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Chapter 18: The multiple routes of photosynthetic electron

transfer in Chlamydomonas reinhardtii

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Non-print items - Abstract

- Like all organisms performing oxygenic photosynthesis, *Chlamydomonas* captures light energy in
- two photochemical steps to drive linear electron flow from water to NADPH and to produce ATP.
- However, this process alone is not sufficient to drive CO₂ fixation in the Calvin-Benson-Bassham
- 14 cycle and to respond to environmental and metabolic constraints, e.g. light availability or
- metabolic needs in term of ATP and NADPH. A complex network of alternative electron flows,
- which comprise the Cyclic Electron Flow around PSI or the various water-to-water cycles utilising
- O₂ as alternative electron acceptor, provide an additional degree of freedom to face this challenge.
- 18 The present chapter presents the various alternative routes of photosynthetic electron transfer in
- 19 Chlamydomonas, describes how they coordinate to optimize photosynthesis and gives a
- 20 retrospective on the early physiology work on those alternative electron flows across model
- 21 photosynthetic organisms.
- Non-print items Keywords: Chlamydomonas, Alternative electron flows, photosynthesis,
- 23 Mehler, flavodiiron proteins, PTOX, Cyclic Electron flow.

24 Abbreviations:

- 25 PETC: Photosynthetic electron transport chain
- 26 PSI/PSII: Photosystem I / II
- 27 cyt. $b_6 f$: cytochrome $b_6 f$ complex

- 28 LEF: linear electron flow
- 29 PQ/PQH₂: plastoquinone/plastoquinol
- 30 PC: plastocyanin
- 31 FNR: Fd:NADP⁺ reductase
- 32 NADP+/NADPH: dinucleotide phosphate
- 33 $\Delta \mu_{\text{H}+}$: electrochemical proton gradient
- 34 Δ pH: proton concentration gradient
- 35 $\Delta \psi$: electric potential
- 36 CBB: Calvin-Benson-Bassham
- 37 NPQ: Non-Photochemical Quenching of chlorophyll fluorescence
- 38 qT: state transition
- 39 qE: energy-dependent quenching
- 40 AEF: alternative electron flows
- 41 CEF: Cyclic Electron Flow
- 42 WWC: Water-to-Water Cycle
- 43 ROS: Reactive Oxygen Species
- 44 LHCII: Light Harvesting Complex II
- 45 PTOX: plastid terminal oxidase
- 46 Fd: ferredoxin
- 47 FQR: Fd-PQ oxidoreductase
- 48 PGR5: proton gradient regulation 5
- 49 PGRL1: PGR5-like 1
- 50 NDH: nucleotide dehydrogenase
- 51 WT: wildtype
- 52 FLV: Flavodiiron protein
- 53 AsA: Ascorbate
- 54 MDA: monodehydroascorbate
- 55 PhQ: phylloquinones

CCM: carbon concentration mechanisms

GlcDH: glycolate dehydrogenase

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Introduction

Like all organisms performing oxygenic photosynthesis, Chlamydomonas captures light energy in two photochemical steps to drive the photosynthetic electron transport chain (PETC) in the thylakoid membrane. Electron transport involves the action of three major molecular complexes embedded in the thylakoid lipid phase: the photosystems (PS) I and II (Volume 2, Chapter 15) and the cytochrome $b_6 f$ complex (cyt. $b_6 f$, Chapter 16). In the main linear electron flow (LEF) pathway (Fig 1), the primary electron donor, water, is oxidized at the PSII reaction center. Both PS work in series (Hill & Bendall, 1960) transferring electrons along redox cascades. Between photosystems, electrons transit through the cyt. $b_6 f$ via two mobile carriers, the hydrophobic and membrane soluble plastoquinone (PQ)-pool connecting PSII to cyt. $b_6 f$ and the water-soluble plastocyanin (PC) shuttle connecting cyt. $b_6 f$ to PSI in the thylakoid lumen. At the PSI acceptor side, Fd:NADP⁺ reductase (FNR) accepts electrons from Fd to reduce dinucleotide phosphate (NADP⁺) into NADPH. The LEF allows water splitting on one side, production of reducing power on the other side, and the generation of an electrochemical proton gradient ($\Delta \mu_{H+}$) across the membrane. Proton accumulation in the lumen is coupled to LEF through water splitting at PSII, and through the Q-cycle at the cyt. $b_6 f$ (Joliot & Joliot, 2006). The proton-motive force $\Delta \mu_{\rm H+}$ comprises two energetic components, a proton concentration gradient ($\Delta p{\rm H}$) and an electric potential ($\Delta \psi$) both driving CF₁F₀-ATP synthase catalytic rotation (Mitchell, 1966; Kramer *et al.*, 2003) (Volume 2, Chapter 16). The intermediate molecules NADPH and ATP are the two energy

sources fueling the Calvin-Benson-Bassham (CBB) cycle (Volume 2, Chapters 7 and 8).

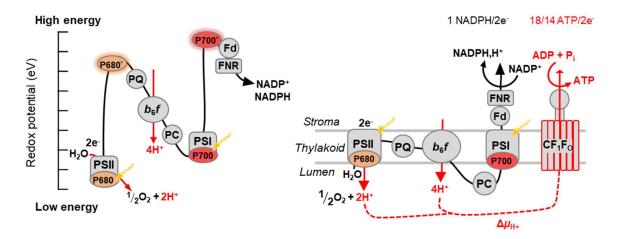


Figure 1: the photosynthetic Linear Electron Flow (LEF). A. LEF in the Z scheme of photosynthesis. B. Representation of the LEF in the thylakoid membranes. Abbreviations: PSII, Photosystem II; PSI, Photosystem I; $b_6 f$, cytochrome $b_6 f$; CF₁F₀, CF₁F₀ ATPase; PC, plastocyanin; PQ, Plastoquinol/Plastoquinone; Fd: ferredoxin; FNR: Ferredoxin/NADP Reductase; $\Delta \mu_H^+$, electrochemical proton gradient.

A description of the photosynthetic electron transfer chain restricted to LEF would give an overly simplistic view of the photochemical phase of photosynthesis. LEF produces a fixed ratio of ATP and NADPH, and in a context were the light input and the metabolic demand in ATP and NADPH are constantly changing, photosynthesis gets the best of LEF only by allowing it to work with some "degrees of freedom". One of them is the biological regulation of the light utilization by the two photosystems, through the non-photochemical quenching (NPQ) at the PSII (Volume 2, Chapter 25) or state transition (qT) (Volume 2, Chapter 24) which is a process particularly important in *Chlamydomonas*. Another main mode of regulation of the photochemical phase of photosynthesis relates to the flexibility of photosynthetic electron flows. In all organisms performing oxygenic photosynthesis, LEF components (PSI, PSII, cyt $b_6 f$) are always involved in

a complex network of alternative electron flows (AEFs) which divert electron transport from NADPH production or assimilation of CO_2 . The present chapter focuses on those AEFs and is structured as follows; in Section 1, we first explain the input and output constraints on LEF operation (light availability and metabolic needs in term of ATP and NADPH) and how AEFs provide an additional degree of freedom to face this challenge. Then we present the various AEFs in Section 2, from the first experimental evidence to recent works more specific to *Chlamydomonas*. We will especially focus on the two main AEFs modes (schematized in Fig 2 and 3), the Cyclic Electron Flow (CEF) around PSI, where electrons at the acceptor side of PSI are reinjected upstream the cyt. $b_6 f$, and the various water-to-water cycles (WWC) (or pseudocyclic electron fluxes), which utilise O_2 as alternative electron acceptor instead of CO_2 (Curien *et al.*, 2016). In Section 3, we discuss how the various AEFs coordinate to optimize photosynthesis in response to changes in environmental conditions. Finally, in relation to the adaptive role of AEFs in green algae, this review ends with a retrospective on the early physiology work on AEFs across model photosynthetic organisms.

1. AEFs provide flexibility to the Linear Electron Flow

The operation of LEF, which uses light as a substrate and synthetizes ATP and NADPH as end-products, is constrained at these two extremities. First, when light fluctuates, light absorption must be adjusted to the electron transport capacity; and second, the ATP/NADPH ratio must adjust to the metabolic needs of the moment. All AEFs share some common features: they play a role of valves, offering an outlet for an additional activity of one photosystem or both. By doing so, they also allow the pumping of extra protons into the lumen, thereby driving an extra $\Delta \mu_{H+}$ and ATP

production. In this first section we will describe first how those common features of AEFs help responding to light and metabolic constraints. Only in the Section 2 which describes AEFs one by one, will their differences and specificities be pointed out, e.g., in terms of photon budget for proton pumping and ATP production.

