Regulation of carotenoid and bacteriochlorophyll biosynthesis genes and identification of an evolutionarily conserved gene required for bacteriochlorophyll accumulation

GREGORY A. ARMSTRONG,* DAVID N. COOK, DZWOKAI MA, MARIE ALBERTI, DONALD H. BURKE and JOHN E. HEARST

Department of Chemistry and Laboratory of Chemical Biodynamics, University of California, Berkeley, CA 94720, USA

(Received 30 October 1992; revised 13 December 1992; accepted 1 February 1993)

The temporal expression of ten clustered genes required for carotenoid (crt) and bacteriochlorophyll (bch) biosynthesis was examined during the transition from aerobic respiration to anaerobiosis requisite for the development of the photosynthetic membrane in the bacterium Rhodobacter capsulatus. Accumulation of.crtA, crtC, crtD, crtE, crtF, crtK, bchC and bchD mRNAs increased transiently and coordinately, up to 12-fold following removal of oxygen from the growth medium, paralleling increases in mRNAs encoding pigment-binding polypeptides of the photosynthetic apparatus. The.crtB and.crtI genes, in contrast, were expressed similarly in the presence or absence of oxygen. The regulation patterns of promoters for the.crtA and.crtI genes and the bchCXYZ operon were characterized using lac2 transcriptional fusion and qualitatively reflected the corresponding mRNA accumulation patterns. We also report that the bchl gene product, encoded by a DNA sequence previously considered to be a portion of.crtA, shares 49% sequence identity with the nuclear-encoded Arabidopsis thaliana Cs chloroplast protein required for normal pigmentation in plants.

Introduction

Carotenoids play a variety of biological roles in both carotenogenic and noncarotenogenic organisms. These pigments protect against the destructive effects of photosensitizing molecules, notably porphyrin derivatives, and against singlet oxygen (Krinsky, 1971). In photosynthetic organisms, all of which synthesize carotenoids, these pigments also supplement the light-harvesting capacity of chlorophyll (Chl) and bacteriochlorophyll (Bchl) (Cogdell & Frank, 1987). Recent findings implicate the carotenoid zeaxanthin in photosynthetic energy dissipation (Demmig-Adams, 1990). The general biosynthetic pathways of carotenoids and Chl/Bchl are described in detail elsewhere (Goodwin, 1980; Castelfranco & Beale, 1983).

The carotenoid and Bchl pigments are bound non-covalently to the polypeptides of the photosynthetic reaction centre (RC), and light-harvesting I and II (LH I and LH II, or B875 and B800–850, respectively) antenna complexes of purple non-sulphur photosynthetic bacteria, such as Rhodobacter species (Kiley & Kaplan, 1988). The RC polypeptides are encoded by the pufL, pufM and puhA genes, the LH I polypeptides by the pufA and pufB genes, and the peripheral antenna LH II polypeptides by the pucA and pucB genes in R. capsulatus (Scolnik & Marrs, 1987). The puf and puh operons and all identified genes required for carotenoid (crt) and Bchl (bch) biosynthesis comprise a 46 kb photosynthesis gene cluster in this organism (Marrs, 1981; Zsebo & Hearst, 1984; Burke et al., 1991a) and in the closely related R. sphaeroides (Coomber et al., 1990). The assignment of.crt genes to specific biosynthetic reactions is summarized in Fig. 1, and a biosynthetic pathway linking bch genes with particular reactions in Bchl biosynthesis has been described (Biel & Marrs, 1983) and recently amended (Yang & Bauer, 1990; Burke et al., 1991b).

