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Redox and light regulation of gene expression in photosynthetic prokaryotes

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All photosynthetic organisms control expression of photosynthesis genes in response to alterations in light intensity as well as to changes in cellular redox potential. Light regulation in plants involves a well-defined set of red- and blue-light absorbing photoreceptors called phytochrome and cryptochrome. Less understood are the factors that control synthesis of the plant photosystem in response to changes in cellular redox. Among a diverse set of photosynthetic bacteria the best understood regulatory systems are those synthesized by the photosynthetic bacterium *Rhodobacter capsulatus*. This species uses the global two-component signal transduction cascade, RegB and RegA, to anaerobically de-repress anaerobic gene expression. Under reducing conditions, the phosphate on RegB is transferred to RegA, which then activates genes involved in photosynthesis, nitrogen fixation, carbon fixation, respiration and electron transport. In the presence of oxygen, there is a second regulator known as CrtJ, which is responsible for repressing photosynthesis gene expression. CrtJ responds to redox by forming an intramolecular disulphide bond under oxidizing, but not reducing, growth conditions. The presence of the disulphide bond stimulates DNA binding activity of the repressor. There is also a flavoprotein that functions as a blue-light absorbing anti-repressor of CrtJ in the related bacterial species *Rhodobacter sphaeroides* called AppA. AppA exhibits a novel long-lived photocycle that is initiated by blue-light absorption by the flavin. Once excited, AppA binds to CrtJ thereby inhibiting the repressor activity of CrtJ. Various mechanistic aspects of this photocycle will be discussed.

Keywords: aerobic repression; photosynthesis; respiration; global regulation

1. INTRODUCTION

All photosynthetic organisms regulate synthesis of their photosystem in response to changes in the environment. Plants control both chloroplast and nuclear gene expression in response to photosynthesis-mediated changes in cellular redox (Pfannschmidt *et al.* 1999; Link 2001). Redox regulation of photosystem genes allows plants to 'fine-tune' synthesis of the photosystem in response to the light intensity. In addition to redox control, plants also contain light-absorbing photoreceptors that control development, several metabolic pathways and circadian rhythms in response to red- and blue-light intensity. The red-light response is mediated by phytochrome that functions as a light-regulated kinase that controls a number of cellular developmental processes such as hypocotyl elongation and cotyledon expansion (Smith 2000; Malakhov & Bowler 2001). Blue-light mediated responses in plants are controlled by flavin-containing photoreceptors, phototropin and cryptochrome. Blue-light absorbency by phototropin is responsible for controlling cell elongation, which mediates bending of plant stems towards or away from light. Blue-light absorption by cryptochrome is responsible for controlling hypocotyl cell elongation, cotyledon/leaf expansion and petiole/flower elongation as well as circadian rhythm (Cashmore *et al.* 1999; Briggs & Huala 1999).

The best-characterized anoxygenic photosynthetic bacteria for which the regulation of photosynthesis gene expression has been studied are *Rhodobacter capsulatus* and *Rhodobacter sphaeroides*. These species exhibit redox control of their photosystem that is characterized by anaerobic, but not aerobic, synthesis of the photosystem, as well as several non-photosynthesis genes such as carbon fixation, nitrogen fixation and respiratory genes, co-regulated by the two-component phosphorylation-dependent signal transduction system, RegB and RegA (Bauer 2001). In addition to RegB and RegA, there is another conserved regulator, known as CrtJ in *R. capsulatus* and PpsR in *R. sphaeroides*, which is responsible for aerobic repression of bacteriochlorophyll, carotenoid, light harvesting and respiratory gene expression (Penfold & Pemberton 1994; Ponnampalam *et al.* 1995; Swem & Bauer 2002).

In contrast to redox regulation of photosynthesis gene expression, for which molecular mechanisms are being revealed, little is known about light regulation of bacterial photosynthesis gene expression. Shimada *et al.* (1992) demonstrated that the most effective high light inhibition

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of *R. sphaeroides* gene expression occurred with blue light at *ca*. 450 nm indicating the existence of a blue-light absorbing photoreceptor in this bacterium.

