A LexA-related protein regulates redox-sensitive expression of the cyanobacterial RNA helicase, *crhR*

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Received April 26, 2006; Revised May 26, 2006; Accepted May 27, 2006

ABSTRACT

Expression of the cyanobacterial DEAD-box RNA helicase, *crhR*, is regulated in response to conditions, which elicit reduction of the photosynthetic electron transport chain. A combination of electrophoretic mobility shift assay (EMSA), DNA affinity chromatography and mass spectrometry identified that a LexA-related protein binds specifically to the *crhR* gene. Transcript analysis indicates that *lexA* and *crhR* are divergently expressed, with *lexA* and *crhR* transcripts accumulating differentially under conditions, which respectively oxidize and reduce the electron transport chain. In addition, expression of the *Synechocystis* lexA gene is not DNA damage inducible and its amino acid sequence lacks two of three residues required for activity of prototypical LexA proteins, which repress expression of DNA repair genes in a range of prokaryotes. A direct effect of recombinant LexA protein on *crhR* expression was confirmed from the observation that LexA reduces *crhR* expression in a linear manner in an *in vitro* transcription/translation assay. The results indicate that the *Synechocystis* LexA-related protein functions as a regulator of redox-responsive *crhR* gene expression, and not DNA damage repair genes.

INTRODUCTION

The ability to adapt to a dynamic light environment is crucial for the survival of photosynthetic organisms and includes both short- and long-term responses. Light sensing occurs either via direct mechanisms involving photoreceptor proteins, or indirectly through light-driven changes in the redox status of the electron transport chain between QA in photosystem II and QO in cytochrome b6f (1–4). Electron carriers in this region of the inter-photosystem electron transport chain perform essential roles in redox-sensing in higher plant chloroplasts, regulating expression of nuclear- and chloroplast-encoded genes involved in photosynthesis (5–9). For example, a direct link between the redox poise of plastoquinone and chloroplast gene expression has been shown for the *psbA* and *psaAB* genes, allowing rapid cellular response to the light environment via sensing of the redox status of the electron transport chain (7). In contrast, the factors responsible for transduction of the electron transport redox poise to transcription regulation remain poorly characterized. Possible transducers identified in spinach chloroplasts include an unidentified 31 kDa dimeric protein shown to bind the *psaA* promoter (10) and the TSP9 thylakoid-associated protein. Redox-mediated phosphorylation of TSP9 on three threonine residues releases the protein from the thylakoid membrane potentially allowing it to play a role as a signaling factor responsible for transducing plastoquinone redox poise to gene expression (11).

In prokaryotic cyanobacteria, the redox status of the electron transport chain carriers also regulates expression of a limited number of photosynthetic and non-photosynthetic genes. Expression of the RNA helicase, *crhR* (1), glutamine synthetase, *glnA* (12), PI protein, *glnB* (13), α and β subunits of phycocyanin, *cpcBA* (14), photosystem proteins (14–16) and a transcriptional regulator (17) has been attributed to the redox poise of plastoquinone and/or cytochrome b6f. Members of the signal transduction pathway(s) associated with sensing and transducing changes in redox status to the transcriptional machinery also remain to be identified in cyanobacteria. Proposed mechanisms in cyanobacteria include a redox-responsive two-component signal transduction pathway (16) and the redox-sensitive transcriptional regulators, NtcA and NblS (17,18). A potential sensor is the membrane-associated sensor histidine kinase NblS, which responds and controls photosynthesis-related gene expression in response to high light and nutrient stress (18). NblS contains a redox-sensing PAS domain potentially involved in the sensing and transduction of high light/nutrient stress induced changes in photosynthetic or cellular redox poise to as yet uncharacterized transcriptional regulators (18). While a number of redox-sensitive transcriptional regulators have been described in prokaryotic systems, the physiological electron donors have not been identified (19–23). NtcA is one transcriptional regulator whose activity has been shown to involve a complex interaction between cellular nitrogen levels, thiol group redox and photosynthetic electron flow although not directly correlated with the redox state of the plastoquinone pool (17). NtcA controls expression of...
genes involved in nitrogen acquisition, repressing gifA and gifB and activating expression of glnA, glnN and glnB in response to both nitrogen levels and electron transport (24).