Diverse factors, including oxygen, light and developmental state of the organism, govern the synthesis and accumulation of carotenoid pigments in plants, algae, fungi and bacteria (Bramley & Mackenzie, 1988), although the regulatory mechanisms remain largely obscure. The regulation of pigment synthesis in purple
data from an (Armstrong 1990). Conversely, the intracytoplasmic membrane harbouring the photosynthetic pigment–protein complexes in facultative photosynthetic bacteria such as Rhodobacter species (Cohen-Bazire et al., 1957; Kiley & Kaplan, 1988). Either the elimination of oxygen from the growth medium accompanied by illumination of a previously dark-grown culture, or a downshift in light intensity during constant anaerobiosis, stimulates carotenoid accumulation in R. capsulatus (Golecki et al., 1980; Kaufmann et al., 1982) and R. sphaeroides (Cohen-Bazire et al., 1957). Lowering the oxygen tension in dark-grown aerobic cultures of R. capsulatus produces a similar result (Schumacher & Drews, 1978; Biel & Marrs, 1985). Several studies report relatively little regulation of mRNA accumulation for the R. capsulatus crt genes during the transition from dark aerobic respiration to low oxygen conditions (Clark et al., 1984; Klug et al., 1985), or of crt promoter activities (Young et al., 1989) and mRNA levels (Zhu & Hearst, 1986) in comparisons between steady-state dark aerobic and anaerobic photosynthetic cultures. Other experiments indicate differences in mRNA levels for some crt genes in comparisons of illuminated steady-state anaerobic and aerobic cultures (Giuliano et al., 1988). These results contrast with the strong regulation of mRNA levels and promoter activities of genes (puf, puh, puc) encoding structural pigment-binding polypeptides of the photosynthetic membrane (Clark et al., 1984; Klug et al., 1985; Zhu & Hearst, 1986; Cook et al., 1989; Young et al., 1989).

The recent molecular characterization of carotenoid biosynthesis genes from R. capsulatus (Bartley & Scolnik, 1989; Armstrong et al., 1989, 1990b, c) provides the basis for more detailed studies of the regulation of individual crt genes by environmental factors. We expect that this approach will lead to a more complete understanding of the mechanisms regulating the entire biochemical pathway.

We have determined the kinetics of mRNA accumulation for eight R. capsulatus crt and two flanking bch genes during the well-defined transition from aerobic respiration to anaerobic photosynthesis using, for the first time, gene-specific probes. These genes form a subcluster within the photosynthesis gene cluster. We have also examined oxygen regulation of promoters for photosynthetic bacteria has been a topic of research for almost 50 years (van Niel, 1944). Both oxygen and light intensity influence the synthesis of carotenoids, Bchl and the intracytoplasmic membrane harbouring the photosynthetic pigment–protein complexes in facultative photosynthetic bacteria such as Rhodobacter species (Cohen-Bazire et al., 1957; Kiley & Kaplan, 1988). Either the elimination of oxygen from the growth medium accompanied by illumination of a previously dark-grown culture, or a downshift in light intensity during constant anaerobiosis, stimulates carotenoid accumulation in R. capsulatus (Golecki et al., 1980; Kaufmann et al., 1982) and R. sphaeroides (Cohen-Bazire et al., 1957). Lowering the oxygen tension in dark-grown aerobic cultures of R. capsulatus produces a similar result (Schumacher & Drews, 1978; Biel & Marrs, 1985). Several studies report relatively little regulation of mRNA accumulation for the R. capsulatus crt genes during the transition from dark aerobic respiration to low oxygen conditions (Clark et al., 1984; Klug et al., 1985), or of crt promoter activities (Young et al., 1989) and mRNA levels (Zhu & Hearst, 1986) in comparisons between steady-state dark aerobic and anaerobic photosynthetic cultures. Other experiments indicate differences in mRNA levels for some crt genes in comparisons of illuminated steady-state anaerobic and aerobic cultures (Giuliano et al., 1988). These results contrast with the strong regulation of mRNA levels and promoter activities of genes (puf, puh, puc) encoding structural pigment-binding polypeptides of the photosynthetic membrane (Clark et al., 1984; Klug et al., 1985; Zhu & Hearst, 1986; Cook et al., 1989; Young et al., 1989).

The recent molecular characterization of carotenoid biosynthesis genes from R. capsulatus (Bartley & Scolnik, 1989; Armstrong et al., 1989, 1990b, c) provides the basis for more detailed studies of the regulation of individual crt genes by environmental factors. We expect that this approach will lead to a more complete understanding of the mechanisms regulating the entire biochemical pathway.

We have determined the kinetics of mRNA accumulation for eight R. capsulatus crt and two flanking bch genes during the well-defined transition from aerobic respiration to anaerobic photosynthesis using, for the first time, gene-specific probes. These genes form a subcluster within the photosynthesis gene cluster. We have also examined oxygen regulation of promoters for prokaryotic homologues of CrtE and CrtB function in GGPP synthesis and catalyse the conversion of GGPP to phytoene, respectively (Chamovitz et al., 1992; Sandmann & Misawa, 1992; Math et al., 1992).
the divergently transcribed \textit{crtA} and \textit{crtI} genes, and for the better characterized \textit{bchCXYZ} operon (Wellington & Beatty, 1989, 1991; Burke \textit{et al.}, 1991a) using plasmidborne \textit{lacZ} (\(\beta\)-galactosidase) transcriptional fusions.