Below is a description of what is currently known about redox and blue-light regulation of gene expression in the purple photosynthetic bacteria, *R. capsulatus* and *R. sphaeroides*.

2. THE GLOBAL REDOX REGULATORS, RegB AND RegA

The *R. capsulatus regB* and *regA* genes are located in a region of the chromosome called the 'photosynthetic regulatory gene cluster' (Sganga & Bauer 1992; Buggy *et al.* 1994; Mosley *et al.* 1994; Buggy & Bauer 1995). This region comprises *regB* divergently transcribed from the *senC–regA–hvrA* genes that form a three-gene operon, as demonstrated by Northern blot analysis (Buggy *et al.* 1994). The same gene clusters have been found in *R. sphaeroides*, although with a different transcriptional organization (Eraso & Kaplan 1994, 1995, 2000), as well as in two other photosynthetic α-Proteobacteria, *Rhodovulum sulfidophilum* and *Roseobacter denitrificans* (Masuda *et al.* 1999).

Genetic experiments demonstrated that inactivation of either *regA* or *regB* affects a similar set of genes, which indicates that the RegA and RegB proteins are cognate *trans*-acting partners that constitute a signal transduction cascade. Sequence analysis demonstrated that the *R. capsulatus regB* gene encodes a 50.1 kDa (460 amino acids) protein containing all the conserved boxes of the histidine protein kinases of the two-component regulatory systems; among them, the putative autophosphorylation site is predicted to be the conserved His225 residue located in the transmitter domain (Mosley *et al.* 1994; Chen *et al.* 2000). Sequence analysis of RegA demonstrated that it codes for a 20.4 kDa protein (184 amino acids) that contains homology with response regulators of the two-component regulatory system. The N-terminal domain is a typical receiver domain with its highly conserved [D D K] amino acid residues, the putative phosphorylation site being the Asp63. This domain is linked by a short hinge of four proline residues to a very short C-terminal effector domain (50 amino acids) that contains a sequence resembling a helix-turn-helix DNA-binding motif (Sganga & Bauer 1992; Du *et al.* 1998). Thus, RegB and RegA appear to constitute a two-component regulatory system.

Topological models predict that RegB is a membrane protein with a N-terminus that contains six hydrophobic regions that constitute six potential membrane-spanning domains (Ouchane & Kaplan 1999; Chen *et al.* 2000). This N-terminal membrane region of RegB is not required for the kinase activity, as evidenced by the ability of a truncated cytosolic portion of the protein (RegB′) to autophosphorylate on a histidine residue *in vitro* in the presence of [γ^{-32}P]ATP (Inoue *et al.* 1995; Bird *et al.* 1999). However, the region seems to be important for sensing and/or transducing the stimulus *in vivo*; indeed, a mutation in a putative non-membranous cytoplasmic loop present between two hydrophobic membrane-spanning domains led to a constitutive oxygen-insensitive PrrB (RegB) protein in *R. sphaeroides* that promotes photosystem synthesis under both anaerobic and aerobic growth conditions (Eraso & Kaplan 1995). Insertion of RegB into the membrane has also been suggested to enhance dimerization of the protein and/or to be important for the regulation of the kinase and/or phosphatase activities (Inoue *et al.* 1995).

RegB′ and RegA are able to communicate *in vitro* by the transfer of phosphate from RegB′ to the conserved Asp63 residue in the receiver domain of RegA (Inoue *et al.* 1995). As dephosphorylation of RegA-P is dependent on the amount of RegB, and is increased with increasing amounts of the histidine kinase *in vitro*, RegB (PrrB) may also possess a phosphatase activity towards its cognate response regulator RegA (PrrA) (Eraso & Kaplan 1995; Bird *et al.* 1999; Comolli *et al.* 2002). Both the kinase and phosphatase activities are essential for a normal *in vivo* regulation of the RegA-controlled promoters, as phosphorylation of the response regulator determines its transcriptional activity.

