S16-015 Substitution of foreign Rubiscos in the cyanobacterium, *Synechococcus* PCC7942

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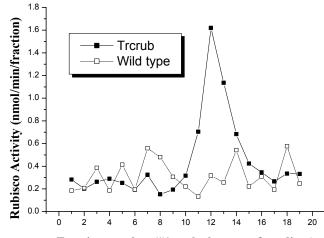
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Introduction

In cyanobacteria, the genes for the central CO₂-fixing enzyme, Rubisco, can be deleted only if they are functionally replaced even when a heterotrophic carbon source is supplied. The so-called "cyanorubrum" version of *Synechocystis* PCC6803 was generated by physically replacing the cyanobacterial *rbc*LS operon with the *Rhodospirillum rubrum rbc*M gene fused to the cyanobacterial *rbc*LS promoter (Pierce *et al.* 1989, Amichay *et al.* 1993). Retarded growth and increased oxygen sensitivity were reported, presumably resulting from the inferior catalytic properties of the *R. rubrum* Rubisco as well as disruption of the carboxysome-based CO₂ concentrating mechanism (Pierce *et al.* 1989). To develop a means for screening foreign Rubiscos for ability to fold and assemble functionally and support the growth of cyanobacteria, we are generating a novel variant of this approach in *Synechococcus* PCC7942. The foreign Rubisco (from *R. rubrum* in the first instance) is encoded on a plasmid in conjunction with inactivation of the cyanobacterial *rbc*LS operon on the chromosome by replacement with an antibiotic resistance gene.

Materials and Methods

The shuttle vector, pTrcrub, was derived from the *Escherichia coli* expression vector, pTrc (Invitrogen). In this construct, expression of *R. rubrum* Rubisco was driven from a Trc promoter, which has the -35 region of the Trp promoter and the -10 region of the lac promoter. The lacI^q gene that encodes the lac repressor is also present in this vector. In the shuttle vector, pTobrub, derived from pTrcrub and pRVRR14 (Whitney & Andrews 2001), the tobacco chloroplast *rbcL* promoter, 5'-UTR and the first 42 coding nucleotides of tobacco *rbcL* are fused to the *R. rubrum rbc*M coding region. Both shuttle vectors have a *Synechococcus* PCC7942 origin of replication as well as an *E. coli* origin of replication, together with a chloramphenicol resistance gene (Price & Badger 1989). Sucrose gradients and Rubisco activity assays were performed as in Andrews (1988) except that 0.5ml of crude extracts (7.5mg ml⁻¹ protein) were loaded onto each gradient and fractions collected from the base of the gradient.



Fraction number (#1 at the bottom of gradient)

B

A

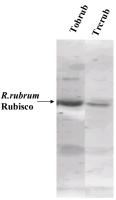
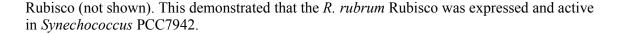


Fig. 1: *R.rubrum* Rubisco is expressed and active in *Synechococcus* PCC7942. **a**) Rubisco activity in soluble extracts from the Trcrub transformant and the wild type sedimented through sucrose gradients. A single peak corresponding to *R. rubrum* Rubisco is present in Trcrub. Most of the cyanobacterial enzyme is sedimented with the carboxysomes to the bottom of the gradient and thus not recovered. **b**) Immunoblot (using antibodies raised against *R. rubrum* Rubisco which do not detect cyanobacterial Rubisco) following SDS-PAGE analysis of soluble extracts isolated from Trcrub and Tobrub (100 μg protein per lane). Levels of *R. rubrum* Rubisco are three-to-five fold greater in Tobrub compared to Trcrub.

Results & Discussion

Expression of R. rubrum Rubisco in Synechococcus PCC7942

Plasmid pTrcrub was transformed into *Synechococcus* PCC7942 and transformants were selected with chloramphenicol. Quantitative immunoblot analysis performed on soluble extracts from transformants revealed that the *R. rubrum* Rubisco was present at levels of approximately 0.4% of the soluble protein, irrespective of the presence of IPTG (not shown). Sucrose-gradient ultracentrifugation of soluble extracts isolated from strain Trcrub revealed a large peak of Rubisco activity which was absent in the wild type (Fig. 1a). Immunoblots confirmed that this activity peak corresponded to the *R. rubrum*



