

Sonani, R. R., Gardiner, A., Rastogi, R. P., Cogdell, R., Robert, B. and Madamwar, D. (2018) Site, trigger, quenching mechanism and recovery of non-photochemical quenching in cyanobacteria: recent updates. Photosynthesis Research, 137(2), pp. 171-180.

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Deposited on: 6 April 2018

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## Site, trigger, quenching mechanism and recovery of non-photochemical quenching in cyanobacteria: Recent updates

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Disclosure of interest: The authors report no conflicts of interest.

### Abstract

Cyanobacteria exhibit a novel form of non-photochemical quenching (NPQ) at the level of the phycobilisome. NPQ is a process that protects photosystem II (PSII) from possible highlight-induced photo-damage. Although significant advancement has been made in understanding the NPQ, there are still some missing details. This critical review focuses on how the orange carotenoid protein (OCP) and its partner fluorescence recovery protein (FRP) control the extent of quenching. What is and what is not known about the NPQ is discussed under four subtitles; where does exactly the site of quenching lie? (*site*), how is the quenching being triggered? (*trigger*), molecular mechanism of quenching (*quenching*) and *recovery* from quenching. Finally, a recent working model of NPQ, consistent with recent findings, is been described.

### Keywords:

Cyanobacteria; Non-photochemical quenching; Orange carotenoid protein; Phycobilisome; Fluorescence recovery protein

### 1. Introduction

Most aerobic photosynthetic organisms frequently encounter situations where the intensity of the incident solar radiation is more than saturating for photosynthesis (Franck and Gaffron 1941; Melis 2009). This situation is potentially damaging, especially for photosystem II (Melis 1999). One of the key defence mechanisms that have evolved to mitigate this problem is non-photochemical quenching (NPQ). In NPQ, the efficiency of the light harvesting system is reduced so that the excess solar energy is dissipated as heat rather than being transferred to the reaction centre (RC) where the major potential site of damage is located (Müller et al. 2001). NPQ in plants occurs in the light harvesting complex II (LHCII) antenna and is triggered by changes in the thylakoid luminal-pH (Ruban et al. 2007; Ruban 2016). Recently, a novel form of NPQ regulating the light harvesting efficiency of the phycobilisome (PB) has been described in cyanobacteria (El Bissati et al. 2000; Wilson et al. 2006). The PB is devoid of chlorophyll and is located proximal to the reaction centre at the outer surface of thylakoid membrane. The PB contains linear tetrapyrrol chromophores covalently attached to its major constituent proteins called phycobiliproteins (PBPs) (Adir 2008; Singh et al. 2015). Typically the PB is composed of two major domains; the core, made up of the low energy absorbing PBP allophycocyanin (APC;  $\lambda_{max}$ , 650-655 nm) that is directly associated with the RCs on thylakoid membrane and the rods, made up of the higher energy absorbing PBP phycocyanin (PC;  $\lambda_{max}$ , 600-620 nm) and/or phycoerythrin (PE;  $\lambda_{max}$ , 540-565 nm) that are arranged perpendicular to the core as mini-rods (Fig. 1A) (Adir 2005). This arrangement of PBPs in the PB creates an energy gradient from  $PE \rightarrow PC \rightarrow APC \rightarrow RC$ , which enables the absorbed-light energy to be 'funnelled' from rods to RC via the core (Fig. 1B) (Gantt and Lipschultz 1973; Adir 2008). NPQ in cyanobacteria occurs at the level of the PB-core and involves a water-soluble protein called the orange carotenoid protein (OCP) (Kirilovsky 2007). This critical review provides an up to date account of what is, and what is not, known

about the *site*, *trigger*, *quenching mechanism* and the *recovery process* of NPQ in cyanobacteria.