\section*{Methods}

\textbf{Plasmid constructions.} \textit{pZM400}, a promoter probe vector suitable for stably maintaining \textit{lacZ} transcriptional fusions in \textit{R. capsulatus} (Ma \textit{et al.}, 1993), was constructed by modification of \textit{pRK290}, a broad host range low copy number plasmid containing an RK2 replicon (Ditta \textit{et al.}, 1980). Briefly, the tetracycline resistance gene of \textit{pRK290} was inactivated by introduction of a kanamycin resistance gene from Tn903 expression, duplicate dark-grown cultures were switched from the aerobic to the anaerobic gas mixture described above, with one culture simultaneously exposed to light. Dark-grown aerobic cultures were sparged with a mixture of \(\text{N}_2:\text{CO}_2\) (80:2, by vol.) supplemented with 200 \(\mu\text{M}\)-chloramphenicol ml\(^{-1}\), 25 mM-\(\text{MgCl}_2\), and an equal volume of ice cold buffer A (80 mM-Tris/HCl, pH 7.5, 10 mM-\(\text{MgCl}_2\)) supplemented with 200 \(\mu\text{g}\) chloramphenicol ml\(^{-1}\), 25 mM-sodium azide and 10 mM-\(\beta\)-mercaptoethanol (Zhu & Kaplan, 1985), cooled for 15 s in a dry ice/ethanol bath and harvested by centrifugation. The pellets were resuspended in lysis buffer, immediately frozen on dry ice and stored at \(-70^\circ\text{C}\) until isolation of the RNA as described (Zhu & Kaplan, 1985).

\textit{pZM} plasmids were introduced into \textit{R. capsulatus} strain SB1003 by triparental matings with \textit{E. coli} plasmid donor and helper strains as described (Zeo \& Hearst, 1984). For \textit{LacZ} activity measurements, exponentially-growing \textit{R. capsulatus} cells were shifted from aerobic to photosynthetic growth as described above. Samples (5 ml) were collected to monitor \textit{LacZ} activities by the method of Miller (1972), with 0.2 ml of cells assayed in 0.8 ml Z-buffer. All \textit{R. capsulatus} cultures were grown at 32 \(^\circ\text{C}\).

\textbf{Preparation of RNA dot-blots, M13 probes and nucleic acid hybridizations.} RNA dot-blots were prepared as described previously, using 5 \(\mu\text{g}\) total RNA per dot (Cook \textit{et al.}, 1989). RNA time courses were probed for specific mRNAs with single-stranded M13 subclones, labelled by primer extension across the insert region with the Klenow fragment of DNA polymerase I as previously described (Armstrong \textit{et al.}, 1990a), except that 5'-\(\alpha\)-\(32\text{P}\)dATP was replaced by 50 pCi 5'-\(\alpha\)-\(32\text{P}\)dCTP (3000 Ci mmol\(^{-1}\)-Amersham). Gene-specific M13 probes for the \textit{crt} genes, \textit{bchC} and \textit{bchD} (Fig. 3) were generated during the sequencing of these regions (Armstrong \textit{et al.}, 1989). The use of the gene-specific M13 probes for the \textit{crt} operon (\textit{puf} operon (\textit{pufL}) and the \textit{puf} operon (\textit{pufA})) (Zhu & Hearst, 1986) to obtain the data plotted in Fig. 2(a) has been described (Cook \textit{et al.}, 1989), as has the gene-specific 15-mer oligonucleotide probe for the \textit{puf} operon (\textit{pufB}) (Zhu & Hearst, 1986). The \textit{puc} oligonucleotide (500 ng) was end-labelled with 50 \(\mu\text{Ci}\) 5'-\(\alpha\)-\(32\text{P}\)dATP (5000 Ci mmol\(^{-1}\)-Amersham) and T4 polynucleotide kinase. To ensure that equivalent amounts of RNA from each sample were applied to the membrane, we prepared dot--blots using about 3 ng total RNA per time point and hybridized these with either radiolabelled \textit{pRC} containing cloned \textit{R. capsulatus} \textit{rRNA} genes (Yu \textit{et al.}, 1982), or with radiolabelled total \textit{R. capsulatus} chromosomal DNA isolated as described previously (Cook \textit{et al.}, 1989). \textit{pRC} (1 \(\mu\text{g}\)) or total chromosomal DNA (1 \(\mu\text{g}\)) was labelled with 50 \(\mu\text{Ci}\) 5'-\(\alpha\)-\(32\text{P}\)dCTP (3000 Ci mmol\(^{-1}\)-Amersham) by nick-translation using a Bethesda Research Laboratories kit. RNA dot-- blot hybridizations with Gene Screen nylon membranes (New England Nuclear), autoradiography, and quantification of the excised dots by scintillation counting (Fig. 2) were performed as described previously (Cook \textit{et al.}, 1989), except that the RNAs to be hybridized with the \textit{puc} oligonucleotide probe were applied to a nitrocellulose membrane (Scheleicher & Schuell). An autoradiogram of the \textit{puc} hybridization was quantitated as above (Fig. 2b). Autoradiograms of membranes probed for \textit{crtC}, \textit{crtD} and \textit{bchD} mRNAs were quantified by densitometry using a Hoefer Scientific Instruments scanning densitometer, Model GS 300 (data not shown).