Expression of the Synechocystis DEAD-box RNA helicase, crhR (Cyanobacterial RNA Helicase-Redox), is also regulated by the redox poise of the electron transport chain (1). crhR transcripts accumulate when the electron transport chain is reduced, either from light-driven electron flow or respiratory electron flow generated by the metabolism of exogenously supplied glucose. In contrast, a reduction in electron flow, leading to oxidation of the electron transport chain, decreases crhR transcript accumulation. These results are corroborated by results obtained using electron transport inhibitors or alteration of light quality which alter crhR induction, confirming redox-regulated expression and identifying the redox poise of the electron transport chain between QA in photosystem II and QO in the cytochrome bc1 complex, as the potential sensor for redox-dependent regulation (1). Biochemically, CrhR exhibits enzymatic activities characteristic of RNA helicases, including RNA-dependent ATPase activity and ATP-stimulated RNA unwinding (25). In addition, CrhR also possesses ATP-dependent RNA annealing activity (26). Thus, CrhR has been proposed to regulate gene expression at the translational level through its ability to rearrange RNA secondary structures of RNA substrates, potentially of other redox-regulated gene transcripts (1,26).

As an initial step to elucidate upstream factors involved in the redox-regulated expression of the crhR gene, we have identified a LexA-related protein that controls crhR transcript accumulation. Treatments known to enhance crhR transcript accumulation reduce lexA levels and vice versa. A direct effect of the recombinant His-tagged LexA protein (rLexA) on crhR expression was confirmed from the observation that rLexA reduces crhR expression in an in vitro transcription/translation assay. LexA thus appears to function as a repressor of crhR transcription when crhR is not required i.e. under conditions which oxidize the electron transport chain. In concurrence with this conclusion, expression of the Synechocystis lexA gene is not DNA damage inducible and its amino acid sequence lacks two of three residues required for the self-cleavage activity of prototypical LexA proteins (27). We discuss the potential significance of a LexA-related repressor in the regulation of redox-responsive gene expression and, consequently, the implications of this novel role performed by LexA in Synechocystis.

MATERIALS AND METHODS

Bacterial strains and growth conditions

Synechocystis sp. strain PCC 6803 was maintained at 30°C on BG-11 agar (28) solidified with 1% (w/v) Bacto-Agar (Difco Laboratories, Detroit, MI) and grown photoautotrophically at 30°C under continuous illumination at a constant intensity of 150 μmol photons m⁻² s⁻¹. Liquid BG-11 cultures were aerated by shaking at 150 r.p.m. and continuous bubbling with humidified air. Dark conditions were created by wrapping the flasks in aluminum foil. Glucose (5 mM) was added where indicated. To induce DNA damage, cells were exposed to short-wave ultraviolet light (UV-C; 254 nm) at a dose rate of 150, 300 or 600 J/m² using a XL-1000 UV crosslinker (Spectronics Corporation) and subsequently incubated in the dark for 1 h prior to harvesting. Escherichia coli strains DH5α and JM109 were used for propagation and protein expression of plasmid constructs, respectively. Cultures were grown in Luria–Bertani (LB) medium at 37°C and aerated by shaking at 200 r.p.m. Ampicillin (100 μg/ml) was added where appropriate.

Plasmid constructs

A deletion series within the crhR promoter/open reading frame (ORF) was created from a 3 kb EcoRI fragment encompassing the crhR promoter, 5'-untranslated region (5'-UTR) and the crhR ORF (1). Plasmid DNA was digested with NotI and SacI, and a deletion series produced using the Erase-A-Base Kit (Promega) according to the manufacturer’s instructions. Two additional deletion constructs were created by restriction enzyme digestion. SphI removed a 328 bp fragment to construct KC+125. The KC+219 construct was created by EcoRI / XmnI digestion to liberate a 2.6 kb fragment containing the crhR ORF downstream of +219 but lacking the promoter region. This fragment was blunt end ligated into EcoRV digested pBlueScript KS+ (Stratagene).