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Exposure to excess light can lead to over-reduction of PS acceptor-side electron carriers (iron-sulfur centers, Fd and NADPH at PSI; QA, QB and the PQ pool at PSII), augmenting the chances for excited chlorophyll a to transition into a highly unstable triplet state reacting with O_2 . The latter can result in the production of Reactive Oxygen Species (ROS) and photooxidative damage, including photoinhibition of the two PSs (Volume 2, Chapter 25). At PSII, the induction of a series of mechanisms, collectively referred to as NPQ allow to diminish the light pressure on PSII (Volume 2, Chapter 25). In Chlamydomonas, the major component of NPQ is the energydependent quenching (qE) which dissipates excess light energy as harmless heat, and prevents photoinhibition of both PS (Roach et al., 2020). Another NPQ process particularly important in Chlamydomonas is state transition (qT) where a reversible kinase-dependent migration of light harvesting antennae LHCII from one photosystem to the other modulates PSII and PSI light harvesting and rebalances energy fluxes (Volume 2, Chapter 24). The two processes are regulated differently since qE depends on the luminal pH whereas the activity of the kinase involved in the qT is regulated by the redox state of the PQ in the Q_0 site of the cyt. $b_0 f$ (Wollman, 2001; Dumas et al., 2017). When considering the necessary adjustment of the light absorption to the capacity of electron transfer, NPQ manages the downregulation of the former where AEFs allow the upregulation of the later. Therefore, by providing an alternative route for excess electrons, AEFs play the role of redox exhaust valves and protect PSs from photoinhibition.

In addition to the response to light changes, the PETC also faces a constraint related to the stoichiometry of NADPH and ATP. The LEF produces ATP from H⁺ accumulated in the lumen and NADPH from e⁻ transfer along the PETC. Because of the H⁺/e⁻ coupling, ATP/NADPH production is fixed in LEF. The water oxidation at the PSII level produces one proton in the lumen per electron transferred. At the level of the cyt. $b_6 f$, 2 protons are pumped per electron transferred along the chain towards PC, thanks to the Q-cycle (Volume 2, Chapter 17). PQH₂, which acquired two protons from the stroma when reduced at the Q_B site, is oxidized to PQ at the luminal facing Q_0 site of cyt. $b_6 f$, where the two transported electrons take bifurcated pathways but both protons are released in the lumen. One electron follows the high potential chain of the Rieske iron-sulphur protein and cyt. f and attains PC. The second electron follows the low potential chain via haem b_L and haem $b_{\rm H}$. In Mitchell's original proposal (1975), this electron in the low potential chain was used to reduce PQ to PQH₂ on the stromal side of the membrane via an electron coming from PSII. However, based on works on the respiratory cyt. bc_1 a modified Q-cycle was proposed where the b haems can act as an electron reservoir and that PQH₂ is solely fully regenerated after two cycles (Zhang et al., 1998; Crofts et al., 2003; Cramer et al., 2011). The modified Q-cycle is largely accepted nowadays, which is constitutively at place and transfers two protons per electron (Sacksteder et al. 2000; but see section Cyclic Electron Flow). Altogether, the LEF produces 3 H⁺ per electron but, from a metabolic perspective, what matters is the relative amount of reducing power and ATP produced by the PETC, often reflected by the ATP/NADPH ratio. Since two electrons are required to reduce NADP⁺, this leads to a value of 6 protons per NADPH. The question mark lies in the proton requirement per ATP synthesized, which can vary between species depending on the stoichiometry of the subunits forming the membrane intrinsic c-ring of the CF₁F₀-ATP synthase (Petersen et al., 2012; Turina et al., 2016). For most authors, each proton

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crossing the CF₁F₀-ATP synthase induces a one incremental step rotation of the c-ring on the F₀ sector transduced via a central stalk to catalytic conformational changes of the $\alpha_3\beta_3$ subunits on the F₁ sector. Although it remains uncertain whether the work accomplished by each translocated proton is homogeneous (Turina et al., 2016), the yield of 3 ATP molecules synthesized/hydrolysed per CF₁F₀ 360° rotation is well established (Adachi et al., 2007). No structural information of the CF₁F₀-ATP synthase allows to give a definitive stoichiometry in *Chlamydomonas*, but the 14 csubunits of the ATP synthase rotor in spinach is usually used as a reference for eukaryotic photosynthetic organisms (Seelert et al., 2000; Hahn et al., 2018). Then 6 protons released in the lumen yield ~1.28 ATP (6*3/14) and the 3 H⁺/e⁻ coupling leads to 1.28 ATP per NADPH. This ratio is below the 3/2 requirement of the CBB cycle (Allen, 2002). Consequently, without additional flexibility, LEF from water to carbon assimilation is condemned to accumulating NADPH until the photosynthetic activity is fully arrested. AEFs permit an additional activity of the photosynthetic complexes involved in proton pumping, PSII and/or the cyt. $b_6 f$. From this point of view, AEFs can be seen as degrees of flexibility for the electron transfer, allowing for proton pumping without net production of NADPH. This, in turn, generates extra ATP and respond to the mismatch between the ATP/NADPH produced by the PETC and the ATP/NADPH requirement for carbon assimilation. Many reports aimed at calculating the required activity of AEFs to adjust the ATP/NADPH ratio of the CBB cycle (Allen, 2002, Amthor, 2010, Alric et al., 2010) and conclude that AEFs should accumulate one additional proton in the lumen per NADPH produced by the LEF (6 +1 = 7 protons per NADPH would produce 7*3/14 = 1.5 ATP). However, it would be naive to see AEFs solely as a balance for the shortcomings of the 14 csubunits of the CF₁F₀ ATP synthase. In the stroma, the reducing power in the form of reduced ferredoxin or NADPH not only drives the CBB cycle but also stromal enzymes involved in

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essential metabolic pathways like nutrients assimilation (Volume 2, Chapter 4) or amino acid biosynthesis (Volume 2, Chapter 6). Moreover, the substrate availability for the PETC (light) and for the CBB cycle (inorganic carbon) can largely and suddenly vary, limiting the general relevance of such a static view. In low CO₂ conditions, carbon concentration mechanisms (CCM) are induced to gather high CO₂ density around Rubisco confined in pyrenoids (reviewed in *Chlamydomonas* in (Wang et al., 2015), see also Volume 2, Chapter 7). Due to the ATP demand of CCMs, the ATP/NADPH ratio for carbon assimilation is further influenced by CO₂ availability. The network of AEFs in organisms performing oxygenic photosynthesis, including *Chlamydomonas*, should be seen as a dynamic flexibility to abiotic conditions and metabolic needs, by fulfilling three major roles: (i) AEFs can dynamically optimize the ATP/NADPH ratio produced by the PETC to the metabolic needs, and thereby avoid the ATP/NADPH stoichiometric cul-de-sac intrinsic to the sole LEF. (ii) They offer electron valves in conditions where light absorption exceeds the capacity of the sole LEF, preventing the over-reduction of the PETC and risks of photoinhibition. (iii) Finally, by generating additional $\Delta \mu H^+$ AEFs participate to the pH-mediated regulation of the PETC under saturating light conditions. The pH control of the PETC comprises the regulation of NPQ (Volume 2, Chapter 15) and the socalled "photosynthetic control". In conditions of electron transfer limitation downstream of PSI (e.g., low temperature or low CO₂), PSI can be photoinhibited (Chaux et al., 2015). The "photosynthetic control" (Volume 2, Chapter 17) which occurs when a low luminal pH slows down PQH₂ oxidation at the Q₀ site of the cyt. b₆ f (Bendall, 1982), prevents this harmful situation by moving the limiting step of the PETC limiting upstream of PSI (Sukenik et al., 1987). The redox regulation of the CF₁F₀-ATP synthase, which is not covered in this chapter (but see Volume 2, Chapter 17), also plays a crucial role in the modulation of the ΔpH (Kramer et al., 1990). The γ -

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subunit of the CF₁F₀-ATP synthase contains a cysteine couple permitting a disulfide formation under light which decreases the $\Delta\mu_{\text{H+}}$ required for CF₁F₀-ATP synthase rotation (Junesch & Gräber, 1987). This mechanism is conserved and restricted to the green lineage, including *Chlamydomonas* (Buchert *et al.*, 2017; Buchert *et al.*, 2021).