### 2. *Site*: APC<sub>660</sub> trimer of the PB-core

Simultaneous reduction in both maximal  $(F_m)$  and minimal  $(F_0)$  fluorescence observed in NPQ is the characteristic hallmark of an antenna based quenching mechanism (El Bissati et al. 2000). Interestingly, this mechanism exists in the strains without Chl antennae CP43, CP47 and RCII (Rakhimberdieva et al. 2004; Scott et al. 2005; Wilson et al. 2006). With these facts, the non-Chl antenna PB was suggested as a possible site of NPQ. This has been confirmed by inability of PB-lacking cyanobacteria to perform NPQ under highlight (Wilson et al. 2006). Furthermore, a mutant whose PB is made up of only PC rods (lacking APC core) was unable to show the quenching, whereas another mutant whose PB is made up of only APC cores (lacking PC rods) does show quenching (Wilson et al. 2006). The room temperature fluorescence decay kinetics during NPQ indicate that the enhanced decay component originates from the APC PB-core, whereas those components that originate from PC remain unaltered (Scott et al. 2006). These results imply collectively that the presumed 'quencher' of NPQ is 'the interaction of OCP with PB-core'. This was later experimentally confirmed by in vitro reconstitution of the cyanobacterial NPQ (Gwizdala et al. 2011). Generally, the PB-core is made up of three APC cylinders; two, attached to the thylakoid membrane and one, positioned on the top of these two. Each of them contains four discs, mainly made up of APC that have their fluorescence emission centred at 660 nm (APC<sub>660</sub>) (Fig. 2). APC cylinders, attached to thylakoid membrane also contain some other proteins called terminal emitters (ApcD, ApcF and ApcE); that along with APC in these discs have their fluorescence emission centred at 680 nm (APC<sub>680</sub>) (Glazer 1984; MacColl 1998; Adir 2005; Singh et al. 2015) (Fig. 2). APC<sub>680</sub> functions as an energy transfer-bridge coupling the PB APC $_{660}$  to the RCs.

It is clear that OCP<sup>r</sup> binds to PB-core very specifically since only one OCP<sup>r</sup> molecule is required to quench the fluorescence of one PB (Gwizdala et al. 2011). The binding of OCP<sup>r</sup> to the PB has been proposed to be with the two basal cylinders of PB-core because the presence of upper cylinder is noticed to be non-essential for NPQ (Jallet et al. 2012). As discussed above (Fig. 2), in basal cylinders of PB-core, two possible candidates APC<sub>660</sub> and APC<sub>680</sub>. have been proposed to be the OCP-binding site. Time resolved fluorescence measurements of NPQ have shown that the fluorescence originating from  $APC_{660}$  is quenched (Tian et al. 2011; Tian et al. 2012) and these make the hypothesis 'OCP<sup>r</sup> binds to APC<sub>660</sub> reasonable. The observation of cross-linked OCP-PB in the quenched state has provided evidence of closer proximity of OCP<sup>r</sup> with APC<sub>680</sub> during NPQ (Zhang et al. 2013). Moreover, the observation of quenching of APC<sub>680</sub> fluorescence (Kuzminov et al. 2012) combined with a docking study suggesting a role of the PB-loop of APC<sub>680</sub> in the OCP-APC interaction (Stadnichuk et al. 2013) opened up the possibility of OCP<sup>r</sup>-APC<sub>680</sub> interaction in NPQ. However, NPQ persists in a Synechocystis ApcE (APC<sub>680</sub>)-mutant (containing chromophore-less ApcE). This suggests that the APC<sub>680</sub> is not a site of quenching but it rather may be a part of the OCPbinding site.

### 3. Trigger: Photo-conversion of OCP<sup>o</sup> to OCP<sup>r</sup>

The OCP, a unique carotenoid-containing water soluble protein, is now widely accepted as the '*trigger*' molecule for NPQ in cyanobacteria. It was first discovered in three cyanobacterial genera by Holt and Krogmann (1981). Its function remained unclear for almost two decades until NPQ in cyanobacteria was discovered. El Bissati et al. (2000) noticed highlight-induced reversible fluorescence quenching in *Synechocystis*, which is the first evidence of NPQ in cyanobacteria. This quenching was found to recover very quickly even in the presence of protein synthesis inhibitors, which does not happen in the other wellknown response to highlight induced damage, the D1 repair cycle (Melis 1999). The involvement of a carotenoid pigment in NPQ was first proposed by Rakhimberdieva et al. (2004) based on the '*quenched-action spectra*' showing typical carotenoid absorption (500, 470 and 430 nm) bands. However, the first report that orange carotenoid protein (OCP) (defined by Holt and Krogmann (1981)) is involved in NPQ was from Wilson et al. (2006). These authors observed the increased vulnerability of an OCP-lacking mutant to highlight. This was further confirmed by the same group when they noticed increased-NPQ activity in an OCP-over-expressing mutant (Wilson et al. 2008).