The lexA gene was amplified by PCR to generate an in frame translational fusion in the pSETB plasmid vector (Invitrogen). The lexA insert DNA was generated using primers LPF-27 (5'-ACTGTTGATCAGGAAACGTACCCG-3'), and LPF-2 (5'-GAAACAAAACCTGAGGAGGCG-3') and Synechocystis chromosomal DNA as template. PCR were performed in a volume of 50 μl, containing 300 nM primer and 0.8 U of Expand High Fidelity enzyme mix (Roche) according to the manufacturer’s instructions. The PCR program consists of 30 cycles of 1 min denaturation at 95°C, 30 s annealing at 55°C and 1 min extension at 68°C; and terminated with 4 min extension at 68°C. Purified DNA was digested with BamHI and HindIII (restriction sites underlined) and cloned into BglII and HindIII digested plasmid XL-1000 UV crosslinker (Spectronics Corporation) and subsequently incubated in the dark for 1 h prior to harvesting. Escherichia coli strains DH5α and JM109 were used for propagation and protein expression of plasmid constructs, respectively. Cultures were grown in Luria–Bertani (LB) medium at 37°C and aerated by shaking at 200 r.p.m. Ampicillin (100 μg/ml) was added where appropriate.

Generation of promoter fragments

Promoter fragments were PCR amplified from the deletion plasmids using the M13 forward primer (5'-GTAACAGGAGGCGCATGATC-3') and GWO-45 (5'-AAGCCAACTTGGCGCGCA-3') (Figure 1A). PCR were performed as described above using an annealing temperature of 45°C. BssHII / BssSI digestion was used to generate fragments corresponding to KC+125 and KC+219. DNA fragments were purified from 1x TAE agarose gels using GENECLEAN® II (BIO 101).

DNA affinity column purification

To purify proteins binding to the crhR promoter region, μMACS Streptavidin magnetic separation was performed (Miltenyi Biotec). Synechocystis cultures (300 ml) were harvested at mid-log phase and resuspended in 2 ml cyano bacterial protein extract buffer [20 mM Tris–HCl (pH 8), 10 mM NaCl, 1 mM EDTA (pH 8) and 5 mM DTT] containing protease inhibitors (Complete Mini Protease Inhibitor Cocktail,
Cells were lysed by eight cycles of sonication for 30 s followed by 30 s cooling in an ice-water bath. Lysed cells were clarified by centrifugation and the supernatant retained. Proteins were quantified by the Bradford assay. Cells were clarified by centrifugation and the supernatant was loaded onto a Ni-NTA column (Qiagen) and incubated with 10 mM imidazole. The column was washed consecutively with steps of increasing salt stringency (0.1 to 1 M KCl). Eluted proteins were concentrated by TCA precipitation, separated on a 10% (w/v) SDS–polyacrylamide gel and visualized by silver staining (BioRad).

Polypeptides of interest were identified by in-gel tryptic digestion and LC/MS/MS of the resulting peptides at the Institute for Biomolecular Design (University of Alberta). Generated LC/MS/MS data were used as queries for Mascot Daemon (Matrix Science, UK) searches of the National Center for Biotechnology Information (NCBI) non-redundant databases. A protein score greater than 73 following Mascot searches was considered significant.

**EMSA**

EMSA were performed using *Synechocystis* soluble protein extract, *E.coli* soluble protein extract or recombinant LexA (rLexA) protein, and the indicated PCR-generated promoter fragments end-labeled with [γ-32P]ATP and T4 polynucleotide kinase (New England Biolabs). Binding reactions were performed for 20 min at 37°C in 1× EMSA buffer, 1 μg poly(dl-dC), 2000 c.p.m. end-labeled DNA (~0.006 pmol) and the indicated protein concentration in a final volume of 20 μl. Reaction products were separated on a 5% TBE non-denaturing polyacrylamide gel and subjected to autoradiography. Two non-specific competitor DNAs were prepared to control for non-specific protein-binding. A vector control target was a 262 bp EcoRV / PvuII fragment containing the pBluescript KS+ multiple cloning site and a 321 bp internal fragment of the *Synechocystis* lexA gene, PCR amplified using primers LPF-4 (5’-ATTTCGATTTCCTCTTCTCCGACC-3’) and LPF-5 (5’-CCTCGATTTCCTCTTCTCCGAC-3’) using an annealing temperature of 45°C as described above.