At first, RegA was thought to be only an intermediate in a multi-component phosphotransfer cascade, as DNA-binding experiments failed, and the protein was even classified among response regulators of the CheY superfamily that contain only a receiver domain (Egger *et al.* 1997). It is only recently that the DNA-binding activity of RegA has been revealed. The demonstration came from the isolation of a mutant version of RegA (RegA*), which is able to promote *in vivo* high-level expression of photosynthesis genes independently of RegB (Du *et al.* 1998). Using DNase I footprint analysis, Du *et al.* (1998) also demonstrated that purified RegA* binds to *puf* and *puc* promoters. In both cases, RegA* binds to two sites, one minor (weaker protection) and one major (strong protection) site, the major site located close or overlapping the −35 region (Du *et al.* 1998). Shortly after, the wild-type form of the protein was also shown to have this DNA-binding ability (Bird *et al.* 1999). The RegA* protein contains a mutation of a single amino acid (A95S); this mutation may alter the structural conformation of the protein mimicking the phosphorylated state thereby facilitating DNA-binding (Bird *et al.* 1999).

Recently, it has been established that RegA and RegB control expression of many additional genes beyond just the light-harvesting and reaction-centre apoproteins. We now know that the RegB and RegA regulon includes genes involved in carbon fixation (Joshi & Tabita 1996; Qian & Tabita 1996; Dubbs *et al.* 2000; Vichivanives *et al.* 2000), nitrogen fixation (Joshi & Tabita 1996; Elsen *et al.* 2000), hydrogen utilization (Elsen *et al.* 2000), several terminal oxidases (Swem *et al.* 2001), DMSO reductase (Kappler *et al.* 2002), nitrite respiration (Laratta *et al.* 2002), as well as expression of cytochromes c_2, c_y and the cytochrome bc_1 complex (Swem *et al.* 2001; figure 1). Thus, RegB and RegA constitute a signal transduction system that is not limited to photosynthesis, but rather functions as a global regulator of many metabolic pathways. One common theme of genes that are controlled by RegB and RegA is that they all affect the redox state of the cell. Specifically, photosynthesis and uptake hydrogenase both generate reducing power in the form of reduced ubiquinone. By contrast, carbon fixation, nitrogen fixation and respiration all utilize reducing power. Thus, one can envision that the main role of RegB and RegA is to mediate the balance of

the generation of reducing power with the utilization of excess reducing equivalents. In many respects, RegB and RegA appear to be functionally similar to the ArcB–ArcA system in *Escherichia coli*, which is also a global regulator of numerous anaerobic processes (Bauer *et al.* 1999).

Another interesting aspect of RegB and RegA is the fact that homologues are present in several different photosynthetic bacteria such as *R. capsulatus* (Sganga & Bauer 1992; Mosley *et al.* 1994), *R. sphaeroides* (Phillips-Jones & Hunter 1994; Eraso & Kaplan 1994, 1995), *Rhodovulvum sulfidophulum* (Masuda *et al.* 1999), *Roseobacter denitrificans* (Masuda *et al.* 1999), as well as in non-photosynthetic bacteria such as *Rhizobium meliloti* (Tiwari *et al.* 1996) and *Bradyrhizobium japonicum* (Bauer *et al.* 1998). Furthermore, the RegB and RegA sequences from these different genera are the most highly conserved members of the large sensor kinase and response regulator family (Masuda *et al.* 1999). Curiously, the putative helix-turn-helix motif of RegA is conserved in all RegA homologues that have been sequenced. This high level of sequence conservation suggests that there are significant constraints in the ability of RegA to genetically drift among these different species. It also suggests that RegB and RegA may have important roles in regulating anaerobic metabolisms in these species.