Generally, OCP is found in two interchangeable conformational isoforms; orange (OCP<sup>o</sup>) and red (OCP<sup>r</sup>) (Wilson et al. 2008). OCP<sup>r</sup> is the active form and has been found to accumulate during NPQ in whole cells (Wilson et al. 2008). *In vitro* binding studies show that only OCP<sup>r</sup> binds to the PB resulting in the quenching of its fluorescence (Gwizdala et al. 2011). Both isoforms contain a single non-covalently bound carotenoid, 3-hydroxyechinenone (hECN) that has a hydroxyl group at one end and keto-group at the other (Kerfeld et al. 2003; Leverenz et al. 2015). Absorption of high intensity light by this carotenoid induces the conversion of OCP<sup>o</sup> to OCP<sup>r</sup> and this then '*triggers*' NPQ in cyanobacteria. However, the key question - 'How exactly does this interconversion occur at molecular level?' is still unanswered.

Most of the detailed information on the changes upon the conversion of OCP<sup>o</sup> to OCP<sup>r</sup> has come from structural studies. In the crystal, OCP<sup>o</sup> is found in the dimeric form, bears an antiparallel association of two OCP<sup>o</sup>-monomers stabilized by both hydrophobic and polar interactions between several conserved or conservatively substituted residues (Kerfeld et al. 2003). In another works, OCP was found as a dimer in solution (Zhang et al. 2013; Bao et al. 2017a). However, the exact oligomeric form of OCP *in vivo* has not been established unequivocally due to the following contradictory results. The OCP was determined to be in the monomeric form through size exclusion chromatography (SEC), Native-PAGE and Small Angle X-ray Scattering (SAXS) analysis (Leverenz et al. 2014; Gupta et al. 2015; Maksimov et al. 2017a; Moldenhauer et al. 2017a). Furthermore, the light-trigged conversion of OCP-dimer into monomer has been described (Zhang et al. 2013). These contradictory results raised the doubt that the OCP-dimer is might be an artefact of the high concentration of protein used for crystallization. Moreover, at higher protein concentration the presence of dimeric form of OCP is as compared to monomeric form (Lu et al. 2016). What is the real functionally relevant state of OCP is, therefore, still an open question?

Structurally, the OCP<sup>o</sup>-monomer comprises of 13  $\alpha$  helices and 6  $\beta$  strands, arranged in two domains, an all helical C-terminal domain (CTD) and the  $\alpha/\beta$  N-terminal domain (NTD). The OCP contains a single carotenoid, which is buried and shared between these two main domains (Fig. 3A). The NTD consists of two clearly distinguished sub-domains, each made up of four α helices, sub-domain 1 and sub-domain 2 (Fig. 3A). The cleft between these subdomains provides the binding pocket for carotenoid's hydroxyl end group. The fold of the CTD belongs to the nuclear transport factor 2 (NTF2) superfamily, and its  $\beta$ -strands are bent to form the hydrophobic binding pocket for the carotenoid's keto end (Fig. 3A). Strong Hbonds between the carotenoid's keto end with conserved Trp290 and Tyr203 (Trp288 and Tyr201 in some cases) residues hold carotenoid more firmly at this keto end (Fig. 3A). These H-bonds have been proposed to have a major role in maintaining the stability of OCP<sup>o</sup> as the other end (hydroxyl end) of carotenoid does not form any direct hydrogen bond with protein, rather only with water molecule. The importance of these H-bonds in the stability of OCP° has been confirmed by removal of either of the amino acids (Tyr201/Trp288 or Carbonyl group of carotenoids) participating in this H-bond. Mutation of Tyr201 and Trp288 has been noticed to decrease the stability of OCP<sup>o</sup> form (Wilson et al. 2011; Sluchanko et al. 2017a). Similarly, the importance of the carbonyl group (of carotenoid) participation in this crucial Hbonds has also been confirmed by the dramatic decrease in stability of OCP°, when