**Recombinant LexA expression and purification**

*E.coli* JM109:pLexA cultures were grown at 37°C to OD600 = 0.6, and LexA expression induced by addition of isopropyl-b-D-thiogalactopyranoside (IPTG) (1.0 mM) and phage (M13/T7 DE3, 5 p.f.u./cell, Invitrogen). After induction for 3 h at 37°C, harvested cells were resuspended in 1/10 volume lysis buffer (50 mM NaH2PO4, 300 mM NaCl and 10 mM imidazole), lysed by sonication (6 × 30 s intervals), and clarified by centrifugation. The supernatant was loaded onto a Ni-NTA column (Qiagen) and incubated with gentle shaking for 60 min at 4°C. The column was washed consecutively with wash buffer (50 mM NaH2PO4 and 300 mM NaCl) containing increasing amounts of imidazole (20 to 50 μM), with bound rLexA eluting in buffer containing 250 mM imidazole. Imidazole was removed from the eluted rLexA buffer by dialysis against lysis buffer lacking imidazole.
Northern analysis

Total RNA was isolated by Synechocystis mechanical lysis, separated on a 1.2% formaldehyde gel, and transferred to a nylon membrane (Hybond N+) as described previously (29). Blots were hybridized overnight at 65°C with the appropriate probe in aqueous buffer (5x SSPE, 5x Denhardt's, 0.5% SDS) and washed for 10 min at 65°C once in 1x SSPE, 0.1% SDS and once in 0.1x SSPE, 0.1% SDS. lexA and crhR DNA fragments were randomly labeled with [α-32P]dCTP using random hexanucleotide primers (Roche). The probes correspond to: lexA, a 750 bp BgIII / HindIII fragment encompassing the entire ORF; crhR, a 784 bp internal BstEI fragment; and recA, a 1091 bp fragment containing the pBluescript KS+ multiple cloning site. Membranes were stripped by incubation in boiling 0.1% SDS and probed with the Synechocystis rnsaeP gene as a control for RNA loading (30).

In vitro transcription/translation assays

In vitro transcription and translation assays were performed using the Promega E.coli S30 extract system for circular DNA in a final reaction volume of 25 µl. The plasmids pCrhR (IV) and pWM3-2 (29) were used for in vitro expression of the crhR and crhC genes, respectively. pCrhR (IV) was prepared by ligating a 2.2 kb BamHI / EcoRI fragment of CS0096-9 (1) into pBluescript KS+ to remove downstream sequences encoding the argC gene. The pCrhR (IV) and pWM3-2 plasmids contain 2.2 and 2.4 kb inserts, respectively encoding the promoters, ORFs, and 5' and 3'-UTRs of crhR and crhC, respectively. Reactions were performed according to manufacturer’s instructions using 1 µg plasmid DNA, corresponding to 0.29 and 0.28 pmol DNA for pCrhR (IV) and pWM3-2, respectively. Reaction products were separated on a 10% (w/v) polyacrylamide gel and subjected to autoradiography. Binding reactions containing rLexA were performed according to manufacturer’s instructions with an initial 5 min incubation to allow protein-binding to the crhR gene. Control reactions were performed to determine the effect of rLexA on crhR expression in the presence of BSA and expression of an unrelated RNA helicase, crhC (30), from its own promoter.