\textbf{Database searches and sequence alignments.} Sequence similarity between the \textit{R. capsulatus} \textit{Bchl} and \textit{A. thaliana} Cs proteins was detected by searching the NBRF database (release 28.0, 3/91) using the \textsc{fasta} program from the GCG software package, version 5.2 (Devereux \textit{et al.}, 1984). The \textsc{nblast} program from this package was used for the initial sequence alignment, which was subsequently optimized by hand.

\section*{Results and Discussion}

\textbf{Accumulation of many \textit{crt} and \textit{bch} mRNAs increases during the transition to photosynthesis}

During the transient cessation of cellular division that follows a rigorous transition from dark aerobic respiration to anaerobiosis in the light, \textit{Rhodobacter} must adapt to photosynthetic growth through the synthesis of carotenoids, Bchl, pigment-binding polypeptides and an intracytoplasmic membrane system harbouring these components (Kiley & Kaplan, 1988). The rates of carotenoid and Bchl synthesis increase rapidly during this lag phase (Cohen-Bazire \textit{et al.}, 1957; Schumacher & Drews, 1978).

We have previously demonstrated that \textit{R. capsulatus} cell division ceases and rRNA levels remain constant during the first hour of such a transition (Cook \textit{et al.},
During the adaptive period (Fig. 2). Probes derived from cultures were shifted from dark aerobic respiratory growth to anaerobic rDNA sequence or total genomic DNA were used to work. A similar hybridization pattern was also obtained using probe mRNA levels for \( rRNA \) and \( bch \) genes plotted relative to an arbitrary value of each mRNA, as determined based on the values at -20, 0, and 20 mins, are as follows: \( \text{crt}A \) (solid line), 0.068; \( \text{crt}B \) (+), 0.350; \( \text{crt}E \) ( ), 0.093; \( \text{crt}F \) (x), 0.320; \( \text{crt}I \) ( ), 0.171; \( \text{crt}K \) ( ), 0.379; \( \text{bch}C \) ( ), 0.151; rRNA ( ), 0.061. (b) Comparison of \( \text{crt}A \) and \( \text{bch}C \) mRNA accumulation with the accumulation of \( \text{puf} \), \( \text{puc} \), and \( \text{puc} \) mRNAs. RNA dot-blot probes for \( \text{puf} \) and \( \text{puc} \) mRNAs (Cook et al., 1989) and \( \text{puc} \) mRNA, with specific DNA probes for each of these sequences (Zhu et al., 1986; 1989), were used for this quantitative presentation. Symbols and standard deviations in the amounts of specific mRNAs not given in (a), as determined based on the values at -20, 0, 10 and 20 mins, are as follows: \( \text{puf}L \) ( ), 0.086; \( \text{puf}A \) ( ), 0.076; \( \text{puf}B \) ( ), 0.198.

In this experiment we also determined mRNA accumulation patterns for the \( \text{crt} \) and two \( \text{bch} \) genes during the adaptive period (Fig. 2). Probes derived from an rDNA sequence or total genomic DNA were used to demonstrate that equivalent amounts of RNA for each time point had been applied to the membrane (Fig. 2 and data not shown). mRNA levels for all \( \text{crt} \) and \( \text{bch} \) genes remained constant prior to the simultaneous removal of oxygen from the growth medium and illumination of the cultures.

