Unusual ribulose-1,5-bisphosphate carboxylase/oxygenase genes from a marine manganese-oxidizing bacterium

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The Gram-negative bacterium strain SI85-9A1 is a novel marine α -proteobacterium that oxidizes manganese(II) to manganese(IV). Initial DNA hybridization screening showed that SI85-9A1 possesses a gene similar to *cbbL*, the gene coding for the large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (RubisCO; EC 4.1.1.39). However, no RubisCO enzyme activity was found in cultures of SI85-9A1. Genes coding for both large (*cbbL*) and small (*cbbS*) subunits of a RubisCO enzyme were identified, isolated and sequenced. When these genes were introduced into an *Escherichia coli* host strain, ribulose-1,5-bisphosphate-dependent CO₂ fixation occurred under control of a *lac* promoter, indicating that the protein is functional in *E. coli*. Although their function is unknown, this is the first direct evidence for the presence of RubisCO genes in a manganese-oxidizing bacterium. Phylogenetic analysis of the RubisCO genes of strain SI85-9A1 showed that they are divergent, but are more related to those from non-chlorophyte algal chloroplasts than are those from other bacteria. The fact that the RubisCO sequence of strain SI85-9A1 is not closely related to any other published RubisCO sequence suggests that the protein may be valuable for studies of the function and evolution of the RubisCO enzyme as well as its activity in the environment.

Keywords: ribulose-1,5-bisphosphate carboxylase/oxygenase, RubisCO, manganese oxidation, autotrophy

INTRODUCTION

Ribulose-1,5-bisphosphate carboxylase (RubisCO; EC 4.1.1.39) is one of two unique enzymes in the Calvin–Benson cycle, the most common pathway for autotrophic CO₂ fixation in plants and bacteria. Two forms (I and II) are known, and form I RubisCOs have been categorized into four types (Tabita, 1995). These forms and types are based on evolutionary relationships, and also reflect common biochemical features among the groups. Chloroplasts of terrestrial plants and green algae together with cyanobacteria contain RubisCOs that form a related group

(Type IB), consistent with the accepted notion of the cyanobacterial origin of chloroplasts. Many marine algal chloroplasts (non-chlorophyte algae) contain RubisCOs (Type ID) that are only distantly related to the cyanobacterial type, and are more closely related to other bacterial RubisCOs (Type IC) than to other chloroplasts. The fourth type (IA) is a group of mostly proteobacterial RubisCOs allied with Type IB, although recently a prochlorophyte was found to have a RubisCO that belongs to this group (Shimada *et al.*, 1995).

Manganese (Mn)-oxidizing bacteria have long been suspected of having autotrophic potential, but the existence of RubisCO genes in these organisms has never been investigated. Such genes may not only provide evidence consistent with the existence of autotrophic Mn oxidation, but may also be useful in understanding the evolution and biochemical function of RubisCO. It was proposed as early as 1913 (Beijerinck, 1913) that the oxidation of reduced Mn [Mn(II)] could provide energy for chemo-

Abbreviations: RubisCO, ribulose-1,5-bisphosphate carboxylase/oxygenase; RuBP, ribulose 1,5-bisphosphate

The GenBank accession numbers for the *cbbS* and *cbbL* sequences, and for the 16S rRNA sequence reported in this paper are L32182 and U53824, respectively.

lithoautotrophic growth. Although autotrophy supported by Mn oxidation is thermodynamically favourable, there is only one report that clearly demonstrates net carbon fixation by a Mn oxidizer (Kepkay & Nealson, 1987). Unfortunately, that organism, *Pseudomonas* sp. strain S-36, does not demonstrate consistent Mn oxidation in our hands. We have screened 45 Mn-oxidizing environmental isolates with probes constructed from *cbbL* (RubisCO large subunit) genes of both an *Anabaena* sp. and *Xanthobacter* strain H4-14, with the aim of finding potential autotrophic strains (Tebo & Haygood, 1989). About 20% of the isolates hybridized positively, and strain SI85-9A1 was selected because of its consistent and reliable Mn oxidation.

Restriction analysis with two enzymes followed by DNA hybridization suggested that this strain has only one copy of the RubisCO form I genes, and hybridization with a probe derived from the *cbbM* gene of *Rhodospirillum rubrum*, which codes for a form II RubisCO, yielded negative results, suggesting that SI85-9A1 has only one copy of RubisCO genes in the genome.

Strain SI85-9A1 was isolated in 1985 from Saanich Inlet, a stratified fjord on the west coast of Canada. The fjord is anoxic below ~130 m for about six months every year, resulting in an O₂/H₂S interface (Tebo & Emerson, 1985). Microbial catalysis of Mn oxidation has been demonstrated in this basin above the interface, where there is an accumulation of particulate Mn (Emerson *et al.*, 1982; Tebo *et al.*, 1984). SI85-9A1 was isolated from water collected at 125 m, within the particulate Mn maximum. When grown on an appropriate seawater-based medium containing Mn(II), the bacteria oxidize Mn(II) and precipitate Mn(IV) manganates on the cell surface, forming a coat around the cell. It is a Gram-negative rod-shaped bacterium, which, according to its 16S rRNA sequence, belongs to the α -subdivision of the proteobacteria. It is not closely related to any of the organisms in the Genbank and RDP databases (GenBank accession number U53824; Maidak *et al.*, 1994). SI85-9A1 grows very slowly, with a doubling time of about 1–2 d, depending on the medium. The final population density in liquid cultures depends on the content of organic nutrients in the medium, and can reach high values (more than 10⁹ cells ml⁻¹) when grown in a rich medium. However, the bacteria also grow with the one-carbon compound formate as the sole organic carbon and energy source. Mn oxidation occurs only when grown in organic-poor media, and at the onset of the stationary phase of growth in batch cultures.

The initial probing results suggested that strain SI85-9A1 possesses a gene similar to *cbbL*, but we were unable to demonstrate *in vitro* ribulose-1,5-bisphosphate-dependent CO₂ fixation activity or autotrophic growth of the organism. We have proceeded by a molecular approach, cloning, sequencing, and expressing the genes, and thus confirming that the RubisCO genes of strain SI85-9A1 do indeed code for a RubisCO enzyme that is functional, and might, under unknown conditions, be expressed to yield a functional protein in the parent organism.

METHODS

Bacterial strains, media and growth conditions. Strains and plasmids used in this study are summarized in Table 1. Strain SI85-9A1 was maintained on solid media K (Krumbein, 1971) and M which consists of artificial sea water (ASW; see below) supplemented with 50 mg yeast extract l⁻¹, 50 mg peptone l⁻¹, 20 mM HEPES buffer (pH 7.8), 100 μ M MnCl₂, 2 mM KHCO₃ and 15 g Bacto Noble agar (Difco) l⁻¹. ASW is prepared in our laboratory at double strength (2 $\times$ ASW) as follows: 24.7 g MgSO₄·7H₂O, 2.9 g CaCl₂·2H₂O, 35.1 g NaCl and 1.5 g KCl are dissolved individually in 250 ml distilled water each and then combined yielding 1 l 2 $\times$ ASW, which is diluted by 50% with distilled water and other components in the final medium.