2. Diversity of AEFs in Chlamydomonas

With the definition used in this chapter for AEFs, i.e. electron routes involving photosynthetic complexes (PSII, PSI, cyt b_6f) without resulting in CO₂ fixation, the diversity of AEFs in *Chlamydomonas* is very large. Some of them are already covered in other chapters: one can consider that the use of photosynthetically reduced ferredoxin or NADPH for nutrient assimilation, e.g., nitrogen or sulfur metabolism (Volume 2, Chapter 4) or for amino acid biosynthesis (Volume 2, Chapter 6) enter that category. This is also the case of the coupling between the PETC and the hydrogenase which uses reduced ferredoxins as substrate, in anaerobic conditions (Volume 2, Chapter 9 and 10). In a way, the recombination events in PSs meet the definition strictly speaking but are covered already in the chapter dedicated to photosystems (Volume 2, Chapter 16) and will not be considered here. Finally, the chlororespiration pathway is a minimal respiratory chain in the thylakoid and cannot be considered an AEF but its components are involved in AEFs. This section will especially cover PSI CEF and the various WWCs.

2.1 Chlororespiratory pathway

A minimal respiratory pathway exists in the thylakoids of most organisms performing oxygenic photosynthesis. Bennoun (1982) first reported that PQH₂ could be oxidised in darkness by a plastid terminal oxidase (PTOX). PTOX, together with a NAD(P)H plastoquinone oxidoreductase, forms a chlororespiratory transport chain using electrons from NAD(P)H to reduce O₂ into H₂O (see

review on PTOX (Nawrocki et al., 2015)). In plants, PTOX was initially investigated to decipher its role in chloroplast development and carotenoids biosynthesis (Wu et al., 1999), presumably by regenerating (oxidized) PQ in darkness, which acts as an electron acceptor to activate the phytoene desaturase upstream of the carotenoids' synthesis pathway (Carol & Kuntz, 2001; Bennoun, 2002). Two PTOX enzymes are expressed by Chlamydomonas, PTOX2 being the main oxidase with a rate ~10 fold faster than PTOX1 (4.5 vs. 0.4 e⁻ PS⁻ s⁻¹) (Houille-Vernes et al., 2011). Chlamydomonas phytoene desaturase mutants show similar phenotypes to plants mutants with regards to carotenoids synthesis (McCarthy et al., 2004; Couso et al., 2011). However, demonstrations of PTOX's involvement in this pathway remain inconclusive, notably because ptox2 Chlamydomonas mutants (see Chlamydomonas AEF mutants strains in Table 1) do not show changes in carotenoids content (Houille-Vernes et al., 2011). This function could be undertaken by PTOX1 (Li et al., 2020) as suggested in the green algae Haematococcus pluvialis (Wang et al., 2009); however, two observations make the role of PTOX in carotenoid synthesis of green algae unclear. Not only the O2 uptake by PTOX during the dark segment of Chlamydomonas' photoperiod is almost null (Strenkert et al., 2019) but, in contrast to plants, most carotenoids seem to be synthesized under light in both Chlamydomonas (Janeiro & Barrnett, 1982) and H. pluvialis (Wang et al., 2009). In plants, the chlororespiratory pathway also involves a chloroplast nucleotide dehydrogenase (NDH) complex, called NDH-1. NDH-1 is closely related to mitochondrial respiration complex I (Sazanov et al., 1998), contains 11 subunits with multiple transmembrane domains and reduces quinones with electrons from reduced Fd. Chlamydomonas and other green algae possess instead the NAD(P)H dehydrogenase 2 (NDA2) (Jans et al., 2008), which exhibit similar function as NDH-1 in cyanobacteria and higher plants. NDA2 also utilizes electrons from NAD(P)H to non-

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photochemically reduce the PQ-pool, thanks to a non-covalently bound flavin mononucleotide cofactor (Jans et al., 2008; Desplats et al., 2009). But it also shows important disparities with NDH-1 (reviewed in (Peltier et al., 2016)): it is a monomeric flavoenzyme membrane-bound on the stromal side of the thylakoid and it uses NAD(P)H as a substrate (Jans et al., 2008). Moreover, NDA2 is non-electrogenic (Melo et al., 2004), opposingly to NDH-1 (Strand et al., 2017). Although Chlamydomonas' NDA2 can utilize NADPH, it favors NADH as a substrate (Desplats et al., 2009). Interestingly Chlamydomonas' plastid genome encodes for a transhydrogenase which could convert NADPH to NADH in the stroma (Mus et al., 2007). Although chlororespiration was initially proposed to generate an electrochemical proton gradient in Chlamydomonas (Bennoun, 2002), this model was later disproven. The electrochemical proton gradient in the dark stems from the hydrolysis by the CF₁F₀-ATPase of ATP from mitochondrial origin or in the absence of ATP hydrolysis by an ATP dependent ionic pump (Bennoun, 1994). Because of the absence of electrogenicity of NDA2 and the position of PTOX on the stromal side of the thylakoid, the chlororespiratory pathway is now considered non-electrogenic in Chlamydomonas. Strictly speaking, chlororespiration cannot be considered a photosynthetic AEF because it does not involve photochemical event. However, the two enzymes NDA2 and PTOX

2.2 Cyclic electron flow around PSI

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Like in other organisms, *Chlamydomonas* shows a fast ($t_{1/2} \sim 100$ ms) reduction of P_{700+} at the offset of an illumination, in the presence of DCMU (Maxwell & Biggins, 1976), but this phase is largely slowed-down in the presence of a cyt. $b_6 f$ inhibitor (Canaani *et al.*, 1989). This was seen as evidence for an electron transfer from the PSI acceptors in the stroma towards P_{700+} via cyt. $b_6 f$. If the existence of a CEF around PSI is well accepted in *Chlamydomonas* (Finazzi *et al.*, 1999,

are independently involved in CEF and WWC, respectively (see 2.2 and 2.3).

Iwai et al., 2010, Alric et al., 2010) the question of the electron transfer pathways from PSI acceptors to the cyt. $b_6 f$, the identity of the molecular players and the maximal rate of CEF have given rise to intense debate in the last decades (recently reviewed in (Nawrocki et al., 2019a)).

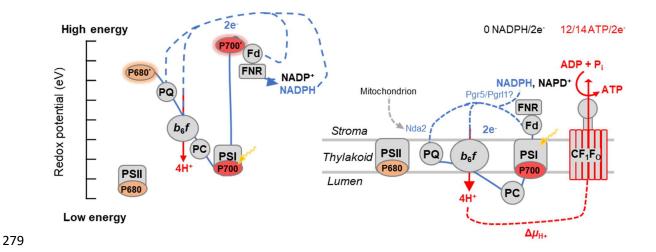


Figure 2: the Cyclic Electron Flow (CEF) around Photosystem I. A. CEF in the Z scheme of photosynthesis. B. Representation of the different routes of the CEF in the thylakoid membranes. Abbreviations: PSII, Photosystem II; PSI, Photosystem I; b_6f , cytochrome b_6f ; CF_1F_0 , CF_1F_0 ATPase; PC, plastocyanin; PQ, Plastoquinol/Plastoquinone; Fd: ferredoxin; FNR: Ferredoxin/NADP Reductase; $\Delta \mu_{H}^+$, electrochemical proton gradient.

