



The Roles of Cytochrome b_{559} in Assembly and Photoprotection of Photosystem II Revealed by Site-Directed Mutagenesis Studies

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Cytochrome b_{559} (Cyt b_{559}) is one of the essential components of the Photosystem II reaction center (PSII). Despite recent accomplishments in understanding the structure and function of PSII, the exact physiological function of Cyt b_{559} remains unclear. Cyt b_{559} is not involved in the primary electron transfer pathway in PSII but may participate in secondary electron transfer pathways that protect PSII against photoinhibition. Site-directed mutagenesis studies combined with spectroscopic and functional analysis have been used to characterize Cyt b_{559} mutant strains and their mutant PSII complex in higher plants, green algae, and cyanobacteria. These integrated studies have provided important *in vivo* evidence for possible physiological roles of Cyt b_{559} in the assembly and stability of PSII, protecting PSII against photoinhibition, and modulating photosynthetic light harvesting. This mini-review presents an overview of recent important progress in site-directed mutagenesis studies of Cyt b_{559} and implications for revealing the physiological functions of Cyt b_{559} in PSII.

Keywords: photosynthesis, photosystem II, cytochrome b_{559} , site-directed mutagenesis, photoprotection, photoinhibition

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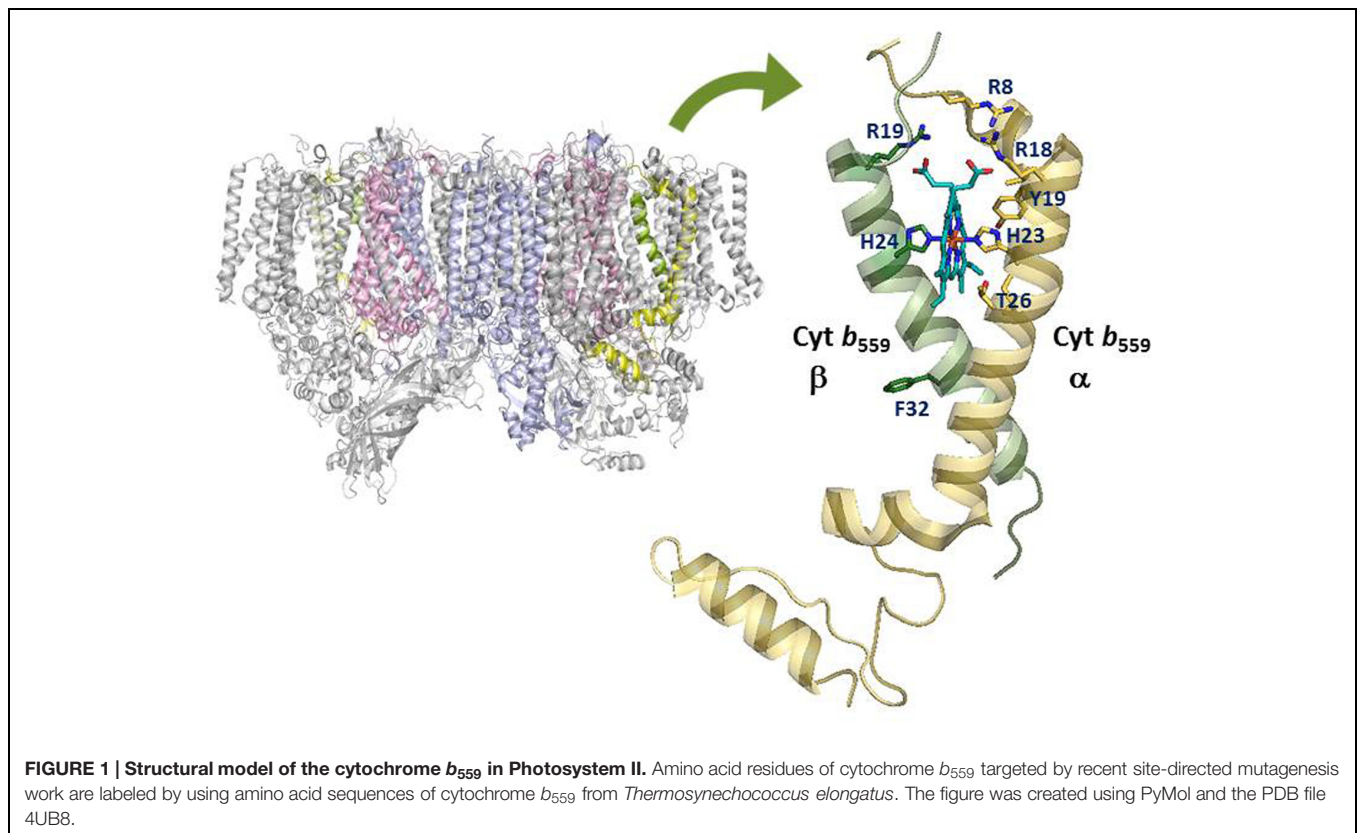
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INTRODUCTION

