fig. 4 B). FDPs that have a unique NADPH flavin reductase domain fused to the C-terminus are present exclusively in several photosynthetic organisms and belong to the so called class C FDPs (Wasserfallen et al., 1998; Vicente et al., 2002; Zhang et al., 2009; Allahverdiyeva et al., 2015b).

Class C FDPs comprise the entire electron transport from NADPH to O<sub>2</sub> in a single protein. Genes encoding class C FDP homologs have been conserved in photosynthetic organisms throughout evolution and are found in cyanobacteria, algae, bryophytes, lycophytes and gymnosperms. It is noteworthy that FDPs have not been detected in diatoms, haptophytes or angiosperms (Ilík et al., 2017; Peltier et al., 2010). FDPs present in oxygenic photosynthetic organisms can be phylogenetically grouped into two clusters, A and B, and at least one FDP of each cluster is always present (Zhang et al., 2009). There are several structural differences between FDPs of cluster A or B. FDPs belonging to cluster A are characterized by the absence of canonical ligands in the FeFe center (Gonçalves et al., 2011). This modification possibly hinders electron transfer in homodimers;

therefore the arrangement in heterodimers, one from each cluster, was suggested (Zhang et al., 2012).

Thus far, the majority of studies have focused on the possible role of cyanobacterial FDPs on photosynthesis and cell metabolism. The non-N<sub>2</sub>-fixing, unicellular cyanobacterium *Synechocystis* sp. PCC 6803 (hereafter *Synechocystis*) expresses four FDPs. The Flv1 and Flv3 proteins are shown to mediate the light-dependent reduction of O<sub>2</sub> downstream of PSI without the production of ROS (Helman et al., 2003). This pathway of O<sub>2</sub> photoreduction is also called the Mehler-like reaction. The same Flv1 and Flv3 proteins are essential for the protection of photosynthesis, particularly the PSI complex, under fluctuating light conditions (Allahverdiyeva et al., 2013; Allahverdiyeva et al., 2015a). Additionally, Flv1 and Flv3 appear to be capable of forming homodimers that have function aside from light-dependent O<sub>2</sub> reduction (Mustila et al., 2016). The involvement of the other two FDPs, Flv2 and Flv4, in O<sub>2</sub> photoreduction and thus, their electron acceptor is still under debate (Helman et al., 2003; Allahverdiyeva et al., 2015b; Shimakawa et al., 2015). However, these proteins are encoded by the *flv4-sll0218-flv2* operon and form a Flv2/Flv4 heterodimer. The *flv4-flv2* operon functions in the photoprotection of PSII under high light and CO<sub>2</sub> limiting conditions. This is likely by discharging excess electron pressure at the PSII acceptor-side (Zhang et al., 2009; 2012) in a process that is dependent on intact phycobilisomes (Bersanini et al., 2014).

*Anabaena* sp. strain PCC 7120 (hereafter *Anabaena*), a filamentous heterocystous N<sub>2</sub>-fixing cyanobacterium, expresses six FDPs. The heterodimer Flv1A/Flv3A is specific to vegetative cells and it was hypothesized that Flv1A/Flv3A and Flv2/Flv4 function similarly to their homologs in *Synechocystis*. The additional set of Flv1B and Flv3B are exclusively expressed in heterocysts. While the function of Flv1B remains unidentified, it has been demonstrated that Flv3B performs light-induced O<sub>2</sub> photoreduction. Therefore, it maintains a microoxic environment and safeguards nitrogenase in heterocysts (Ermakova et al., 2013; 2014).

Recent studies have confirmed the essential role of FDPs as a rapid electron sink protecting PSI in the moss *P. patens* under fluctuating light conditions (Gerotto et al., 2016) and at the onset of light in the liverwort *Marchantia* (Shimakawa et al., 2017). Furthermore, the heterologous expression of *P. Patens* FDPs in *A. thaliana* resulted in functional O<sub>2</sub> photoreduction that could, in part, complete the phenotype of the *pgr5* knock-out mutant (Yamamoto et al., 2016).

*C. reinhardtii* possesses two *flv* genes, *flvA* (Cre12.g531900) and *flvB* (Cre16.g691800). The high homology between the cyanobacterial Flv1 and Flv3 and

the two *C. reinhardtii* FDPs suggests that FLVA and FLVB are also involved in O<sub>2</sub> photoreduction downstream of PSI (Zhang et al., 2009; Peltier et al., 2010; Allahverdiyeva et al., 2015a). Immune-pull-down has shown an interaction of Fd with FLVB, indicating that Fd could also act as an electron donor for FDPs in *C. reinhardtii*, as indicated in Fig. 3 (Peden et al., 2013).

### **1.3.2. Chloroplast O<sub>2</sub> photoreduction processes other than flavodiiron proteins**

Besides FDP-mediated O<sub>2</sub> photoreduction there are three additional mechanisms which use O<sub>2</sub> as a final electron acceptor of PET: O<sub>2</sub> photoreduction by RuBisCo; WWC; and O<sub>2</sub> photoreduction by PTOX.

The active center of RuBisCo can perform a dual function: carboxylation and oxygenation of ribulose-1,5-bisphosphate (RuBP). This oxygenation reaction of RuBisCo is called photorespiration. In plants, photorespiration is considered a physiologically significant process that reduces redox pressure in the stroma when CO<sub>2</sub> assimilation is low (Ort & Baker, 2002; Peltier & Cournac, 2002). However, due to an active CCM, which favors RuBP carboxylation (Moroney & Ynalvez, 2007), it is unlikely that this pathway plays an important role in the cell metabolism in *C. reinhardtii*.

It is also known that O<sub>2</sub> can be directly reduced at the acceptor side of PSI in a process called the Mehler reaction (Mehler, 1951). This process results in the production of superoxide radicals that are then converted to H<sub>2</sub>O<sub>2</sub> and O<sub>2</sub> by a superoxide dismutase (FeSOD). An ascorbate-specific peroxidase (APX) reduces the H<sub>2</sub>O<sub>2</sub> to H<sub>2</sub>O (Fig. 3). This entire process is called the water-water-cycle (WWC) and is able to dissipate excess reducing equivalents from the photosynthetic apparatus under high light or CO<sub>2</sub> limiting conditions (Asada, 1999). As WWC works at the acceptor side of PSI, it contributes to the generation of ΔpH, possibly balancing the ratio of ATP and NADPH in a similar way to CET. The APX reaction also creates a monodehydroascorbate radical (MDA) that is extremely reactive (Miyake & Asada, 1992). This MDA can, in turn, be reduced by an MDA reductase using NADPH as a substrate, or by a glutathione/NADPH system (Asada, 1999). The WWC is not considered a safe way to dissipate excess electrons because of the potential for cell damage by production of ROS (Ort & Baker, 2002). Although, some ROS is required for stress signaling (Baxter et al., 2014).

Another pathway for O<sub>2</sub> photoreduction is the re-routing of electrons from PSII, via the PQ-pool, to a reaction catalyzed by PTOX (Fig. 3), reducing O<sub>2</sub> to H<sub>2</sub>O at the expense of CO<sub>2</sub> fixation (Kuntz, 2004). PTOX cannot compete with PSI under

steady-state photosynthetic conditions; however it likely plays an important role under stress conditions (Trouillard et al., 2012) and thus, PTOX is able to act as a safety valve for photosynthesis. Additionally, PTOX can promote ROS production (Heyno et al., 2009). While higher plants possess only one PTOX gene, *C. reinhardtii* has two, although it has been shown that PTOX2 mostly functions in O<sub>2</sub> photoreduction. Moreover, *C. reinhardtii* PTOX2 is not involved in chloroplast biogenesis or carotenoid biosynthesis like the plant enzyme is (Houille-Vernes et al., 2011). The PTOX reaction directly affects the redox state of the PQ-pool and therefore influences PQ-pool dependent regulative mechanisms, such as state transitions.

#### **1.4. Additional mechanisms regulating photosynthetic electron transport**

Fast changes in light availability and other environmental conditions create the need to constantly adjust the electron flow via the PET chain. In addition to the AET pathways and electron sinks described above, there are also other short-term mechanisms regulating photosynthesis and supporting the dissipation of excess electron pressure. These photoprotective mechanisms include non-photochemical quenching, photosynthetic control, and state transitions (Rochaix, 2013).

##### **1.4.1. Non-photochemical quenching**

Non-photochemical quenching (NPQ) is the portion of absorbed light energy that exceeds the capacity of the PET chain and therefore has to be dissipated harmlessly as heat. In green algae and plants, NPQ can be separated into three components (Horton et al., 1994; Müller et al., 2001). One component depends on the photoinhibition of PSII (qI) induced by excess light damage; another is credited to state transitions (qT) involving the detachment of phosphorylated LHCII antenna from PSII (Minagawa, 2011), described in more detail below.

However, the main component of NPQ is called energy dependent quenching (qE) and is regulated by the  $\Delta$ pH over the thylakoid membrane (Niyogi et al., 2000). As already described,  $\Delta$ pH increases because of a boost in photosynthetic activity and this increased  $\Delta$ pH in turn down-regulates PET. The qE component involves the reversible conversion of the carotenoid violaxanthin to antheraxanthin and subsequently to zeaxanthin (xanthophyll cycle) under high light conditions (Niyogi et al., 1997). In *A. thaliana*, the xanthophyll cycle makes up a large portion of qE, while its contribution in *C. reinhardtii* is minor (Niyogi et al., 1997; Kawabata & Takeda, 2014; Quaas et al., 2015).

In *A. thaliana*, the protein responsible for qE is a LHC-family protein, PsbS (Li et al., 2002). It is constitutively expressed but only activated by an increase in luminal pH, leading to a rapid and efficient induction of NPQ (Niyogi & Truong, 2013). In *C. reinhardtii*, another stress-related three-helix LHC family protein, LHCSR3, is known to sense  $\Delta\text{pH}$  and quench excited Chl molecules in LHCII (Peers et al., 2009). LHCSR3 expression and activation is triggered by high light and low carbon conditions (Maruyama et al., 2014). Furthermore, protonation of LHCSR3 leads to the activation of the quenching process, linking  $\Delta\text{pH}$  formation with LHCSR3-mediated qE (Bonente et al., 2011). A blue-light photoreceptor and calcium signaling may also promote LHCSR3 expression (Petroustos et al., 2016). Recently, it was shown that a PSBS protein is present also in *C. reinhardtii*, and is likely involved in the induction of qE (Correa-Galvis et al., 2016). Unlike LHCSR3, the PSBS protein is much less abundant and accumulates transiently during stress conditions (Tibiletti et al., 2016). The contribution of PGRL1-Fd-mediated CET to  $\Delta\text{pH}$  links CET with the induction of NPQ (Kukuczka et al., 2014). Furthermore, a possible cooperation and compensation of LHCSR3-dependent and PGRL1-dependent photoprotection has been proposed (Chaux et al., 2017), demonstrating the importance of the interplay between short-term response mechanisms and AET.

#### **1.4.2. Photosynthetic control at Cytochrome *b<sub>6</sub>f***

Photosynthetic control describes an additional  $\Delta\text{pH}$ -dependent photoprotective mechanism which functions at Cyt *b<sub>6</sub>f* level (Tikhonov, 2014). Although photosynthetic control in the PET chain between PSII and PSI was first proposed long ago (Rumberg & Siggel, 1969), its importance and mechanism have only recently become clearer (Colombo et al., 2016).

It has been suggested that the increase in  $\Delta\text{pH}$  at the thylakoid membrane blocks the reaction between  $\text{PQH}_2$  and the Cyt *f* subunit of Cyt *b<sub>6</sub>f* (Nishio & Whitmarsh, 1993). The mechanism of  $\text{PQH}_2$  oxidation includes the formation of hydrogen bonds between the hydroxyl group of  $\text{PQH}_2$  and the  $\text{H}^+$ -accepting residues inside the  $\text{Q}_0$ -center (Crofts et al., 1999). When  $\Delta\text{pH}$  increases, these  $\text{H}^+$ -accepting residues may be protonated, making them unavailable for  $\text{PQH}_2$  oxidation. This photoprotective mechanism is triggered under high light by increased  $\Delta\text{pH}$ , which down-regulates Cyt *b<sub>6</sub>f* activity and limits electron flow, thus protecting PSI under high light stress.