For large scale DNA preparations the cells were grown in seawater complete (SWC) medium (Nealson, 1978) at room temperature for 1 week. For RubisCO activity assays cells were grown at room temperature for 1 week in J medium [ASW supplemented with 20 mM HEPES buffer (pH 7.8), 1.5 mM NH₄Cl, 2 mM KHCO₃, 10 ml vitamin mix (Kepkay, 1985), 73 μ M KH₂PO₄ and 0.1 ml of a stock solution of 3 mg ferrous ammonium citrate (ml ASW)⁻¹] supplemented with 20 mM formate. *Escherichia coli* strains were grown at 37 °C in LB medium (Sambrook *et al.*, 1989). *Thiobacillus neapolitanus* cells were grown in TMN-2 medium (Starr *et al.*, 1981) at room temperature.

Probing of environmental isolates. Forty-five strains of Mn-oxidizing bacteria isolated from a variety of marine environments were screened with probes constructed from fragments of the *cbbL* genes from four organisms: a 1.5 kb *Pst*I–*Eco*RI fragment of the plasmid pANP1155, which contains a 2.3 kb *Pst*I fragment of the *cbbL* gene of *Anacystis nidulans* 6301 (Shinozaki & Sugiura, 1983), a 0.95 kb *Hpa*I–*Hind*III fragment internal to *cbbL* from the plasmid pAn600, which contains a 17 kb fragment including the *cbbL* gene of *Anabaena* 7120 (Curtis & Haselkorn, 1983), a 1.4 kb *Eco*RI–*Bgl*II fragment of the plasmid pRR2119, which contains a 2.4 kb fragment of the *cbbM* gene of *Rs. rubrum* (Somerville & Somerville, 1984), and a 0.9 kb *Sma*I–*Sal*I fragment from the plasmid pLL417R, which contains a 1.7 kb region of the *cbbL* gene of *Xanthobacter* sp. strain H4-14 (Lehmiche & Lidstrom, 1985). Hybridization conditions were adjusted to the highest stringency that would still allow detection of a *T. neapolitanus* positive control with the *Anabaena* probe.

Construction of a genomic DNA library and subcloning the RubisCO genes. Strain SI85-9A1 cells are very difficult to lyse. In order to obtain large quantities of high molecular mass DNA we used the following procedure. Cells were grown in 1 l SWC medium without Mn to stationary phase (in the presence of Mn the cells become coated with Mn oxides, making them even more difficult to lyse). The cells were spun down and resuspended in 95 ml TE buffer pH 8.0 (50 mM Tris buffer pH 8.0, 10 mM EDTA). The suspension was divided into 10 tubes and 200 μ l lysozyme solution (50 mg ml⁻¹) was added to each. The cells were stored on ice for 10 min, then 0.5 ml 10% (w/v) SDS and 50 μ l proteinase K solution (20 mg ml⁻¹) were added to each tube and the cells incubated at 37 °C for a few hours, until clear. The clear lysate was extracted with CTAB (hexadecyltrimethylammonium bromide, Sigma) and chloroform (Ausubel *et al.*, 1987) and the DNA precipitated, dissolved in TE buffer, and purified on a CsCl density gradient. The DNA was partially digested with the restriction enzyme *Sau*3A, and fragments larger than 20 kb were purified on a sucrose gradient. The size-fractionated DNA was ligated to pMMB33 cosmid arms as described by Frey *et al.* (1983), and packaged with a Gigapack XL packaging kit (Stratagene). The packaged library

Table 1. Bacterial strains and plasmids used in this work

Strain or plasmid	Genetic characteristic(s)	Source or reference
Strains		
SI85-9A1	Manganese oxidizer	This study
<i>Thiobacillus neapolitanus</i> ATCC 23638	Autotroph	Parker & Prisk (1953)
<i>Escherichia coli</i> DH1	<i>supE44 hsdR17 recA1</i>	Hanahan (1983)
XL1-Blue	<i>lacI^q lacZAM15</i>	Stratagene
Plasmids		
pLL417R	Contains the <i>cbbL</i> gene of <i>Xanthobacter</i> strain H4-14	Lehmick & Lidstrom (1985)
pANP1155	Contains the <i>cbbL</i> gene of <i>Anacystis nidulans</i> 6301	Shinozaki & Sugiura (1983)
pAn600	Contains the <i>cbbL</i> gene of <i>Anabaena</i> 7120	Curtis & Haselkorn (1983)
pRR2119	Contains the <i>cbbL</i> gene of <i>Rhodospirillum rubrum</i>	Somerville & Somerville (1984)
pMMB33	IncQ broad host range, Km ^r cosλ	Frey <i>et al.</i> (1983)
pMMB33-7	pMMB33 containing a 29 kb fragment of SI85-9A1 chromosome	This study
pBluescript II KS- /SK-	Phagemid, <i>bla lacZ^c</i>	Stratagene
pRC1	pBluescript containing a <i>XhoI</i> fragment of pMMB33-7	This study
pRC1R	As pRC1 with the <i>XhoI</i> fragment in the opposite orientation	This study
pRC3	pBluescript containing a <i>PstI</i> fragment of pMMB33-7	This study
pRC3R	As pRC3 with the <i>PstI</i> fragment in the opposite orientation	This study
pRC4	pBluescript containing a <i>SaI</i> fragment of pMMB33-7	This study
pRC10	pBluescript containing both <i>cbbL</i> and <i>cbbS</i>	This study
pRC11	pBluescript containing both <i>cbbL</i> and <i>cbbS</i> fused to the <i>lac</i> promoter	This study

was transduced into *E. coli* XL1-Blue cells. The resulting library had about 200 000 c.f.u. and a mean insert size of 20 kb.

Ten thousand colonies representing the gene library were probed by Southern hybridization with the *Xanthobacter* sp. strain H4-14 probe described above, and seven positive colonies were isolated. The cosmid of one of them, pMMB33-7, which contained an insert of ~29 kb, was digested with different restriction enzymes and reprobated. Two positive bands were isolated: a 2013 bp *XhoI* fragment, which was cloned into *XhoI*-digested pBluescript KS- in both orientations, resulting in pRC1 and pRC1R, and a 1678 bp *PstI* fragment, which was cloned into *PstI*-digested pBluescript KS- resulting in pRC3 and pRC3R (Fig. 2). A similarly digested chromosomal DNA yielded positive bands of the same size, suggesting that no rearrangement had occurred. Both pRC1 and pRC1R were subjected to nested deletions, using an Erase-a-Base kit (Promega), resulting in plasmids pRC1-1 to pRC1-10 and pRC1R-1 to pRC1R-10, respectively. Since it was found that plasmids pRC1 and pRC3 did not contain the whole *cbbL* gene, a synthetic oligonucleotide was prepared from the sequence at the end of the *PstI* fragment (*cbbL*1), and used to probe pMMB33-7 again. A positive *SaI* fragment of 2.5 kb was isolated and cloned into pBluescript KS-, resulting in pRC4. This plasmid contained the rest of the *cbbL* gene, and also the *cbbS* gene.