The \( \text{crt} \) and \( \text{bch} \) mRNAs fall into two groups depending on their response to this change in environmental conditions. The accumulation of mRNAs for \( \text{crt}A \), \( \text{crt}B \), \( \text{crt}C \), \( \text{crt}D \), \( \text{crt}E \), \( \text{crt}F \), \( \text{crt}K \), \( \text{bch}C \) and \( \text{bch}D \) (not shown) increased 2- to 12-fold, while mRNA levels for \( \text{crt}B \) and \( \text{crt}I \) remained constant (Fig. 2a). In the same experiment, accumulation of \( \text{puf} \) and \( \text{puc} \) (LH I and RC) mRNAs increased comparably (6- to 8-fold; Cook et al., 1989), while \( \text{puc} \) (LH II) mRNA increased 25-fold (Fig. 2b). The results of the \( \text{crt} \) and \( \text{bch} \) mRNA accumulation studies and the locations of the DNA probes used are summarized in Fig. 3.

Our results thus indicate that regulated \( \text{crt} \) and \( \text{bch} \) mRNA accumulation may play as significant a role in the expression of pigment biosynthesis enzymes as in the expression of pigment-binding polypeptides during the rigorous transition from dark aerobic respiration to anaerobic photosynthesis. Three important features combined in this study distinguish it from previous efforts, discussed below, in this area: (i) the use of gene-specific probes for each mRNA studied, including mRNAs representing both pigment biosynthetic enzymes and pigment-binding polypeptides, (ii) the measurement of both mRNA accumulation and promoter activities using identical and well-defined growth conditions to obtain two independent measures of gene regulation, (iii) the detailed sampling of time points during the early stages of the adaptation to photosynthetic growth.

Several earlier studies, including work from this laboratory, had indicated relatively small changes in \( \text{R. capsulatus} \) \( \text{crt} \) mRNA levels (Clark et al., 1984; Klug et al., 1985; Zhu & Hearst, 1986) or promoter activities (Young et al., 1989) in response to low oxygen tensions or anaerobic photosynthetic conditions, in contrast to the \( \text{puf} \) operon. Discrepancies between our results and earlier comparative studies of mRNA accumulation probably result in large part from the previous unavailability of gene-specific probes for \( \text{crt} \) mRNAs and the absence, with one exception (Clark et al., 1984), of detailed kinetic data. Differences in the experimental techniques, bacterial strains, or the growth conditions used could also be contributing factors. \( \text{puf} \) and \( \text{puc} \) mRNAs, for example, accumulate to significantly higher levels in dark-grown \( \text{R. capsulatus} \) cultures shifted from 20% to 3% oxygen tension (Leach et al., 1991) than in cultures shifted to completely anaerobic conditions (Fig. 2b; Cook et al., 1989).

Some evidence for the regulation of certain \( \text{crt} \) mRNAs was obtained by comparing anaerobic versus aerobic...
cultures under constant illumination (Giuliano et al., 1988), a condition which allows Rhodobacter species to use both photosynthetic and respiratory growth modes simultaneously (Cohen-Bazire et al., 1957; Keister, 1978). Our quantitative data on the temporal regulation of mRNA accumulation (Fig. 2a) do, despite the difference in growth conditions used, agree with the qualitative steady-state results previously reported (Giuliano et al., 1988). The measured increases in crtE and crtF mRNAs during the transition to photosynthesis (Fig. 2a) also agree with the oxygen regulation attributed to an inducible promoter for the crtEF operon using plasmid-borne LacZ translational fusions (Young et al., 1989).

The constitutive patterns of ctfI and ctfB mRNA expression detected using three different DNA probes (Fig. 3) are consistent with the proposed cotranscription of these genes (Giuliano et al., 1988; Armstrong et al., 1989). In contrast, ctfK mRNA accumulation increased 8-fold during the shift from aerobic respiration to photosynthetic growth (Fig. 2a), suggesting that ctfK may form a distinct operon. An alternative explanation would be the differential regulation of mRNA stability within the same transcript, as documented for the R. capsulatus puf operon (Belasco et al., 1985; Chen et al., 1988).