3. THE AEROBIC REPRESSOR CrtJ/PpsR

Mutational analyses of the *R. capsulatus* and *R. sphaeroides* photosynthesis cluster suggested that an open reading frame termed *crtJ* in *R. capsulatus* and *ppsR* in *R. sphaeroides* codes for a *trans-acting* repressor of photopigment biosynthesis genes (Penfold & Pemberton 1991, 1994; Bollivar *et al.* 1994; Ponnampalam *et al.* 1995). Spectral analyses of aerobically grown cultures demonstrated that the steady-state level of bacteriochlorophyll is elevated 2.6-fold in a *crtJ* mutant compared with wild-type cells (Bollivar *et al.* 1994). Aerobic expression of various photopigment biosynthesis genes is also elevated twofold higher in a *crtJ* mutant strain suggesting that CrtJ functions as an aerobic repressor of *bch* and *crt* genes (Ponnampalam *et al.* 1995; Gomelsky & Kaplan 1995*a*). Interestingly, the effect of CrtJ is not limited to the pigment biosynthesis genes. Aerobic expression of the *puc* operon, which codes for the light-harvesting II structural apoproteins, is also twofold higher in a *crtJ* mutant despite the fact that *puf* and *puh* expression levels are essentially the same as in the wild-type (Ponnampalam *et al.* 1995). The *puc* operon is therefore subjected to activation by RegB–RegA as well as repression by CrtJ. A CrtJ binding site in the *puc* operon overlaps that of the RegA binding site (Du *et al.* 1998; Elsen *et al.* 1998; Bowman *et al.* 1999). It has also been demonstrated that these two sites cannot be co-occupied by RegA and CrtJ invoking competition for binding as the mechanism of *puc* repression by CrtJ (Bowman *et al.* 1999). CrtJ has also been shown to control aerobic repression of ubiquinol oxidase (Swem & Bauer 2002), which is thought to be the high affinity respiratory oxidase (Thöny-Meyer *et al.* 1994; figure 1).

CrtJ is a soluble protein (52 kDa) with a deduced amino acid sequence that exhibits a putative helix-turn-helix DNA binding domain (Penfold & Pemberton 1991, 1994; Alberti *et al.* 1995). An examination of the DNA sequences of promoters that are regulated by CrtJ reveals a consensus sequence of TGT–N_{12}–ACA (Alberti *et al.* 1995; Elsen *et al.* 1998). Gel mobility shift and DNA footprint experiments have demonstrated that CrtJ binds to this palindrome's sequence (Ponnampalam & Bauer 1997; Ponnampalam *et al.* 1998; Elsen *et al.* 1998). In the *bchC* promoter region there are two CrtJ-binding palindromes 8 bp apart, one that straddles the –35 region and the other at the –10 region (Ponnampalam & Bauer 1997). Binding of CrtJ to the *bchC* promoter is co-operative, with protein bound to the –35 palindrome interacting with protein bound to the –10 palindrome (Ponnampalam *et al.* 1998). *In vitro* and *in vivo* experiments have demonstrated that CrtJ is unable to effectively bind to the *bchC* promoter if the spacing between the two *bchC* palindromes is altered by adding or removing just a few base pairs (Ponnampalam *et al.* 1998).

Unlike the *bchC* operon, other CrtJ-repressed genes in *R. capsulatus* contain only a single palindrome within the –10 to –35 promoter region (Alberti *et al.* 1995; Elsen *et al.* 1998). However, in every case that has been examined, an additional palindrome has been found in close proximity, usually 100–150 bp upstream of the transcription start site. *In vivo* and *in vitro* experiments have demonstrated that CrtJ bound to the 'distant palindrome' co-operatively interacts with CrtJ bound to the –10 or –35 promoter region (Elsen *et al.* 1998). This indicates that DNA looping must be occurring, which permits CrtJ interactions between palindromes separated by 100 bp or more. Interestingly, CrtJ is known to exist in solution as a tetramer, suggesting that each monomer binds to single palindrome half site (Gomelsky *et al.* 2000).

In vitro gel-mobility shift experiments have demonstrated that the CrtJ effectively binds to the target palindrome under oxidizing, but not under reducing, conditions (Ponnampalam & Bauer 1997; Masuda *et al.* 2002). Studies failed to detect the presence of metal as a redox-responding co-factor that has been found in other redox-sensing proteins (Ponnampalam & Bauer 1997). Recently, it has been demonstrated that oxidizing conditions promote the formation of an intramolecular disulphide bond in CrtJ that is stimulated by direct interaction with oxygen (Masuda *et al.* 2002) (figure 2). Disulphide bond formation in CrtJ was also shown to occur *in vivo* when *R. capsulatus* cells are grown under oxidizing conditions but not when grown under reducing conditions. Presumably, the formation of the disulphide bond causes CrtJ to adopt a conformational form that allows it to effectively bind DNA. Interestingly, one of the Cys that is involved in disulphide bond formation is located very near the CrtJ helix-turn-helix motif (Masuda *et al.* 2002).