carotenoids (like zeaxanthin) that do not contain a keto-group are incorporated (Punginelli et al. 2009; Wilson et al. 2011). The carotenoid is ~24 Å long in OCP and adopts a transconfiguration with an average deviation of 16° from planarity between its two end rings (Kerfeld et al. 2003). This deviation from planarity is thought to be the major tuner of OCP's spectral properties (Kerfeld et al. 2003). The conformation of the carotenoid is due to interactions with the protein. A slight twist (with 28 Å radius of curvature) is imposed on carotenoid along its length due to the protein-carotenoid interactions (Kerfeld et al. 2003). It has been suggested that this twisting stabilizes an intramolecular charge transfer state in carotenoid, which makes it a more effective energy dissipater (Polívka et al. 2005; Kirilovsky and Kerfeld 2012). The charged and polarizable residues in OCP have been proposed to play a major role in the large bathochromic shift observed between the free and the protein boundcarotenoid.

Unfortunately, the structure of OCP<sup>r</sup> is not available. Leverenz et al. (2015) and Gupta et al. (2015) have suggested that the OCP<sup>o</sup> is converted to OCP<sup>r</sup> under highlight by adopting substantial changes in its conformation. The OCP, after conversion, seems to be more elongated based on low resolution SAXS data (Gupta et al. 2015). Therefore, the conversion of OCP<sup>o</sup> $\rightarrow$ OCP<sup>r</sup> is believed to possibly involve the dissociation of the NTD and CTD domains of OCP<sup>o</sup> (Leverenz et al. 2015). The 'domain separation hypothesis' for OCP photoconversion is also supported by increased hydrodynamic radius of activated-OCP (Moldenhauer et al. 2017b). Further, the fact 'OCP<sup>o</sup> is converted into OCP<sup>r</sup> by chaotropes without light'(King et al. 2014) also suggests that the OCP<sup>o</sup> needs to unfold for its conversion in to OCP<sup>r</sup>. Recently, structures of OCP NTD (binding canthaxanthin) (PDB IDs: 4xb4, 4xb5), which are presumed to be equivalent to the dissociated NTD of OCP<sup>r</sup>, have been solved and studied (Leverenz et al. 2015). These structures show that the carotenoid moves 12 Å further into the NTD (as compared to OCP<sup>o</sup>), in a way that the polyene chain becomes

matrix and the β-ionone rings are solvent-exposed (Fig. 3B). The network of proteincarotenoid contacts reconfigures drastically in these structures (Leverenz et al. 2015) and this substantially alters the carotenoid's conformation. The polyene chain, which is now entirely within NTD, adopts a planner conformation as compared to that in OCP<sup>o</sup>. The out of plane torsion of both  $\beta$ -ionone rings (in OCP<sup>o</sup>) is reduced significantly (Leverenz et al. 2015). The reduced torsions between the  $\beta$ -ionone rings and the increased polyene planarity in OCP<sup>r</sup> have been confirmed by Raman-spectroscopy (Wilson et al. 2008; Leverenz et al. 2014; Kish et al. 2015). However, the ultimate cause for this change has yet to be definitively confirmed. Several causes like all-cis to all-trans isomerization, relaxation of the degree of bending (Kish et al. 2015) and dipole moment-induced conformation change (Mori 2016) are the most feasible to explain the photoconversion of OCP<sup>o</sup> to OCP<sup>r</sup>. Upon photoactivation when the carotenoid is encased in NTD due to dramatic rearrangement of carotenoid-proteins Hbonding network, its effective conjugation length is increased giving red colour to the OCP<sup>r</sup> (Niedzwiedzki et al. 2014; Liu et al. 2016). These authors (Niedzwiedzki et al. 2014) also suggest that the photoactivation of OCP is associated with its monomerization that was already described by Zhang et al. (2013).