Cytochrome b_{559} is one of the essential components of Photosystem II in all oxygenic photosynthetic organisms (Whitmarsh and Pakrasi, 1996; Stewart and Brudvig, 1998; Guskov et al., 2009; Umena et al., 2011). Cyt b_{559} is a heme-bridged heterodimer protein comprising one α - and one β - subunit (encoded by the *psbE* and *psbF* genes) of 9 and 4 kDa, respectively (see **Figure 1**). Each subunit provides a His ligand (His-22 residue of the α - or β -subunit of Cyt b_{559} in *Synechocystis* sp. PCC 6803, corresponding to His-23 residue of α - or His-24 residue of the β -subunit of Cyt b_{559} in *Thermosynechococcus elongatus*) for the non-covalently bound heme, which is located near the stromal side of PSII. In addition, Cyt b_{559} has different redox potential forms depending on the type of PSII preparations and treatments: a HP form with a midpoint redox potential of about +400 mV, an IP form of about +200 mV, and a LP form with a midpoint redox potential of about 0–80 mV (Stewart and Brudvig, 1998; Roncel et al., 2001 and references therein). In intact PSII preparations, Cyt b_{559} is mostly in the reduced HP form under

Abbreviations: APC, allophycocyanin; Car, β -carotene; Cyt b_{559} , cytochrome b_{559} ; HP, high potential; IP, intermediate potential; LP, low potential; NPQ, non-photochemical fluorescences quenching; PQ, plastoquinone; PQH₂, plastoquinol; PSII, Photosystem II; Q_A, primary quinone electron acceptor in PSII; Q_B, the secondary quinone electron acceptor in PSII; Q_C, the third plastoquinone-binding site in PSII.



ambient conditions. In inactive or less intact PSII preparations, Cyt *b*₅₅₉ is typically in the LP or IP form and mostly oxidized (presumably by molecular oxygen) under ambient conditions (Barber and De Las Rivas, 1993; Poulson et al., 1995; Pospíšil et al., 2006).