4. LIGHT REGULATION OF CrtJ/PpsR

Early physiological studies of purple bacteria demonstrated that when photosynthetic cultures are shifted from high- to low-light conditions they exhibit a distinct growth lag that correlated with increased rates of photopigment production (Cohen-Bazire *et al.* 1957). This indicates that cells compensate for a decline in light intensity by increasing synthesis of the photosystem to maintain an adequate supply of energy. Careful investigations into this phenomenon revealed that cells adapt to a drop in light intensity

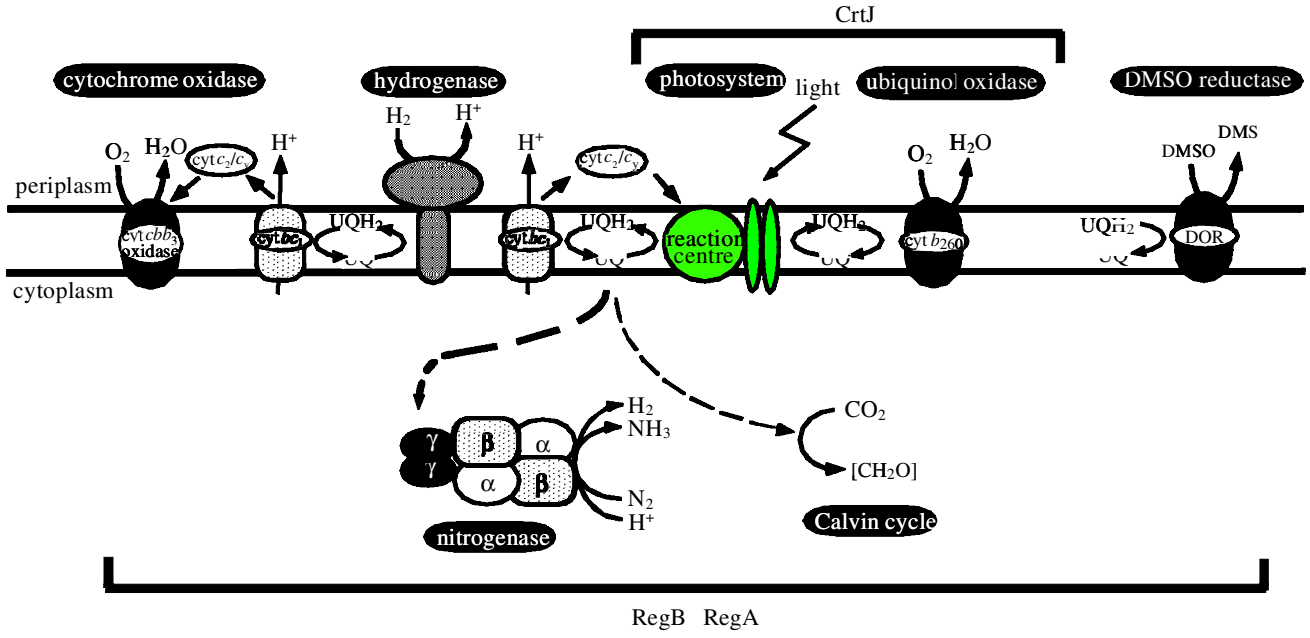

Figure 1. Systems regulated by RegB–RegA and CrtJ. Parentheses denote specific energy-generating and energy-utilizing systems that are controlled by the RegB–RegA signal transduction cascade as well as by CrtJ.