The possible routes for CEF in Chlamydomonas

Like in plants (Shikanai, 2007), two major CEF routes have been described in *Chlamydomonas* (Figure 2). The "major one" corresponds to the original pathway postulated by Arnon and co-workers (Arnon *et al.*, 1954) following the observation of light-dependent ATP phosphorylation in isolated chloroplasts, mediated by the stromal electron carrier ferredoxin (Fd) A membrane-bound Fd-PQ oxidoreductase (FQR) was proposed to reinject electrons from the PSI

acceptor side to the inter-system ETC (Moss & Bendall, 1984; Bendall & Manasse, 1995). This pathway was serendipitously "rediscovered" almost 50 years later in a screening for Arabidopsis qE-defective mutants, lacking a small, stromal-soluble protein named PGR5 (for proton gradient regulation 5) (see Table 1) (Munekage et al., 2002). Shortly after, the molecular partner of PGR5, PGRL1 (PGR5-like), was discovered, which is an integral thylakoid protein with both termini stroma-exposed and six redox-active cysteine residues (DalCorso et al., 2008). In Arabidopsis, Hertle and co-authors (2013) (but see also (Szymańska et al., 2011)) reported in vitro FQR activity from PGRL1 (albeit on a non-physiological quinone species) which they attributed to its redoxactive cysteine residues presenting a binding site for a Fe-containing cofactor and triggered by PGRL1 heterodimerization with PGR5 (however see (Strand et al., 2016) for critical discussion on this hypothesis). While both PGR5 and PGRL1 have been shown to modulate *Chlamydomonas* CEF regulation (Alric, 2014; Johnson et al., 2014; Jokel et al., 2018; Buchert et al., 2020), their direct involvement in electron recycling from PSI acceptor to the PQ-pool remains debated (Nawrocki et al., 2019a). Although this PGR5/PGRL1 pathway was sensitive to inhibition by antimycin-A (a mitochondrial Complex III inhibitor) in plants, it is not the case in *Chlamydomonas* (Iwai et al., 2010, Antal et al., 2013).

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The second CEF pathway was first described in *Synechocystis* mutated in the membrane-bound, nucleotide dehydrogenase (NDH) gene (Ogawa, 1991; Mi *et al.*, 1995). In the mutants the PQ-pool remained oxidized after illumination in the presence of PSII inhibitor DCMU, as opposed to the wildtype where PQ re-reduction was attributed to NDH-1 (Mi *et al.*, 1995). In *Chlamydomonas* and other green algae, the secondary CEF pathway involves a different NAD(P)H dehydrogenase, NDA2 (Jans *et al.*, 2008), already described in the chlororespiratory section (see 2.1). In CEF, NDA2 utilize electrons from NAD(P)H to non-photochemically reduce the PQ-pool

and *nda2* mutants show a shorter post-illumination fluorescence rise than wild-type because NAD(P)H can not be mobilized to reduce PQ (Jans *et al.*, 2008).

The light sensitivity of *Arabidopsis* mutants lacking both NDH and PGR5/PGRL1 pathways confirmed the essential role of CEF in photosynthesis (Munekage *et al.*, 2004). It also suggested that these two routes, functionally redundant, represented the only possibilities for CEF in plants. However, emerging structural information on cyt. $b_6 f$ (Stroebel *et al.*, 2003; Malone *et al.*, 2019) have stimulated the emergence of a third potential pathway for CEF in *Chlamydomonas*. In this model, the CEF cycle could be completed via the direct reinjection from a stromal electron donor to the cyt. $b_6 f$ following the classical Q-cycle originally proposed by Mitchell (1975). This model, first proposed by Chain (1982) and reconsidered more recently on the basis of kinetic considerations (Joliot & Johnson, 2011; Nawrocki *et al.*, 2019a; Buchert *et al.*, 2020), does not involve the lateral diffusion of PQ in the thylakoid membrane. It supposes that the reduction of the quinone at the Q_i site is bifurcated, one electron coming from a stromal reductant, the other from the low-potential chain.

The maximal rate of CEF in Chlamydomonas

To evaluate the physiological importance of the CEF around PSI, the value of the maximal rate of CEF, relatively to the maximal rate of the LEF, has been a long-lasting question. In *Chlamydomonas*, the maximal rate of LEF is usually in the 100-150 electron per second per photosystem (Maxwell and Biggins 1976, Alric, 2010; Nawrocki *et al.*, 2019b). In the presence of DCMU, the rate of P_{700}^+ re-reduction at the offset of a saturating light was used as a direct measure of the rate of CEF and provided typical values of 5-15 electrons per second per PSI in oxic conditions (Maxwell & Biggins, 1976, Alric *et al.*, 2010; Takahashi *et al.*, 2013). Such a rate of CEF would be insufficient to supply the LEF with the additional ATP required for carbon

assimilation, alone. However, the rate of CEF in the presence of DCMU is not always a valid estimation of the rate of CEF in physiological conditions. If LEF and CEF are in competition for a common substrate, oxidized PQ or reduced ferredoxin, inhibition of LEF would increase CEF (Fan et al, 2016). In contrast, CEF can be limited by the lack of reduced ferredoxin / NADPH (Alric et al., 2010; Lucker & Kramer, 2013). This latter hypothesis is supported by higher rates of CEF measured in anoxic conditions, where the reducing power generated by glycolysis in the chloroplast maintain reducing pressure on the PETC. In these conditions (DCMU and anoxia), rates as high as 60 electrons per second per PSI were measured (Alric et al., 2010), which were further corroborated during the first seconds following a dark-to-light transition in the absence of DCMU (Nawrocki et al, 2019b).

With this value in mind, it becomes possible to evaluate the relevance of the NDA2 and PGR5/PGRL1 pathways for CEF on a kinetic basis. The slow rate of NDA2 under aerobic conditions (2-4 e PSI-1 s-1 (Houille-Vernes *et al.*, 2011) suggested that its role may be restricted to chlororespiration (Nawrocki *et al.*, 2015). However, during N-deprivation inhibiting the CBB and leading to the accumulation of stromal reductants, a doubling of the rate of P₇₀₀+ re-reduction, dependent upon NDA2 but not upon PGR5/PGRL1, was reported (Saroussi *et al.*, 2016). This discrepancy could stem from a different redox state of the stromal reductants in the two experiments: the rate of NDA2 would be limited by the availability of NAD(P)H in oxic conditions. In *Chlamydomonas*, PGRL1 mutants were shown to exhibit transiently the same maximal CEF rate as wildtype (Nawrocki *et al.*, 2019b). This was also the case in PGR5 mutants of *Arabidopsis* where the CEF maximal rate was not affected compared to the wild type (Nandha *et al.*, 2007). In both cases, it was suggested that PGR5 and PGRL1 could play a regulatory role in CEF, possibly via the redox poising of the chloroplast, instead of playing a direct FQR function.

The supposed low rate of NDA2, together with the unchanged maximal rate of CEF in pgrl1 mutants, were taken as clues for the existence of another CEF pathway involving the reinjection of electrons in the Q_i site of the cyt. b_6f and able to take in charge the high rates of CEF measured in Chlamydomonas. It is to note, however, that a compensation by NDA2 in Chlamydomonas pgrl1 mutants can not be fully excluded yet. A NDA2/PGRL1 double mutant in Chlamydomonas would help testing the redundancy of NDA2 and PGR5/PGRL1 pathways and/or the hypothesis that none of them represent the major route of CEF.

A classical (Mitchellian) Q-cycle involved in CEF?

Independently from the kinetics analysis discussed above, a regain of interest for a classical Q-cycle mediated CEF model comes from crystallography and structural analysis of the differences between cyt. $b_6 f$ and cytochrome bc_l (see also Volume 2, Chapter 11 and Chapter 17). Notably cyt. $b_6 f$ possesses three unique prosthetic groups per monomer: one chlorophyll a, one β -carotene and one special haem c_l (Stroebel et al., 2003) which could be involved in direct electron transfer from reduced ferredoxin to the quinone in the Q_i site (Stroebel et al., 2003; Malone et al., 2019). Haem c_l is unique by its lack of coordination of the haem iron (no amino acid axial ligand) and by being covalently bound in the vicinity of the high potential b_H at the Q_i site (Stroebel et al., 2003; Alric et al., 2005; Yamashita et al., 2007) yielding strong magnetic dipolar coupling between the two haems (Baymann et al., 2007). Interestingly, FNR is known to interact with cyt. $b_6 f$ stromal surface (Clark et al., 1984; Zhang et al., 2001; Mosebach et al., 2017) and FNR has been proposed to tether reduced Fd in proximity to the two high potential haems enabling PQ reduction which would assign the FQR function to cyt. $b_6 f$ (Joliot & Johnson, 2011; Goss & Hanke, 2014; Nawrocki et al., 2019a). New structural insights on cyt. $b_6 f$ so far seems to support this model (Malone et al., 2019) which resembles the Mitchellian Q cycle model with one electron coming