RESULTS

Promoter deletion series delineates the protein-binding site within the crhR gene

EMSA assays were performed using nine plasmid constructs containing deletions of the crhR promoter (Figure 1A) to delineate the protein-binding region. Intact crhR promoter (KC-179) and deletions up to position +77 of the crhR transcript (KC+77) exhibited decreased mobility on a native PAGE gel upon incubation with Synechocystis protein extract (Figure 1B, lanes 1–14). The KC+125 DNA target, deleted to +125 of the transcript, exhibited a reduced amount of shift (Figure 1B, lanes 15 and 16), while deletion to +219 completely abolished the mobility shift (Figure 1B, lanes 17 and 18). Together, these results indicate that the protein-binding site is located downstream of the translational start codon (+110) in the region of DNA surrounding an Spel site (+125). Sequence specificity of binding was shown by competition assays in the presence of increasing amounts of either specific or non-specific competitor DNA (Figure 1C).

Addition of specific competitor DNA (KC-179) progressively challenged formation of the shifted complex (Figure 1C, Specific competitor). Conversely, inclusion of a similar sized fragment containing the pBluescript KS+ multiple cloning site had no effect on the mobility shift (Figure 1C, non-specific competitor). Taken together, these results indicate that at least one soluble Synechocystis protein interacts with the crhR gene in a sequence-specific manner.

Synechocystis LexA-related protein binds within the crhR ORF

To identify the protein responsible for altered mobility of the crhR gene, DNA affinity column chromatography was performed using light-grown Synechocystis soluble protein extracts and biotinylated KC+5 DNA (239 bp). A single polypeptide with an apparent molecular weight of 28 kDa was recovered in the high stringency 1 M KCl elution (Figure 2A). The single significant hit (score 92) identified by in-gel tryptic digestion and LC/MS/MS corresponded to the Synechocystis gene sll1626, which has been annotated as encoding the transcriptional repressor LexA (http://www.kazusa.or.jp/cyanobase/). Analysis of the deduced Synechocystis LexA amino acid sequence revealed that the sequence lacks the Ala-Gly self-cleaveage site and the serine of the Ser-Lys dyad active site present in E.coli LexA, both of which are required for LexA self-cleavage (Figure 2B: (31)]. Furthermore, an SOS-like box, similar to those identified as LexA binding sites in E.coli (32,33), Bacillus subtilis (34) and Mycobacterium tuberculosis (35) could not be identified within the upstream sequence of either lexA or crhR (data not shown). However, a sequence related to the putative cyanobacterial SOS box (36), matching 7 of 9 essential residues with required spacing between essential residues, was identified within the protein-binding domain in crhR (Figure 2C). This sequence includes the SpeI site, possibly explaining the reduced shift observed with the SpeI generated KC+125 fragment (Figure 1B).

Synechocystis lexA, crhR and recA transcript accumulation

crhR transcript accumulation is regulated by the redox poise of the plastoquinone pool with treatments leading to reduction of plastoquinone correlating with an increase in crhR transcript accumulation, whereas conditions that lead to the oxidation of the plastoquinone pool result in decreased crhR accumulation (1). Northern analysis was therefore performed to determine the relationship between lexA and crhR transcript accumulation under varying redox conditions (Figure 3A). Growth in the light (Figure 3A, lane 1), conditions favoring crhR transcript accumulation, correlate with reduced levels of lexA transcript. Conversely, growth in the dark (Figure 3A, lane 2) reduces crhR while enhancing lexA transcript accumulation. The addition of glucose (5 mM) to light-grown cells enhanced crhR and lexA transcript accumulation (Figure 3A, lane 3). crhR expression was significantly induced in response to cold stress (20°C; Figure 3A, lane 4), concomitant with the complete repression of lexA transcript accumulation. The data indicates
under all conditions tested, requiring riboprobe detection and extended exposure times. lexA transcript accumulation was also not altered by DNA damage-induced by mitomycin C (data not shown). Similarly, expression of crhR was not UV-inducible (data not shown); rather, it followed the expected decrease in transcription that occurs in wild-type cells in the dark (1). The lack of induction of the Synechocystis recA, lexA and crhR genes following DNA damage suggests these gene products are not required during the cellular response to DNA damage.