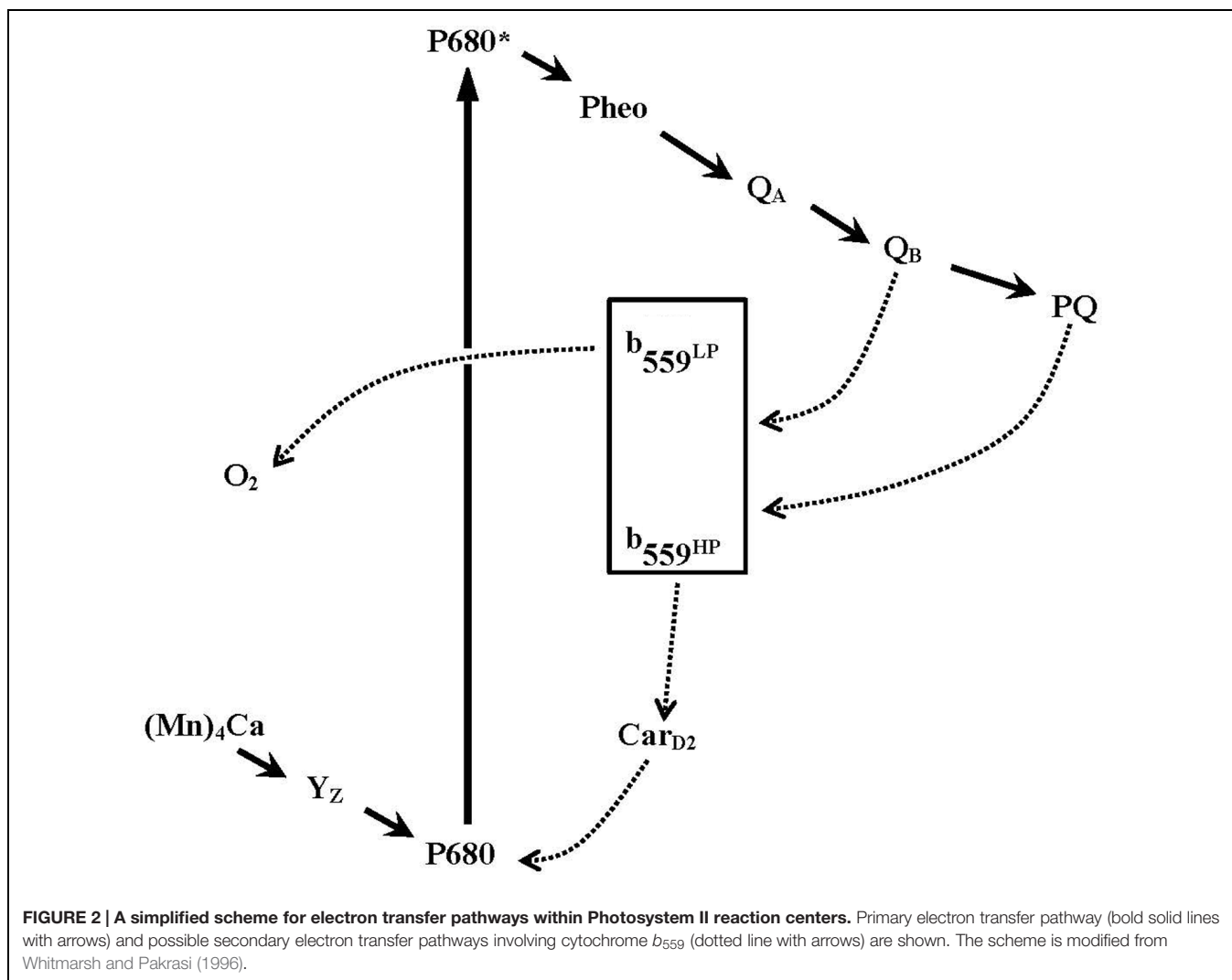
Several studies have proposed that Cyt *b*₅₅₉ participates in secondary electron transfer pathways that protect PSII against photoinhibition (see **Figure 2**; Heber et al., 1979; Falkowski et al., 1986; Thompson and Brudvig, 1988; Barber and De Las Rivas, 1993; Poulson et al., 1995; Magnuson et al., 1999; Faller et al., 2001; Tracewell and Brudvig, 2008 and references therein). In these models, the HP form of Cyt *b*₅₅₉ is thought to donate its electron, via a β -carotene molecule (Car_{D2}), to reduce highly oxidized chlorophyll radicals in PSII under donor-side photoinhibitory conditions (e.g., the oxygen-evolving complex is impaired or under assembly). Oxidized Cyt *b*₅₅₉ may accept an electron from the acceptor side of PSII (Q_B⁻, or reduced PQH₂ from the pool), thus forming a cyclic pathway of electron transfer within PSII. On the other hand, when the electron transfer on the acceptor side of PSII is inhibited (e.g., under high-light conditions), the oxidized Cyt *b*₅₅₉ might accept an electron from the acceptor side of PSII to prevent the formation of damaging singlet oxygen species (Nedbal et al., 1992; Vass et al., 1992; Barber and De Las Rivas, 1993; Bondarava et al., 2010). In addition, several different enzymatic functions of Cyt *b*₅₅₉ have been proposed, such as superoxide dismutase (Ananyev et al., 1994) and PQH₂ oxidase in intact PSII (Kruk and Strzalka, 1999, Kruk and Strzalka,

2001; Bondarava et al., 2003, 2010) and superoxide oxidase and reductase in tris-washed PSII (Tiwari and Pospíšil, 2009; Pospíšil, 2011). Moreover, a novel quinone-binding site (Q_C) was identified close (about 15 Å) to the heme of Cyt *b*₅₅₉ in the 2.9-Å PSII crystal structure from *T. elongatus* (Guskov et al., 2009). The occupancy of this Q_C site with PQ (or PQH₂) has been proposed to modulate the redox equilibration between Cyt *b*₅₅₉ and the PQ pool (Kaminskaya et al., 2006, 2007; Kaminskaya and Shuvalov, 2013) or be involved in the exchange of PQ on the Q_B site from the pool (Guskov et al., 2009). However, the Q_C site was not detected in the more recent 1.9-Å PSII crystal structure (Umena et al., 2011). Despite the recent remarkable progress in understanding the structure and function of PSII, the exact function of Cyt *b*₅₅₉ in PSII remains unclear.