### 1.4.3. State transitions

In green algae and plants, peripheral light harvesting complexes (LHCs) harvest and transfer light energy to the reaction centers of the photosystems. These LHC antennas consist mostly of chlorophyll (Chl) *a* and *b* and span the thylakoid membrane (Minagawa & Takahashi, 2004; Tokutsu et al., 2004). In *A. thaliana*, the LHCII comprise three types of major antenna proteins, LHCB1-3, organized as heterotrimers. The peripheral LHCII trimers are connected to the PSII core by CP26, CP29 and CP24 monomers. Additional pigments, i.e. neoxanthin, lutein, and carotenoids, are connected with LHCII and work in the dissipation of excess energy. The peripheral antenna of PSI in *A. thaliana* consists of six LHCI subunits, mostly LHCA1-4, with much lower levels of LHCA5 and 6, forming a half-ring on one side of the PSI core (Rochaix, 2011). In *C. reinhardtii*, the monomeric LHCII protein CP24 is missing and CP26 and CP29 are located close to the PSII core complex and connect the major LHCII proteins, LHCBM1-9, to PSII (Drop et al., 2014; Minagawa & Takahashi, 2004). The PSI core is associated with nine LHCI subunits, LHCA1-9, that form a half-ring similar to that in *A. thaliana* (Takahashi et al., 2004; Drop et al., 2011).

The LHCII and LHCI antennae possess different light absorption characteristics. PSII can absorb blue and red light, while PSI can absorb blue and far-red light. These differences result in an imbalance between the excitation of PSII and PSI, especially under rapidly changing light conditions. For optimal photosynthetic electron transport under stress conditions, an adjustment of the relative absorption cross-section is required. Therefore, photosynthetic organisms have developed a mechanism, referred to as a state transition, which balances excitation by connecting LHCs to either PSII or PSI, as required (Murata 1969; Wollman, 2001).

State transitions rely on the interplay between phosphatases and kinases, regulated by the PQ-pool redox status. Under high light conditions, PSII becomes overexcited and the PQ-pool is reduced. In *C. reinhardtii*, this leads to the binding of PQH<sub>2</sub> to the Q<sub>0</sub>-centre of Cyt *b<sub>6</sub>f* and in turn activates protein kinases, Stt1 and Stt7 (Bonardi et al., 2005). Respective orthologues in *A. thaliana* are called STN8 and STN7. Subsequently, Stt7 phosphorylates several Lhcb subunits and Stt1 phosphorylates PSII core subunits. Part of LHCII then connects to the PSI-LHCI complex. The formation of this PSI-LHCI-LHCII complex is called state-2 and is reversible, back to state-1. In state-1 the PQ-pool is oxidized, followed by the inactivation of the kinases and then the dephosphorylation of LHCII, which

reconnect to PSII (Minagawa, 2011). The antagonistic phosphatases are not well studied in *C. reinhardtii*. However, in *A. thaliana*, PHOTOSYSTEM II CORE PHOSPHATASE (PBCP) is responsible for the dephosphorylation of PSII core subunits and as such, is the antagonist of STN8 (Samol et al., 2012). The STN7 antagonistic protein phosphatase is PPH1/TAP38 that dephosphorylates several Lhcb subunits (Pribil et al., 2010; Shapiguzov et al., 2010).

As state transitions are regulated by the redox status of the PQ pool, the mechanism can be affected by environmental conditions other than high light. It appears that sulfur-deprivation, ATP deficits and dark anoxia also induce state-2 transitions in *C. reinhardtii* (Wykoff et al., 1998; Cardol et al., 2009; Ghysels et al., 2013). In this context, it is also important to note that both CET and state transitions are redox-regulated, although independently from each other (Takahashi et al., 2013).

Whilst well studied, a consensus on the significance of state-transitions is yet to be reached by the research community. Earlier studies suggested that in green algae about 80% of the LHCII antennae are involved in state transitions, while only about 20% of LHCII participate in this process in plants (Delosme et al., 1996). More recent studies in *C. reinhardtii* indicate that only about 10% of LHCII connect to PSI during state-2. In thylakoids, a major fraction of phosphorylated LHCII detach from PSII but do not attach to PSI, thus forming a self-quenching antennae pool dissipating excess energy (Nagy et al., 2014; Ünlü et al., 2014). Contrary to this, another study has suggested that state transitions redistribute energy between PSI and PSII instead of dissipating it (Nawrocki et al., 2016). Although the role of LHCII and PSII core protein phosphorylation remains unclear in *C. reinhardtii*, research on *A. thaliana* has progressed significantly and has demonstrated a key role for thylakoid protein phosphorylation in light-intensity-dependent interactions and energy distribution between PSII and PSI (Tikkanen et al., 2011; Grieco et al., 2012). Dephosphorylation of thylakoid proteins plays also a significant role in the regulation of photosynthesis (Mekala et al., 2015).

## 1.5. Hydrogen production in green algae

The largest available energy source on Earth is solar power with ~1300 ZJ of photosynthetically active radiation (PAR) received per year (Oey et al., 2016). This amount of energy is much more than the current global demand of only 0.56 ZJ every year, and is more than all fossil fuel and uranium reserves on earth combined (Stephens et al., 2013). Therefore, the ability to efficient harness solar power for

renewable and sustainable energy sources is highly desirable in resolving problems of global warming and fossil fuel depletion.

The exploitation of biologically produced H<sub>2</sub> is a promising renewable alternative to carbon-based fossil fuels. It has immense advantages in that it is a clean fuel that has the potential to be carbon negative (Dubini & Ghirardi, 2015; Melis & Happe, 2001). The combustion of H<sub>2</sub> generates water as the only product and, when generated by aquatic phototrophs, it does not compete with food production for fertile land, which is a common problem for land-based first- or second-generation biofuels (Ghirardi et al., 2000; Stephens et al., 2013). Furthermore, it has a very high energy density (~120 kJ/g) compared to other hydrocarbon fuels (Gupta, 2014). Currently, commercial H<sub>2</sub> production is based on fossil fuels and is mostly produced via steam methane reforming (SMR), but also coal gasification, industrial oil and naphtha reforming, and fossil fuel driven water electrolysis (Gupta, 2014; Lam & Lee, 2012). These technologies require high energy input, are expensive and emit high levels of CO<sub>2</sub>.

Over the past decades, biological H<sub>2</sub> photoproduction by cyanobacteria via the nickel hydrogenase (H<sub>2</sub>ase) or the bi-directional H<sub>2</sub>ase and by green algae via the [FeFe]-H<sub>2</sub>ase has become a focus of research. However, there are several bottlenecks which need to be resolved before H<sub>2</sub> photoproduction becomes economical feasible. One of them is the sensitivity of the [FeFe]-H<sub>2</sub>ase to O<sub>2</sub> (Ghirardi et al., 1997; Happe et al., 2002; Ghirardi, 2015). Since O<sub>2</sub> is a byproduct of photosynthesis, H<sub>2</sub> production is only a transient process under natural conditions.

*C. reinhardtii* is one of the most studied microalga in regards to H<sub>2</sub> production (Eroglu & Melis, 2016; Melis & Happe, 2001; Oey et al., 2016). Furthermore, progress in metabolic engineering and synthetic biology has led to advances in establishing *C. reinhardtii* as a biotechnological platform (Scaife et al., 2015). Most of the strategies employed to reach sustainable H<sub>2</sub> photoproduction in *C. reinhardtii* nowadays follow a common concept. The photosynthetic activity and thus, O<sub>2</sub> evolution, has to be reduced and respiratory processes have to be increased in the cell to establish the anoxic or microoxic conditions that induce H<sub>2</sub> production.

There are three different pathways directing electrons towards the [FeFe]-H<sub>2</sub>ase (Fig. 5), of which two are connected with the PET chain. The direct pathway is PSII-dependent (Chochois et al., 2009) and the indirect pathway bypasses PSII, with electrons originating from starch breakdown arriving at the PQ pool via NDA2 (Jans et al., 2008). However, the starch accumulation is PSII-dependent. The third pathway functions under dark anoxic conditions and is linked to fermentation. It involves

electron transfer via a pyruvate-ferredoxin-oxidoreductase (PFR) from pyruvate to [FeFe]-H<sub>2</sub>ase (Hemschemeier & Happe, 2011; Noth et al., 2013). The direct PSII-dependent pathway is the most desirable because it exhibits the most efficient conversion of solar energy into H<sub>2</sub> without intermittent products like starch or pyruvate (Chochois et al., 2009; Eroglu & Melis, 2016; Volgusheva et al., 2013).

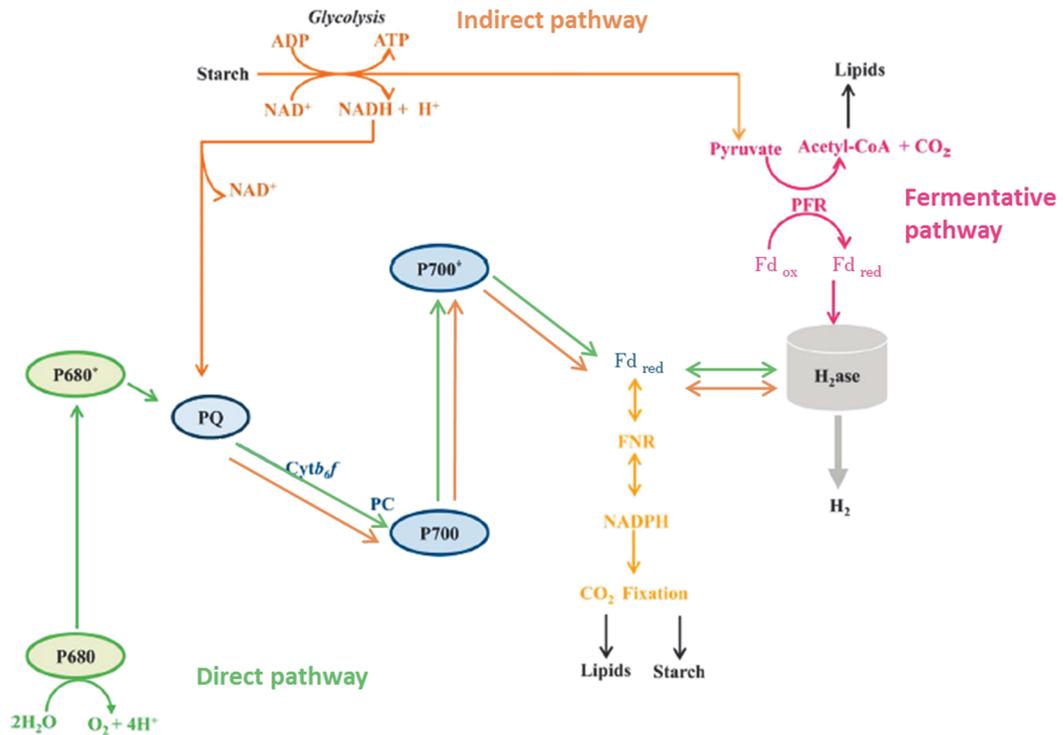


Figure 5: Metabolic pathways fueling H<sub>2</sub> photoproduction. The direct PSII-dependent pathway is depicted in green and the indirect starch-dependent pathway in orange. The third pathway depending on fermentation is shown in pink (adapted from Catalanotti et al., 2013).

### 1.5.1. The role of hydrogenases as an alternative electron sink

Several microalgae, including *C. reinhardtii*, possess O<sub>2</sub>-sensitive [FeFe]-H<sub>2</sub>ases that use electrons from Fd to produce H<sub>2</sub> (Fig. 3, orange arrows). These enzymes have been lost in terrestrial plants. It is possible that [FeFe]-H<sub>2</sub>ases act as an additional alternative electron sink under anoxic conditions (Melis & Happe, 2001; Melis, 2007; Hemschemeier & Happe, 2011), thus providing a similar dissipation of excess reducing power from the PET chain as PTOX or FDPs under oxic conditions. In cyanobacteria, a bidirectional H<sub>2</sub>ase may act as a safety valve during dark to light transitions under anoxic conditions (Appel et al., 2000). This is physiologically

important due to the natural exposure of cyanobacteria and green algae to anoxic or microoxic conditions in their aquatic or wet soil habitats (Clowez et al., 2015), whereas terrestrial plants are constantly surrounded by atmospheric O<sub>2</sub> levels.

The enzymes responsible for H<sub>2</sub> production in *C. reinhardtii* are plastidial soluble [FeFe]-H<sub>2</sub>ases located in the stroma (Ghirardi et al., 1997; 2007; Atteia et al., 2013; Stiebritz et al., 2012). The catalytic domain (H-cluster) in *C. reinhardtii* [FeFe]-H<sub>2</sub>ases contains only one 4Fe-4S-cluster domain binding one 2Fe-2S cluster, without the addition of a further 4Fe-4S-cluster as found in bacterial H<sub>2</sub>ases (Ghirardi et al., 2007; Stripp et al., 2009; Shepard et al., 2014). The [FeFe]-H<sub>2</sub>ases mainly accept electrons from FDX1 (Winkler et al., 2010), fueling a double reduction of the proton bound to the distal iron of the 2Fe-2S catalytic center and a subsequent recombination of the resulting hydride anion H<sup>-</sup> with another proton bound to the bridging dithiomethylamine ligand. This recombination reaction results in the formation of H<sub>2</sub> (Nicolet et al., 2001). During this reaction the H-cluster becomes accessible to O<sub>2</sub>, which inhibits any further H<sub>2</sub>ase-activity (Stripp et al., 2009).