To generate a clone containing the intact *cbbL/cbbS* region, the *SaI* fragment of pRC4 was cut and cloned into the 5.1 kb *SaI* fragment from pRC3. The resulting plasmid was named pRC10. In order to fuse this insert to the *lac* promoter of pBluescript, the whole insert of pRC10 was cut by simultaneous digestion with

KpnI and *SacI*, which cut outside the insert but within the multiple cloning site of pBluescript, and cloned into a *KpnI*-*SacI*-digested pBluescript SK-. The resulting plasmid was named pRC11.

Southern hybridization. DNA probes were either prepared from double-stranded DNA using a Random Primed DNA Labeling kit (Boehringer Mannheim), or oligonucleotides were synthesized by a DNA synthesizer (Applied Biosystems, model 391) and tailed by a DNA Tailing kit (Boehringer Mannheim) using high specific activity ($> 111 \text{ TBq mmol}^{-1}$) [α - ^{32}P]dATP (ICN Biochemicals). DNA was transferred to membranes using a downward transfer protocol (Koersier *et al.*, 1993).

16S rRNA sequencing and analysis. Overlapping fragments of the 16S rRNA gene were obtained by PCR amplification using standard methods and primers (Lane, 1990). Sequencing was done with an automated DNA sequencer (ABI model 373A) using a PRISM Ready Reaction DyeDeoxy Terminator Cycle Sequencing Kit (Applied Biosystems). The sequence was aligned to other sequences using the RDP World Wide Web server (Maidak *et al.*, 1994). Aligned sequences were imported into PAUP version 3.0s (Swofford, 1991) and a phylogenetic tree was generated by a heuristic search using 10 replications of random stepwise additions.

RubisCO sequencing and analysis. Sequencing was done either manually or by an automated sequencer. Single-stranded DNA for manual sequencing was obtained from pBluescript phagemids (Stratagene) according to the manufacturer's instructions, and both strands sequenced with Sequenase version 2.0 (United States Biochemicals). Double-stranded DNA for automated sequencing was obtained with Magic Mini

Prep Columns (Promega). Resulting DNA sequences were analysed and translated by the MacVector Sequence Analysis Software version 3.5 (International Biotechnologies), and translated sequences were analysed by PAUP. Sequence alignments were performed manually using Microsoft Excel colour macros (Haygood, 1993). Nucleotide sequence identity was calculated using the alignment feature of the MacVector program. Pairs of SI85-9A1 and each of the other taxa were aligned, identical nucleotides were determined, and percentage identity calculated as the number of identical nucleotides divided by the length of the shorter sequence. Phylogenetic trees were generated from aligned amino acid sequences by heuristic searches, using 10 replications of random stepwise additions with the PROTPARS step matrix, and evaluated by bootstrap analysis. The sequence of the *R. rubrum cbbM* gene, which belongs to the Type II group, was used as an outgroup.

The rooted tree diagram was generated by the TreeDraw program (a version of Drawgram and Drawtree by J. Felsenstein, ported to the Macintosh by D. G. Gilbert, Biology Dept, Indiana University, IN, USA) using branch information generated by PAUP. Branch lengths indicate the inferred number of character state changes on each branch.

Sequences of RubisCO genes from other organisms used in this paper were chosen from those for which the sequence is available for both subunits, and so will represent all the major groups of RubisCO. The following sequences were used (GenBank accession numbers are given in parentheses): *Alcaligenes eutrophus* (M17744) (Andersen & Caton, 1987), *Anacystis nidulans* strain 6301 (X03220) (Shinozaki & Sugiura, 1983; Shinozaki *et al.*, 1983), *Chromatium vinosum* (D90204) (Kobayashi *et al.*, 1991), *Chlamydomonas reinhardtii* (X04471, J01399) (Dron *et al.*, 1982; Goldschmidt-Clermont & Rahire, 1986), *Cryptomonas* Φ (X14171, X62349) (Douglas & Durnford, 1989; Douglas *et al.*, 1990), *Cyanidium caldarium* strain RK-15 (X55524) (Valentin & Zetsche, 1990a), *Cylindrotheca* sp. strain N1 (M59080) (Hwang & Tabita, 1991), *Ectocarpus siliculosus* (X52503) (Valentin & Zetsche, 1990b), *Olisthodiscus luteus* (M24288, X61918) (Boczar *et al.*, 1989; Hardison *et al.*, 1992), *Porphyridium aeruginosum* (X17597) (Valentin & Zetsche, 1989), *Rhodobacter sphaeroides* (M64624) (Gibson *et al.*, 1991), *R. rubrum* (X00286) (Nargang *et al.*, 1984), *Synechococcus* sp. strain a-1 (D13539) (Yaguchi *et al.*, 1993), *Thiobacillus ferrooxidans* (M85061) (Kusano *et al.*, 1991), *Xanthobacter flavus* (X17252) (Meijer *et al.*, 1991), and *Zea mays* (Y00322, V00171) (M. Lebrun, G. Waksman & B. Freyssinet, Genbank submission; McIntosh *et al.*, 1980).

RubisCO assays. These were modified from a previously published assay (Glover & Morris, 1979). Strain SI85-9A1 cultures were grown for 1 week, *T. neapolitanus* cultures were grown for 3 d, and *E. coli* cultures were grown overnight. In the morning of the experiment two aliquots of 6 ml of each *E. coli* culture were transferred into sterile tubes. One millilitre of LB medium containing 14 mM IPTG was added to one of the aliquots (2 mM final concentration), while 1 ml of LB medium without IPTG was added to the other. The tubes were incubated at 37 °C for 2 h to allow expression of genes fused to the *lac* promoter. Assay mixtures were prepared by filtering two duplicates of each culture onto Whatman GFF filters. The volumes used were 1 ml for *E. coli* cultures, 10 ml for *T. neapolitanus* and 25 ml for strain SI85-9A1. The filters were placed in scintillation vials, 400 μ l 10% (v/v) Triton X-100 added and the filters incubated for 10 min. An exception was with strain SI85-9A1 cells, when 200 μ l lysozyme in TE (5 mg ml⁻¹) were added first, the cells incubated on ice for 10 min, and then 200 μ l 20% Triton X-100 was added and the cells incubated

for 2 h at room temperature. When the assay mixtures were ready, 0.93 ml reaction buffer (70 mM Tris pH 8, 25 mM glutathione, 25 mM MgCl₂, 40 mM NaHCO₃, 3.071 $\times$ 10⁵ Bq H¹⁴CO₃ ml⁻¹) was added to each vial and the vials were incubated at room temperature for 10 min to activate the enzyme. For each sample, 50 μ l of a solution containing 4 mg ribulose 1,5-bisphosphate (RuBP) ml⁻¹ (dissolved in 1:5-diluted reaction buffer without radiotracer and adjusted to pH 6) was added to one duplicate (360 μ M final concentration), while 50 μ l of the same buffer without RuBP was added to the second duplicate.