Although changes in light intensity during photosynthetic growth can influence carotenoid content in Rhodobacter species (Cohen-Bazire et al., 1957; Golecki et al., 1980; Kaufmann et al., 1982), pigment accumulation can also be triggered solely by a downshift in oxygen tension in dark-grown cultures (Schumacher & Drews, 1978; Biel & Marrs, 1985). To address directly the possible regulation of R. capsulatus ctf genes by light we examined the expression of ctfA, a gene strongly regulated by oxygen tension, during the transition from
dark aerobic respiration to either dark anaerobic or anaerobic photosynthetic conditions. Cells shifted in the presence of light displayed a transient 10-fold increase in crtA mRNA, versus a 5-fold increase in the absence of light (data not shown). The patterns of mRNA accumulation versus time were equivalent in both of these experiments to the results presented in Fig. 2. Thus, the removal of oxygen from the growth medium suffices qualitatively for the induced accumulation of crtA mRNA, although the presence of light may play a modulating role.

**mRNAs for different classes of genes required for photosynthesis accumulate coordinately**

mRNAs for all regulated crt genes, and for bchC and bchD, accumulated coordinately during the first 45 min of the adaptation to photosynthetic growth (Fig. 2a). puf, puh, and puc mRNAs accumulated with time courses roughly similar to those of the regulated crt, and bch mRNAs, although their accumulation continued up to 60 min into the transition, in some cases (Fig. 2b). This temporal pattern of mRNA accumulation may reflect a coordinated programme of gene expression during the development of a functional photosynthetic membrane. The stable assembly of the pigment–protein complexes relies on the presence of the pigments in R. capsulatus (Zsebo & Hearst, 1984; Klug et al., 1985), suggesting the biological significance of such an expression pattern.

One mechanism for a rapid and transient increase in carotenoid and Bchl production to meet the demands of the cell would be the accumulation of those mRNAs encoding enzymes governing rate-limiting reactions in the respective biosynthetic pathways (Fig. 1; see Biel & Marrs (1983) for an outline of the Bchl biosynthetic pathway). The intracellular levels of CrtI are apparently not a limiting factor in carotenoid biosynthesis (Bartley & Scolnik, 1989). Consistent with this, we did not observe regulation of crtI mRNA accumulation or transcriptional activity. Although the different R. capsulatus carotenoid biosynthesis enzymes have not yet been biochemically characterized and their relative enzymic activities have not been measured, the constitutive expression of crtB and crtI mRNAs indicates that biosynthetic capacity for the conversion of GGPP to neurosporene (Fig. 1) is not regulated at the level of mRNA. The regulated crt genes encode products required both early in carotenoid biosynthesis (before GGPP) and late in the pathway (after neurosporene). The increase in crtE expression could, for example, reflect an increased requirement for GGPP in the synthesis of both carotenoids and of the phytol moiety of Bchl in response to photosynthetic conditions. Expression of a homologue of crtE from another bacterium significantly increases GGPP accumulation in E. coli (Sandmann & Misawa, 1992).

**Oxygen regulation of crtI, crtA and bchCXYZ promoter activities determined using lacZ transcriptional fusions**

The oxygen regulation of crtI, crtA, and bchCXYZ expression was further studied by fusion of promoter-containing restriction fragments (Fig. 3) 5′ to a promoterless lacZ gene resident in the low copy number plasmid pZM400. The crtI, crtA and bchCXYZ promoter constructs, pZM422, pZM432 and pZM410, respectively, were introduced into R. capsulatus strain SB1003. Cells were assayed for LacZ activity at different times during the adaptation to photosynthetic growth under the same conditions used to measure mRNA accumulation.

When R. capsulatus cultures were shifted from dark aerobic growth to anaerobic photosynthetic conditions, LacZ activity driven by the crtA and bchCXYZ promoter regions increased 2- and 3.5-fold, respectively, reaching a plateau approximately 60 min after the maximal mRNA accumulation (Fig. 4). This lag may reflect the translation of the lacZ mRNA and the gradual accumulation of active LacZ enzyme. crtI promoter-driven LacZ activity remained roughly constant during the same time course, in agreement with the RNA data. The background level of LacZ activity from the promoter-less control, pZM400, was an order of magnitude lower than that observed in the promoter-containing constructs under photosynthetic conditions. The difference between the increases in crtA promoter activity (two-fold; Fig. 4) and
mRNA accumulation (12-fold; Fig. 2) in response to anaerobiosis could reflect either post-transcriptional regulation, or differences in expression between the chromosomal and plasmid-borne copies of the \textit{crtA} promoter due to DNA structure or plasmid copy number.