from the stroma. Especially, the propionate of haem c_i can switch conformation upon PQ binding to the Q_i pocket, which could reflect the previously documented decrease in c_i redox potential in dark-adapted algae (reducing conditions) (Alric et al., 2005) and give a mechanistic basis for electron channelling from the FNR:Fd complex to PQ mediated by haem c_i (Malone et al., 2019). Highlighting the homodimer structure of cyt. $b_6 f$, its central cavity and the edge-to-edge distance allowing electron transfer between opposing haems b_L (Lanciano et al., 2013), Nawrocki et al. (2019a) proposed that oxidized PQ in the Q₀ site of one monomer could be shuttled to the Q_i site of the other monomer. In this model, CEF and LEF would not compete for a common pool of oxidized PQ; instead PSII would reduce the PQ pool freely diffusing in the thylakoid membrane, whereas the CEF would inject an electron in a PQ located in the cyt. $b_6 f$ cavity, allowing high CEF even under conditions where the PQ pool is highly reduced by LEF. Interestingly, a natively bound PQ molecule was observed by cryo-electron microscopy between haems c_i and b_H of opposing cyt. $b_6 f$ monomers, which could represent a glimpse at this putative trans-monomer shuttle (Malone et al., 2019). By measuring redox kinetics associated to the different haems of cyt. b₆ f, Buchert et al. (2020) proposed that the switch between the modified Q-cycle associated to LEF and a classical Q-cycle driving CEF requires PGR5, explaining the different reports of CEF phenotypes in pgr5 mutants (Munekage et al., 2002; Alric, 2014; Johnson et al., 2014; Godaux et al., 2015).

Influence of Supercomplexes and State transitions on CEF

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Various early studies (Canaani *et al.*, 1989; Herbert *et al.*, 1990; Finazzi *et al.*, 2002) indicated a relationship between state transitions, which regulates the attachment of LHCII to PSII (state 1) or PSI (state 2) (see Volume 2, Chapter 24), and CEF in *Chlamydomonas*. While PSII sets the redox poise of the chain, only PSI participates to the CEF. Because the formation of State 2 increases

PSI antenna size, it expectedly increases PSI turnover and CEF if the later is light-limited. During the formation of state 2, a fraction of the cyt b_6f complex also moves from the PSII-enriched appressed regions of the thylakoid membrane to the stroma lamellae where PSI is localized (Vallon *et al.*, 1991). Because the co-localization of PSI and cyt b_6f and the increase of PSI antenna size coincide during state transitions, the question of their relative effects on CEF was rather difficult to address.

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In 2010, Iwai and collaborators isolated a PSI-LHCI-LHCII-cyt.b₆ f-PGRL1-FNR supercomplex (but lacking PGR5) under state 2. At first, the "Supercomplex model proposed CEF activation upon state 1 to state 2 transition, allowing for i) compartmentalization between CEF and LEF limiting their competition for the mobile electron carriers (PQ, PC, Fd) (Joliot & Joliot, 2002; Alric et al., 2010) and, ii) tight interactions between Fd-FNR, cyt b₆ f and the PQ-pool favoring fast electron transfer and high CEF rates in vivo (Iwai et al., 2010; Joliot & Joliot, 2002; Alric et al., 2010). However, those experiments could not disentangle the effect of state transitions per se, and the one of the anaerobic treatment used for their induction (which also lead to a decrease of the cellular ATP and an increase of the reducing power). When a mutant specifically devoid of state transition were used as a control, the link between state transitions and increased CEF or supercomplex formation was ruled out: increase in CEF and supercomplex formation is therefore induced by redox rather than state transitions (Lucker & Kramer, 2013; Takahashi et al., 2013). Accordingly, whether it involves supercomplexes or not, electron fluxes partitioning between the LEF and the PGR5/PGRL1 CEF pathway seem to obey a competition model regulated by the stromal ATP/NADPH ratio (Alric et al., 2010; Johnson et al., 2014). Based on the absence of the PSI antennae subunits LHCA2 and LHCA9 in supercomplex, Steinbeck and collaborators (2018) recently proposed a mechanistical model for CEF supercomplex assembly driven by the dissociation of these LHC under anoxia. Remarkably, $\Delta lhca2$ knockout mutants exhibited higher CEF rate under aerobic conditions than wildtype (WT) under either aerobic or anaerobic conditions (Steinbeck *et al.*, 2018). In any case, direct electron transfer from FNR:Fd to cyt. $b_6 f$ seems possible whether cyt $b_6 f$ forms a supercomplex with PSI or not. Furthermore, rates of CEF in supercomplexes remain to be measured experimentally as *in vivo* experiments in yeast showed that bc1-CcOx supercomplex do not display a faster kinetics of cytochrome c mediated electron transfer between the two complexes (Trouillard *et al.*, 2011; see however Berndtsson *et al.*, 2020).

Proton pumping and regulatory role of CEF

At present we can only speculate on the path of electrons in the CEF pathway, but through the Q-cycle, it undoubtedly participates to the pumping of extra protons into the lumen. In plants, the yield of protons pumped per electron recycled around PSI is different between PGR5/PGRL1 (2 H⁺/e⁻) and NDH-1 (3 or 4 H⁺/e⁻) pathways, due to the electrogenicity of the NDH-1 complex (Strand et al 2017; Strand et al., 2019). Because NDA2 is non-electrogenic (Melo *et al.*, 2004), the NDA2 CEF pathway in *Chlamydomonas* participates to the $\Delta\mu_{H^+}$ only to the same extent as the PGR5/PGRL1 pathway or the CEF based on the classical Q cycle, i.e. 2 H⁺/e⁻.

2.3 Water-to-water cycles

Electrons extracted from water at the PSII level can be rerouted from the LEF to various chloroplastic oxidases which utilise O₂ as electron acceptor and produce water (Curien *et al.*, 2016). This creates various AEFs linking the photo-oxidation of water into O₂ at one extremity to

the reduction of O₂ into water on the other, creating a water-to-water cycles (WWC) (or pseudocyclic electron fluxes).

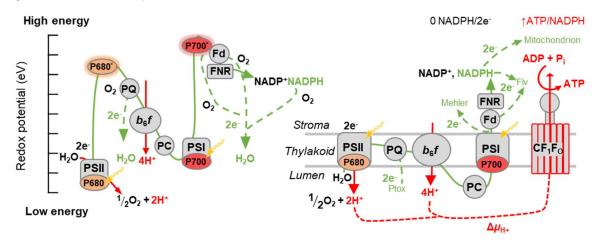


Figure 3: the Water-to-Water Cycles (WWC). A. Water-to-water cycles in the Z scheme of photosynthesis. B. Representation of the different water-to-water cycles in the thylakoid membranes. Abbreviations: PSII, Photosystem II; PSI, Photosystem I; b₆f, cytochrome b₆f; CF₁F₀, CF₁F₀ ATPase; PC, plastocyanin; PQ, Plastoquinol/Plastoquinone; Fd: ferredoxin; FNR: Ferredoxin/NADP Reductase; Δμ_H⁺, electrochemical proton gradient.

PSII-PTOX pathway

By reoxidizing PQ, PTOX can divert electrons from the main transport chain. Therefore, it has been suggested to have a function of safety-valve relieving excitation pressure on PSII under light exposure (Cournac *et al.*, 2000; Niyogi, 2000; McDonald *et al.*, 2011). It may indeed fulfill such function in organisms inhabiting harsh environments and accumulating large PTOX content (Stepien & Johnson, 2009; Laureau *et al.*, 2013; Ghotbi-Ravandi *et al.*, 2019). Because electrons are initially extracted from H₂O at PSII in LEF, oxidation of PQH₂ coupled to O₂ photoreduction by PTOX form a WWC. However, a photoprotective role for PTOX seems contradictory with its pro-oxidant activity (Heyno *et al.*, 2009; Krieger-Liszkay & Feilke, 2016) although we can not discount that those ROS may serve signaling purposes (Rea *et al.*, 2018). It is also hard to reconcile

with its much slower rate compared to PSII turnover under light in *Chlamydomonas* (Houille-Vernes *et al.*, 2011) and *Arabidopsis* (Joliot & Joliot, 2002). Indeed, comparable electron transport rates measured between *Chlamydomonas* WT and *ptox2* mutants under steady illumination suggests that PTOX main function is not a photoprotective valve (Nawrocki *et al.*, 2019c). Additional observations that WT and *ptox2* mutants have similar growth rates under continuous illumination but that the mutants are severely impaired under intermittent light, prompt the authors to posit PTOX's role is to balance the PQ-pool redox state during transient light fluctuations to avoid hampering PSII driven LEF (Nawrocki *et al.*, 2019c) (see also (Houyoux *et al.*, 2011)). Slower growth of *ptox2* mutants compared to WT under intermittent light further reveals the crucial role of this pathway in the redox modulation of the PQ-pool and PSI acceptors in this condition. Heterotrophic and phototrophic metabolism intersect at the PQ-pool of which the redox state is a major electron transport regulation hub. Therefore interplay between NDA2 and PTOX influence LEF and CEF respective rates (Nawrocki *et al.*, 2019c), state transition (Houille-Vernes *et al.*, 2011) and metabolic exchanges (Wei *et al.*, 2014).