This mini-review gives an overview of important progress in recent site-directed mutagenesis studies performed to reveal the physiological function(s) of Cyt *b*₅₅₉ in PSII. More comprehensive reviews on the structure and functions of Cyt *b*₅₅₉ are available (Whitmarsh and Pakrasi, 1996; Stewart and Brudvig, 1998; Faller et al., 2005; Pospíšil, 2011; Shinopoulos and Brudvig, 2012).

FUNCTION IN ASSEMBLY AND STABILITY OF PSII REACTION CENTERS

Prior mutagenesis studies with *Synechocystis* sp. PCC 6803, *Chlamydomonas reinhardtii* or *Nicotiana tabacum* showed no



stable PSII reaction centers assembled in the absence of either Cyt *b*₅₅₉ subunit (Pakrasi et al., 1988, 1989, 1990; Morais et al., 1998; Swiatek et al., 2003; Suorsa et al., 2004). Several authors proposed that Cyt *b*₅₅₉ plays an important structural role, such as being a nucleating factor, during the early stage of PSII assembly (Pakrasi et al., 1988; Morais et al., 1998; Komenda et al., 2004).

In addition, mutagenesis studies with *Synechocystis* sp. PCC 6803 showed that substituting either of the heme axial ligands (His22 of the α -subunit or His22 of the β -subunit of Cyt *b*₅₅₉ in *Synechocystis* sp. PCC 6803) with Leu, Met, Glu, Gln, Tyr, Lys, Arg, or Cys abolished the photoautotrophic growth and severely diminished the assembly or stability of PSII in the mutant cells, except for H22K α mutant cells, which were able to grow photoautotrophically and accumulated stable PSII reaction centers (~81% as compared with wild-type cells; Pakrasi et al., 1991; Hung et al., 2007, 2010). Electron paramagnetic resonance results indicated the displacement of one of the two axial ligands to the heme of Cyt *b*₅₅₉ in H22K α mutant reaction centers, at least in isolated reaction centers (Hung et al., 2010). In addition, H22K α and Y18S α (corresponding to Y19S α in *T. elongatus*)

in mutant PSII core complexes contained predominately the LP form of Cyt *b*₅₅₉. The findings support the concept that the redox properties of Cyt *b*₅₅₉ are strongly influenced by the hydrophobicity and ligation environment of the heme (Krishtalik et al., 1993; Gadjieva et al., 1999; Roncel et al., 2001; Pospíšil and Tiwari, 2010).

Spectroscopic and functional characterizations of the cyanobacterium *Synechocystis* sp. PCC 6803 with mutation of charged residues on the cytoplasmic side of Cyt *b*₅₅₉ in PSII have been reported (Chiu et al., 2013). All mutant cells grew photoautotrophically and assembled stable PSII. However, R7E α , R17E α , and R17L β mutant cells grew significantly slower and were more susceptible to photoinhibition as compared with wild-type cells. In addition, the PSII core complexes from R7E α and R17L β cells contained predominantly the LP form of Cyt *b*₅₅₉. Electron paramagnetic resonance results indicated the displacement of one of the two axial ligands to the heme of Cyt *b*₅₅₉ in the reaction centers of the R7E α and R17L β mutants. In recent PSII crystal structural models (Guskov et al., 2009; Umena et al., 2011), the side chains of

these Arg residues of Cyt *b*₅₅₉ (corresponding to Arg8 and Arg18 residues of the α -subunit and Arg19 residue of the β -subunit of Cyt *b*₅₅₉ in *T. elongatus*) are in close contact with the heme propionates of Cyt *b*₅₅₉ (see **Figure 1**). Thus, the electrostatic interactions between these Arg residues and the heme propionates of Cyt *b*₅₅₉ may affect the ligation structure and redox properties of the heme in Cyt *b*₅₅₉ (Chiu et al., 2013).