In agreement with our results, chromosomal (Biel & Marrs, 1983) and plasmid-borne (Wellington & Beatty, 1989, 1991; Young \textit{et al}., 1989) \textit{lacZ} transcriptional and translational fusions in \textit{R. capsulatus} have indicated that the steady-state activity of the \textit{bchCXYZ} promoter (Burke \textit{et al}., 1991\textit{b}) increases between 3- and 8-fold when comparing growth under high and low oxygen tensions or photosynthetic conditions with respiration. Although transcripts initiated upstream of the \textit{bchCXYZ} promoter (Fig. 3) can read through into the \textit{bchC} gene (Wellington & Beatty, 1991), the magnitude of \textit{bchC} mRNA accumulation (3-fold) corresponds closely with the increase in transcription initiation from the \textit{bchCXYZ} promoter in our experiments (compare Figs 2 and 4). A thorough characterization of the \textit{bchCXYZ} promoter will be presented elsewhere (Ma \textit{et al}., 1993). The data presented here on the temporal expression of \textit{bchCXYZ} promoter activity and \textit{bchC} and \textit{bchD} mRNAs, combined with measurements made by other researchers (Biel \& Marrs, 1983; Hunter \& Coomber, 1988; Young \textit{et al}., 1989; Yang \& Bauer, 1990; Wellington \& Beatty, 1991), demonstrate moderate regulation of many \textit{bch} genes by oxygen tension.

\textbf{Identification of the \textit{bchI} gene and conservation of the predicted gene product in more evolved photosynthetic organisms}

Previous experiments with \textit{R. capsulatus} had established that the Tn5.7 insertion mutation defining the \textit{bchI} locus as an entity distinct from \textit{bchD} and \textit{crtA} by complementation (Zsebo \& Hearst, 1984) mapped physically within the 3' portion of the ORF assigned to the \textit{crtA} gene (Armstrong \textit{et al}., 1990\textit{c}). This Tn5.7 mutation abolished the accumulation of Bchl or its visibly absorbing precursors (Zsebo \& Hearst, 1984). In the course of the current study, we determined that the C-terminal half of the predicted \textit{crtA} gene product displays a high degree of sequence similarity with the \textit{Arabidopsis thaliana} Cs protein (Koncz \textit{et al}., 1990). \textit{cs} (ch-42) is a light-regulated nuclear gene which encodes a protein destined for the chloroplast and required for normal pigmentation in plants. These data led us to consider the possibility that the published nucleotide sequence of \textit{crtA} might contain an error (Armstrong \textit{et al}., 1989).

Redetermination of the nucleotide sequence of the entire \textit{crtA} coding region revealed one change, the absence of a single nucleotide at position 1733 (Fig. 5), with respect to the original sequence. As a consequence, the long ORF of 591 amino acids thought to encode CrtA is split into two segments. 21 amino acids of the 5' ORF following the frameshift error (Thr-221 to Ala-241) differ from those originally reported for CrtA before an in-frame stop codon is reached. Overlapping the stop codon, an AUG start codon preceded by a potential ribosome binding site (Fig. 5) could be used to initiate translation of a 3' ORF of 350 amino acids, corresponding to residues 242 to 591 originally deduced for CrtA. In accordance with the above considerations, we propose that the 5' and 3' ORFs encode CrtA and BchI, respectively. Based on the gene order in this region (Zsebo \& Hearst, 1984; Burke \textit{et al}., 1991\textit{a}), previous data from \textit{in vivo} complementation studies (Taylor \textit{et al}., 1983; Zsebo \& Hearst, 1984; Giuliano \textit{et al}., 1988), and the rough mapping of \textit{bchD} transposon-induced mutations (Zsebo, 1984), we propose that the ORF downstream from \textit{bchI} corresponds to \textit{bchD}. Absolute confirmation of these proposals will, however, require
characterization of the gene products derived from this region of the chromosome (Fig. 3).

Mutations in the \textit{bchD} gene also disrupt the accumulation of Bchl or its immediate precursors (Zseo & Hearst, 1984; Giuliano et al., 1988). BchD is thought to be required either for insertion of magnesium or for the coupled methylation reaction required for the conversion of protoporphyrin IX into magnesium protoporphyrin IX monomethyl ester in \textit{Euglena gracilis}, an alga, has also recently been found to encode a BchI/Cs-like product (Orsat et al., 1992). This observation indicates the export of the \textit{cs} (\textit{ch-42}) gene from the chloroplast to the nucleus in the course of evolution from algae to higher plants.