*C. reinhardtii* possesses two genes encoding H<sub>2</sub>ases: HydA1, mainly responsible for H<sub>2</sub> production; and HydA2, whose exact function is still under debate (Forestier et al., 2003; Meuser et al., 2012). At least three maturation factors are needed, HydEF and HydG, for the maturation of the H-cluster, that is also O<sub>2</sub>-sensitive (King et al., 2006). Whilst early studies indicated that H<sub>2</sub>ases are only expressed under anoxic conditions (Happe & Kaminski, 2002), it now appears that O<sub>2</sub> is not the only factor involved in H<sub>2</sub>ase expression. It is possible that the redox state of the PQ pool, influenced by starch metabolism or nutrient deprivation, also induces H<sub>2</sub>ase expression. Additional factors that may influence H<sub>2</sub>ase expression include light-dark photoperiods, the cell cycle (Whitney et al., 2011), and the ΔpH created by CET (Chochois et al., 2009). Whilst H<sub>2</sub>ase activity has been well documented under anoxic conditions, a recent study has suggested that H<sub>2</sub>ases are also present and able to sustain H<sub>2</sub> production in algal cells under oxic conditions (Liran et al., 2016)

### ***1.5.2. Different protocols to induce hydrogen production***

The fermentation driven production of H<sub>2</sub> by green algae under dark anoxic conditions in cooperation with fermentation has been known since the publication of Gaffron and Rubin, (1942). In the same work, light-dependent H<sub>2</sub> production was also demonstrated, following a dark to light shift. Nowadays, a two-stage process involving sulfur-deprivation is the most commonly applied protocol to induce H<sub>2</sub>

production in *C. reinhardtii* (Melis et al., 2000). In the first step, *C. reinhardtii* is grown to increase biomass,  $O_2$  is evolved from photosynthesis and reducing power is stored as carbohydrates. During the second step the cells are deprived of sulfur, which initiates specific metabolic changes, leading to  $H_2$  production. Sulfur-deprivation impairs protein synthesis and as a consequence, photodamaged PSII centers are not repaired which severely inhibits electron transport from PSII (Wykoff et al., 1998; Melis et al., 2000; Zhang et al., 2002). Moreover, sulfur-deprivation induces state-2 transition and a simultaneous elevation of CET, which further reduces PSII activity and consequently,  $O_2$  evolution (Wykoff et al., 1998; Melis, 2007). Mitochondrial respiration works at the same level as during sulfur-replete conditions, which allows rapid removal of  $O_2$  from the culture (Melis et al., 2000; Zhang & Melis, 2002). Due to these processes, the culture passes through five stages (Fig. 6): photosynthetically active (I),  $O_2$ -consuming (II), anaerobic (III),  $H_2$  producing (IV) and termination (V) (Kosourov et al., 2002; Volgusheva et al., 2013).

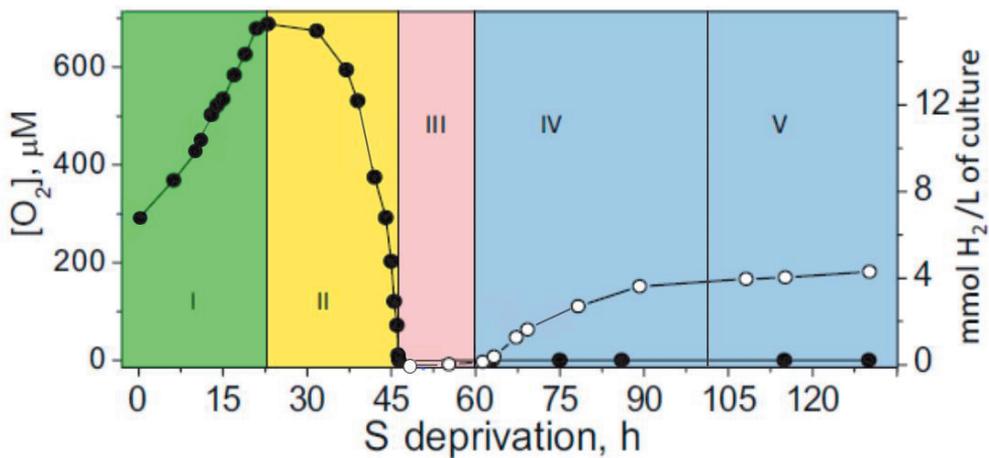


Figure 6: Stages of  $H_2$  photoproduction under sulfur-deprivation; photosynthetic (I),  $O_2$ -consumption (II), anaerobic (III),  $H_2$  production (IV) and termination (V).  $O_2$  levels are marked with closed circles and  $H_2$  levels with open circles (adapted from Volgusheva et al., 2013).

Efforts have been made to improve  $H_2$  production yields further by testing deprivation protocols of other nutrients like nitrogen, phosphorus, potassium and magnesium (Philipps et al., 2012; Batyrova et al., 2012; 2015; He et al., 2012; Papazi et al., 2014; Volgusheva et al., 2015). Similar to sulfur-deprivation, the depletion of these nutrients induces a reduced photosynthetic activity, accumulation of starch, the establishment of anoxia and subsequently,  $H_2$  production.

Nitrogen deprivation results in the degradation of numerous proteins of the PET chain and therefore, results in less H<sub>2</sub> production than sulfur-deprivation (Philipps et al., 2012). Phosphorous deprivation is also a less effective stimulus for H<sub>2</sub> production in *C. reinhardtii* (Batyrova et al., 2012). In contrast, magnesium-deprived cells are capable of producing H<sub>2</sub> at similar rates, but for considerably longer periods of time, compared to sulfur-deprived cells (Volgusheva et al., 2015). Magnesium is a component of Chl molecules, therefore its deprivation decreases LHC antenna sizes, which promotes light utilization efficiency in dense cultures. Furthermore, PSII activity remains higher during magnesium-deprivation than during sulfur-deprivation, which may account for the enhanced H<sub>2</sub> production (Volgusheva et al., 2015).

All long-term nutrient deprivation protocols are ultimately terminal for microalgae cultures. Therefore, a periodical two-stage protocol that alternates between aerobic photosynthetic recovery phases and anaerobic H<sub>2</sub> production phases should be applied. This can be realized by transferring cells from the complete growth medium to the nutrient deprivation medium and back (Ghirardi et al., 2009). This is a difficult and expensive task in liquid cultures, which may be improved by the immobilization of cells (Laurinavichene et al., 2006; Kosourov & Seibert, 2009). Moreover, the immobilization of *C. reinhardtii* cells in e.g. Ca<sup>2+</sup>-alginate films has several advantages in that it substantially increases the conversion efficiency of solar energy to H<sub>2</sub> by accelerated PSII inactivation, altered starch metabolism and thus, enhanced contribution of the indirect pathway to H<sub>2</sub> production (Kosourov & Seibert, 2009). Immobilization possibly also protects the [FeFe]-H<sub>2</sub>ase from remaining O<sub>2</sub> in the growth medium.

To date, none of the proposed H<sub>2</sub> production protocols have indicated the potential for an economically feasible process. Thus, more research is required and technical advances are needed to increase current efficiencies.

### **1.5.3. Improving hydrogen production via genetic modifications**

Improvement of H<sub>2</sub> production efficiencies and new insights into production mechanisms have been achieved through genetic engineering approaches. A major target of these approaches has been the generation of an O<sub>2</sub>-insensitive H<sub>2</sub>ase. However, neither random mutagenesis, nor targeted engineering of the catalytic centre have led to large improvements in O<sub>2</sub>-tolerance (Ghirardi et al., 1997; Stiebritz et al., 2012). Another approach is to engineer the heterologous expression of O<sub>2</sub>-tolerant H<sub>2</sub>ases, such as the clostridial [FeFe]-H<sub>2</sub>ase, in *C. reinhardtii* (Noone et

al., 2017). Appealing new candidates are H<sub>2</sub>ases able to produce H<sub>2</sub> in the presence of low level O<sub>2</sub> that have recently been identified in two green algae (Hwang et al., 2014).

An alternative approach is to induce anoxic conditions by genetically modifying PSII activity, or by elevating O<sub>2</sub> uptake pathways in the cell. Down-regulation of the O<sub>2</sub> evolution capacity of PSII (Scoma et al., 2012; Torzillo et al., 2009) and the reversible copper-induced regulation of PSII D2 protein synthesis (Surzycki et al., 2007) are strategies demonstrating improved H<sub>2</sub> production. The truncation of LHC antennae (TLA mutants) improved photon conversion efficiencies and altered photoinhibition of PSII, leading to higher H<sub>2</sub> production rates than wt (Kosourov et al., 2011). The reduced LHC antennae make the TLA mutants well-suited to immobilization, as light can penetrate further through the layers of cells. Indeed, immobilized *tlal* mutant cells have been shown to produce H<sub>2</sub> with a maximum specific rate 4–8 times higher than the wt. Similar results were achieved by RNAi knock-down targeting the LHCBM1, 2, 3 and 9 antenna proteins (Grewe et al., 2014; Oey et al., 2013).

To increase O<sub>2</sub> uptake, leghemoglobins that sequester O<sub>2</sub> and are originally found in N<sub>2</sub>-fixing rhizobia, have been introduced into *C. reinhardtii* and improved H<sub>2</sub> production compared to wt (Wu et al., 2011). An O<sub>2</sub> consuming *E. coli* enzyme (pyruvate oxidase, PoX) has also been successfully introduced into *C. reinhardtii*, producing double the amount of H<sub>2</sub> than the wt (Xu et al., 2011). In this regard, FDPs could also be considered an interesting target, as they consume O<sub>2</sub> and are endogenous to *C. reinhardtii*.

H<sub>2</sub> production may also be limited by electron competition with other pathways like FNR, nitrate reductase, sulphite reductase, glutamate synthase or fatty acid desaturases (Hemschemeier & Happe, 2011). Thus, the fusion of PSI, FDX1 and HydA1 has resulted in efficient electron transfer towards H<sub>2</sub>ase and subsequently enhanced H<sub>2</sub> production (Eilenberg et al., 2016; Yacoby et al., 2011). Indirect pathways also compete with H<sub>2</sub>ase for electrons, and mutants targeting the down-regulation of RuBisCo (Hemschemeier et al., 2008; Pinto et al., 2013), starch degradation (Chochois et al., 2009), respiration and CET (Kruse et al., 2005; Steinbeck et al., 2015; Tolleter et al., 2011) have all demonstrated increased H<sub>2</sub> production over the wt. The *pgrl1* and *pgr5* mutants hold particular promise in demonstrating the highest yields of H<sub>2</sub> reported thus far (Steinbeck et al., 2015).

The *stm6* mutant, which is locked in state-1 and has an impaired CET, also produces more H<sub>2</sub> than its wt (Kruse et al., 2005), possibly due to an increased

contribution of the direct pathway to H<sub>2</sub> production, via PSII (Volgusheva et al., 2013). To further increase H<sub>2</sub> yields in *stm6*, a hexose symporter from *Chlorella kessleri* was introduced (Doebbe et al., 2007). This mutant, called *stm6glc4*, can uptake externally supplied glucose and use it for heterotrophic growth, supplying more electrons for the H<sub>2</sub>ase.

Currently, work is being done to genetically combine several of the above described mutants to push H<sub>2</sub> production yields even further. In addition, new targets for overcoming the bottlenecks of H<sub>2</sub> production are constantly identified.

## 2. AIMS OF THE STUDY

The green alga *C. reinhardtii* is exposed to variable environmental conditions in its natural habitat and, for that reason, it possesses flexible and efficient acclimation mechanisms to avoid excess electron pressure and the consequent production of harmful ROS. In my thesis, I have focused on the function and regulation of several AET pathways in the protection of photosynthesis under various challenging environmental conditions. In order to gain further insight into the AET network, I used wt and several knock-out mutants of *C. reinhardtii*. A particular emphasis was placed on the evaluation of strategies arising from the findings of my work for the photoproduction of H<sub>2</sub> as a renewable bioenergy source.

My thesis objectives included the following aspects of AET pathways in *C. reinhardtii*:

1. The significance of FDPs as a part of the AET network in protecting the photosynthetic apparatus in *C. reinhardtii*
2. Interplay of the main AET pathways mediated by FDPs, PGRL1 and PGR5 during naturally occurring fluctuations in light intensity
3. Crosstalk between FDP-mediated O<sub>2</sub> photoreduction and H<sub>2</sub> photoproduction

### 3. METHODOLOGY

#### 3.1. Growth conditions and *C. reinhardtii* strains

Table 1: *C. reinhardtii* strains used in this research. The construction of the mutants is described in detail in the references.