Furthermore, mutagenesis studies of *C. reinhardtii* showed that the H23Y α , H23M α , and H23C α mutant cells were unable to grow photoautotrophically, were sensitive to photoinhibition, accumulated 10–20% of the PSII (compared to wild-type cells), and contained a disrupted heme pocket while still retaining significant O₂ evolution activity (Morais et al., 2001; Hamilton et al., 2014). Thus, the heme of Cyt *b*₅₅₉ was not required for photosynthetic water oxidation by PSII (Morais et al., 2001). A recent study also presented evidence to ascribe the photoinhibition phenotype of H23C α mutant cells to a faster rate of photodamage and an impaired PSII repair cycle (Hamilton et al., 2014). Hence, Cyt *b*₅₅₉ may play important roles in the assembly, repair and maintenance of the PSII complex *in vivo*.

In the other recent mutant study of *T. elongatus* that took advantage of the robustness of the PSII variant with PsbA3 as the D1 subunit, the four constructed Cyt *b*₅₅₉ mutants (H23A α , H23M α , Y19F α , and T26P α) grew photoautotrophically (*T. elongatus* is an obligate photoautotroph; Sugiura et al., 2015). Although the H23A α and H23M α mutants assembled only an apo-Cyt *b*₅₅₉, the steady-state level of active PSII was comparable to that in the wild-type control. The results suggest that the heme has no structural role in the assembly of PSII in the presence of α - and β -subunits of Cyt *b*₅₅₉. This finding is in strong contrast to the *Synechocystis* sp. PCC 6803 mutant showing that proper coordination of the heme cofactor in Cyt *b*₅₅₉ is important to the assembly or stability of PSII (Pakrasi et al., 1991; Hung et al., 2007). In addition, Cyt *b*₅₅₉ mutant cells of *T. elongatus* showed no correlation between the rate of photoinhibition and the redox potential of the heme. However, the recovery of the oxygen-evolving activity of PSII after photoinhibition was significantly slower in these mutant cells. PsbA3 is the D1 isoform expressed in *T. elongatus* under high-light conditions (Nakamura et al., 2002; Kós et al., 2008). The high-light D1 isoform in cyanobacteria has a Glu instead of a Gln residue (for the low-light D1 isoform) at position 130 in the D1 protein sequence (for a review, see Mulo et al., 2009) and this Glu residue forms hydrogen-bonding interactions with pheophytinD1 (Dorlet et al., 2001; Shibuya et al., 2010). Cyanobacterial PSII with the high-light D1 isoform showed increased photo-tolerance and accelerated non-radiative charge recombination (Tichy et al., 2003). This phototolerant property has been attributed to a photoprotection mechanism involving the redox potential of pheophytinD1, which enhances the probability for non-radiative recombination of the singlet radical pair and prevents the formation of potentially damaging ³P680 and singlet oxygen species (Vass and Cser, 2009; Sugiura et al., 2014). Further investigation could determine whether PsbA3 may compensate the photoprotective function of Cyt *b*₅₅₉

in the assembly and stability of PSII in these Cyt *b*₅₅₉ mutant cells.