Nonetheless, the question "how is the OCP<sup>o</sup> $\rightarrow$ OCP<sup>r</sup> conversion being triggered in response to highlight?" remains to be answered. Some plausible ideas for the molecular basis of this *'trigger'* reaction have been proposed. The light activated carotenoid could drive the OCP<sup>o</sup> $\rightarrow$ OCP<sup>r</sup> conversion by adopting a less-constrained conformation in OCP<sup>r</sup> as discussed above (Fig. 4A). The  $\alpha$ A- helix (2-18 residues) of OCP<sup>o</sup> that appears to play a major role in bridging the NTD and the CTD could then act as the primary site of conformation changes. Light-induced structural changes in this region would result in loss of the important bridging-interaction of this helix with the CTD (Fig. 4B). This idea has been proposed based on two lines of evidence. This helix showed the largest conformational movement during NPQ and

its fold bears similarities with that seen in the Per-Arnt-Sim photo-sensor family (Gupta et al. 2015). A change in pH, clearly potentiates the conversion of  $OCP^{o} \rightarrow OCP^{r}$ . This conversion process becomes 8 fold faster at pH 12 than at pH 8 (Wilson et al. 2011). At higher pH, Tyr203 (to which the carotenoid is H-bonded) is suggested to be de-protonated and this could result in the detachment of carotenoid, thereby facilitating the dissociation of NTD from CTD (Fig. 4C) (Wilson et al. 2011). It also has been suggested recently that light-mediated excitation of the conjugated carbonyl group in ionone ring of carotenoid could disrupt its hydrogen bond linkage with Trp290 and Tyr203, which in turns could then release the strain of carotenoid, unlocking the aA- helix of NTD from CTD and so initiate domain separation (Bandara et al. 2017). This most recent model, obtained through dynamic crystallography (Bandara et al. 2017), is plausible as it explains the key question 'how is the light being sensed and operated in photo-activation of OCP?' It is also supported by other evidence, such as increased 'Trp' fluorescence in OCPr (Maksimov et al. 2015). Recently, spectroscopic interrogation of the OCP photocycle on a faster time scale has revealed the existence of a very short-lived OCP<sup>oI</sup> intermediate (having partially joined NTD and CTD domains) during the reversion of OCP<sup>r</sup> in to OCP<sup>o</sup> (Maksimov et al. 2017c). However, even if one of these ideas is true it is still unclear how these changes are induced by carotenoid photochemistry, especially when this reaction has such a low quantum yield.

# 4. *Quenching mechanism*: Structural change in the PB-*core or* direct bilin to carotenoid energy transfer

The exact molecular mechanism of how OCP<sup>r</sup> induces NPQ in the PB is still obscure. Since, the strong correlation between OCP-PB binding and fluorescence quenching is clear (Gwizdala et al. 2011), two important and obvious questions arise, 'where does the OCP bind on PB-*core*?' (Described in section 2) and 'how does the OCP-PB interaction translate into quenching?' Two major theories have been proposed for how OCP-mediated NPQ take place. First, OCP<sup>r</sup> introduces a structural change in PB-core upon binding. This change then results in the bilin pigment being converted into a form that has much faster fluorescence decay. Second, the carotenoid of OCP may directly interact with the bilin pigment and quench excess energy through three different possible mechanisms, excitation energy transfer (Berera et al. 2013), charge transfer (Holt et al. 2005; Tian et al. 2011) or excitonic interactions (Bode et al. 2009). At present, either one or indeed both of these mechanisms seem possible. These mechanisms neither have been ruled out nor have been unequivocally proven. The spectral properties of APC<sub>660</sub>, believed to be the major site of quenching, appears to be highly susceptible to even minor conformational changes because PCB is embedded in an unique hydrophobic pocket within the APC structure (McGregor et al. 2008). This could favour the PB-core structural change theory. However, it has been shown that singlet-singlet annihilation rate in PB during NPQ does not change very much. This suggests that any conformational changes in the PBcore must be quite subtle rather than very extensive (Kuzminov et al. 2012). Docking studies of OCP with APC complex suggested that the distance between carotenoid and closest PCB, in case of APC<sub>680</sub> is ~24.7 Å and in case of APC<sub>660</sub> is ~21 Å (Stadnichuk et al. 2013; Stadnichuk et al. 2015; Zlenko et al. 2016). With these distances, assuming the carotenoid in this conformation has a stable intramolecular charge-transfer (ICT) and a lower energy S1excited states in OCP<sup>r</sup>, direct energy transfer from PCB to the carotenoid seems possible (Berera et al. 2012; Berera et al. 2013). Nevertheless, one cannot ignore the apparently unfavourable distance between carotenoid and PCB. Recently, recognising that the carotenoid moves significantly within NTD of OCP during photo-conversion, the possibility of further change in OCP<sup>r</sup> structure (after binding to PB-core) that may place carotenoid closer for direct energy transfer has been proposed (Leverenz et al. 2015). This idea would also require that the PB-core undergo a conformational change to allow the carotenoid to pierce PB-core,