Flavodiiron proteins

Flavodiiron proteins (FLV) were first identified in cyanobacteria (Helman *et al.*, 2003) but have since been documented in all green lineages groups except angiosperms (Ilik et al, 2017). In red algae, *flv* genes have never been observed. They are also absent from most brown algae genomes (see reviews (Peltier *et al.*, 2010; Alboresi *et al.*, 2019)), even though homologs in the dinoflagellate *Symbiodinium* were reported (Roberty et al, 2014; Shimakawa *et al.*, 2021). *Chlamydomonas* synthesizes both FLVA and FLVB isoforms (homologous to FLV1 and FLV3 respectively in cyanobacteria (Peltier *et al.*, 2010)) which are believed to associate in hetero-dimer to perform a WWC by photo-reducing O₂ at PSI acceptor side (Mustila *et al.*, 2016; Chaux *et al.*,

2017). So far, only a partial structural resolution of FLV1/3 lacking the C-term domain has been revealed in Synechocystis (Borges et al., 2019). Using in silico modeling, Alboresi and co-authors (2019) suggested distinct catalytic sites organisation between FLVA and FLVB (in the bryophyte Physcomitrella patens), enabling their action as a dimer and a possible conformational change allowing swift regulation answering to external cues like stromal redox-state. The electron donor for FLVs has been matter of debate in recent years. In Synechocystis, it was first proposed that FLVs may be able to receive electrons directly from NAD(P)H via a C-terminal flavin oxidoreductase-like module (Vicente et al., 2002). However, FLVs were also reported to possibly interact with Fd in both Chlamydomonas (Peden et al., 2013) and Synechocystis (Cassier-Chauvat & Chauvat, 2014). Most recently, evidence from comparison between re-oxidation kinetics of NADPH and of the iron sulfur cluster comprising Fd, F_X and F_AF_B (the terminal PSI acceptors) between WT and flv1/3 Synechocystis mutants, strongly suggested that reduced Fd-FAFB and not NADPH is the redox partner of FLVs (Sétif et al., 2020). Interestingly, the P₇₀₀ re-oxidation signal of Chlamydomonas WT, flv and CEF mutants (Jokel et al., 2018) have similar kinetics as Synechocystis homologous strains (Sétif et al., 2020), which possibly indicate both organisms' FLVs receive electron via reduced Fd-FAFB as previously proposed by Jokel and co-authors (2018).

FLVs act as a safety valve to alleviate PSI acceptor limitation and pertaining photodamage, hence accurate regulations is essential to avoid futile competition for reducing power with the CBB (Alboresi *et al.*, 2019). Interestingly, FLVs are an extremely efficient immediate electron sink upon sudden light intensity shifts (e.g. while CBB's enzymes are activating), but their activity under steady state illumination is barely detectable (Chaux *et al.*, 2017).

The Mehler reaction

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The Mehler reaction was postulated following the observation that isolated pea thylakoids can photo-reduce O₂ to peroxide (H₂O₂) (Mehler, 1951). Later seminal investigations by Asada and co-workers led to the identification of O₂⁻⁻ as the initial transient product generated by charge transfers from an internal PSI transporter on its acceptor side to O₂ (Asada & Kiso, 1973; Takahashi & Asada, 1988). The superoxide O₂⁻⁻ anion is instantly disproportionated to H₂O₂ and O₂ by the thylakoid bound superoxide dismutase and both products are released in the stroma (Ogawa *et al.*, 1995). Although less toxic and a more efficient cellular messenger than O₂⁻⁻ (Rea *et al.*, 2018), H₂O₂ remains harmful in excessive concentrations and it is scavenged in the stroma via an ascorbate peroxidase using two ascorbate (AsA) molecules as electron acceptors and yielding two water (thus making the Mehler reaction a WWC) and monodehydroascorbate (MDA) molecules as products (Asada, 1999). Afterward, a MDA-reductase use NADPH to recycle MDA back to AsA and play a role in *Chlamydomonas* 'photooxidative stress tolerance (Yeh *et al.*, 2019). Alternatively, MDA can spontaneously disproportionate to AsA and dehydroascorbate, which is converted to a supplemental AsA via the glutathione cycle also consuming NADPH (Lin *et al.*, 2018).

The PSI pigment-protein complex encompasses two symmetrical bifurcated electron chains spanning from P₇₀₀ and converging to F_X, the phylloquinones (PhQ) A and B, located on PSI heterodimer PsaA and PsaB, respectively (Volume 2, Chapter 15). Due to differences in protein interactions, the electron transfer to F_X is slower from PhQ_A than from PhQ_B, with lifetimes of ~300 and ~15 ns respectively, making PhQ_A•- much more susceptible to yield electrons to exogenous O₂ and generate ROS (Cherepanov *et al.*, 2017). However, a residue mutation delaying even further PhQ_A•- decay does not affect the quantum yield of PSI as electron overflow is redistributed to the PhQ_B chain (Santabarbara *et al.*, 2015). Recently, Kozuleva and co-authors

(2021) proposed a novel mechanistic model for the Mehler reaction after measuring the lightdependent second-order rate of O2 photoreduction in various Chlamydomonas PSI complex isolates showing mutations in different electron carriers (see other crucial works which led to the following model proposal (Kozuleva & Ivanov, 2010; Kozuleva et al., 2014; Santabarbara et al., 2015)). In this new model, F_AF_B participates to some extent to O₂ photoreduction but its rate saturates under moderate irradiance intensities and the major O₂ photoreduction sites is located at PhQ_A.- (Kozuleva et al., 2021). The alternative classical view is that the sole electron donor is reduced Fd and that O₂ photoreduction is favored by limited NADP+ availability (Furbank & Badger, 1983). While the Mehler reaction can partake to the $\Delta \mu_{\rm H+}$, quantifying its contribution in vivo is challenging due to its transient products and interactions with other AEFs and electron flux regulation mechanisms (see conflicting views on its significance in plants (Heber, 2002; Ort & Baker, 2002)). For example, in *Chlamydomonas* exposed to high light intensity, it was, counterintuitively, reported that the Mehler action is most active when CO2 concentration is elevated and LEF optimally functioning. When CO₂ is low, qE induction and state transition are sufficient to limit excitation pressure and H₂O₂ evolution (Roach et al., 2015). Based on experimental data and the thermodynamics parameters of electron transfers within PSI redox chains, Cherepanov and co-authors (2017) developed a model predicting more that 0.3% of total electron flux could be diverted to the Mehler reaction, although it is not clear how that electron flux could be affected in the presence of FLV in Chlamydomonas (Chaux et al., 2017). Likewise, it is likely that some, if not most, of the light-dependent O₂ uptake attributed to the Mehler reaction in previous works on Chlamydomonas (Peltier & Thibault, 1985, Forti & Caldiroli, 2005, Franck & Houyoux, 2008) was in fact due to the action of the then unknown FLVs (sometime called Mehler-like reaction, as FLVs do not generate H₂O₂) (see section 3.1). Simultaneous quantification

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of O₂ uptake and H₂O₂ evolution in FLVs mutants will be necessary to determine substantial of an electron sink the Mehler reaction can be in *Chlamydomonas*.