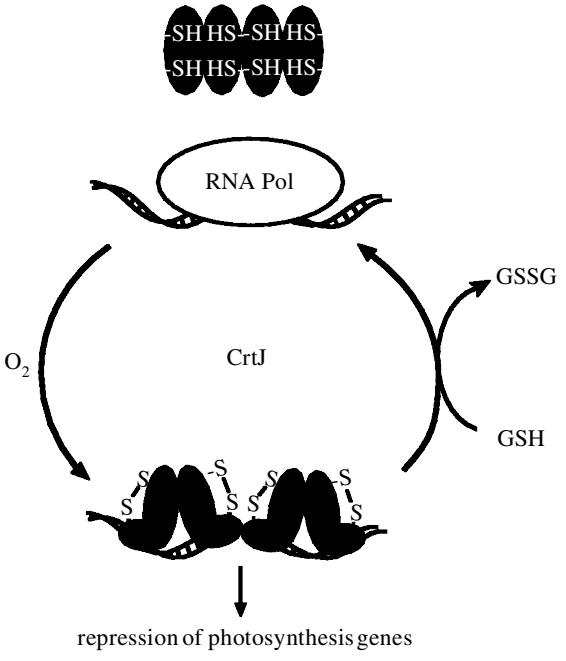

Figure 2. The control of CrtJ/PpsR repressor activity through disulphide bond formation.

by increasing the number of core photosynthetic units per cell (up to 5-fold) while simultaneously increasing the ratio of light-harvesting II antenna complexes to reaction centres (up to 2-fold) (Shumacher & Drews 1979; Golecki *et al.* 1980; Drews 1985). Molecular and genetic investigations later confirmed that high light intensities promote a reduction in photopigment production caused by diminished levels of *puf*, *puh* and *puc* transcripts (Zhu & Kaplan 1985; Zhu & Hearst 1986; Zhu *et al.* 1986; Buggy *et al.* 1994).

Shimada *et al.* (1992) used Northern hybridization experiments to examine the dependence of *R. sphaeroides puf* and *puc* gene expression on specific light wavelengths and found that the largest inhibition occurred under blue light (*ca.* 450 nm). This suggested that a flavin-containing transcription factor might sense light intensity and modulate photosynthesis gene expression accordingly. The authors later reported that a factor present in cell extracts of cultures grown photosynthetically under various light conditions bound to the *puf* promoter at a site previously identified as a *cis*-acting oxygen control element (Shimada *et al.* 1993, 1996). Gel-mobility shift and footprint experiments indicated that binding appeared to be enhanced when cell extracts were made from cultures grown semi-aerobically under blue light indicating that the factor might be a repressor of *puf* transcription.

A null mutation in *R. sphaeroides ppsR* was shown to be deficient in redox-regulated repression as well as in high light repression of photosystem synthesis. This suggests that PpsR may be involved in both redox and light-dependent regulation of *R. sphaeroides* photosynthesis gene expression (Gomelsky & Kaplan 1997). Surprisingly, there is only a modest amount of high light repression of photosystem gene expression in the closely related bacterium *R. capsulatus*. Deleting CrtJ has no effect on light regulation in this species. This indicates that there are fundamental differences between *R. capsulatus* and *R. sphaeroides* in respect of the mechanism of high light repression of the photosystem.

Recently, it was shown that different light-control mechanisms between *R. capsulatus* and *R. sphaeroides* involve a PpsR antagonist called *appA* (Gomelsky & Kaplan 1997; Masuda & Bauer 2002). This protein, which has no known homologue in the sequenced genome of *R. capsulatus*, has several interesting structural features (Gomelsky & Kaplan 1995*b*, 1998). The amino-acid terminal region of AppA binds FAD, which is used as a blue-light absorbing chromophore by cryptochrome (Gomelsky & Kaplan 1998; Masuda & Bauer 2002). The carboxy-terminal region contains a cysteine-rich motif that is also characteristic of disulphide-bond-reducing proteins