Strain	Description	Paper	Reference
<b>cc 406</b>	Wild-type (wt), cell wall deficient	I	
<b>137c</b>	wt, also CC-124, progenitor of <i>pgr5</i> and <i>pgrl1</i>	I, II, III, IV	
<b>CC-4533</b>	wt, progenitor of <i>flv</i> mutant lines	III	
<b><i>pgr5</i></b>	Knock-out of <i>pgr5</i>	III	Johnson et al., 2014
<b><i>pgr5 c1</i></b>	Complementation of <i>pgr5</i>	III	Johnson et al., 2014
<b><i>pgrl1</i></b>	Knock-out of <i>pgrl1</i>	II, III	Tolleter et al., 2011
<b><i>flv 208</i></b>	Knock-out of <i>flvB</i> , LMJ.RY0402.242208	III	Li et al., 2016
<b><i>flv 308</i></b>	Knock-out of <i>flvB</i> , LMJ.RY0402.229308	III	Li et al., 2016
<b><i>flv 321</i></b>	Knock-out of <i>flvB</i> , LMJ.RY0402.052321	III	Li et al., 2016

The *C. reinhardtii* wild-type strains and mutants (Table 1) were maintained in Erlenmeyer flasks under mixotrophic conditions in Tris/Acetate/Phosphate (TAP) medium (Gorman & Levine, 1965). The cultures were kept at ambient air, 25°C, agitation of 90 rpm and under a continuous white fluorescent light (L30W/865 Osram) at an intensity of 50  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ . For preparing experimental cultures the cells were harvested at  $\text{OD}_{750} = \sim 1.2$ , diluted to high salt medium (HSM; Sueoka, 1960) to an  $\text{OD}_{750} = \sim 0.1$  and cultivated photoautotrophically at 25°C. Various light intensities from 50  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  (growth light, GL) to 200  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  or 600  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  (high light, HL) were used to grow experimental cultures. In some experiments, the cultures were subject to bubbling with sterile air (low  $\text{CO}_2$ , LC) or sterile air supplemented with 2% (Paper II) or 3% (paper I)  $\text{CO}_2$  (high  $\text{CO}_2$ , HC). Experiments for paper II were performed in growth chambers (AlgaeTron AG 130-ECO, PSI) equipped with LED white lights at a continuous light intensity of 20  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  (CL 20) or at fluctuating light (FL) where 20  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  background light was interrupted every 5 min by 30 s high light phases of 200  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  (mild FL 20/200) or 600  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  (harsh FL 20/600) for 7 days. Protein and transcript samples were

taken directly from the Erlenmeyer flasks. Prior to biophysical analysis, the cells were transferred into fresh HSM and the Chl *a* and *b* concentration was adjusted to 5 or 10  $\mu\text{g mL}^{-1}$ , depending on the experiment. The Chl concentration was measured spectrophotometrically following pigment extraction with 95% ethanol (Lichtenthaler, 1987).

### 3.2. Photosynthetic activity measurements

#### 3.2.1. Chl *a* fluorescence and P700 measurements

A Dual-pulse amplitude modulated (PAM)-100 fluorometer (Walz, Germany) was used for simultaneous measurement of PSII and PSI activity, based on Chl *a* fluorescence and the P700 absorbance changes, respectively (Klughammer & Schreiber, 2008). The  $P_m$  value was calibrated and normalized as described in paper II. Saturating pulses (4,000  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  white light, 500 ms) were used to measure maximal fluorescence from dark adapted cells,  $F_m$ , and from light adapted cells,  $F_m'$ . For mimicking fluctuating light with the DUAL-PAM, the actinic light was set at 5 min 22  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  and 30 s 210  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  for the high light phase. In this case the cells were not dark-adapted. PSII parameters were calculated as following: the maximum quantum yield of PSII,  $F_v/F_m=(F_m-F_0)/F_m$ ; the effective PSII yield under actinic light,  $Y(II)=(F_m'-F_s)/F_m'$ ; NPQ= $(F_m-F_m')/F_m'$ . PSI parameters were calculated as: the effective PSI yield under actinic light,  $Y(I)=1-Y(ND)-Y(NA)$ ; acceptor-side limitation of PSI,  $Y(NA)=(P_m-P_m')/P_m$ ; and donor-side limitation of PSI,  $Y(ND)=1-P700 \text{ red}$ . The analysis of the P700 reduction curves were recorded at 1000  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  actinic white light for 5 s. In this case, the cells were pre-adapted in the dark for 45 min.

#### 3.2.2. Electrochromatic shift analysis

The electrochromatic shift (ECS) absorbance change at 515 nm was measured by using a DUAL-PAM-100 paired with a P515/535 emitter-detector module (Walz, Germany)(Schreiber & Klughammer, 2008). The ECS dark relaxation after 2.5 min of illumination at 210  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  actinic white light was analyzed to estimate the proton motive force (*pmf*). The total amplitude of the rapid decay of the ECS signal represents the total *pmf* and its partitioning in  $\Delta\text{pH}$  and  $\Delta\Psi$  was analyzed according to Kramer and Sacksteder, (1998) and Cruz et al., (2001).

### **3.2.3. Low temperature fluorescence emission spectroscopy**

Low temperature (77 K) fluorescence emission spectra of whole cells were determined using a USB4000-FL-450 (Ocean Optics) spectrofluorometer. The cells for analysis were frozen in liquid nitrogen and excited by 440 nm light obtained via 10 nm width interference filters. The spectra were normalized to PSII emission at 682 nm.

### **3.2.4. Oxygen exchange/evolution and H<sub>2</sub>O<sub>2</sub> analysis**

O<sub>2</sub> exchanges were analyzed in the presence of [<sup>18</sup>O]-enriched O<sub>2</sub> in a thermo-regulated (25°C) reaction chamber connected to a mass spectrometer (model Prima dB; Thermo Electron) via a membrane inlet system (Tolleteer et al., 2011). The cell suspensions were treated and the O<sub>2</sub> evolution and uptake rates were determined as described in paper II. For some measurements the mitochondrial respiratory inhibitors myxothiazol (2 mM) and salicylhydroxamic acid (SHAM) (0.4 mM) were added. Extracellular H<sub>2</sub>O<sub>2</sub> was detected as described in paper III, using the Amplex Red reagent (Invitrogen). The fluorescence emission at 580 nm (excitation 540 nm) was measured with a SAFAS Xenius fluorescence spectrophotometer.

In paper IV, the O<sub>2</sub> evolution and consumption rates were measured with a Clark-type O<sub>2</sub> electrode (Oxygraph plus system, Hansatech, GB) at 24°C. The net O<sub>2</sub> evolution (photosynthesis rate) was measured in the presence of 10 mM NaHCO<sub>3</sub> and under saturating light (2000 μmol photons m<sup>-2</sup> s<sup>-1</sup>). Light-saturated O<sub>2</sub> evolution (max. PSII activity) was recorded in the presence of the artificial electron acceptors, 0.5 mM 2,5-dichloro-1,4-benzoquinone (DCBQ) and 0.5 mM ferricyanide (FeCy). Respiration was calculated as the O<sub>2</sub> consumption rate in the dark and chlororespiration was calculated when the mitochondrial respiratory inhibitors myxothiazol (2 μM) and SHAM 0.9 (mM) were added.

## **3.3. Transcript analysis**

### **3.3.1. Quantitative Real-time PCR**

Total RNA was extracted using TRIsure (Bioline) reagent and further purified by phenol/chloroform/isoamylalcohol (25:24:1) extraction. Genomic DNA was removed using the Ambion Turbo DNase kit. The RNA quality and concentration was determined with a NanoDrop ND-1000 spectrophotometer (Thermo Scientific). The cDNA was reverse transcribed with poly(dT)(20) primers and SuperScript III

Reverse Transcriptase (Invitrogen). For the quantitative real-time (qRT) PCR iQ SYBR Green Supermix (Bio-Rad) in 96-well plates was used in a Bio-Rad IQ5 system. The PCR protocol and primers used can be found in paper I. The qbase<sup>+</sup> software by Biogazelle was used to calculate relative changes in the gene expression and to normalize them to the appropriate reference genes. The selection process of the reference genes is described in full detail in paper I.

### **3.3.2. Next-generation RNA sequencing**

Total RNA was extracted and treated as described above. The RNA samples were submitted for next-generation RNA sequencing (RNAseq) using a HiSeq 2000 (Illumina) to the Turku Centre for Biotechnology (Turku, Finland). The RNAseq reads were aligned to the genome of *C. reinhardtii* (version 5.1.) downloaded from Phytozome. The alignment using the Tophat algorithm and read-depth quantification was performed using the open source analysis software Chipster (CSC, Finland). Differentially expressed genes were identified by a log<sub>2</sub> fold change of 1 with a p-value <0.05.

## **3.4. Protein analysis**

Total and membrane proteins were extracted as described in paper I and separated using 14% SDS-PAGE without urea. Samples were loaded on the gels on equal protein basis, measured by Bradford assay (Bio-Rad, USA) and visualized with Coomassie Brilliant Blue (Bio-Rad, USA). Proteins were then transferred onto a polyvinylidene difluoride membrane (Millipore, USA) and examined with protein-specific antibodies. Antibodies were either purchased from Agrisera (Sweden), provided by collaborators, or newly raised against peptides, as stated in the relevant publication. Protein levels were analyzed using a secondary anti-rabbit antibody linked with horseradish peroxidase (HRP) and visualized with ECL.

## **3.5. Hydrogen production**

### **3.5.1. Sulfur-deprivation protocol**

*C. reinhardtii* cells cultivated in standard TAP medium and a light intensity of 50  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  were harvested at a Chl concentration of  $\sim 25 \mu\text{g mL}^{-1}$ , washed from sulfur and resuspended in TAP medium without sulfur (TAP-S). The cultures were adjusted to a Chl concentration of  $20 \mu\text{g mL}^{-1}$  and placed into custom-made cylindrical photobioreactors (550 ml) with an inner diameter of 60 mm. The

bioreactors were kept sealed with rubber stoppers and were placed under  $75 \mu\text{mol photons m}^{-2} \text{ s}^{-1}$  illumination from white fluorescent light (L 30W/865 Osram) at  $25^\circ\text{C}$ . Production of  $\text{H}_2$  was monitored by gathering the gas in an upside-down graduated cylinder submerged in water. For more detailed continuous monitoring of the  $\text{O}_2$  levels, the S-deprivation was performed in a microprocessor-controlled photobioreactor system (Tsygankov et al., 2006). In paper IV, S-deprivation was performed in gas-tight glass vials (total volume of 14 ml,  $\varnothing$  22 mm).

### ***3.5.2. Magnesium-deprivation protocol***

Mg-deprived cultures were obtained via a three-stage process which has been previously described (Volgusheva et al., 2015). In Stage 1, cells were grown under standard conditions in TAP medium (as described above). Stage 2 involved the transfer of cells into TAP-Mg for an aerobic pre-incubation lasting 7 days. For the 3<sup>rd</sup> stage, cells pre-conditioned to Mg-deprivation were harvested and transferred into fresh TAP-Mg at a concentration of  $\sim 4 \times 10^6 \text{ cells ml}^{-1}$  ( $\sim 7 \mu\text{g Chl mL}^{-1}$ ). Aliquots of 11 ml were then placed into gas-tight glass vials (total volume 14 ml,  $\varnothing$  22 mm) and incubated for 230 h, with constant shaking at 100 rpm, under the temperature and illumination conditions described above.

## 4. MAIN RESULTS

### 4.1. The interplay of O<sub>2</sub> photoreduction and cyclic electron transport protects photosynthesis

Genes encoding FDPs were reported in *C. reinhardtii* (Zhang et al., 2009), leading to questions concerning their expression levels and physiological function. Subsequent phylogenetic analysis of *C. reinhardtii* FDP protein structures indicated that FLVA and FLVB could function in a Mehler-like reduction of O<sub>2</sub>, in a similar manner to Flv1 and Flv3 in cyanobacteria. I decided to investigate this hypothesis and to explore the cooperation of FDP-mediated O<sub>2</sub> photoreduction with other AET routes like PGRL1-mediated CET and PGR5.

#### 4.1.1. Flavodiiron proteins are up-regulated when there is an excess of electrons in the photosynthetic electron transport chain

To assess the physiological role of FDPs in *C. reinhardtii*, the expression of FDPs on transcript and protein level was studied under different environmental conditions. Prior to analyzing the transcript level of *flvA* and *flvB* with qRT-PCR, I selected the most suitable set of reference genes under the tested conditions required for normalization (Paper I, Fig. 1). The most stable transcript levels under the three studied conditions were found for *cblp* and *ubc8*. Therefore, these were selected as reference genes for transcript analysis.