Other WWCs

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Other O₂ photoreduction processes can occur in the photosynthetic process, which are described in more detail in other chapters of this volume and will be only briefly described here. One of them is photorespiration (see Volume 2, Chapter 7 and 8). When O₂ rather than CO₂ enters Rubisco's catalytic site, it can trigger the oxidation of ribulose 1,5 biphosphate and generate 3phosphoglycerate (3PGA) and 2-phophoglycolate (2PG). The subsequent suite of enzymatic reactions recycling these products (also called the C2 cycle in reference to these two carbon intermediates) is described in Volume 2, Chapters 7 and 8. A crucial trickle-down effect of 2PG recycling to 3PGA, is that along the enzymatic reactions cycle, terminal acceptors like NADP+, NAD+, ADP and oxidized Fd are restored, fostering non-CO₂-assimilatory electron transport, which makes photorespiration a key response to harsh conditions in plants (chill, high light, CO₂ limitation) by limiting the otherwise associated overreduction of the PETC (reviewed in (Voss et al., 2013)). Rubisco's oxygenase activity is unavoidable but its output tends to be limited in microalgae due to carbon concentration mechanisms (CCM) which consume ATP to gather high CO₂ density around Rubisco confined in pyrenoids (reviewed in *Chlamydomonas* in (Wang et al., 2015)). The photorespiration pathway is conserved across photosynthetic phyla with two major divergences (i) reactions compartmenting in different organelles as peroxisomes and pyrenoids are not presents in all taxa, Chlamydomonas possesses pyrenoids but no peroxisomes and, (ii) the nature of the enzyme which oxidizes glycolate to glyoxylate. It is currently accepted that Chlamydomonas (and all Chlorophytes) replaced the Glycolate oxydase of plants by a glycolate dehydrogenase (GlcDH) similar to cyanobacteria (which possess both Glycolate oxydase and GlcDH) (Esser et al., 2014). Chlamydomonas' GlcDH harbors three spanning regions likely bound to the mitochondrion membrane and potentially feeds electrons to the ubiquinone pool of the respiratory transport chain (Beezley et al., 1976; Nakamura et al., 2005; Aboelmy & Peterhansel, 2014). Cross-talk between photorespiration and mitochondrial activity was hypothesized to explain the simultaneously up-regulated transcription of their related genes under high light, which could reflect enzyme synthesis for glyoxylate conversion to malate in the mitochondria (Davis et al., 2013). A study by Nakamura and co-workers (2005) strongly supported a photorespiratory function to be dependent on GlcDH by characterizing a high CO2 requiring phenotype in a Chlamydomonas mutant with a disrupted GlcDH gene, very similar to typical photorespiration defects in higher plants. Moreover, GlcDH mutants showed exacerbated glycolate excretion in the medium (Nakamura et al., 2005). To a lesser extent, increase in glycolate exudation was reported in Chlamydomonas WT exposed to high light, low CO2, in which the photorespiration pathway was inhibited (Moroney et al., 1986; Nakamura et al., 2005) and in immobilized cells (for which slowly diffusing O₂ concentration is high due to photosynthetic activity) (Garbayo et al., 2005). However, increased extracellular glycolate accumulation is often short-lived (Moroney et al., 1986; Garbayo et al., 2005; Günther et al., 2012). This is possibly due to overcompensation by enhanced CCM to limit photorespiratory carbon loss, as exemplified by steady up-regulation of CCM genes compared to transient increase for photorespiration genes upon transition to low CO₂ concentrations (Tirumani et al., 2019). In hope of developing sustain methane bioproduction from glycolate, Wilhelm and co-workers (Günther et al., 2012; Taubert et al., 2019) demonstrated that acclimating Chlamydomonas to low O2/CO2 conditions before a shift to scarce CO2 availability with addition of the CCM and GlcDH inhibitor 6-ethoxy-2-benzothiazolesulfonamide can yield elevated glycolate production sustained for up to 21 d.

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Another kind of WWC consists in a cooperation between photosynthesis and respiration, whereby the rerouting of the reducing power generated by the PETC towards the mitochondrial electron transfer chain eventually fuels the cytochrome oxidase (complex IV) and Alternative Oxidase. Such WWCs, described in *Chlamydomonas* and in plants (Lemaire *et al.*, 1988; Krömer & Heldt, 1991) involves the malate/oxaloacetate valve as well as other metabolic shuttles, which enable the transport of reducing power from the chloroplast to the mitochondrion via the cytosol (Scheibe *et al.*, 2005). Reversely, the extra ATP generated thereby in the mitochondrion can be imported back in the chloroplast through mitochondrial ATP/ADP translocators and potentially DHAP/3-PGA shuttle (Hoefnagel *et al.*, 1988). The study *Chlamydomonas* mutants affected in mitochondrial respiration point to an important role of those energetic exchanges between organelles (Cardol *et al.*, 2009). Such a cooperation can restore photoautotrophic growth in a *Chlamydomonas* strain lacking the chloroplastic CF₁Fo-ATPase, by rerouting excess reducing power from the chloroplast to the mitochondrion and by importing mitochondrial ATP for CO₂ fixation (Lemaire et al., 1988).

3- An integrated and historical view of the AEFs

We now identify the importance of alternative electron transfer pathways in their common functions: poising the redox state of the electron transfer chain, playing the role of exhaust valves, or increasing the proton-motive force and ATP production. AEFs actions are integrated within a cohesive response to limit photosynthetic electron transport bottlenecks. In the last two decades, the extensive use of mutants has revealed that while interplays and redundancies are inherent to the AEFs network, it makes-up for bioenergetic resilience rather than a weakness, giving plasticity to photosynthesis to operate under changing environmental conditions and metabolic demands.

Some redundancy between AEFs is indeed observed, especially in the recent years between CEF around PSI and WWCs mediated by FLVs. Artificial introduction of Flv genes in Arabidopsis (Yamamoto et al., 2016) or rice (Wada et al., 2018) can partially increase growth in pgr5 mutants. In *P. patents* double mutants exhibit exacerbated defects under fluctuating light compared to single pgrl1 or FlvA mutants (Storti et al., 2019). The redundancy of those two AEFs seems to be at place in Chlamydomonas too, where the pgrl1 mutants compensate deficient CEF by up-regulating FLVs synthesis (Dang et al., 2014). The light-dependent O₂ uptake was increased in this mutant, reflecting a higher activity of FLVs together with an energetic cooperation with mitochondria (Dang et al., 2014). Recently, it was shown that the rate of carbon fixation in Chlamydomonas decreases under low inorganic carbon in the double mutant of PGRL1 and FLVs compared to the wild type, but not in the respective single mutants (Burlacot et al., 2021). This indicates that the supplementary ATP demand for CO₂ concentrating mechanisms is met by the synergistic action of FLVs and PGRL1-mediated CEF (Burlacot et al., 2021). Moreover, it is likely that accelerated CEF historically reported for Chlamydomonas under anoxia are not only the result of a more reduced photosynthetic electron chain (Alric et al., 2010) but also caused by the decrease of electron leaks towards FLVs (Nawrocki et al., 2019b). This raises the question of the relative importance of the different AEFs: what are the rates of the different pathways under steady-state photosynthesis? How do they change with the environmental conditions (CO₂, temperature) or metabolic status of the cell? Because of this redundancy, comparing mutants of the different AEFs will not be sufficient to answer such questions; methodological advances in measuring and distinguishing the different electron pathways in photosynthesis are needed to address these questions. During the pioneering era of photosynthesis research, scientists were aiming at measuring precisely the maximum quantum yield of the

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photosynthetic process. At that time, in order to estimate what the photochemical reactions were at the molecular level, it was crucial to decide on precise values, to quantify the minimum number of photons required for the production of an O₂ molecule (or the assimilation of a CO₂ molecule). If we take the Emerson and Lewis value of 0.09 for the quantum yield (Emerson & Lewis, 1943), it means that ~11 photons are needed (quantum requirement) to produce one molecule of O₂ or to fix one molecule of CO₂. We now know that 8 electrons transferred linearly through PSI and PSII are required for one O₂, that the quantum yield of PSI is close to 1 and that of PSII is about 0.8, so there would remain about 1-2 reducing equivalents rerouted to "alternative pathways". Now that we know the molecular players of photosynthesis, and that we have mutants of AEFs, it might be worth revisiting these studies; the maximum quantum yield of photosynthesis is expected to depend on the relative participation of the alternative pathways compared to the linear electron transfer, and on the energy-requirement of the CO₂-concentrating mechanism. Another fundamental question relates to the kinetics of activation/deactivation of the different AEFs in transitory conditions. While both the PGR5/PGRL1 and FLVs help limit PSI photodamage during growth under rapidly fluctuating lights, FLVs have been shown to be particularly crucial because of their more rapid induction compared to CEF (Jokel et al. 2018). Comparison between pgr5, pgrl1 and Flv Chlamydomonas mutants showed that FLVs are essential for survival under fluctuating light while pgr5/pgrl1 growth was only slowed-down (Jokel et al., 2018). It was therefore posited that FLVs act as a frontline defense in the first few seconds following light shifts which also promote rapid ΔpH and NPQ development (Chaux et al., 2017), while CEF takes longer to reach sustained high functioning rates under excess light (Jokel et al., 2018; Storti et al., 2019). The best example of the sequential coordination of the different AEFs is probably the dark-to-light transition in anaerobic Chlamydomonas cells, which has been