and move closer to PCB. Recently, Harris et al. (2016) has provided a clearer picture about interaction of OCP<sup>r</sup> and PB. The LC/MS-MS analysis of cross-linked OCP-PB complex suggested that the NTD of OCP<sup>r</sup> burrows into PB-*core* leaving CTD outside and ApcC stabilizes this interaction (Harris et al. 2016). This then could move the carotenoid close enough for quenching via energy transfer.

### 5. *Recovery*: Fluorescence recovery protein (FRP)

The quenching of PB fluorescence recovers rapidly when highlight goes away. Boulay et al. (2010) discovered that fluorescence recovery protein (FRP), a non-chromophoric ~15 kDa protein, plays an important role in the fluorescence recovery process. The specific occurrence of FRP encoding gene, *slr1964*, in all OCP-containing cyanobacteria strongly supports its role in the reversal of NPQ. Interestingly, though the genes *slr1964* and *slr1963* (the OCP gene) are found on same mRNA, the relationship between their expression is still unclear (Boulay et al. 2010). Later, the proposal by Gwizdala et al. (2011) that there are two distinct promoters for these two genes provides an explanation for the separate regulation of OCP and FRP transcription. By interacting with OCP<sup>r</sup>, FRP promotes fluorescence recovery by detaching OCP<sup>r</sup> from the PB and converting the free OCP<sup>r</sup> to OCP<sup>o</sup>.

Three different models have been proposed for FRP-OCP interactions. The first model of FRP-OCP interaction was proposed by the Kirilovsky-Kerfeld group (Sutter et al. 2013). These authors found two different forms of FRP, a dimer and a tetramer in its crystal structure (Sutter et al. 2013). Sutter et al. (2013) and Thurotte et al. (2017) also demonstrated the strong interaction of a patch of conserved residues (W50, D54, H53, and R60) of FRP with the CTD domain of OCP through docking simulations and co-immunoprecipitation. As these residues are buried inside in the FRP-tetramer, this oligomeric form of FRP is as an inactive form. This was confirmed later by the recently described *Fremyella* FRP crystal

structure (PDB ID: 5tz0) that only showed a dimeric form of FRP (Bao et al. 2017b). Furthermore, the inability of FRP in binding to the OCP NTD-analogue affirmed that the FRP binding does not involve NTD. According to this model, the FRP dimer is the biologically active form.

The Blankenship group (Lu et al. 2016; Lu et al. 2017) suggests that dimeric-FRP first binds with the CTD of OCP<sup>r</sup> and induces conformational changes in dimeric-FRP that enabls its binding to the NTD domain. This, in turn, induces monomerization of dimeric-FRP, bridging and pulling of the CTD and NTD together and thereby promoting the conversion of OCP<sup>r</sup> in to OCP<sup>o</sup>. The rejoining of the NTD and the CTD results in the detachment of monomeric-FRP and its subsequent dimerization. This model describes a concerted interaction between FRP and OCP in which the binding of FRP to OCP<sup>r</sup> destabilizes each other and where detachment of FRP from OCP<sup>o</sup> stabilizes each other.