Cells grown under 50  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  (GL) and 3% CO<sub>2</sub> (HC) were shifted to 150  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  (HL) or air level CO<sub>2</sub> (LC). The cells were also shifted from GLHC conditions to combined HLLC. A sudden shift from GLHC to HL and/or LC creates an accumulation of excess electrons in the PET chain, creating an overreduction of the system. This was confirmed by the reduced effective PSII yield under these conditions, especially during the shift from GLHC to combined HLLC (Paper I, Fig. 2). The shift of *C. reinhardtii* wt cells from HC to LC led to a strong increase in *flvA* and *flvB* transcripts and a moderate increase in the amounts of corresponding proteins (Paper I, Fig. 3). It is noteworthy that the accumulation of the FLVB protein was relatively higher than FLVA. The shift from GL to HL conditions only induced a slight increase in both *flv* transcripts (Paper I, Fig. 4). Under this condition, FLVA accumulation was more strongly induced than FLVB. The shift to combined HLLC conditions resulted in the transient increase of both *flv* transcripts (Paper I, Fig. 5). Interestingly, the protein level of FLVA stayed almost unchanged, whereas FLVB was strongly up-regulated. Overall, it appears that *flv* transcription is

more induced by LC than by HL. This is in line with results from *flv1* and *flv3* in *Anabaena* (Ermakova et al., 2014). However, the amount of protein translation did not always follow transcription levels. Overall, the protein accumulation of FDPs was more stimulated by HL than LC. Under HL conditions, FLVA accumulation was more strongly up-regulated, whilst FLVB was more strongly induced by the shift to combined HLLC.

#### **4.1.2. O<sub>2</sub> photoreduction via flavodiiron proteins is crucial for survival under fluctuating light**

Reports of O<sub>2</sub> photoreduction performed by FDPs protecting cyanobacteria and also the moss *P. patens* from FL conditions (Allahverdiyeva et al., 2013; Gerotto et al., 2016) lead to the question whether the same function is possible in *C. reinhardtii*. The availability of *C. reinhardtii flv* knock-out mutants made it possible to study the impact that the lack of FDPs has on photosynthesis. The knock-out mutants missing both FDPs were subjected to photoautotrophic growth conditions and two different light regimes, 5 min of 20  $\mu\text{mol photon m}^{-2} \text{s}^{-1}$  interrupted by 30 s of 200  $\mu\text{mol photon m}^{-2} \text{s}^{-1}$  (mild FL 20/200) or constant illumination of 20  $\mu\text{mol photon m}^{-2} \text{s}^{-1}$  (CL 20). The growth of both *flv* mutants was strongly impaired as compared to the wt under FL 20/200 conditions, while there was no difference under CL 20 illumination (Paper II, Fig. 1). Due to the inability of *flv* mutants to grow under FL 20/200 conditions, all measurements were performed on CL 20 grown cells only.

Analysis of the *flv* mutants with pulse-amplitude fluorometer (PAM) mimicking FL 20/200 conditions revealed that the effective PSII yield, Y(II), and the yield of PSI, Y(I), were drastically reduced at the onset of the HL phase, as compared to the wt progenitor (Paper II, Fig. 4). The lack of FDPs in the mutants created a strong acceptor-side limitation at PSI, Y(NA), that in turn led to a lack of donor-side limitation during the HL phase. Analysis of the P700 oxidation kinetics in wt cells during a shift from darkness to HL illumination resulted in a wave phenomenon - the fast oxidation of P700, then its reduction and re-oxidation within 1 s at the onset of light (Paper II, Fig. 5). In previous studies, this fast P700 “re-oxidation rise” was described as a FDP-mediated electron sink acting after PSI (Allahverdiyeva et al., 2013; Ilík et al., 2017). Accordingly, the anaerobic incubation of wt cells resulted in the loss of this P700 “re-oxidation rise” and this trend was also missing from the P700 oxidation kinetics of the *flv* mutants. Next, the proton motive force (*pmf*) and its partitioning into a proton gradient ( $\Delta\text{pH}$ ) and an electric potential ( $\Delta\Psi$ ) were analyzed by measuring the electrochromic shift (ECS) at the thylakoid membrane

(Joliot and Joliot, 1989; Kramer and Sacksteder, 1998; Cruz et al., 2001). The *flv* mutants displayed a smaller *pmf* than the wt, which was caused by a decrease in the  $\Delta\text{pH}$  component, while the  $\Delta\Psi$  component was comparable to that of the wt (Paper II, Fig. 6). The reduced  $\Delta\text{pH}$  in the *flv* mutants demonstrates that FDP-mediated  $\text{O}_2$  photoreduction contributes to the establishment of  $\Delta\text{pH}$ , similar to the water-water cycle. Accordingly, the buildup of NPQ is delayed in the *flv* mutants (Paper II, Suppl. Fig. 4). However, contribution of FDPs to  $\Delta\text{pH}$  must be a transient effect. This is also supported by the fact that the *flv* mutants were able to accumulate LHCSR3 protein and establish NPQ similar to the wt (Paper II, Fig. 7). The *flv* mutant cells appeared to compensate for the loss of FDPs via up-regulation of RbcL and  $\text{O}_2$ -consuming processes, as indicated by the elevated protein level of FeSOD and COXIIb. It appears that CET is not one of the compensatory processes, because accumulation of NDA2 did not change and PGRL1 even decreased slightly in the *flv* mutants compared to the wt. Interestingly, the accumulation of PGR5 increased, indicating that PGR5 may have an additional, yet unknown function besides CET.

#### **4.1.3. PGRL1-mediated cyclic electron transport is essential during high light transitions**

Another AET pathway in *C. reinhardtii* photosynthesis is CET mediated by PGRL1, and the availability of a *pgrl1* knock-out mutant (Tollete et al., 2011) made it possible to study this pathway and its cooperation with other AET routes. In paper III, similar environmental conditions were applied as in paper I, although in steady-state mode: low light (LL,  $50 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ ); high light (HL,  $200 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ ); high  $\text{CO}_2$  (HC, 2%  $\text{CO}_2$  in air); and low  $\text{CO}_2$  (LC, air). Under HCLL, HCHL and LCLL conditions, the electron transport rate (ETR) and NPQ of *pgrl1* and the wt showed no significant differences (Paper III, Fig. 1). In contrast, under LCHL conditions, *pgrl1* had a reduced ETR and stronger NPQ. To investigate which component was responsible for this elevated NPQ, state transitions (qT) were analyzed by low temperature (77K) chlorophyll fluorescence emission and LHCII phosphorylation (Paper III, Fig. 2). Under LCHL conditions, *pgrl1* showed a strongly increased transition to state-2 and a stronger phosphorylation of the LHCII proteins CP29, CP26 and LHCP11 than the wt (Paper III, Fig. 2). Thus, the high NPQ in *pgrl1* under LCHL conditions is likely due to increased state-2 transition. Nevertheless, the fast induction of NPQ was reduced within 1 min in *pgrl1*.

The growth of *pgrl1* in 1 L photobioreactors, operated as turbidostats, was not affected under the steady-state conditions described (Paper III, Fig. 3). However,

the observation that *pgrl1* showed impaired growth under LCHL conditions on solid media (Paper III, Fig. 3), led to the question of whether *pgrl1* is sensitive to changes in light intensity during the plating of cells from liquid culture onto solid medium. Indeed, the growth of *pgrl1* in photobioreactors was severely impaired during the first 4 h after the shift to HL (800  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ ). Under FL (5 min 50  $\mu\text{mol photon m}^{-2} \text{s}^{-1}$  and 1 min 800  $\mu\text{mol photon m}^{-2} \text{s}^{-1}$ ) and LC conditions, *pgrl1* also showed impaired growth as compared to wt. These results together suggest that PGRL1-Fd-mediated CET is important during transitions to HL when CO<sub>2</sub> levels limit photosynthesis, but is not strictly necessary during steady-state growth.

#### **4.1.4. The loss of PGRL1 leads to increased mitochondrial respiration and elevated O<sub>2</sub> photoreduction**

Under LC and HL conditions, which usually invoke increased ATP demand for metabolic processes, the wt up-regulated PGRL1 protein amounts (Paper III, Fig. 7 and Suppl. Fig. 3). Thus, it could be expected that growth of the *pgrl1* mutant would be impaired in these circumstances. However, as already described, the *C. reinhardtii pgrl1* mutant and wt demonstrated approximately equal growth under LC and HL conditions. This indicates that there are other compensatory mechanisms contributing to the ATP production in *pgrl1*. One possible compensatory mechanism is an elevated cooperation with mitochondrial respiration. Thus, the effect of respiratory inhibitors on photosynthetic activity was analyzed (Paper III, Figure 4). Indeed, when salicylhydroxamic acid (SHAM) (inhibitor of the alternative oxidase) and myxothiazol (inhibitor of the mitochondrial cytochrome *bc*<sub>1</sub> complex) were added to the cells, *pgrl1* exhibited a reduced PSII yield, accompanied with more reduced PSII electron acceptors (1-qP), than the wt progenitor. These results suggest that the loss of PGRL1 makes the *C. reinhardtii* photosynthetic activity more dependent on the cooperation with mitochondrial respiration.

The light-dependent O<sub>2</sub> exchange in wt and *pgrl1* were analyzed by Membrane Inlet Mass Spectrometer (MIMS) with [<sup>18</sup>O] labelled O<sub>2</sub> in order to dissect the nature of the O<sub>2</sub> reducing processes involved in the compensatory mechanisms. The net O<sub>2</sub> production did not notably differ between wt and *pgrl1*, except under the LCHL condition, where less activity was shown in *pgrl1*. The light-dependent O<sub>2</sub> uptake was slightly higher in *pgrl1* than in wt under LCLL conditions (Paper III, Fig. 5). To estimate the contribution of mitochondrial respiration and O<sub>2</sub> photoreduction to the light-dependent O<sub>2</sub> uptake, the same inhibitors of mitochondrial respiration were used as for the photosynthetic activity analysis described above. Under LCHL

conditions, the light-dependent O<sub>2</sub> uptake in *pgrl1* was clearly less affected by the inhibitors than in the wt, suggesting that O<sub>2</sub> photoreduction pathways other than mitochondrial respiration are also active. The LCHL condition also increased extracellular H<sub>2</sub>O<sub>2</sub> levels compared to the other conditions. This indicated increased activity of the true Mehler reaction and was observed for both wt and *pgrl1* cultures, although in *pgrl1* the increase was more prominent (Paper III, Fig. 6). Immunoblot analysis showed that both FDPs are strongly up-regulated in *pgrl1* during all conditions except for LCHL. Under LCHL conditions, FLVB was moderately up-regulated and FLVA protein levels were unchanged as compared to the wt (Paper III, Fig. 6). A shift from HC to LC at 500 μmol photon m<sup>-2</sup> s<sup>-1</sup> (HL) revealed large increases in both FDP levels over the first 6 h, but levels had lowered again by 24 h. However, FLVB accumulation remained at higher levels than FLVA (Paper III, Fig. 7). Collectively, these results show that O<sub>2</sub> photoreduction processes, the true Mehler reaction and FDP-mediated O<sub>2</sub> photoreduction are activated in the *pgrl1* mutant. It is likely that FDPs function under conditions that create a moderate electron pressure on the PET chain, while the true Mehler reaction becomes the main compensatory O<sub>2</sub> photoreduction mechanism under LCHL, when the electron pressure on the PET chain is higher.

#### ***4.1.5. Underlying mechanisms behind the phenotypes of the *pgrl1* and *pgr5* mutants under fluctuating light***

To evaluate the function of PGR1 and PGR5 in protecting photosynthesis during fluctuating light, the knock-out mutants of *pgr5* and *pgrl1* were subjected to the same mild FL 20/200 illumination regime as described in section 4.1.2. The *pgr5* mutant showed severely impaired growth under mild FL 20/200 conditions, whereas the growth of *pgrl1* was not affected. It was only under harsh FL 20/600 conditions that inhibition of the growth of *pgrl1* cells was observed (Paper II, Fig. 1). Under mild FL 20/200 conditions, the wt and *pgrl1* mutant exhibited very similar effective PSII and PSI yields (Paper II, Fig. 2 and Fig. 3). The *pgrl1* mutant grown in mild FL 20/200 showed only a slightly lower PSI yield than the wt under the HL phase. Additionally, the PSI donor-side limitation and PSI acceptor-side limitation were only mildly affected under mild FL 20/200 conditions. Immunoblot analysis showed an increased accumulation of FDPs in the *pgrl1* mutant (Paper II, Fig. 7). Remarkably, this increased accumulation of FDPs in *pgrl1* even caused a decrease in PSI acceptor-side limitation during the HL phase when the cells were grown in CL 20 conditions (Paper II, Fig. 3). Immunoblot analysis also revealed a low

accumulation of Cyt *f* in *pgr11* under FL 20/200 illumination, suggesting limited electron flow to PSI. This, together with increased FDP accumulation, allows *pgr11* to protect PSI and to cope with mild FL stress.