FUNCTION IN PROTECTING PSII AGAINST PHOTOINHIBITION

Numerous site-directed mutagenesis studies have investigated the role of Cyt *b*₅₅₉ in protecting PSII against photoinhibition under high light. In the photoprotective models, oxidized Cyt *b*₅₅₉ may accept an electron from the acceptor side of PSII (Q_B⁻, Q_C, or reduced PQH₂ from the pool). Previous mutant studies of dark-adapted leaves of the F26S β Cyt *b*₅₅₉ tobacco mutant showed a greatly reduced PQ pool, conversion of the redox-potential form of Cyt *b*₅₅₉ to the LP form, and photosynthetic activities sensitive to high light (Bondarava et al., 2003, 2010). In addition, R7E α and R17L β Cyt *b*₅₅₉ mutant cells of *Synechocystis* sp. PCC 6803 and R18S α Cyt *b*₅₅₉ mutant cells of *T. elongatus* showed markedly reduced PQ pools, altered redox-potential forms of Cyt *b*₅₅₉, and high susceptibility to light stress (Chiu et al., 2013; Guerrero et al., 2014). A defect in PQH₂ oxidase activity of Cyt *b*₅₅₉ due to altered redox-potential forms of Cyt *b*₅₅₉ in these mutant strains could explain their high susceptibility to strong light and greatly reduced PQ pools. Therefore, Cyt *b*₅₅₉ may function as a PQH₂ oxidase to keep the PQ pool and the acceptor side of PSII oxidized in the dark, thereby preventing PSII from acceptor-side photoinhibition (Kruk and Strzalka, 1999; Kruk and Strzalka, 2001; Bondarava et al., 2003, 2010). However, one recent study reported no defect in PQH₂ oxidation in the dark in H23C α mutant cells of *C. reinhardtii*, even though H23C α mutant cells contained a disrupted heme-binding pocket of Cyt *b*₅₅₉ and were sensitive to photoinhibition (Hamilton et al., 2014). Further studies are required to clarify this discrepancy. In addition, study of the 2.9-Å resolution PSII crystal structure reported the binding of Q_C at a hydrophobic cavity near Cyt *b*₅₅₉ (Guskov et al., 2009). Several spectroscopic studies have provided evidence that the occupancy of the Q_C site by PQ (or PQH₂) may modulate the redox potential of Cyt *b*₅₅₉ and mediate the redox equilibration between Cyt *b*₅₅₉ and the PQ pool (Kaminskaya et al., 2006, 2007; Kaminskaya and Shuvalov, 2013). A recent study provided evidence of a possible one-electron oxidation of PQH₂ by Cyt *b*₅₅₉ at the Q_C site involved in the formation of a superoxide anion radical (Yadav et al., 2014). The above results are consistent with Cyt *b*₅₅₉ possibly accepting an electron from PQH₂ via the Q_C site in PSII. However, the Q_C site was not present in the more recent 1.9-Å PSII crystal structure (Umena et al., 2011). Further investigations are needed to solve this important issue.

Spectroscopic and functional characterization of the H22K α and Y18S α Cyt *b*₅₅₉ mutant cells of *Synechocystis* sp. PCC 6803 showed that both mutants have functional PSII and exhibited the normal period-four oscillation in oxygen yield (Hung et al., 2010). However, both mutants were more susceptible to photoinhibition than the wild type under high-light conditions. In addition, PSII core complexes from the H22K α and Y18S α

mutants predominantly contained the oxidized LP form of Cyt *b*₅₅₉ (~79 and 86%, respectively). A defect in the photoprotective function of Cyt *b*₅₅₉ in H22K α and Y18S α mutants could explain their high susceptibility to strong light. Furthermore, H22K α and Y18S α Cyt *b*₅₅₉ mutants in a D1-D170A genetic background that prevented assembly of the Mn cluster showed almost completely abolished accumulation of PSII even under normal-growth-light conditions. The data support an important redox role of Cyt *b*₅₅₉ in protecting PSII under donor-side photoinhibition conditions (Hung et al., 2010).

Furthermore, under low light, the H23C α Cyt *b*₅₅₉ mutant showed more rapid assembly of the Mn₄CaO₅ cluster than the wild-type control in *C. reinhardtii* (Hamilton et al., 2014). However, the photoactivation of oxygen-evolving PSII in the H23C α mutant was inhibited under high light. The results suggest that reduction of P680⁺ via cyclic electron flow within PSII (via Cyt *b*₅₅₉ and Car_{D2}, **Figure 2**) may compete with the photoactivation process and provides important *in vivo* evidence for a photoprotective role of Cyt *b*₅₅₉ in photo-assembly of the Mn₄CaO₅ cluster in PSII (Hamilton et al., 2014).

A recent mutant study involving *T. elongatus* showed that the midpoint redox potential of the HP form of Cyt *b*₅₅₉ was significantly destabilized (converted to the IP form) in mutant PSII core complexes of Cyt *b*₅₅₉ mutant strains (I14A α , I14S α , R18S α , I27A α , I27T α , and F32Y β ; Guerrero et al., 2014). When the oxygen-evolving complex was inactive, the yield of dark-reduction of Cyt *b*₅₅₉ was lower and the kinetics was slower in the R18S α mutant than in wild-type cells. The results support the concept that the HP form of Cyt *b*₅₅₉ may function as a PQH₂ oxidase to keep the PQ pool oxidized and also as an electron reservoir for the cyclic electron flow within PSII when the donor-side of PSII is impaired (Guerrero et al., 2014).