The reactions were allowed to proceed for 1 h at room temperature, then terminated by adding 3 ml acetic acid/methanol (1:20, v/v) and dried at 65 °C overnight. Total radioactivity was measured by adding 5 μ l of the stock solution to 0.5 ml β -phenylethylamine, then adding 10 ml Scintillation cocktail (ScintiVerse BD, Fisher Scientific) to all samples and counting for 5 min in a Beckman LS 6000TA scintillation counter.

Total protein concentrations. These were determined using the BCA Protein Assay kit (Pierce), according to the manufacturer's instructions. Samples were taken immediately before filtering cells for the RubisCO activity assay, centrifuged and the pellets frozen. The pellets were later resuspended in TE buffer, and NaOH and SDS were added to 0.1 M and 1%, respectively. Strain SI85-9A1 cells were incubated at 55 °C overnight; *T. neapolitanus* and *E. coli* cells lysed immediately.

RESULTS

16S rRNA sequence

The 16S rRNA sequence analysis placed strain SI85-9A1 within the α -subdivision of the proteobacteria. It is not closely related to any known species, but the closest organisms as determined by the Similarity Rank test are members of the rhizobia group, such as *Rhizobium ciceri* (*S*_{ab} 0.763) and *Rhizobium huakuii* (*S*_{ab} 0.750) (Fig. 1).

Fig. 1. Relationships among different proteobacteria based on their 16S rRNA sequences, as determined by maximum parsimony (PAUP; Swofford, 1991). Strain SI85-9A1 belongs to the α -subdivision of that group. The closest organism to strain SI85-9A1 as determined by the Similarity Rank test is *Rh. ciceri* (*S*_{ab} 0.763). The arrow indicates position of root (determined with *Bacillus subtilis* as outgroup). Branch lengths indicate the inferred number of character state changes on each branch. Sequences other than strain SI85-9A1 were obtained from the RDP World Wide Web Server (Maidak *et al.*, 1994).

Fig. 2. Restriction maps of *cbb* regions of plasmid constructs. Restriction fragments were cloned into pBluescript vectors and sequenced using universal and reverse primers or synthetic oligonucleotides. Small arrows show length and direction of sequencing runs. P, *Pst*I; S, *Sal*I; X, *Xho*I.

RubisCO sequence

The region sequenced is shown in Fig. 2. The region containing the *cbbL* and *cbbS* genes was fully sequenced on both strands (Fig. 3). Two additional ORFs were identified from the partial sequence (Fig. 2). The first (partial) ORF contains 762 bp which encode the carboxyl-terminus 254 amino acids of a putative Calvin cycle aldolase (*cbbA*). The nucleotide sequence of this gene (not shown) closely resembles (75% identity) that of the *cbbA* gene of *Rb. sphaeroides* (Gibson *et al.*, 1991). This putative gene ends with a TGA codon and is followed by a non-coding region of 173 bp.

The second ORF is 1461 bp long (bases 176–1636), and encodes a 486 amino acid CbbL subunit. This ORF is preceded by a Shine–Dalgarno sequence (GAAGGA-GGA) upstream from ATG, the start codon. The *cbbL* gene is followed by a non-coding region of 114 bp (bases 1637–1750).

The third ORF is 423 bp long (bases 1751–2173), and encodes a 140 amino acid CbbS subunit. This ORF is preceded by a Shine–Dalgarno sequence (GAAGAGGA) located upstream from the ATG starting codon. The *cbbS* gene is followed by a non-coding region of 129 bp.

The fourth (partial) ORF (*orfX*) is 100 bp long, and encodes the amino-terminal 33 amino acids (not shown)

of an unidentified protein. This ORF is also preceded by a Shine–Dalgarno sequence (GAGGAG).

The DNA sequence of the *cbb* genes is most similar to RubisCO genes belonging to the Type IC group, namely *Rb. sphaeroides*, *X. flavus* and *Al. eutrophus*. Table 2 shows the percentage identity of these genes to RubisCO genes from the various groups.

Parsimony analysis

In order to analyse these genes, we have aligned the amino acid sequences generated by translation of the *cbbL* and *cbbS* genes to published sequences from several organisms (Fig. 4). The amino acid sequence generated by translation of strain SI85-9A1 *cbbL* gene possesses all the amino acids that were found to be implicated in activation and catalysis of the enzyme (Knight *et al.*, 1990). The aligned sequences were analysed by maximum parsimony to generate phylogenetic trees. We generated trees for CbbS, CbbL, and CbbL and CbbS combined, but only the tree constructed for CbbL is shown (Fig. 5) since the information contained in the CbbS region alone was not sufficient to resolve phylogenetic relationships among some of the organisms, and the result for the combined sequence was similar to that obtained from CbbL alone. The tree was generated using the CbbM protein of *R. rubrum* (which belongs to the Type II group) as an outgroup. The tree has the following parameters: length