When *pgr5* was grown under FL 20/200 conditions, the effective yields of PSII and PSI were reduced as compared to the wt (Paper II, Fig. 2). PSI acceptor-side limitation was greatly increased and the donor-side of PSI was not limited. This led to greatly increased electron pressure on PSI in the *pgr5* mutant under FL 20/200 conditions. The increased electron pressure on PSI results in a decrease of PSI over time, as was evidenced by reduced levels of PsaA protein under FL 20/200 (Paper II, Fig. 7). Next generation RNA sequencing (RNAseq) showed the down-regulation of several photosynthesis related transcripts including *psaH*, *lhcbm6*, *lhcbm7* and *lhcbm9* in *pgr5* (Paper II, Suppl. Tab.1). Furthermore, the *curt1* transcript level is reduced in the *pgr5* mutant, indicating the possibility of a disturbed thylakoid architecture. Immunoblot analysis revealed that the problem in *pgr5* is likely associated with the missing donor-side limitation, given that proteins working as electron acceptors downstream of PSI (FDX1, RbcL and FDPs) were up-regulated (Paper II, Fig. 7). The *pgr5* and *pgr11* mutants exhibited an increased level of proteins involved in O<sub>2</sub> consuming processes (COXIIb, FeSOD and FDPs) under CL 20 conditions and, to a lesser extent, under FL 20/200 conditions (Paper II, Fig. 7). These results were similar to the observations made for *pgr11* under steady-state conditions in paper III and thus could indicate similar compensation mechanisms involving mitochondrial respiration and O<sub>2</sub> photoreduction for *pgr5*.

Interestingly, the P700 redox kinetics revealed that, similar to the *flv* mutants, the fast “re-oxidation rise” was almost completely lacking in the *pgr5* mutant (Paper II, Fig. 5). This finding suggests that although FDPs are present, they are not capable to cope with the high electron flux towards P700 in *pgr5*. Low temperature (77K) fluorescence emission analysis showed an increased transition to state-2 in *pgr5* under FL 20/200 conditions, that was not observed for wt or *pgr11* cells. Thus, *pgr5* stromal electron carriers are likely over-reduced and may be influencing FDP-activity.

Analysis of the ECS signal in *pgr5* revealed that the total *pmf* was diminished due to the reduction of both  $\Delta pH$  and, particularly,  $\Delta\Psi$  components (Paper II, Fig. 6). Therefore, NPQ and LHCSR3 accumulation were also drastically reduced (Paper II, Suppl. Fig. 4 and Fig. 7). Surprisingly, the *pgr11* mutant exhibited a slightly higher *pmf* than the wt. However,  $\Delta pH$  was reduced under FL 20/200 conditions due to the lack of PGRL1-mediated CET and thus, the accumulation of NPQ and LHCSR3 were

also reduced. The increased *pmf* in *pgrl1* was a result of an increased  $\Delta\Psi$  component. This result indicates that ion channels in the thylakoid membrane may be differently regulated in *pgrl1* than in wt or the *pgr5* mutant.

## **4.2. Impact of alternative electron transport on hydrogen production**

Hydrogen (H<sub>2</sub>) production represents an additional AET pathway because it can work as an electron sink for photosynthesis under specific conditions, e.g. during the shift from dark anoxia to light (Appel et al., 2000; Happe et al., 2002). It has been shown that the knock-out of *pgrl1* and *pgr5* enhances H<sub>2</sub> photoproduction during sulfur (S)-deprivation (Steinbeck et al., 2015). Therefore, the impact of other pathways in the AET network on H<sub>2</sub> production is an area of increased interest.

### ***4.2.1. Flavodiiron proteins are transiently up-regulated during the shift to sulfur-deprivation***

In order to understand the impact of FDP-mediated O<sub>2</sub> photoreduction on H<sub>2</sub> production, gene transcription and protein expression of FDPs were studied during cell acclimation to S-deprivation. S-deprived *C. reinhardtii* cultures go through five successive stages during the acclimation process: active photosynthesis, increased O<sub>2</sub> consumption, anaerobic lag phase, H<sub>2</sub> production and termination (see Introduction, Fig. 6). The samples for transcript and protein analysis were collected at representative time points for each acclimation stage (Paper I, Fig. 6). Both *flvA* and *flvB* transcripts were greatly up-regulated after only 2 h of S-deprivation (Paper I, Fig. 6). The *flvA* transcript amount decreased only after 40 h, whilst *flvB* had decreased by 24 h. Immunoblot analysis demonstrated a strong up-regulation of FLVA over the first 24 h of the shift to S-deprivation followed by a return to initial levels. In contrast, FLVB levels were elevated during the first 24 h, but then declined to become undetectable by the end of the experiment. These results indicate that FDPs are important during the early hours of S-deprivation and possibly accelerate the acclimation to anoxic conditions.

### ***4.2.2. Comparison of H<sub>2</sub> production in sulfur- or magnesium-deprivation protocols***

Sulfur (S)-deprivation is one of the regularly used protocols to establish anoxic conditions needed for H<sub>2</sub> photoproduction in *C. reinhardtii* (Melis et al., 2000). However, in a recent study a magnesium (Mg)-deprivation protocol has been tested and the Mg-deprived *C. reinhardtii* cells were able to produce more H<sub>2</sub> than known from S-deprived

cells (Volgusheva et al., 2015). Therefore, the reasons for this enhanced H<sub>2</sub> production were studied by comparing side by side the two different protocols.

The H<sub>2</sub> production capacities of *C. reinhardtii* cells during both S- and Mg-deprivation exhibited the typical five acclimation stages described above. The Mg-deprived cells produced H<sub>2</sub> at a similar rate to the S-deprived cells and were able to maintain the production for a longer time (Paper IV, Fig. 1). Excluding the pre Mg-deprivation stage, the O<sub>2</sub> evolution phase was shorter in the Mg-deprived cells and the overall O<sub>2</sub> yield was also lower. Accordingly, anoxia was established earlier in the Mg-deprived cells. The effective PSII yield showed a sharp drop when O<sub>2</sub> was entirely consumed from the media, possibly because of a redox-dependent inactivation of PSII. Instead, in Mg-deprived cells,  $\Delta F/Fm'$  decreased much more slowly than in S-deprived cells. The starch content was also lower in Mg-deprived cells, and the starch break-down began earlier (Paper IV, Fig. 1). Low temperature (77K) fluorescence analysis showed that Mg-deprivation induced a transition to state-2. This indicated that CET was possibly increased, as both phenomena are induced by the redox status of the PQ-pool (Paper IV, Fig. 6).

The apparent increase in PSII activity in Mg-deprived cells, as compared to S-deprived cells, led to a more thorough study of O<sub>2</sub> exchange. The net O<sub>2</sub> evolution in light, or photosynthesis rate, and maximal PSII activity were measured using a Clark-type O<sub>2</sub> electrode. The photosynthesis rate and maximal PSII activity exhibited a rapid drop after 24 h in S-deprivation (Paper IV, Fig. 3). In contrast to this, Mg-deprivation resulted in a higher photosynthesis rate and PSII activity, which only dropped after 120 h. These results correlate with the higher levels of PsbA, Cyt *f* and RbcL found in Mg-deprived cells and their rapid decline in S-deprived cells (Paper IV, Fig. 5).

Respiration increased during the first 48 h in S-deprivation and then slowly decreased, whilst respiration in Mg-deprived cells remained constant and only decreased after 120 h. The contribution of chlororespiration to dark O<sub>2</sub> consumption was estimated by adding the mitochondrial respiratory inhibitors myxothiazol and SHAM to the cells (Paper IV, Fig. 4). It is probable that the remaining O<sub>2</sub> uptake activity mainly represents the activity of PTOX (Antal et al., 2009), which was enhanced during Mg-deprivation. Immunoblot analysis suggested that other O<sub>2</sub>-consuming processes were also up-regulated during Mg-deprivation, as FeSOD levels were elevated under both conditions and FDPs remained at higher levels than during S-deprivation. These results indicate that a combination of different O<sub>2</sub> reduction processes create a micro-oxic environment inside the chloroplast to protect the O<sub>2</sub>-sensitive hydrogenase under Mg-deprivation.

## 5. DISCUSSION

### 5.1. The importance of alternative electron transport for photoprotection in dynamic light environments

Many laboratory studies concerning photosynthesis are carried out under steady state environmental conditions, or changes are tracked following a change in only one environmental factor. However, in nature, photosynthetic organisms are repeatedly exposed to changing environmental conditions, such as light intensity, temperature or nutrient availability. In particular, aquatic photosynthetic microorganisms experience frequent fluctuations in light due to turbulence, the lens effect of waves and the shading caused by clouds or leaves (Allahverdiyeva et al., 2015a). Resulting sudden shifts to high light create an electron pressure in the PET chain that leads to harmful side products like reactive oxygen species (ROS) and as a result, oxidative damage of the photosynthetic apparatus. Therefore, oxygenic photosynthetic organisms developed elaborate and efficient mechanisms to fine-tune the photosynthetic apparatus and cope with changing light conditions.

In cyanobacteria, Flv1 and Flv3 (the homologs of *C. reinhardtii* FDPs) protect PSI from excess electron pressure under FL conditions by forming a heterooligomer and acting as an electron sink downstream of PSI (Allahverdiyeva et al., 2013). It is noteworthy that cyanobacteria do not possess a Pgr11 homolog and only have a Pgr5-like protein. The Pgr5-like protein is believed to be involved in CET (Yeremenko et al., 2005), but it is not involved in the protection of *Synechocystis* during fluctuations in light intensity (Allahverdiyeva et al., 2013). In contrast, for higher plants that do not possess homologous genes of FDPs, the PGR5 protein is crucial for survival under FL conditions. This is the case for *A. thaliana* (Suorsa et al., 2012) and rice (Yamori et al., 2016). Higher plants also possess PGRL1 which is likely involved in CET and this pathway could also be beneficial during fluctuating light. To my knowledge, the impact of PGRL1 on the photosynthesis of higher plants under FL conditions has not yet been studied. In the moss *P. patens* and the liverwort *Marchantia*, which are lower in the evolutionary tree, the important photoprotective function of FDPs under fluctuating light conditions has been previously shown (Gerotto et al., 2016; Shimakawa et al., 2017). These organisms, like *C. reinhardtii*, possess all of the proteins already discussed as important under FL: FDPs, PGR5 and PGRL1. However, a comparative study determining which of these proteins is the main player in the photoprotection of PSI, has yet to be published. Therefore, my doctoral research focussed on the function and interplay of these AET pathways, to

identify which pathway is most important and if these pathways can complement each other.

## **5.2. Flavodiiron proteins work on a faster time-scale than PGR5 or PGRL1 and are indispensable for survival under fluctuating light**

FDPs are up-regulated during the acclimation process to stress conditions that lead to the reduction of the PET chain, i.e. HL and/or LC (Paper I Fig. 3, 4 and 5). Furthermore, the accumulation levels of FLVA and FLVB do not necessarily correlate with each other, indicating that besides functioning as heterooligomers, these proteins possibly also form homooligomers as demonstrated for *Synechocystis* Flv3 and Flv1 (Mustila et al., 2016). Indeed, alignment of the flavodoxin domain demonstrated specific changes in the amino acid sequence of the flavodoxin domain in cluster B (Fig. 7). This suggests that homooligomers of FLVA or FLVB would exhibit different features, rather than heterooligomers, and thus may be involved in different processes than Mehler-like O<sub>2</sub> photoreduction. Apparently, the protein accumulation of FLVB also affects either the stability or the translation of FLVA, because the *flvB* knock-out mutant lines are not able to accumulate FLVA in the absence of the heterodimer with FLVB (Paper II Suppl. Fig. 2).

Compared to the *pgr5* and *pgrl1* mutants, the *flv* mutants showed the most severe phenotype even under mild FL 20/200 conditions (Paper II Fig. 1). During the HL phase, the PET chain is completely blocked, demonstrated by a fully limited PSI acceptor-side in the *flv* mutants (Paper II Fig. 4). These results and the fast P700 oxido-reduction kinetics (Paper II Fig. 5) led to the conclusion that FDPs work as a fast electron sink, within 1 second of the onset of HL, similar to previous studies in cyanobacteria, the moss *P. patens* and the liverwort *Merchantia* (Allahverdiyeva et al., 2013; Gerotto et al., 2016; Shimakawa et al., 2017). Furthermore, the important contribution of this rapid electron sink to the fast induction of photoprotective mechanisms, i.e. NPQ and photosynthetic control of Cyt *b<sub>6</sub>f*, via the establishment of ΔpH was demonstrated (Paper II Fig. 7 and Suppl. Fig. 4).

From these data, I concluded that the soluble nature of FDPs makes a fast interaction with available reduced donors, NADPH or FDX, possible. Thus, FDP-mediated O<sub>2</sub> photoreduction could provide a strong sink for the majority of electrons arriving from PSI over a short time period, at the onset of HL. On the other hand, the redox-dependent activation of PGRL1-mediated CET via thioredoxin and the reduction of PGRL1 likely need several seconds to activate (Hertle et al., 2013). Due

to this time difference between FDP-, PGR5- and PGRL1-mediated AET, a lack of FDPs cannot be rescued by PGR5 or PGRL1-mediated CET.