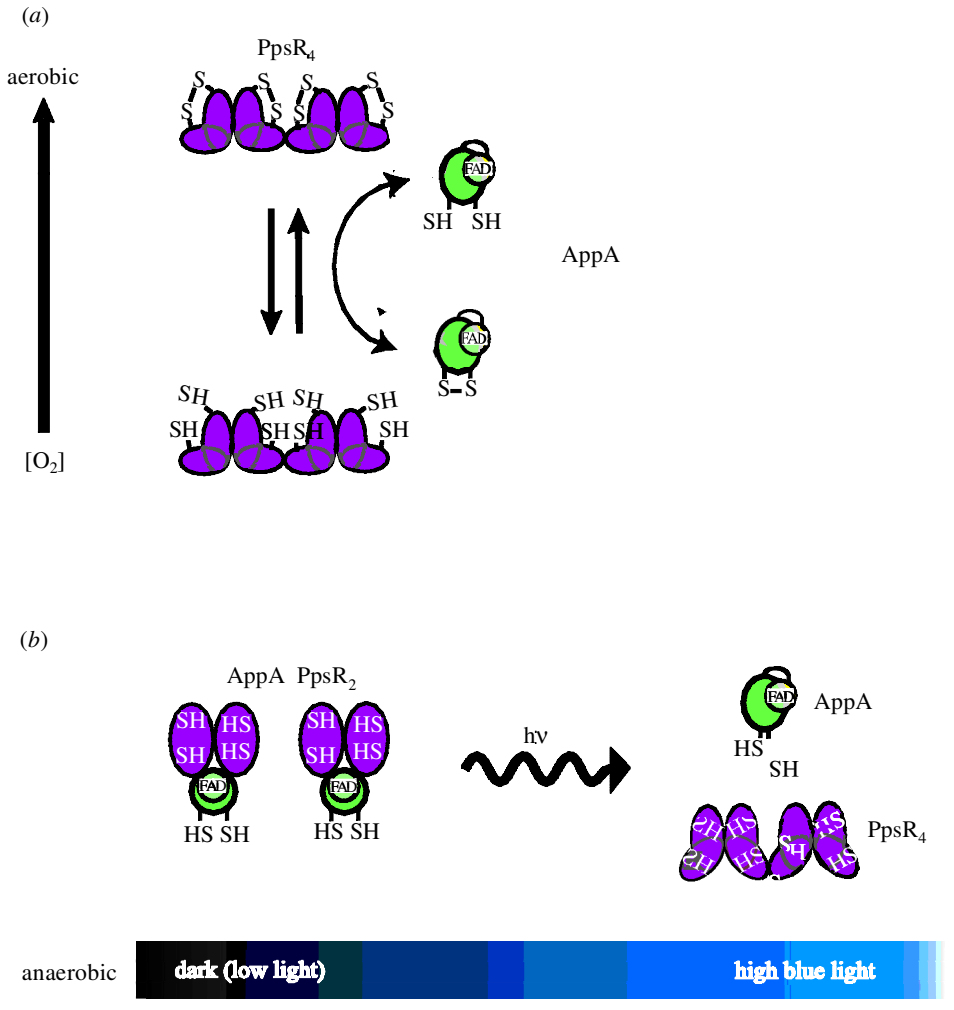

Figure 3. The role of AppA in the regulation of PpsR repressor activity. As discussed in the text, AppA has two activities, one to reduce a disulphide bond in PpsR (*a*) and the other to convert the PpsR tetramer into an AppA–$PpsR_2$ complex that is incapable of binding DNA (*b*). The later reaction is inhibited by excitation of the flavin by blue light.

such as thioredoxin reductase and glutaredoxin reductase (Holmgren 1989). Deletion of *appA* results in greatly increased repression of PpsR-regulated genes (Gomelsky & Kaplan 1995*b*) with secondary null mutations in PpsR relieving this repressing effect. This indicates that AppA functions as an antagonist of PpsR repressor activity (Gomelsky & Kaplan 1997). Recently, Masuda & Bauer (2002) used purified PpsR and AppA proteins to demonstrate that AppA inhibits DNA-binding of PpsR by two mechanisms (figure 3). One mechanism involves AppA-mediated reduction of the disulphide bond in PpsR. The second mechanism involves the light-regulated formation of a stable AppA–$PpsR_2$ antirepressor–repressor complex that inhibits DNA-binding. The flavin in AppA was shown to undergo a novel photocycle involving a long-lived blue-light-induced red shift in the flavin spectrum. The light-induced spectral shift appears to cause a conformational change in AppA that inhibits formation of the AppA–$PpsR_2$ complex. These results provide the first molecular mechanism of blue-light control of photosystem synthesis in a photosynthetic bacterium.

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Discussion

R. E. Blankenship (*Department of Chemistry and Biochemistry, Arizona State University, AZ, USA*). Your redox data were really beautiful, Carl, but I am confused, because it seems like the effect takes over at too low a potential. At –300 mV you are going to have to shut down photosynthesis by reducing the quinone acceptors, so I do not understand how that part of the story works.