The \textit{R. capsulatus}, \textit{E. gracilis}, and \textit{A. thaliana} proteins all contain putative ATP-binding sites (Fig. 6). We note that chelation of magnesium into protoporphyrin IX is an ATP-requiring process in higher plants and that this reaction has been proposed to require at least two components, a soluble stromal protein and a membrane-associated protein (Castelfranco & Beale, 1983; Walker & Weinstein, 1991). It will be of interest to determine whether BchI/Cs-like gene products have been conserved in other photosynthetic organisms, and whether analogous homologues exist between BchI and BchD from \textit{Rhodobacter}.

### Fig. 6. The \textit{R. capsulatus} BchI and \textit{A. thaliana} Cs proteins are highly conserved and contain putative ATP-binding sites. Numbers at the left indicate the amino acid positions. Identities between the two sequences are shown by asterisks. Dashes indicate gaps inserted to maximize the sequence alignment. A putative ATP-binding site is shown in bold, compared to a consensus (Walker et al., 1982; Husain et al., 1986) in which h is a small hydrophobic residue and X is any residue. NBRF database accession numbers for BchI and Cs are S04401 (the former CrtA sequence, residues 242–591) and S08654, respectively.

<table>
<thead>
<tr>
<th>BchI</th>
<th>1 MITAVARLQP9ASGAKTRP6VFPSAVGQEDMKLLALLTTAVDGP16GLVLFVCDRGDSGKTAVRALAALLP5E1EEVEQCPVSSPNEPMPF</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cs</td>
<td>70 SISQVGRFDSKSSA-PRVPFFAIAVQGQMKLCNLVDP15KG5VHG3N16YMG12TSXVSHOILVPEKNAVGDPY55P3DQEFM</td>
</tr>
<tr>
<td>BchI</td>
<td>91 WATVLSTW1RKP7V-VDLPLGVEDRVGADILERAKISNKEAFGELLLARANGSYL1DECNLEDHDBLVLDDLVDVAGSN</td>
</tr>
<tr>
<td>Cs</td>
<td>158 GVEVRESEVEQGEQ6VATXKNMPLDGTEDRVCKTIDEIKALTEVGAFEPGELLAKANGRLYLVDEKNLDDLVLDLSASAGWN</td>
</tr>
<tr>
<td>BchI</td>
<td>174 GVEVRESEVEQGEQ6VATXKNMPLDGTEDRVCKTIDEIKALTEVGAFEPGELLAKANGRLYLVDEKNLDDLVLDLSASAGWN</td>
</tr>
<tr>
<td>Cs</td>
<td>248 TVERGJSHFAPFILIGSNPEEGELRPQLLDRGMAQVGTADLRKSVEERARFSDNPKNRFD9TFKTYEQDLOI1SARANL</td>
</tr>
<tr>
<td>BchI</td>
<td>264 PKVEAPNTALYDCAALCIALGQAGLGKELTTLKSSA1ALLEGATVQGRDHKLKVATMALSRLRBDLDEAGSTHVARVARTVEETLP</td>
</tr>
<tr>
<td>Cs</td>
<td>338 SSVQIDRE6LVK1SRVCSELNVDDLGRDG1VTROAKALAKGLKDRVTDFDVTVIPNCLRRHLKDPLES1DSVGLVSEKFAEIPS</td>
</tr>
</tbody>
</table>

**Consensus ATP-binding site:**  
\[ hhhhhGXGYGKT \]

**Fig. 6.** The \textit{R. capsulatus} BchI and \textit{A. thaliana} Cs proteins are highly conserved and contain putative ATP-binding sites. Numbers at the left indicate the amino acid positions. Identities between the two sequences are shown by asterisks. Dashes indicate gaps inserted to maximize the sequence alignment. A putative ATP-binding site is shown in bold, compared to a consensus (Walker et al., 1982; Husain et al., 1986) in which h is a small hydrophobic residue and X is any residue. NBRF database accession numbers for BchI and Cs are S04401 (the former CrtA sequence, residues 242–591) and S08654, respectively.
evolved photosynthetic organisms, including *E. gracilis* and *A. thaliana*.

We thank Drs G. Drews (Universität Freiburg, FRG) for supplying the plasmid pRC1, Y. S. Zhu for invaluable advice on RNA isolation techniques, and E. Stutz (Universität de Neuchatel, Switzerland) for communicating data prior to publication. We also thank Dr C. Maulbecker for critical reading of this manuscript. This material is based upon work supported by a National Science Foundation Biology Energy Division, Department of Energy under contract DE-AC03-76SF00098.

References