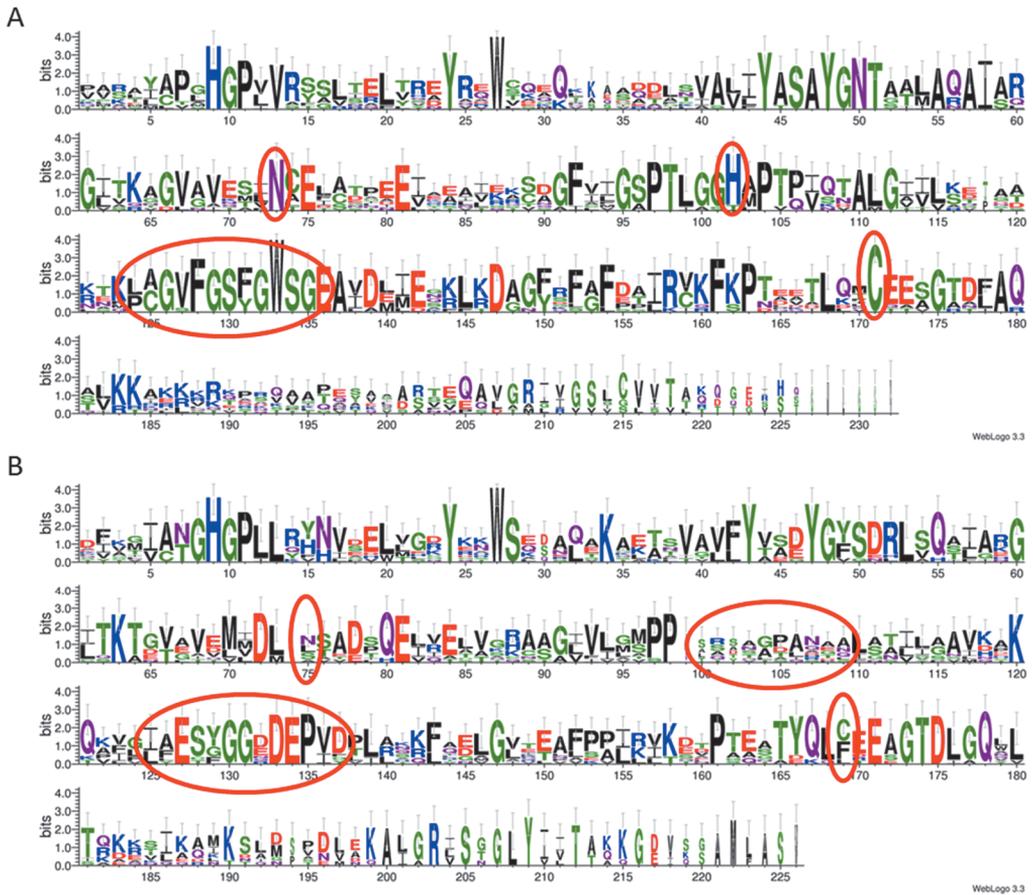


Fig. 7: Sequence logo of the flavodoxin domain of cluster A (A) and B (B). The alignments were performed with the FDP aminoacid sequences from *Synechocystis* sp. PCC 6803, *Anabaena* sp. PCC 7120, *Chlamydomonas reinhardtii*, *Micromonas pusilla* CCMP1545, *Ostreococcus lucimarinus*, *Physcomitrella patens* and *Selaginella moellendorffii*. Red circles indicate conserved aminoacids that are missing in the cluster B flavodoxin domain and the hydrophobic area from position 126 to 135, which is also missing in flavodoxin B.

### 5.3. PGR5 and PGRL1 proteins have different impacts on photosynthesis

The ability of *C. reinhardtii* cells to grow under different cultivation modes – mixotrophic, heterotrophic and photoautotrophic, and the common tradition to favour heterotrophic growth, makes the interpretation of photosynthesis research, particularly that focused on CET, challenging. CET rates have been estimated from cells grown in the presence of acetate (Petroustos et al. 2009; Alric 2014; Johnson et

al. 2014) and from short (2 h) shifts in TAP medium to minimal medium (Terashima et al., 2012; Tolleter et al., 2011). Complications arise because in mixotrophic grown *C. reinhardtii* cells, up to 50% of the carbon is actually acquired from acetate and not from photosynthetic driven CO<sub>2</sub> fixation (Heifetz et al., 2000). Furthermore, the effective PSII yield and O<sub>2</sub> evolution are reduced in mixotrophic grown cells, while respiration remained unchanged (Endo and Asada, 1996). The presence of acetate in the medium also reduces the expression of several photosynthesis related genes in *C. reinhardtii* (Kindle, 1987; Sheen, 1994). To avoid masking photosynthetic responses to FL conditions by acetate metabolism, I undertook experiments in completely photoautotrophic conditions, growing cells for 7 days in minimal medium.

My data show the importance of PGRL1 during the transition to HL, especially under LC conditions (Paper III Fig. 3). These data also correlate with the impaired growth of the *pgrl1* mutant under harsh FL 20/600 conditions (Paper II Fig. 1). The following modifications in the photosynthetic apparatus of *pgrl1* are able to rescue the loss of PGRL1-mediated CET under steady state conditions and under mild FL 20/200: The up-regulation of FDPs (Paper II, Fig. 7); with an increased mitochondrial respiration (Paper III, Fig. 4 and 5); and protection of PSI by the down-regulation of Cyt *f* under FL 20/200 conditions (Paper II, Fig. 7). It is possible that the loss of PGRL1 destabilizes the Cyt *b<sub>6</sub>f* complex and creates this down-regulation of Cyt *f*.

While the role of PGRL1 in CET is relatively clear, that of PGR5 is not so straightforward. The *pgr5* mutant shows a more severe phenotype even under mild FL 20/200 conditions. This cannot be simply ascribed to impaired CET, because the *pgrl1* mutant can still cope under these conditions (Paper II Fig. 1 and 2). It is noteworthy that Cyt *f* accumulation is not altered in the *pgr5* mutant and therefore electrons reach PSI unhindered (Paper II Fig. 2 and 7). The induction of NPQ is reduced in *pgr5* and *pgrl1*, although more severely in *pgr5*. This correlates with the LHCSR3 protein accumulation in these mutants (Paper II Fig. 7 and Suppl. Fig. 4). In contrast to wt and *pgrl1*, the 77K low temperature spectroscopy of FL 20/200 grown cells showed that the *pgr5* mutant is mostly in state-2 (Paper II Suppl. Fig. 5). This indicates a more reduced redox status of stromal components in the absence of PGR5 and thus, hints towards a possible role for PGR5 as a redox- regulator of photosynthetic electron transport.

This different redox status of the *pgr5* mutant compared to wt or *pgrl1* under FL 20/200 illumination could also explain the differences in the electric potential

component ( $\Delta\Psi$ ) of the *pmf* (Paper II Fig. 6). While the *pgr11* mutant demonstrates increased  $\Delta\Psi$ , the *pgr5* mutant exhibits a decreased  $\Delta\Psi$  component. This could indicate a modification of ion fluxes over the thylakoid membrane (Finazzi et al., 2015; Höhner et al., 2016). The redox-regulated thylakoid  $K^+/H^+$  antiporter KEA3 has been shown to increase  $\Delta\Psi$  while decreasing  $\Delta pH$ , and thus accelerate NPQ relaxation during a transition from HL to LL in *A. thaliana* (Armbruster et al., 2014). A homolog of KEA3 is present in *C. reinhardtii* and could thus be a candidate for the difference observed in  $\Delta\Psi$  between *pgr5* and *pgr11*.

It is interesting that FDP-mediated  $O_2$  photoreduction cannot rescue the loss of PGR5. The fast P700 oxido-reduction kinetics of the *pgr5* mutant closely resembles that of the *flv* mutants (Paper II Fig. 5). Thus, even though FDPs accumulate in *pgr5*, their activity as an electron sink downstream of PSI seems to be insufficient to contribute to the oxidation of P700. It is possible that despite high FDP accumulation (Paper II Fig. 7) and an increased light-induced  $O_2$  uptake (Steinbeck et al., 2015), the elevated influx of electrons to PSI cannot be quenched in the *pgr5* mutant. However, this also does not exclude a possible redox-dependent down-regulation of FDP-activity via one or more of the conserved cysteins present in FDPs in the *pgr5* mutant, which exhibits an altered redox status (Paper II Suppl. Fig. 5).

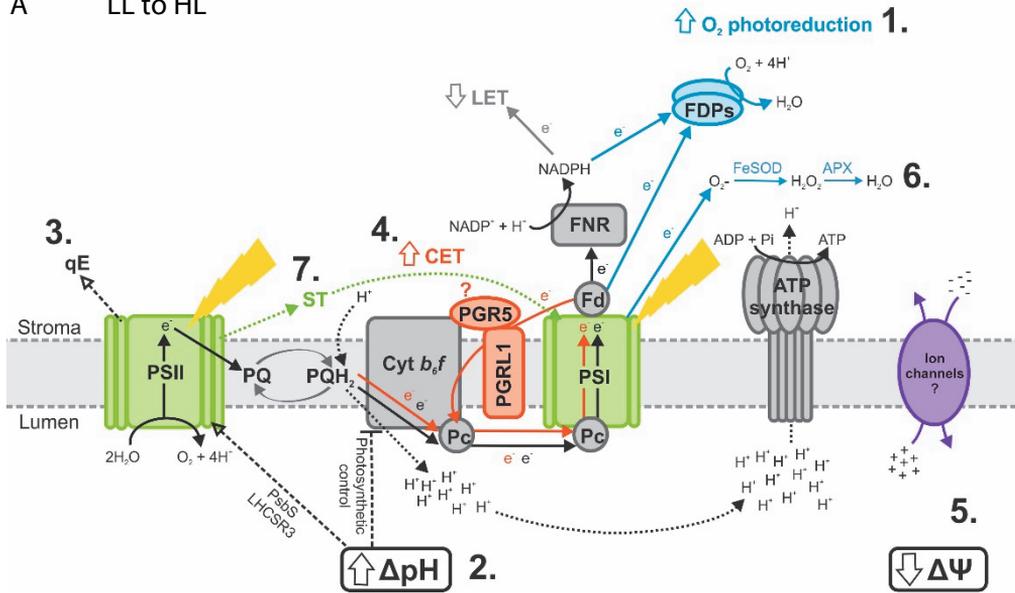
The results of my own doctoral research and other recently published work on the function of PGRL1 and PGR5 show distinct differences in the regulation of the knockout mutants. I observed differences in growth performance under FL conditions, the induction and partitioning of *pmf*, and the redox state of the cells between the two mutants. In other works, the CET rate has been reported as drastically reduced in the *pgr11* mutant, whilst altered only under anoxia in *pgr5* (Tolter et al., 2011; Alric, 2014; Johnson et al., 2014). Moreover, the *pgr5* mutant has been demonstrated to produce  $H_2$  much more efficiently than the *pgr11* mutant (Steinbeck et al., 2015). In the same work, the *pgr5* mutant also showed stronger PSI photoinhibition than *pgr11*, similar to the results presented in this thesis. The apparent differences between the two mutants indicate that PGRL1 and PGR5 do not have exclusive function together in the same pathway. In *A. thaliana*, the PGR5 protein plays a crucial role in the protection of PSI under FL conditions (Suorsa et al., 2012; Tiwari et al., 2016) and thus, the data for the *pgr5* mutant presented here suggests a similar role for *C. reinhardtii*.

The function of PGRL1 in *C. reinhardtii* is closely linked to CET under oxic and anoxic conditions (Iwai et al., 2010; Petroustos et al., 2009; Terashima et al., 2012;

Tolleteer et al., 2011) and it was proposed to be the elusive FQR, functioning in a redox-dependent manner in *A. thaliana* (Hertle et al., 2013). In that study, the function of the six conserved cysteins in PGRL1 was elucidated *in vitro*. While the first two cysteins are important for the dimerization of PGRL1, these cysteins, together with two more, bind the iron in the active centre. The last two cysteins appear to be necessary for the structural stability of the protein. It was also suggested that the last four cysteins are involved in the interaction of PGRL1 with PGR5 (Hertle et al., 2013; Dang, 2015). In PGR5, only one cystein is conserved, thus the interaction via disulfide bonds is probably not very strong (Dang, 2015). It is likely that PGR5 is not directly involved in CET via PGRL1, but is actually more of a redox sensor, manipulating the efficiency of electron transport via PGRL1. In this regard, it is also possible to explain the fairly extensive consequences that the lack of PGR5 has on many different processes in *C. reinhardtii*, as described in this doctoral thesis. As a redox sensor, PGR5 may also interacts with other targets and influence several metabolic pathways, such as: thylakoid ion channel activity; ATP synthase H<sup>+</sup> conductivity; and the functionality of FDPs. The stimulating effect that the lack of PGR5 has on ATP synthase H<sup>+</sup> conductivity has been reported in *A. thaliana* (Avenson et al., 2005; Wang et al., 2015). Interestingly, a recent study in *A. thaliana* showed the redox-dependent regulation of the ATP synthase H<sup>+</sup> conductivity by the chloroplast NADPH thioredoxin reductase C (Carrillo et al., 2016). It is possible that the redox sensing function of PGR5 is connected to the thioredoxin regulative system in the chloroplast.