**Synechocystis LexA interacts with the crhR gene**

Recombinant His-tagged LexA (rLexA) was purified to near homogeneity and used to test interaction with the KC+5 crhR promoter fragment (Figure 4). KC+5 crhR promoter DNA mobility was reduced by incubation with total Synechocystis protein extracts (Figure 4A, lane 8 versus lane 1). Mobility of the KC+5 DNA target was also altered by incubation with non-specifically bound proteins removed by increasing KCl washes. Silver staining of eluted proteins were removed by increasing KCl washes. Silver staining of eluted proteins separated by a 10% SDS–PAGE reveals a single polypeptide in the 1 M KCl lane. 2, low molecular weight standards (BioRad); lane 3, 1 M KCl wash. (*LexA binding was demonstrated by competition assays in the presence of increasing concentrations of either specific or non-specific competitor DNA. Addition of unlabeled specific competitor (KC+5) challenged formation of the shifted complex at all concentrations tested (Figure 4B, lanes 2–5), with addition of >50-fold excess of unlabeled target abolishing shift of the DNA target. In contrast, incubation with non-specific competitor DNA, an internal lexA fragment similar in size to the specific competitor, did not significantly alter mobility shift at comparable concentrations (Figure 4B, lane 3, 1 M KCl wash, lane 2, low molecular weight standards (BioRad); lane 3, 1 M KCl wash. (*LexA binding was demonstrated by competition assays in the presence of increasing concentrations of either specific or non-specific competitor DNA. Addition of unlabeled specific competitor (KC+5) challenged formation of the shifted complex at all concentrations tested (Figure 4B, lanes 2–5), with addition of >50-fold excess of unlabeled target abolishing shift of the DNA target. In contrast, incubation with non-specific competitor DNA, an internal lexA fragment similar in size to the specific competitor, did not significantly alter mobility shift at comparable concentrations (Figure 4B, lane 3, light plus 5 mM glucose; lane 4, cold stress for 3 h (20°C). (B) recA, lexA and maseP transcript accumulation in response to increasing levels of UV-irradiation. Lane 1, 1 h dark; lane 2, UV irradiated with 150; lane 3, 300; lane 4, 600 J/m² followed by a 1 h incubation in the dark.

**Figure 3.** Transcript analysis. Total RNA (30 μg) was isolated from Synechocystis cells grown as indicated. RNA was separated on a 1.2% formaldehyde agarose gel, transferred to Hybond N* and hybridized with the indicated 32P-labeled probe. (A) lexA, crhR and maseP transcript accumulation following incubation in the light. Lane 1, 3 h light; lane 2, 3 h dark; lane 3, light plus 5 mM glucose; lane 4, cold stress for 3 h (20°C). (B) recA, lexA and maseP transcript accumulation in response to increasing levels of UV-irradiation. Lane 1, 1 h dark; lane 2, UV irradiated with 150; lane 3, 300; lane 4, 600 J/m² followed by a 1 h incubation in the dark.

**Figure 2.** Isolation and characterization of a crhR regulatory protein by affinity chromatography and LC/MS/MS. (A) A 28 kDa polypeptide interacts with the crhR ORF. A single polypeptide was isolated by DNA affinity chromatography using KC+5 as the target. Non-specifically bound proteins were removed by increasing KCl washes. Silver staining of eluted proteins separated by a 10% SDS–PAGE reveals a single polypeptide in the 1 M KCl elution. LC/MS/MS identified this polypeptide as the Synechocystis crhR gene product. Residues essential for E.coli LexA association with the crhR gene (SpeI site is underlined) with the consensus cyanobacterial LexA binding sequence (32). Conserved residues with appropriate spacing. (C) Alignment of the putative LexA binding region of the crhR gene (Spel site is underlined) with the consensus cyanobacterial LexA binding sequence (32). Conserved residues are bolded. The LexA binding sequence within the crhR matches at 7 of 9 conserved residues with appropriate spacing.
lanes 7–10). Together, the results indicate that recombinant LexA interacts with the crhR gene in a sequence-specific manner.