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1   GAGGCCAGCTCCAGCCCGCGGTCGCTGACCGGCGGTCCCCGCGGCACCGAACTGACAGAATTGNCCTGAATGGACGGCGCGAACCCCTTTCGCGCC
101  GAAGGGAGACGCTTGTCCGAAATTCGCCGAAACGGCGCTGCGGACGCAACCGGGATCAACGAAGGAGGACCGTATGGATCAGGGCTCGGACACCATCA
    M D Q G S Q T I K 9
    G K D R Y K S G V M E Y R K M G Y W E P D Y E P K E T D V I A C F 42
201  AGGGCAAGGACCGCTACAAGTCAGGTGTTCATGGAATACCGCAAGATGGGCTATTGGGAGCCCGACTACGAACCCAAGGAGACGGACGTCATCGCTGT
    R I T P Q D G V D P I E A A A A V A G E S S T A T W T V V W T D R 75
301  CCGGATCAGCCCCAGGACGGCGTCGATCCGATCGAGGCGGCGGCGGTGGCGCGGAATCTCCACCGCGACATGGACCGTCGTGGACCGACCGG
    L T A A E K Y R A K A Y R V D Q V P N T D D Q Y F A Y I A Y D L D L 109
401  CTGACGGCGGCGGAGAAGTACCGGCCAAGGCTTACCGGTGTCAGGTGCCGAACACCGACGACAGTATTTCGCTTATATCGCTACGACCTCGACC
    F E N G S I A N L T A S I I G N V F G F K P L K G L R L E D M R L 142
501  TGTTCGAGAGCTCGATCGCAATCTGACGGCGTCGATCGGCAATGTCTTCGGCTTCAAGCCGCTGAAGGGCTGCGGCTGCGGCTGCGCCT
    P T A Y V K T F Q G P A T G I V V E R E R L D K F G R P L G A T 175
601  GCGGACCGCTTATGTGAAGACCTTCCAGGGGCGGCGACCGGATCGTCGTCGAGCGCAACGCTCGACAAGTTCGGCCGCGCTGCTCGGCGCGACG
    V K P K L G L S G R N Y G R V V Y E A L K G G L D F T K D D E N I N 209
701  GTGAAGCCCAAGCTCGGCTGTGCGGCGCAATTACGGCGCGTCGTCACGAGGCGCTGAAGGGCGGCTCGACTTCACCAAGGACGACGAGAATCA
    S Q P F M D W R E R F L Y C M E A V N K A Q A A T G E I K G T Y L 242
801  ACTCGAGCCCTTTCATGGATTGGCGCGAGCGGTTCTCTACTGTCATGGAGGCGGTGAACAAGGCCAGGCGCCACCGGCGAGATCAAGGGAACCTATCT
    N V T A A T M E D M Y E R A E F A R D L G S N I I M I D L V I G W 275
901  CAACGTCACCGCGCCACCATGGAGGACATGTACGAGCGCGCGAGTTCGCCAGGACCTGGGCTCCACATCATCATGATCGACCTCGTCATCGGCTGG
    T A M Q S M A K W A R R N N M I L H L H R A G H S T Y T R Q K T H G 309
1001 ACCGCCATCGAGTCCATGGCCAAATGGGCGCGCGCAACAACATGATCTGTCATGCAACGGCGGCGGCACTCGACCTATACCGCGCAGAAGACCCACG
    Sali
    V S F R V I A K W A R L A G V D H I H A G T V V G K L E G D P A T 342
1101 GCGTGTCTGTTCCGGGTGATCGCCAAATGGGCGCGGCTGGCGGTCGACCATGCCGCGCACGGTCGTCGGCAAGCTGGAGGGCGATCCGGCGAC
    XhoI
    T K G Y Y D I C R D E F T H R K L E N G I F F D Q P W A S L N K M 375
1201 GACCAAGGGCTATTACGACATCTGCCGCGACGAGTTCACCCACCGGAAGCTCGAGAACGGCATCTTCTTCGACCGCCCTGGGCTTCGCTGAACAAGATG
    PstI
    M P V A S G G I H A G Q M H Q L L D L L G D D T V L Q F G G G T I G 409
1301 ATGCCGGTGGCTCGGGCGGCATCCATGCCGCGCAGATGCACCAACTCCTTGATCTTCGCGCGACGACACCGTGTGTCAGTTCGGCGGCGGCACGATCG
    H P M G I A A G A T A N R V A L E C M V L A R N E G R D I V N E G 442
1401 GCCATCCCATGGGCTCGCGCGCGCGCGACGCCAACCGGTGGCGCTGGAATGCATGGTTCTTGCCCGCAACGAGGCGCGGACATCGTCAATGAGGG
    P E I L Q E A A R S C T P L Q Q A L E T W K D V T F N Y T S T D S 475
1501 ACCGGAGATCCTGACGAGGCGGCAAGGAGCTGCACGCGCTGCAGCAGGCGCTCGAGACGTGAAGGACGTGACCTTCAACTACACCTCGACCGATTCC
    P D Y A V T A T A S V * 486
1601 CCCGACTACGGGTGACGGCGACGGCTCGGTCTGATCCATCCCGCTCAGGACGGGCGAGCCTCCCAACGCCCGTCTCCCATCGATCGAACCCGG
    M R I T Q G A F S F L P D L T D T 17
1701 CCGGCGCTGCTTSCAAAGGCTGGCGCGCAACCTGAAGAGGATATCGACCATGCGCATCACCCAAGGGGCTTCTCGTTTCTGCCCGACCTACCGACAC
    Q I T A Q I Q Y C L D N G W A V N L E H T D D P H P R N T Y W D M 51
1801 GCAGATCACCGCACAGATCCAGTACTGCCTCGACAATGGCTGGGCGGTGAATCTGGAGCACACCGACGACCCGATCCGCGCAATACCTACTGGGACATG
    W G H P M F D I A D A G G V M M E L S E C R K V H G E R Y I R M S A 85
1901 TGGGGGACCCGATGTTTCAGATCGCGGATGCGGGCGGCTGATGATGAGTTGTCCGAGTGCCCAAGGTCATGGCGAACGCTACATCCGATGTCTGG
    F D S T A G W E S V K L S F I V N R P A N E P G F R L R R S E M E 118
2001 CCTTCGATTCCACGGCGCGCTGGGAGTCGGTGAAGCTGCTTCATCGTCAACGGCGCGGCAACGACCGGCTTCCGGTGCGCCGCTCGGAAATGGA
    G R T I R Y T T E S Y A T D K P E G G E R Y A E * 140
2101 AGGCGCGACTATTCGCTACACGACGAATCCTACGCCACCGACAAGCGGAGGCGGAACGCTACGCCGAGTAGCCGTGCGGTGAGCCGCTCCCTCTCCCG

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Fig. 3. Nucleotide sequence and deduced amino acid sequence of the *cbbL* and *cbbS* region of the insert in pRC10. Predicted amino acid residues are shown above the respective codons. Putative ribosome-binding sites are overlined and stop codons are indicated with asterisks. There is no restriction site at the end of the sequence.

1253, consistency index (CI) 0.773, homoplasy index (HI) 0.227, retention index (RI) 0.746 and rescaled consistency index (RC) 0.576.

Expression of SI85-9A1 RubisCO in *E. coli*

Because we were unable to detect RubisCO enzyme activity in cells of strain SI85-9A1 we thought that the SI85-9A1 RubisCO genes might be nonfunctional. To

test this possibility we cloned the genes into an expression system in *E. coli* and assayed for activity (Table 3). The RubisCO expression experiment included the bacterium *T. neapolitanus* as a positive control, and the *E. coli* strain XL1-Blue carrying the plasmid pBluescript as a negative control. The control cells, together with XL1-Blue cells carrying the plasmids pRC10 and pRC11, were incubated for 1 h with and without the *lac* gene inducer IPTG, and with and without RuBP, in the presence of $\text{H}^{14}\text{CO}_3^-$.