From the new data presented in this thesis, together with current literature on the topic, a model of the mechanisms regulating photosynthesis during the exposure to fluctuating light is proposed (Fig. 8).

## A LL to LL



## B HL to LL

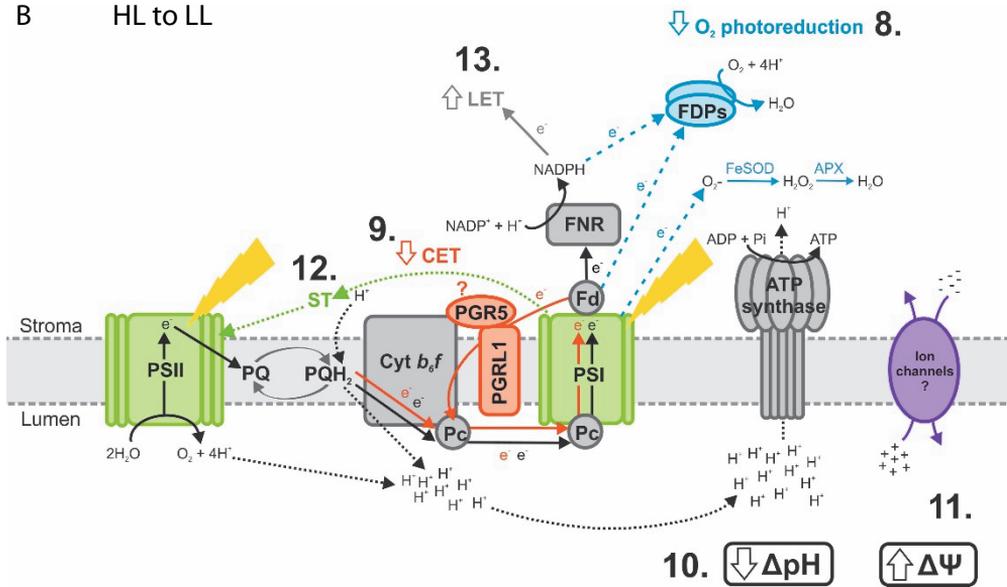


Fig. 8: Schematic representation of photosynthetic and alternative electron transport pathways demonstrating events occurring during a shift from LL to HL (A) and from HL to LL (B) in *C. reinhardtii*. LET is indicated by black and grey arrows; CET by red arrows. Blue arrows indicate O<sub>2</sub> photoreduction, mediated by FDPs or the true Mehler-reaction. Proton translocation is indicated by black dashed arrows and ion movement over the thylakoid membrane by purple arrows. Green dashed arrows represent state transitions. At the onset of HL (A), FDP-mediated O<sub>2</sub> photoreduction functions within seconds and forms a strong electron sink downstream of PSI (1). Thus, FDPs support the entire PET and contribute to proton pumping into the thylakoid lumen (2). Subsequently, increased ΔpH induces other photoprotective mechanisms including photosynthetic control at Cyt *b<sub>6</sub>f* level (Colombo et al.,

2016) and the activation of LHCSR3 and PsbS (Correa-Galvis et al., 2016; Peers et al., 2009), which in turn induce NPQ (3). After several seconds, PGRL1-mediated CET accelerates, possibly influenced by the redox-sensor PGR5. Elevated CET contributes further to the establishment of  $\Delta\text{pH}$  (4). At this point, PGRL1-mediated CET probably replaces FDP-mediated  $\text{O}_2$  photoreduction as the major AET route. To balance *pmf* and regulate the  $\Delta\Psi$  component, counter ions are translocated across the thylakoid membrane (Finazzi et al., 2015; Höhner et al., 2016) by ion channels, which either release cations into the stroma or transport anions into the lumen (5). After a prolonged period of HL, possibly several minutes, the excess electron pressure leads to ROS production at PSI which activates true Mehler reaction and subsequently the WWC (6), ultimately making FDPs redundant as an electron sink. Also after several minutes, the reduced PQ-pool, responsible for activating specific kinases, leads to the transition of LHClI from PSII to PSI (Minagawa, 2011) into state-2 (7). On returning from HL to LL illumination (B), these processes are reversed. Limited electron availability causes a decrease in FDP-mediated  $\text{O}_2$  photoreduction (8) and PGRL1-mediated CET (9). The transition to LL also requires rapid dissipation of NPQ and photosynthetic control at Cyt *b<sub>6</sub>f*, this happens via the dissipation of  $\Delta\text{pH}$  (10). Proton translocation performed solely via ATP synthase is probably not fast enough, thus the KEA3 channel may also releases protons from the thylakoid lumen (Armbruster et al., 2014) and ion channels operate so that  $\Delta\Psi$  is increased (11). On a slower time-scale, probably in the range of minutes, state transitions are reversed (12), the PET chain returns to its balanced state and LET becomes the major PET pathway (13). For simplicity reasons, NDA2-mediated CET is not depicted in this figure.

#### 5.4. Hydrogen production is influenced by the activity of other alternative electron transport pathways

Several microalgae, including *C. reinhardtii*, are able to use solar energy and photoproduce  $\text{H}_2$  metabolically. However, direct conversion of light to  $\text{H}_2$  is very low, because the  $\text{H}_2$ ase is  $\text{O}_2$ -sensitive (Ghirardi et al., 1997; 2007; Stripp et al., 2009). Consequently,  $\text{H}_2$  production yields are not high enough for commercialization of this process. Thus, different  $\text{H}_2$  production protocols and genetic modifications of *C. reinhardtii* have been tested for their  $\text{H}_2$  production capability.

An increased understanding of photosynthesis in microalgae has led to the discovery of new targets for enhancing  $\text{H}_2$  production via genetic manipulation. The knockout mutant of PGRL1, lacking CET, is able to produce about 5-times more  $\text{H}_2$  than the wt (Steinbeck et al., 2015; Tolleter et al., 2011). The *pgr5* mutant is, even more impressive, able to produce 8-times more  $\text{H}_2$  compared to the wt, making it the best biological  $\text{H}_2$  producer up-to-date. This enhanced  $\text{H}_2$  production in *pgr1* and *pgr5* has been explained by more remaining PSII activity and increased  $\text{O}_2$  consumption (Steinbeck et al., 2015). The data obtained during my doctoral research corroborates the increased  $\text{O}_2$  consumption in *pgr1* and suggests that this is due to a combined effect of enhanced mitochondrial respiration and  $\text{O}_2$ -photoreduction via

FDPs (Paper III Fig. 5 and 6). However, whether FDP-mediated O<sub>2</sub>-photoreduction contributes to the enhanced O<sub>2</sub> consumption in *pgr5* is still under question, because there is the possibility that FDPs are not fully active in *pgr5* under certain conditions (Paper II Fig. 5). It is possible that the redox status of the *pgr5* mutant favors the formation of FDP homooligomers which could function in a different AET route to the Mehler-like reaction as proposed for Flv1 and Flv3 homooligomers in *Synechocystis* (Mustila et al., 2016).

The data presented in this doctoral thesis also suggest that FDP-mediated O<sub>2</sub> photoreduction is an important factor accelerating the acclimation of algal cells to anaerobiosis induced by S-deprivation (Paper I Fig. 6). To sustain the metabolism of the cell under anoxia, the activity of the H<sub>2</sub>ase and of fermentative pathways is needed (Hemschemeier and Happe, 2011; Catalanotti et al., 2013). Several enzymes of these pathways are sensitive to O<sub>2</sub> (Atteia et al., 2013). Therefore, a rapid shift to complete anoxia in the cell and subsequent efficiency of fermentation and H<sub>2</sub>ase are important for the survival of *C. reinhardtii*, which regularly faces microoxic or anoxic conditions in its natural aquatic habitat. Because of their possible role in the acclimation process to anoxia, FDPs are an interesting target for genetic modification towards improved H<sub>2</sub> production yields.

Different production protocols, used to induce anaerobiosis via the depletion of nutrients like nitrogen, phosphorus, potassium and magnesium, have been the focus of much of the recent research on *C. reinhardtii* H<sub>2</sub> production (Philipps et al., 2012; Batyrova et al., 2012; 2015; He et al., 2012; Papazi et al., 2014; Volgusheva et al., 2015). Indeed, Mg-deprivation has resulted in the production of about twice as much H<sub>2</sub> as S-deprivation, this being due to a prolonged H<sub>2</sub> production phase (Paper IV Fig. 1). The contribution of FDP-mediated O<sub>2</sub> photoreduction to the removal of remaining O<sub>2</sub> inside the chloroplast is indicated by a greater accumulation of FDPs during H<sub>2</sub> production in Mg-deprived cells than in S-deprived cells (Paper IV Fig. 5). Recently, it was shown that H<sub>2</sub> production is also possible under micro-oxic conditions (Liran et al., 2016). Under these conditions, FDPs may be particularly useful in the removal of O<sub>2</sub> from the chloroplast to ensure the activity of the H<sub>2</sub>ase. In Mg-deprived cells, mitochondrial respiration and PTOX activity are also increased (Paper IV Fig. 3 and 4). The enhancement of these O<sub>2</sub> consumptive processes is necessary because the activity of PSII remains higher in Mg-deprived cells than in S-deprived ones (Paper IV Fig. 1, 2 and 3). Although the energy for H<sub>2</sub> production is mostly supplied by the indirect pathway via starch breakdown, it is highly likely that the enhanced PSII activity in Mg-deprived cells has positive effects on the

metabolism and viability of the cells and is the reason for the prolonged H<sub>2</sub> production phase.

Biological H<sub>2</sub> production by microalgae holds both challenge and promise for the future. Further advances in molecular engineering, such as the deployment of the CRISPR/Cas9 method, novel H<sub>2</sub> production protocols and bioreactor design are needed to feasibly employ solar fuel systems in the context of a sustainable energy economy. A combination of several of the discussed mutations with the right production protocol will be required to ensure efficient long-term production of clean H<sub>2</sub> fuel, which has the potential to be an important step toward the reduction of global green house gas emissions.

## 6. CONCLUSIONS AND FUTURE PERSPECTIVES

The data presented in this doctoral thesis give valuable new insight into the regulation of photosynthesis via AET in the green algae *C. reinhardtii*. My results suggest that the regulation of photosynthesis via AET under dynamic light environments is a more complex process than is currently understood. Through my doctoral research, I have demonstrated that in *C. reinhardtii*;

- FDPs are indispensable for survival under FL and function as a strong and transient electron sink of the PET chain downstream of PSI
- Following FDPs, PGR5 is the next important player to act under FL conditions. In the absence of PGR5, FDPs are not sufficient to fully rescue cells from FL stress
- PGRL1 is dispensable under mild FL conditions, but becomes more important during periodic shifts from low background light to very strong HL transients and thus, contributes to growth under harsh FL conditions
- The successive function of all three AET pathways; FDPs, PGR5, and PGRL1-mediated CET, together with the cooperation of mitochondrial respiration are necessary to protect photosynthesis under changing environmental conditions
- FDPs function as O<sub>2</sub> quenchers during S-deprivation and contribute to the maintenance of anoxia inside the chloroplast during the acclimation phase
- Mg-deprivation results in prolonged H<sub>2</sub> production due to the positive effect of increased PSII activity and O<sub>2</sub> consumption via FDPs and other pathways on the metabolism of the cell

Additional research is needed to clarify the exact role of PGR5 as a possible redox-regulator of PET and/or its function in establishing photosynthetic control. In particular, more extensive studies on the different possible targets of PGR5 are needed to understand how PGR5 regulates photosynthesis. Additionally, *in vivo* experiments with cystein substitution mutants of PGR5 and PGRL1 remain to be performed. My doctoral research indicates a close link between PGR5, PGRL1 and the regulation of ion fluxes over the thylakoid membrane. Further studies are

needed to identify thylakoid ion channels in *C. reinhardtii* and evaluate their impact on PET.

The protection of photosynthesis via the FDP-mediated O<sub>2</sub> photoreduction pathway is evolutionarily conserved in cyanobacteria, green algae, bryophytes, lycophytes and gymnosperms. Therefore, the question arises as to why this pathway is lost in angiosperms, and what mechanism compensates for this loss. More work is needed to properly address this question, although efficient CET was proposed as a possible candidate mechanism in *A. thaliana* (Yamamoto et al., 2016).

The discovery of the function of FDPs in AET and the fact that the H<sub>2</sub>ases are also part of this network, led to the identification of FDPs as a new target for improving H<sub>2</sub> photoproduction in microalgae. Whether the knockout of FDPs and thus, the removal of an electron competitor to the H<sub>2</sub>ase, is beneficial for H<sub>2</sub> photoproduction is yet to be established. However, the approach demonstrates the value in better understanding photosynthesis and AET toward the employment of microalgae for efficient bioenergy production.

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