LexA represses crhR gene expression in vitro

An in vitro transcription and translation system was used to confirm LexA regulation of crhR gene expression from its native promoter. As shown in Figure 5A, CrhR protein accumulation decreased in response to increasing rLexA concentration. Quantification of these results indicated that the rLexA inhibition of CrhR expression was linear with respect to rLexA concentration (Figure 5B). The specificity of repression was demonstrated by the lack of change in the levels of the plasmid-encoded β-lactamase protein, a non-LexA regulated protein. Similarly, crhR expression was unaffected by incubation in the presence of 1 pmol BSA (Figure 5C), a protein concentration at which rLexA significantly altered crhR expression. Furthermore, in vitro transcription and translation of a second cyanobacterial RNA helicase, crhC (29,30), was also unaffected by 1 pmol rLexA (Figure 5C). Together, these results indicate that LexA specifically regulates crhR transcription in a negative fashion.

DISCUSSION

We have begun investigation of the signal transduction pathway transducing the redox poise of the electron transport system to the transcription apparatus in cyanobacteria. In this paper we show that a LexA-related protein regulates expression of the redox-responsive RNA helicase, crhR. This identification implies a novel function for LexA in Synechocystis, a conclusion consistent with previous studies suggesting that LexA may regulate expression of carbon metabolism...
and bidirectional hydrogenase genes in *Synechocystis* (37–39).

The LexA binding site is located downstream of the *crhR* transcription start site, requiring sequences surrounding +125 of the *crhR* transcript. This localization suggests a regulatory mechanism for the *Synechocystis* LexA-related protein that differs from LexA regulation of DNA damage inducible genes in *E. coli* and other bacteria, where the LexA binding site (SOS box) surrounds the transcriptional start (32,33). Similar regulatory element arrangements, where transcription factors bind downstream of the transcription start site, have been observed in the cyanobacterium *Synechococcus* sp. strain PCC 7942 (40). In fact, the light responsive transcription of the *psbA* and *psbD* gene families in *Synechococcus* requires enhancer elements located downstream of the transcription start (40–42). The LexA DNA binding site within the *crhR* ORF is therefore consistent with regulatory protein-binding sites localized in other genes whose expression is known to be regulated by either light or redox signals. Unfortunately, the DNA binding proteins interacting with these other sites remain to be identified.

A combination of DNA affinity chromatography and mass spectrometry identified the protein interacting with the *crhR* gene as being related to LexA. Northern blot analysis showed that *Synechocystis* lexA transcripts accumulate when cells are grown under conditions correlating with the repression of *crhR* accumulation. Based on these results, it appears that LexA functions as a negative regulator of *crhR* expression. Negative regulation was confirmed using an *in vitro* transcription/translation assay, which demonstrated that LexA binding interferes with *crhR* expression possibly through interference with promoter recognition and/or transcription initiation. Based on these results, it appears that *Synechocystis* LexA functions as a repressor of *crhR* expression. LexA activity is well studied in *E. coli* and other prokaryotes where it regulates expression of ~20 unlinked genes associated with DNA damage repair, the SOS regulon, which include *recA* and *lexA* (27). Derepression occurs following DNA damage, and requires RecA-stimulated LexA autocleavage and subsequent derepression of *lexA*, *recA* and other regulon members (27). Induction following DNA damage ranges between regulon members; *recA* and *lexA* are induced 10 and 2- to 5-fold, respectively (43-45). Similarly, DNA damage caused by UV-irradiation or mitomycin C treatment strongly induces *recA* transcript and protein accumulation in another cyanobacterium, *Anabaena variabilis* (46,47). Levels of both the *recA* transcript and its protein remain elevated until the damaging agents are removed and/or the DNA repaired, as observed for *E. coli* *recA* transcripts (27). In contrast, expression of the *Synechocystis* *recA* and *lexA* genes was not induced by UV-irradiation. Rather, our results show that *recA* and *lexA* levels decrease following UV-treatment, in agreement with other studies (39,48). These results indicate that the DNA damage induction of *recA* is variable among not only cyanobacteria but also prokaryotes in general. Our observation that *lexA* is not induced following UV-irradiation further suggests that *Synechocystis* LexA is not required for survival following DNA damage, and therefore potentially regulates expression of genes not associated with DNA repair. We therefore refer to this protein as being LexA-related.