Table 2. Nucleotide sequence identity of RubisCO genes from strain SI85-9A1 with those from other organisms

Organism*	RubisCO group	Identity (%)	
		<i>cbbL</i>	<i>cbbS</i>
<i>Rhodobacter sphaeroides</i>	IC	77	72
<i>Xanthobacter flavus</i>	IC	76	65
<i>Alcaligenes eutrophus</i>	IC	75	66
<i>Chromatium vinosum</i>	IA	63	43
<i>Porphyridium aeruginosum</i> cp	ID	61	52
<i>Cryptomonas</i> Φ cp	ID	61	48
<i>Anacystis nidulans</i>	IB	60	48
<i>Olisthodiscus luteus</i> cp	ID	59	49
<i>Cyanidium caldarium</i> cp	ID	59	49
<i>Ectocarpus siliculosus</i> cp	ID	59	50
<i>Thiobacillus ferrooxidans</i>	IA	59	39
<i>Synechococcus</i> sp. strain a-1	IB	59	44
<i>Cylindrotheca</i> sp. strain N1 cp	ID	56	52
<i>Chlamydomonas reinhardtii</i> cp	IB	50	35
<i>Zea mays</i> cp	IB	50	30
<i>Rhodospirillum rubrum</i> (<i>cbbM</i>)	II	38	NA

NA, Not applicable.

* cp, chloroplast.

Clone pRC10, which contains the *cbbL/S* genes in an opposite orientation from the *lac* promoter of pBluescript, did not show any RuBP-dependent CO₂-fixing activity, while clone pRC11, in which the *cbbL/S* genes are controlled by the *lac* promoter, demonstrated IPTG- and RuBP-dependent CO₂ fixation at a rate of 18 nmol CO₂ min⁻¹ (mg total soluble protein)⁻¹ (Table 3). The positive control cells (*T. neapolitanus*) fixed CO₂ in the presence of RuBP at a rate of 51.3 nmol CO₂ min⁻¹ (mg total soluble protein)⁻¹. Strain SI85-9A1 showed no RubisCO activity.

DISCUSSION

The RubisCO genes of strain SI85-9A1 are unique, and are not closely related to any other published RubisCO sequences. The most parsimonious tree (Fig. 5) shows that the strain SI85-9A1 genes are about equally closely related to the members of Type IC and Type ID groups. Although the grouping of SI85-9A1 RubisCO with non-chlorophyte algal chloroplast RubisCOs (Type ID) was the most parsimonious with this data set, it was not strongly supported by bootstrapping (the alternative grouped SI85-9A1 at the base of the Type IC group). Nonetheless, all of the analyses support the RubisCO genes of strain SI85-9A1 being closest to Type ID RubisCO genes of non-chlorophyte algal chloroplasts among the bacterial RubisCO genes that have been sequenced to date. This result was obtained by analysing either the sequence of both genes together, or the sequence of *cbbL* alone.

The Type ID enzymes are the subject of intense current interest because they have a much higher specificity factor (lower susceptibility to the competing oxygenase reaction) than enzymes of Type IB from terrestrial plants (Tabita, 1995). The bacterial enzymes of Type IC have specificity factors in the range of terrestrial plants. The loop 6 region of the large subunit of RubisCO is believed to influence the specificity factor (Read & Tabita, 1994), and the SI85-9A1 enzyme shares some amino acids with the Type ID enzymes, some with the Type IC and is unique at other positions. Clearly, the specificity factor and other biochemical properties of the SI85-9A1 RubisCO are important subjects for future investigation.

The issue of autotrophy is particularly interesting in the case of strain SI85-9A1 because of its ability to oxidize Mn. For many decades scientists have been debating whether Mn oxidation could provide the necessary energy for autotrophic growth (Ali & Stokes, 1971; Beijerinck, 1913; Ghiorse, 1984; Kepkay & Neelson, 1987; Neelson *et al.*, 1988; van Veen, 1972). Although we have not yet been able to demonstrate autotrophic growth of strain SI85-9A1, it is apparent that this strain has some of the required genes. This, and the fact that strain SI85-9A1 oxidizes Mn only on organic-poor media, suggest that there might be a link between Mn oxidation and CO₂ fixation in this strain.

The sequence data, together with the expression of the genes in an *E. coli* host, suggest that strain SI85-9A1 might have the capability for synthesizing an active RubisCO enzyme. It remains unclear, though, under what

(a)

S185-9A1 MDQGSQTIKGDYKSYMEYRKMGVWEPDTEPKETVIVACFRITPDGNDPIIAAAGVAGSS-TAIWVVTTRIAAEK 81
A. eutrophus MNAPEITQAKPKRYDAGVMKYKEMGYWDGIVPKDITVLALFRITPDGNDPIIAAAGVAGSS-TAIWVVTTRIAACDM 82
R. sphaeroides MDTKTTEIKGKERYKAGVLKYAQMGYWDGIVPKDITVLALFRITPDGNDPIIAAAGVAGSS-TAIWVVTTRIAACDS 81
O. luteus MSNNVYERNRIKNDRYESGVIPYAKMGVWDANISVKDITLLALFRITPDGNDPIIAAAGVAGSS-TAIWVVTTRIAACDV 83
C. caldarium MAQSVQERTRLKNRYESGVIPYAKMGVWDPNVYVKDITLLALFRITPDGNDPIIAAAGVAGSS-TAIWVVTTRIAACDV 83
T. ferrooxidans MAVKTYEAGVKDY-RQTVWAPENVPLDSILACFKITPDGNDPIIAAAGVAGSS-TAIWVVTTRIAACDV 72
A. nidulans MPKTQSAAG-YKAGVKDY-KLTNYTTPDITPKDITLLALFRITPDGNDPIIAAAGVAGSS-TAIWVVTTRIAACDV 76
Z. mays MSPQTETKASVG-FKAGVKDY-KLTNYTTPDITPKDITLLALFRITPDGNDPIIAAAGVAGSS-TAIWVVTTRIAACDV 80

S185-9A1 RAKARVDQSPNTDDQYFAYIAYDLDTIINGSIANLTAIIGNSIATKPLKAVRITDMELITAYVTSRGGATIIIVTERLD 165
A. eutrophus RAKARVDQSPNTDDQYFAYIAYDLDTIINGSIANLTAIIGNSIATKPLKAVRITDMELITAYVTSRGGATIIIVTERLD 166
R. sphaeroides RAKARVDPVPGNTPGQYFCYVAYDLDTIINGSIANLTAIIGNSIATKPLKAVRITDMELITAYVTSRGGATIIIVTERLD 165
O. luteus RAKARVDQSPNADQYFAYIAYDLDTIINGSIANLTAIIGNSIATKPLKAVRITDMELITAYVTSRGGATIIIVTERLD 167
C. caldarium RAKARVDQSPNPDQYFAYIAYDLDTIINGSIANLTAIIGNSIATKPLKAVRITDMELITAYVTSRGGATIIIVTERLD 167
T. ferrooxidans KGRARIEDPGDDTCFYAFVAYPIDIIEEGSVNLTSLVNGSIGKAVRALRITDVEFLAYVTSRGGATIIIVTERLD 156
A. nidulans KGRARIEDPGDDTCFYAFVAYPIDIIEEGSVNLTSLVNGSIGKAVRALRITDVEFLAYVTSRGGATIIIVTERLD 156
Z. mays KGRARIEDPGDDTCFYAFVAYPIDIIEEGSVNLTSLVNGSIGKAVRALRITDVEFLAYVTSRGGATIIIVTERLD 160