The model, proposed by the Maksimov group (Sluchanko et al. 2017a; Sluchanko et al. 2017b) also proposed that the FRP-monomerization is crucial for recovery from NPQ. Their most recent conclusion regarding the FRP-active form is *'The dimer form of FRP may be of importance for binding with OCP; after binding, the FRP is converted in to monomer, an active form*'. This model suggests that the FRP monomer contains the site for CTD and NTD binding, which is hidden at FRP dimer interface. The binding of dimeric-FRP at the same site where the  $\alpha$ A- helix of NTD binds induces its monomerization, and opens the hidden OCP-binding region that has affinity for both CTD and NTD (Sluchanko et al. 2017b). Unlike the Blankenship group's model, this model is only based on the monomerization of FRP, no conformation change (except monomerization) in FRP structure is suggested. The MS analysis of cross-linked FPR and OCP and the analysis of the flash-induced absorption transients of FRP and  $\Delta$  NTE OCP (NTD-deleted OCP) suggested that FRP binds to the CTD

of OCP and brings the CTD and the NTD together inducing recovery (Sluchanko et al. 2017a; Sluchanko et al. 2017b; Maksimov et al. 2017b). This model also explains the lower affinity of FRP for OCP<sup>o</sup> because the FRP binding site is hidden in the compact state of OCP<sup>o</sup> (Sluchanko et al. 2017a). Clearly this area needs further detailed study to get to an accepted mechanism of FRP's mode of action.

It should also be noted that the fluorescence recovery depends on the FRP/OCP ratio. Fluorescence recovery is achieved rapidly or fluorescence quenching is completely inhibited if this ratio is high (Boulay et al. 2010; Gwizdala et al. 2013). The amplitude of the NPQ depends on the concentration of OCP<sup>r</sup>. As FRP decreases the concentration of OCP<sup>r</sup>, it is clear that the amplitude of NPQ depends on OCP<sup>r</sup> concentration and the FRP/OCP ratio. (Gwizdala et al. 2013; Boulay et al. 2010).

### 6. Working model of cyanobacterial NPQ

The recent model of NPQ in cyanobacteria based on the available facts is shown in Fig. 5. In minimal light or darkness, the NTD and CTD of OCP<sup>o</sup> interact and carotenoid molecule is encased between them. Here, the oligomeric state of OCP is still uncertain. Orange OCP has a low affinity for the PB-core. Therefore, OCP in its orange form does not interact with the PB-core and transfer of excitation energy to reaction centre occurs with high efficiency. Under highlight, the NTD and CTD of OCP<sup>r</sup> dissociate from each other and there is a dramatic reordering of the carotenoid-protein H-bonding network induced by excitation of the carotenoid. It remains uncertain how strong light, absorbed by the carotenoid in OCP<sup>o</sup>, sensitises the triggering process that induces this major conformational event. The dissociation results in a substantial movement of the carotenoid so that it is now buried inside the NTD of OCP<sup>r</sup>. The separation of NTD and CTD make the OCP structure more elongated resulting in a form that is able to burrow into the space between basal core cylinders of PB.

The NTD of OCP<sup>r</sup> interacts with PB-*core* in such a way that the bilin-carotenoid distance becomes shorter and may, or may not, allow direct participation of the carotenoid in the quenching process. The exact details of interaction between the NTD-OCP<sup>r</sup> and the PB-core remain to be determined. The energy transfer efficiency of the PB is restored by FRP, which performs two major functions, detachment of OCP<sup>r</sup> from PB-*core* and back-transformation of OCP<sup>r</sup> into OCP<sup>o</sup>. The recovery process starts with binding of FRP dimer to OCP<sup>r</sup>, which in turn results in OCP<sup>r</sup> detachment from the PB-*core*. However, the site of FRP-OCP interaction is still an open question although it is clear that the position of the N-terminal helix in OCP<sup>o</sup> hinders this interaction. It is thought to be coupled with the monomerization of FRP and release of a FRP monomer from the OCP<sup>r</sup>-FRP dimer complex. The other OCP<sup>r</sup>-attached FRP monomer is then proposed to bring NTD and CTD closer together, relocating the carotenoid and transforming OCP<sup>r</sup> back into OCP<sup>o</sup>. It will be interesting to re-evaluate this general model when more detailed mechanistic information becomes available.