Moreover, a previous spectroscopic study showed that different spectral forms of Car were oxidized in PSII samples containing different redox forms of Cyt *b*₅₅₉ (Tracewell and Brudvig, 2008). The authors proposed that the quenching properties of PSII may be controlled by the redox form of Cyt *b*₅₅₉ by modulating the different type of oxidized Car species (radical cation or neutral radical) formed in PSII. Future study could investigate the quenching properties of PSII in the wild type versus Cyt *b*₅₅₉ mutant strains of cyanobacteria with different redox forms of Cyt *b*₅₅₉ to validate this proposal.

EFFECTS ON PHOTOSYNTHETIC LIGHT HARVESTING

Recent mutant studies revealed a novel role of Cyt *b*₅₅₉ in modulating photosynthetic light harvesting in PSII reaction centers. A spontaneously generated mutant from *Synechocystis* sp. PCC 6803 wild-type cells grown in BG-11 agar plates containing 5 mM Glu and 10 μ M DCMU carried an Arg7 to Leu mutation on the alpha-subunit of Cyt *b*₅₅₉ in PSII (Chiu et al., 2009). Results of 77-K fluorescence and room-temperature chlorophyll *a* fluorescence spectra indicated that the energy transfer from phycobilisomes to PSII reaction centers was partially inhibited or uncoupled in this mutant. In

addition, the cytoplasmic side of Cyt *b*₅₅₉ is located within the predicted contact sites in PSII for the APC core complex of the phycobilisome (Barber et al., 2003). The Arg7 to Leu mutation of Cyt *b*₅₅₉ may alter the interaction between the APC core complex and PSII reaction centers, thereby reducing energy delivery from the antenna to the reaction center and protecting mutant cells against DCMU-induced photo-oxidative stress (Rutherford and Krieger-Liszkay, 2001).

Many cyanobacteria including *Synechocystis* sp. PCC 6803 have a novel blue-green light-induced NPQ mechanism to protect PSII reaction centers against photodamage under high-light stress (Kirilovsky and Kerfeld, 2012). Under high-light conditions, a soluble orange carotenoid protein is able to absorb blue-green light and undergoes photo-conversion into the active red form, which interacts with the APC core of the phycobilisome and dissipates excess excitation energy from the phycobilisome as heat. Interestingly, several *Synechocystis* sp. PCC 6803 mutant cells (e.g., R7L α and R17L β) with mutations on the cytoplasmic side of Cyt *b*₅₅₉ in PSII showed significant inhibition of the effects of blue-green light-induced NPQ and apparent acceleration on its recovery (Chiu et al., 2013). These results are consistent with the proposal that the mutations on Cyt *b*₅₅₉ may alter the interaction between the phycobilisome and PSII reaction centers, thereby affecting the regulation of photosynthetic light harvesting in *Synechocystis* sp. PCC 6803.

CONCLUSION AND PERSPECTIVES

Site-directed mutagenesis studies combined with spectroscopic and functional characterization have revealed multiple roles of Cyt *b*₅₅₉ in the assembly and photoprotection of PSII reaction centers. The findings provide convincing evidence for the physiological role(s) of Cyt *b*₅₅₉ in a photoprotective secondary electron transfer pathway within PSII reaction centers, as was suggested from earlier studies of isolated PSII complexes (reviews in Whitmarsh and Pakrasi, 1996; Stewart and Brudvig, 1998; Shinopoulos and Brudvig, 2012). In the near future, site-directed mutagenesis studies combined with advanced high-resolution protein crystallography and spectroscopic and functional analysis will provide further new insights (e.g., structure and function relationships for different redox forms of Cyt *b*₅₅₉) and possibly the final proof of the molecular mechanisms of Cyt *b*₅₅₉ in PSII.

AUTHOR CONTRIBUTIONS

H-AC wrote the major part of the manuscript. Y-FC wrote the minor part of the manuscript, contributed the **Figure 1** and edited the references.

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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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