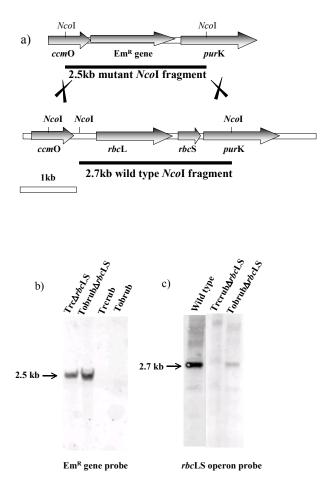


Fig. 2: Strategy for insertional inactivation of the *rbc*LS operon in *Synechococcus* PCC7942 and genomic analysis of transformants grown in 5%CO₂/95% air. **a**) The construct used for insertional inactivation by homologous recombination of the *rbc*LS operon in *Synechococcus* PCC7942, and the *NcoI* sites used in DNA blot analysis. **b**) DNA blot analysis of erythromycin-resistant transformants using the erythromycin resistance gene as probe. c) DNA blot analysis of erythromycin resistant transformants and the wild type using the *rbc*LS gene as probe. Equal loadings of DNA were used. The faint 2.7 kb signals indicate the heteroplasmic state of Trcrub Δrbc LS and Tobrub Δrbc LS.expressed and active in *Synechococcus* PCC7942.

In cyanorubrum strain of *Synechocystis* PCC6803, *R. rubrum* Rubisco expression was driven from the endogenous *rbc*LS promoter and the amount of *R. rubrum* enzyme predicted to be roughly equivalent to the amount of cyanobacterial enzyme (Pierce *et al.*, 1989). Cyanobacterial Rubiscos are typically present at levels of 1-2% of the soluble protein. To attain higher levels of expression of *R. rubrum* Rubisco, plasmid pTobrub, in which expression of *R. rubrum* Rubisco is driven constitutively from the tobacco *rbc*L promoter, was transformed into *Synechococcus* PCC7942. A similar construct transformed into the tobacco chloroplast leads to levels of *R. rubrum* Rubisco of 5% of total soluble protein (Whitney & Andrews 2001). Quantitative Western analysis on Tobrub transformants showed the *R. rubrum* enzyme to be present at levels three-to five-fold greater than in the Trcrub transformants (Fig. 1b).

Insertional inactivation of the Synechococcus PCC7942 rbcLS operon

The entire *rbc*LS operon (including the promoter) of the *Synechococcus* PCC7942 chromosome was replaced with an erythromycin resistance gene (Elhai & Wolk 1988) to produce the chromosome-transforming construct shown in Fig. 2a. This construct was sequenced to ensure that no errors had been introduced into the flanking *ccm*O or *purK* genes by the PCR manipulations and then transformed into both Trcrub and Tobrub. Transformants were selected with erythromycin (15µg ml⁻¹). Resistant transformants (Trcrub Δrbc LS and Tobrub Δrbc LS) were detected after four weeks and were restreaked and grown photoautotrophically in liquid culture with 15 µg ml⁻¹ erythromycin sparged with 5%CO₂/95% air. DNA-blot analysis of transformants using the erythromycin resistance gene as a probe revealed that correct insertion of the erythromycin resistance gene had taken place (Fig. 2b). However, similar blots using the *rbc*LS operon as a probe showed that traces of the wild type *rbc*LS operon persisted in the transformants (Fig. 2c), indicating a heteroplasmic condition with both wild-type and transformed chromosomes co-existing. Growth under increasing concentrations of erythromycin (up to 1000 µg ml⁻¹) failed to drive transformants to homoplasmicity (data not shown). The cyanorubrum strain of Synechocystis PCC6803 could grow photoautotrophically in the presence of 5%CO₂/95% air once homoplasmic. To drive cells to this homoplasmic state, however, heterotrophic growth in 5%CO₂/95% air or photoautotrophic growth in 5%CO₂/95% N₂ was required (Pierce et al. 1989, Amichay et al. 1993). Therefore, the Synechococcus PCC7942 ArbcLS transformants are now being grown in the presence of 5%CO₂/95%N₂ to drive the *rbc*LS deletion to homoplasmicity.

Conclusion

Here we demonstrate that the tobacco chloroplast *rbc*L promoter and 5'UTR can drive expression of *R. rubrum* Rubisco in *Synechococcus* PCC7942 from a plasmid to levels of ~1% soluble protein. Expression of *R. rubrum* Rubisco from a similar construct in the tobacco chloroplast led to levels of ~5% total soluble protein (Whitney & Andrews 2001). This presumably highlights similarities in the transcriptional/translational machinery between chloroplasts and cyanobacteria. Indeed, it has previously been observed that expression of the chloroplast *rbc*LS operon of the non-green alga *Galdieria sulphuraria* can also occur from its own promoter in *Synechococcus* PCC7942 (unpublished observation). The generation of this new system for expressing foreign Rubiscos in *Synechococcus* PCC7942 will provide new information about folding and assembly of Rubisco and may also give new insights into the plasticity of the carbon concentrating and fixing mechanisms of cyanobacteria.

References

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