S185-9A1 KFGRLPLGAIIVKPLGLGSKNYGRVYVIGIKGGGLDITKDDININSQPIIMRWDRILYCMCAVNNAAQQTGTIKEHYISVYATM 249
A. eutrophus KFGRLPLGAIIVKPLGLGSKNYGRVYVIGIKGGGLDITKDDININSQPIIMRWDRILYCMCAVNNAAQQTGTIKEHYISVYATM 250
R. sphaeroides KFGRLPLGAIIVKPLGLGSKNYGRVYVIGIKGGGLDITKDDININSQPIIMRWDRILYCMCAVNNAAQQTGTIKEHYISVYATM 249
O. luteus KFGRLPLGAIIVKPLGLGSKNYGRVYVIGIKGGGLDITKDDININSQPIIMRWDRILYCMCAVNNAAQQTGTIKEHYISVYATM 251
C. caldarium KFGRLPLGAIIVKPLGLGSKNYGRVYVIGIKGGGLDITKDDININSQPIIMRWDRILYCMCAVNNAAQQTGTIKEHYISVYATM 251
T. ferrooxidans KYGRPMIGCIIKPLGLGSKNYGRVYVIGIKGGGLDITKDDININSQPIIMRWDRILYCMCAVNNAAQQTGTIKEHYISVYATM 240
A. nidulans KYGRPMIGCIIKPLGLGSKNYGRVYVIGIKGGGLDITKDDININSQPIIMRWDRILYCMCAVNNAAQQTGTIKEHYISVYATM 244
Z. mays KYGRPMIGCIIKPLGLGSKNYGRVYVIGIKGGGLDITKDDININSQPIIMRWDRILYCMCAVNNAAQQTGTIKEHYISVYATM 248

S185-9A1 EDNYERREFAKDLASNTIIVIGW T AMQSMKAWARNMIILHHRAGHLYTYIQKTHVSRVIAEWLRLACVDDIITACTV 332
A. eutrophus EDNYERREFAKDLASNTIIVIGW T CIQSMNWCRODMIIHHRAGHLYTYIQKTHVSRVIAEWLRLACVDDIITACTV 333
R. sphaeroides EDNYERREFAKDLASNTIIVIGW T CIQSMNWCRODMIIHHRAGHLYTYIQKTHVSRVIAEWLRLACVDDIITACTV 332
O. luteus EDNYERREFAKDLASNTIIVIGW T CIQSMNWCRODMIIHHRAGHLYTYIQKTHVSRVIAEWLRLACVDDIITACTV 334
C. caldarium EDNYERREFAKDLASNTIIVIGW T CIQSMNWCRODMIIHHRAGHLYTYIQKTHVSRVIAEWLRLACVDDIITACTV 334
T. ferrooxidans EDNYERREFAKDLASNTIIVIGW T CIQSMNWCRODMIIHHRAGHLYTYIQKTHVSRVIAEWLRLACVDDIITACTV 334
A. nidulans EDNYERREFAKDLASNTIIVIGW T CIQSMNWCRODMIIHHRAGHLYTYIQKTHVSRVIAEWLRLACVDDIITACTV 328
Z. mays EDNYERREFAKDLASNTIIVIGW T CIQSMNWCRODMIIHHRAGHLYTYIQKTHVSRVIAEWLRLACVDDIITACTV 331

S185-9A1 VGKIEGDPATTKYVDICRDEFTHRKL E NGIITDQDWASLNKMMPPVASSGTHAGQHQLDLLEDTYVLOIGGGHLDHGMIAA 416
A. eutrophus VGKIEGDPATTKYVDICRDEFTHRKL E NGIITDQDWASLNKMMPPVASSGTHAGQHQLDLLEDTYVLOIGGGHLDHGMIAA 417
R. sphaeroides VGKIEGDPATTKYVDICRDEFTHRKL E NGIITDQDWASLNKMMPPVASSGTHAGQHQLDLLEDTYVLOIGGGHLDHGMIAA 416
O. luteus VGKIEGDPATTKYVDICRDEFTHRKL E NGIITDQDWASLNKMMPPVASSGTHAGQHQLDLLEDTYVLOIGGGHLDHGMIAA 418
C. caldarium VGKIEGDPATTKYVDICRDEFTHRKL E NGIITDQDWASLNKMMPPVASSGTHAGQHQLDLLEDTYVLOIGGGHLDHGMIAA 418
T. ferrooxidans VGKIEGDPATTKYVDICRDEFTHRKL E NGIITDQDWASLNKMMPPVASSGTHAGQHQLDLLEDTYVLOIGGGHLDHGMIAA 408
A. nidulans VGKIEGDPATTKYVDICRDEFTHRKL E NGIITDQDWASLNKMMPPVASSGTHAGQHQLDLLEDTYVLOIGGGHLDHGMIAA 412
Z. mays VGKIEGDPATTKYVDICRDEFTHRKL E NGIITDQDWASLNKMMPPVASSGTHAGQHQLDLLEDTYVLOIGGGHLDHGMIAA 415

S185-9A1 GATANRVAIICMVLARNIGRDIVNIGPEILQEAARSCTPIQQALETWKDVTIN-YTSTSPDYAVTATASV 486
A. eutrophus GATANRVAIICMVLARNIGRDIVNIGPEILQEAARSCTPIQQALETWKDVTIN-YTSTSPDYAVTATASV 487
R. sphaeroides GATANRVAIICMVLARNIGRDIVNIGPEILQEAARSCTPIQQALETWKDVTIN-YTSTSPDYAVTATASV 486
O. luteus GATANRVAIICMVLARNIGRDIVNIGPEILQEAARSCTPIQQALETWKDVTIN-YTSTSPDYAVTATASV 488
C. caldarium GATANRVAIICMVLARNIGRDIVNIGPEILQEAARSCTPIQQALETWKDVTIN-YTSTSPDYAVTATASV 488
T. ferrooxidans GATANRVAIICMVLARNIGRDIVNIGPEILQEAARSCTPIQQALETWKDVTIN-YTSTSPDYAVTATASV 488
A. nidulans GATANRVAIICMVLARNIGRDIVNIGPEILQEAARSCTPIQQALETWKDVTIN-YTSTSPDYAVTATASV 473
Z. mays GATANRVAIICMVLARNIGRDIVNIGPEILQEAARSCTPIQQALETWKDVTIN-YTSTSPDYAVTATASV 472