The discrepancies in *lexA* regulation may also imply differences at the protein level, where LexA self-cleavage may not be required for derepression of gene expression. This appears to be the case, as *Synechocystis* LexA possesses modifications in two sites important for LexA function in *E. coli*; an altered cleavage site, and the absence of the nucleophile serine of the Ser-Lys dyad. In *E. coli*, LexA self-cleavage and derepression of the SOS regulon requires a catalytic serine/lysine dyad and an Ala-Gly cleavage bond (31). In the absence of these residues, as indicated by mutational studies, LexA self-cleavage in *E. coli* is defective (31). These modifications to the *Synechocystis* protein have been previously noted as a potential explanation for the absence of a ‘cyanobacterial’ SOS box within the upstream regions of *Synechocystis* DNA repair genes (36), and further imply an unique cellular function for the *Synechocystis* LexA protein.

Novel roles for LexA have been implied in other bacteria, including *Mycobacterium tuberculosis* (49,50) and *Deinococcus radiodurans* (51), although the alternative function has not been identified. In *D. radiodurans*, RecA protein levels remain unchanged regardless of the *lexA* status (52), which is unexpected if LexA is required to regulate *recA* expression and is similar to the results reported here. DNA damage induction of repair genes in *M. tuberculosis* also occurs predominately via a LexA- and RecA-independent mechanism as shown by mitomycin C induction of DNA repair gene expression in *recA* mutants (49,50). Evidence for separation of *recA* expression from *lexA* regulation may also exist in higher plant chloroplasts, which possess a DNA damage-induced *recA* homologue (53), while *lexA* has not been reported to be encoded by plant genomes. This evidence suggests that conservation of the LexA/RecA regulation of the SOS response may be less widespread than previously anticipated, and furthermore, homologues of these proteins may fulfill different roles in their respective hosts.

*crhR* encodes an RNA helicase proposed to regulate RNA metabolism through its modification of RNA secondary structure (1,26). The redox-responsive regulation of *crhR* expression suggests that its cellular capacity to catalyze RNA secondary structure modifications is regulated by the redox status of the electron transport chain. The observed induction of *crhR* resulting from respiratory electron flow suggests that *crhR* may regulate the function of RNAs associated with photosynthesis (light harvesting and/or carbon metabolism) (1) or the cellular response to the predominating light/redox environment. The implication of *crhR* in carbon metabolism is consistent with both a proposed role for LexA in the regulation of carbon uptake and utilization genes (39) and observations demonstrating reduction in *lexA* transcript accumulation following a downshift in inorganic carbon availability (54). Further to our hypothesis suggesting LexA may ensure cells express the necessary gene products to respond to a dynamic light environment, one of the proposed functions for the bidirectional hydrogenase, a recently identified LexA-activated gene (37,38), is as an electron valve during photosynthesis (55). LexA regulation of *crhR* and the *boxEFUYH* bidirectional hydrogenase may ensure continued maximal photosynthetic capabilities in response to changing cellular redox conditions.

Identification of a LexA-related protein as the regulator of *crhR* transcription provides unique insights into the
mechanism by which redox-regulated gene expression is controlled in photosynthetic cyanobacteria. The observations suggest a unique regulatory role for Synechocystis LexA in regulating gene expression in response to environmental cues other than DNA damage. These insights also imply the ubiquitous nature of the Lex/RecA DNA repair dogma is not conserved in Synechocystis, raising questions regarding the mechanisms by which DNA repair gene expression is regulated in this organism.

ACKNOWLEDGEMENTS

The authors would like to thank Dr Danuta Chamot and Troy Locke for their invaluable help through the course of this study. This study was supported by grants from the Natural Sciences and Engineering Research Council of Canada (NSERC grant 171 319 to G.W.O.) and NSERC PG5 A and Alberta Ingenuity Fund studentships to L.P.F. Funding to pay Open Access publication charges for this article was contributed by the Alberta Ingenuity Fund studentships to L.P.F. Funding to pay the Open Access publication charges for this article was contributed by the Natural Sciences and Engineering Research Council of Canada.

Conflict of interest statement. None declared.

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