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extensively studied for biohydrogen production. In these conditions, the initial photosynthetic activity is entirely associated to an electron transfer from water oxidation at the PSII level toward the hydrogenase, downhill of PSI, and is fully arrested in hydrogenase mutants (Godaux et al, 2015; Burlacot et al, 2021). This electron flow from PSII to the hydrogenase does not last more than one or two minutes in the wild type and is then replaced by other AEFs that play the role of relay between hydrogenase activity and CO₂ fixation. Interestingly, Godaux and collaborators, who measured PSI and PSII activity at the onset of light but did not consider WWCs, concluded that CEF was the relay (Godaux et al, 2015). Later, Burlacot and collaborators performed a similar experiment including FLV mutants and light-induced O2 uptake measurements (but no CEF measurements) and concluded that FLVs were the major relay (Burlacot et al, 2019). Concomitant measurements of CEF, H₂ production, CO₂ fixation and FLV mediated O₂ uptake at the dark-tolight transitions would be useful to reconcile those reports, which however suggest that, again, a synergic action of CEF and FLVs allow the transition from hydrogen production to carbon fixation. How does Chlamydomonas relate to the great diversity of organisms performing oxygenic photosynthesis, in terms of alternative photosynthetic electron routes? It is difficult to judge in which species or for which kind of stress condition a particular pathway plays a more important role: why should a regulatory pathway, identified as important for drought resistance in plants, be conserved in oceanic algae that do not experience drought stress? Perhaps here we should recognize the "chance" in the scientific approach: some AEFs have been identified and extensively studied in a specific organism for practical or historical reasons. For example, the genes of the chloroplast NADPH:dehydrogenase complex involved in chlororespiration were identified in tobacco by homology with mitochondrial complex I (Matsubayashi et al., 1987) after the whole chloroplast genome sequencing in tobacco (Shinozaki et al., 1986), not because of the study of

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chlororespiration in tobacco. Similarly, CEF around PSI was not detected as a proton-motive force dependent on PSI excitation, but as an ATP production in spinach thylakoid membranes (broken chloroplasts) reconstituted with Fd (Tagawa et al., 1963). In algae like Chlamydomonas (or Chlorella), the detection of AEFs involving O₂ as a terminal electron acceptor instead of CO₂ was favored because (i) from an experimental point of view, while it is difficult to assess the flow along a cyclic pathway where the reaction intermediates do not change concentration over time, it is relatively easy to measure the accumulation of an end-product of photosynthesis, like the net O₂ evolution induced by a continuous illumination, (ii) they are aquatic species and the detection of dissolved O₂ is easy and inexpensive, and (iii) there is no, or little photorespiration (high-CO₂ conditions or active CCM). Chlamydomonas is adapted to the measurements of dissolved O2, an accurate and sensitive technique using a polarographic method (Clark electrode) independent of the mass transfer of O₂ between the liquid and the gas phase. These O₂ exchange measurements are done more cheaply and more easily in a liquid suspension of unicellular algae than on plant leaves where the gas flow through a measuring chamber must be carefully controlled, and the detection of CO₂ is often monitored using an infrared gas analyzer. In addition to the observation of the red drop (Emerson & Lewis, 1943) and enhancement effect (Brody & Emerson, 1959), which suggested the existence of two different photochemical centers, other observations, often based on the transient gush and gulps of O2, showed the existence of pools of carriers in the electron transport chain (Joliot 1965). O2 exchange was not only used to detect O2 evolution but was also a pathfinder for O₂ photoreduction reactions. Perhaps the most illustrative example of the sensitivity of oxygen exchange measurements in liquid suspensions was the observation of the "Kok effect" in the green alga *Chlorella*, a break in the slope of light-response curve of the net O₂ exchange near the light compensation point (Kok 1949), suggesting an inhibition of respiration

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under weak illumination, a first insight into the interaction between photosynthesis and respiration. In O₂ exchange measurements, membrane inlet mass spectrometry (Hoch et al., 1963) allowed for significant progress in identifying alternative pathways using isotopic discrimination of different O₂ species. The PSII-dependent oxygen evolution from water (E₀) is monitored at a mass-tocharge ratio (m/e = 32, unlabeled $^{16}O_2$) while the oxygen uptake rate (U_O), corresponding to mitochondrial respiration, photorespiration, chlororespiration, Mehler reaction, are measured at m/e = 36 from labeled $^{18}O_2$ added to the sample before the measurement. These experiments, more specific to respiration, confirmed the light-induced changes in O₂ exchange observed earlier (Kok, 1949). In the case of Scenedesmus, O₂ photoreduction can compete with CO₂ reduction to the point it replaces it (Radmer & Kok, 1976), a similar phenomenon was also later observed in Chlamydomonas and hypothesized to contribute to the energy requirement of the CO₂concentrating mechanism (Sültemeyer et al., 1993). We now know that such large O2 photoreduction is dependent on FLVs proteins (Chaux et al., 2017) and is mostly restricted to terrestrial plants (gymnosperms), green algae (Chlorophyceae and Prasinophyceae), mosses and cyanobacteria (Peltier et al., 2010). Chlororespiration was also evidenced very early on using nonlabelled oxygen (Diner & Mauzerall, 1973), and later confirmed using membrane inlet mass spectrometry (Peltier et al., 1987, Vermeglio et al., 1990, Cournac et al., 2000). Because of this part of "chance" in the studies of AEFs in different model species, a comparative approach may be appropriate to understand the physiological role of alternative pathways in the photosynthetic diversity. It also suggests that comparisons between models or species should not be restricted to concepts and experimental results, but also take into account the materials and methods used in the work.

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	Gene	CreNumber	Protein	Protein localization	Mutants	Transcription up-regulation	Literature
CEF PSI	pgr5	Cre05.g242400	PGR5	Stroma	Crpgr5, hpm91	-Fe	1*, 2**, 3, 4
	pgrl1	Cre07.g340200	PGRL1	Thylakoid	pgrl1	-Fe	1*, 5**,6, 7
	nda2	Cre19.g750547	NDA2	Thylakoid	Nda2-RNAi	-N, -S	8*, 9**,10
WWC	flvA	Cre12.g531900	FLVA	Stroma	flvB	-CO ₂ , -S, HL	4, 11*,12**, 13
	flvB	Cre16.g691800	FLVB	Stroma	flvB	-CO ₂ , -S, HL	4, 11*,12**, 13
	PTOX1	Cre07.g350750	PTOX1	Thylakoid	ptox1i		14*,15**,16
	PTOX2	Cre03.g172500	PTOX2	Thylakoid	ptox2, ptox2i	-N	14*,15**,16,17

Literature: 1: Arnon et al., 1954, J. Am. Chem. Soc.; 2: Munekage et al., 2002, Cell; 3: Johnson et al., 2014, Plant Physiol.; Am. Soc. Plant. Biol. 4: Jokel et al., 2018, Plant J.; 5: Dal'Corso et al., 2008, Cell; 6: Petroustos et al., 2009 J. Biol. Chem.; 7: Nawrocki et al., 2019b, BBA-Bioenergetics; 8: Ogawa et al., 1991 Proc. Natl. Acad. Sci.; 9: Jans et al., 2009 Proc. Natl. Acad. Sci.; 10: Desplats et al., 2009 J. Biol. Chem.; 11: Radmer and Kok 1976 Plant Physiol.; 12: Gerotto et al., 2016 Proc. Natl. Acad. Sci.; 13: Chaux et al., 2017 Plant Physiol.; 14: Bennoun 1982 Proc. Natl. Acad. Sci.; 15: Wu et al., 1999 Plant Cell; 16: Houilles-Vernes et al., 2011 Proc. Natl. Acad. Sci.; 17: Nawrocki et al., 2019 Plant Physiol.

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