C. E. Bauer. Yes, that section we were doing *in vitro* when we actually dumped in the reducing agent. I do not think that RegB itself is a sensor. The reason I say this is because there is another protein (protein X) inside the cell that we mutated. RegB is refractory to changes in the redox potential, and is essentially constitutively active. Protein X actually sits in the membrane; it has a beautiful membrane-spanning domain, so I think that it is the actual sensor that is going to sit in the membrane section sending electrons into RegB. Now one of the things that is rather interesting for both RegB and CrtJ is the potential of the RegB and CrtJ. RegB, for example, should always be in its oxidized state *in vivo*. CrtJ should always be in its reduced state *in vivo*, because we have done a redox titration and CrtJ has a redox potential of –190 mV and we know the cell potential is –220 mV. However, we know CrtJ undergoes oxidation–reduction so I am not sure if the potential is changing or if the environment inside the protein is changing the potential differently *in vivo* from what we are actually measuring *in vitro*.

R. E. Blankenship. Yes, but the one thing you want to avoid, of course, are conditions in which you are making chlorophyll but not making the apoproteins; that would be disastrous. It is a little surprising, I guess, that the two regulatory circuits are not a little bit more locked together, in terms of turning those things on and off at the same time.

C. E. Bauer. Yes, it is surprising, but it is rather interesting. Barry Marrs back in the late 1970s did a very careful analysis of turning on the genes for photosynthesis, both the chlorophyll biosynthesis genes and the reaction-centre

genes, at various oxygen tensions, and it was clearly biphasic. The chlorophyll biosynthesis genes are actually turned on before the reaction-centre genes. So what we are actually seeing here is that our *in vitro* results are mimicking the *in vivo* analysis.

J. F. Allen (*Plant Biochemistry, Lund University, Lund, Sweden*). Thank you, you were not invited just to say I was right you know, and in fact, of course, you just proved I am wrong because RegB does not have a homologue. On the other hand, the moment you say it is sensing the redox state, something outside the membrane is actually disqualified. A better model for what I am talking about is the Arc system of Linn, which is now demonstrated to be a quinone redox sensor.

C. E. Bauer. Well I was going to say, John, that RegB is interacting with another protein, called protein X right now, just for the sake of argument. We know that another protein binds a cofactor, and it is either a modified flavin or a quinone, we do not know which yet, but the spectrum indicates that there is definitely another cofactor there. That protein is present from bacteria all the way to humans; you have it yourselves. It is present in bacteria, it is present in plants, it is present in eukaryotes and it is associated with cytochrome oxidase in mitochondria, so that may be your 'magic bullet'.

J. F. Allen. Ah, but then a hundred questions arise immediately.

C. E. Bauer. I will talk to you about that later.

W. Martin (*Institute of Botany III, Heinrich-Heine Universität Düsseldorf, Düsseldorf, Germany*). That was exactly my question. This protein can modulate your RegA–RegB activity with oxygen or what have you, but what is really sensing redox is protein X, and that is everywhere. And so you are saying that this is the candidate to take the signal out of the quinone pool or out of flavin–adenosine dinucleotide or out of something and transfer it to RegA–RegB.

C. E. Bauer. RegB is not the sensor itself; it is just the output. I mean it basically gets a signal, an electron from this other protein.

W. Martin. OK. In contrast with a standard two-component system, this one is a two-component system taking a signal from a protein.

C. E. Bauer. Absolutely. I was just at a meeting in France, where the hydrogen utilization to sense hydrogen involves a two-component system where the sensor kinase docks with hydrogenase. It is the electrons going through the hydrogenase that control the sensor kinase.

J. F. Allen. A brief comment. Of course, my original proposal was that redox sensors are such a great idea; it would be a very good idea to have one at each of a number of different specific midpoint potentials reporting on the redox state of a number of key points in electron transport chains; so it is not quinone or nothing, quite on the contrary. There is important redox information, which must be doing something, arising from a number of different key locations in respiratory and photosynthetic chains, I would say.

GLOSSARY

FAD: flavin adenosine dinucleotide