### 7. Acknowledgement

Ravi R Sonani is deeply thankful to the Department of Science and Technology (DST), New Delhi, Indo-French Centre for the Promotion of Advance Research (IFCPAR), New Delhi and British Council for the financial support. Datta Madamwar acknowledges University Grants Commission (UGC), New Delhi for BSR Faculty Grant.

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### **Figure captions**

**Figure 1**: Schematic cartoon representation of phycobilisome (A) and the unique downhill energy gradient (B) within it, created by overlapping spectral characteristics of its constituent phycobiliproteins. Light energy (Yellow arrows), absorbed by outer most high energy absorbing phycoerythrin (PE) is successively transferred to reaction centre (RC)-chlorophyll (*chl*) via comparatively intermediate and low energy absorbing phycocyanin (PC) and allophycocyanin (APC), respectively.

**Figure 2**: Schematic view of phycobilisome core (PB-core). APC discs absorbing at 660nm and 680nm are represented by dark and light blue colour, respectively. APC<sub>660</sub> disc is made up of only APC, whereas APC<sub>680</sub> contains ApcD or ApcF and ApcE along with APC. 'A' denotes the heterogeneous APC-cylinders made up of two APC<sub>660</sub> and two APC<sub>680</sub> discs. 'B' denotes the homogeneous APC-cylinders made up of only APC<sub>660</sub> discs.

**Figure 3: Cartoon representation of OCP structure (A) and truncated-OCP structure containing only NTD (B)**. The NTD and CTD are represented by violet and cyan colour, respectively. Pigments and its H-bonded residues (Tyr203 and Trp290) are represented by red coloured stick model. Figure is prepared using protein data bank-retrieved OCP structures coordinates (PDB ID: 5ul2, 4xb4).

Figure 4: Schematic of  $OCP^{o} \rightarrow OCP^{r}$  photo-conversion. The Yellow and red bars between NTD and CTD represents the constrained and non-constrained carotenoid in  $OCP^{o}$  and  $OCP^{r}$ , respectively. Yellow arrows represent the highlight. (A) The more constrained-carotenoid of  $OCP^{o}$  senses the highlight and transform into less-constrained conformation which causes dissociation of CTD and NTD in  $OCP^{r}$ . (B) The  $\alpha$ A-helix (2-18 aminoacid) of NTD senses the highlight and undergoes structural rearrangement and loses interaction with CTD results in dissociation of CTD and NTD in  $OCP^{r}$ . (C) The H-bonds between carotenoids and protein

(Tyr203) is broken due to highlight induced pH-alteration. The loss of this H-bond causes detachment of CTD from carotenoid and thus from NTD.

**Figure 5:** Working model of cyanobacterial NPQ. **(1)** Upon highlight exposure, OCP adopts more extended conformation (OCP<sup>r</sup>), in which, NTD and CTD dissociates from each other and the hECN translocate to be buried in NTD protein matrix. This structural conformation increases the OCP-affinity towards PB-core; OCP<sup>r</sup> interacts with PB-core causing decreased-excitation energy transfer from PB-core to photosystem (represented by thin red arrow as compared to thick arrow under normal condition). **(2-4)** The quenching is recovered under normal light with the help of soluble protein call fluorescence recovery protein (FRP). **(2)** FRP dimer interacts with OCP<sup>r</sup> and cause dissociation of OCP<sup>r</sup> from PB-*core* by forming OCP<sup>r</sup>-FRP dimer complex. Simultaneous to this phenomenon, **(3)** monomerization of FRP occurs and one monomer from OCP<sup>r</sup>-FRP dimer complex is released. **(4)** Remaining FRP-monomer brings NTD and CTD domains of OCP together, relocates carotenoid and restores the orange conformation of OCP. After formation of OCP<sup>o</sup>, FRP-monomer detaches form OCP<sup>o</sup>.

Figure 1A





Figure 2