(b)

S185-9A1 MRITQGAFFIFDLTDTQITATIQICLND 30
A. eutrophus MRITQGAFFIFDLTDTQITATIQICLND 30
R. sphaeroides MRITQGAFFIFDLTDTQITATIQICLND 30
O. luteus VRLTQGAFFIFDLTDTQITATIQICLND 30
C. caldarium VRLTQGAFFIFDLTDTQITATIQICLND 30
T. ferrooxidans MADIQDYNSTPKYETEFYIIPAMQPKMRRIALINQ 38
A. nidulans MSMTKLPKERRFETEFYIIPPLSDRQIAAGIEMIEQ 37
Z. mays MAPTYVMASATAVAPFQGLKSTASLPVARRSSRLGNVSNNGRIRCMQVVPAYGNKKFETLNYIPLSTDDLLKQVDFLR-NG 83

S185-9A1 WAVNLTHTDDPHPRNT-----YWMWGLIMDIADAGGVMMILSECRKVHGERYIRMSAFDSTAGWESVKLSIVNRP 103
A. eutrophus WAVNLTHTDDPHPRNT-----YWMWGLIMDIADAGGVMMILSECRKVHGERYIRMSAFDSTAGWESVKLSIVNRP 103
R. sphaeroides WAVNLTHTDDPHPRNT-----YWMWGLIMDIADAGGVMMILSECRKVHGERYIRMSAFDSTAGWESVKLSIVNRP 103
O. luteus WSVGVYHTDDPHPRNT-----YWMWGLIMDIADAGGVMMILSECRKVHGERYIRMSAFDSTAGWESVKLSIVNRP 103
C. caldarium WSVGVYHTDDPHPRNT-----YWMWGLIMDIADAGGVMMILSECRKVHGERYIRMSAFDSTAGWESVKLSIVNRP 103
T. ferrooxidans WNPGLHVE-PE-RASTY-----YWMWGLIMDIADAGGVMMILSECRKVHGERYIRMSAFDSTAGWESVKLSIVNRP 109
A. nidulans FHPLIFNEHSNPEEF-----YWMWGLIMDIADAGGVMMILSECRKVHGERYIRMSAFDSTAGWESVKLSIVNRP 108
Z. mays WIPCLIFSKVGFVYRENSTSPCYDGR-----YWMWGLIMDIADAGGVMMILSECRKVHGERYIRMSAFDSTAGWESVKLSIVNRP 165

S185-9A1 ANEPGFRLRRSEMEGRTIRYTTESYATDK-PEGERYAE 140
A. eutrophus ANEPGFRLRRSEMEGRTIRYTTESYATDK-PEGERYAE 135
R. sphaeroides EPEPSLRMERTEVDGRSIRYTHSIVR 129
O. luteus KSEPGFYLERTEAEGRMIRYTHSYAVARNPEGSRY 139
C. caldarium AHEPGFVLRRIESNDRVQRYQIHSYAT 130
T. ferrooxidans R 110
A. nidulans G-----RY 111
Z. mays PGSD 169

Fig. 4. Amino acid sequence comparison of the RubisCO large (a) and small (b) subunits of different organisms. Identical residues are shown in white lettering on a black background. Active site residues are labelled with an asterisk (Knight et al., 1990).

Fig. 5. Relationships among different RubisCO large subunits based on amino acid sequences determined by maximum parsimony (PAUP; Swofford, 1991). The arrow indicates position of root (determined with *Rs. rubrum* as outgroup). Nodes significantly supported by bootstrap analysis (> 80%) are labelled with the percentage of bootstrap replicates that supported the node. Branch lengths indicate the inferred number of character state changes on each branch. cp, chloroplast.

Table 3. Expression of the RubisCO enzyme

Results are given as nmol CO₂ fixed min⁻¹ (mg total soluble protein)⁻¹. *T. neapolitanus* was used as a positive control and *E. coli* XL1-Blue carrying the plasmid pBluescript with no insert was used as a negative control.

	-IPTG		+IPTG	
	-RuBP	+RuBP	-RuBP	+RuBP
pBluescript (no insert; negative control)	0.6	0.6	1.3	1.2
pRC10 (no <i>lac</i> promoter)	0.9	1.2	1.0	1.2
pRC11 (<i>lac</i> promoter)	0.6	1.4	1.1	18
<i>T. neapolitanus</i> (positive control)	1.9	51.3	NA	NA
SI85-9A1	1.2	0.4	NA	NA

NA, Not applicable.

circumstances the genes might be expressed. Clone pRC10, in which the genes are not controlled by the *lac* promoter, did not demonstrate any RubisCO-dependent CO₂-fixing activity. However, in most organisms the *rbcL/S* genes are part of a larger operon that contains other CO₂-fixation-related genes (*cbhR*, *cbhF*, *cbhP* and *cbhA*). Since there clearly is a *cbhA* gene upstream of the *cbhL* gene in strain SI85-9A1, it is possible that the promoter for this operon is located upstream from the cloned fragment, and is thus missing in clones pRC10 and

pRC11. Alternatively, the promoters might be present, but not recognized by the *E. coli* transcription machinery. The fact that the Mn-oxidizing strain SI85-9A1 has genes coding for a functional RubisCO enzyme and other carbon fixation genes, suggests that SI85-9A1 is either autotrophic for some energy source, or a heterotrophic descendant of a previously autotrophic organism that lost some of the genes required for autotrophy. In the latter case, the fact that functional RubisCO genes are still present could be explained if the RubisCO genes were

linked to other essential genes. A similar case has been reported for freshwater *Beggiatoa* strains (Nelson *et al.*, 1989) that have apparently lost the ability to grow autotrophically, while maintaining the RubisCO genes. Another similar case is that of *Thiobacillus intermedius* in which two sets of RubisCO genes are present, coding for both form I and a form II enzymes. However, all attempts to demonstrate the presence of a form II RubisCO enzyme in *T. intermedius* failed (Stoner & Shively, 1993). After cloning the genes of *T. intermedius* into *E. coli*, a low level of activity was present, and as in our case, a higher level [$32 \text{ nmol CO}_2 \text{ fixed min}^{-1} (\text{mg protein})^{-1}$] was observed under the control of an external *lac* promoter.

On the other hand, strain SI85-9A1 may be the first representative of a novel group of organisms that fix CO_2 in the environment. A sequence similar to the strain SI85-9A1 RubisCO was recently obtained from a water column mRNA sample from the Gulf of Mexico at a depth of about 90 m (Paul & Pichard, 1996), representing a different ocean basin to that from which strain SI85-9A1 was isolated. The wide distribution and relative abundance of this type of gene implied by the finding, and the fact that the gene was apparently transcribed, underscore the importance of further studies on strain SI85-9A1 and other representatives of this group.

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