Enhanced translation of a chloroplast-expressed RbcS gene restores small subunit levels and photosynthesis in nuclear RbcS antisense plants

Amit Dhingra*, Archie R. Portis, Jr.,†, and Henry Daniell‡‡

*Department of Molecular Biology and Microbiology, University of Central Florida, 4000 Central Florida Boulevard, Biomolecular Science, Building 20, Room 336, Orlando, FL 32816-2364; and †Photosynthesis Research Unit, Agricultural Research Service, United States Department of Agriculture, and Departments of Crop Sciences and Plant Biology, University of Illinois at Urbana–Champaign, Urbana, IL 61801

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Ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) is the most prevalent enzyme on this planet, accounting for 30–50% of total soluble protein in the chloroplast; it fixes carbon dioxide, but oxygenase activity severely limits photosynthesis and crop productivity. Consequently, Rubisco is a primary target for genetic engineering. Separate localization of the genes in the nuclear and chloroplast genomes and a complex assembly process resulting in a very low catalytic activity of hybrid Rubisco enzymes have rendered several earlier attempts of Rubisco engineering unsuccessful. Here we demonstrate that the RbcS gene, when integrated at a transcriptionally active spacer region of the chloroplast genome, in a nuclear RbcS antisense line and expressed under the regulation of heterologous (gene 10) or native (psbA) UTRs, results in the assembly of a functional holoenzyme and normal plant growth under ambient CO2 conditions, fully short-circuiting nuclear control of gene regulation. There was ~150-fold more RbcS transcript in chloroplast transgenic lines when compared with the nuclear RbcS antisense line, whereas the wild type has 7-fold more transcript. The small subunit protein levels in the gene 10/RbcS and psbA/RbcS plants were 60% and 106%, respectively, of the wild type. Photosynthesis of gene 10/RbcS plants was approximately double that of the antisense plants, whereas that of psbA/RbcS plants was restored almost completely to the wild-type rates. These results have opened an avenue for using chloroplast engineering for the evaluation of foreign Rubisco genes in planta that eventually can result in achieving efficient photosynthesis and increased crop productivity.

It is evident that a completely functional eukaryotic Rubisco has never been assembled in any foreign host. Therefore, in this study, RbcS cDNA was engineered into a transcriptionally active spacer region of the chloroplast genome of nuclear RbcS antisense tobacco plant. In addition, two different 5’ UTRs were used to facilitate enhanced translation of the RbcS cDNA. This report demonstrates successful Rubisco expression and assembly from plastid-derived SSUs and LSUs of Rubisco to achieve normal plant growth under ambient CO2 conditions and photosynthesis.

Materials and Methods

Construction of Chloroplast Transformation Vectors. The RbcS cDNA was amplified by using PCR from the vector pTSa (a kind gift from Xing-Hai Zhang, University of Illinois at Urbana–Champaign, Urbana) incorporating an NcoI restriction enzyme site at the 5’ end to facilitate its cloning downstream to gene 10 and psbA 5’ UTRs. The gene 10 5’-UTR/RbcS cDNA and psbA promoter/5’-UTR/RbcS cDNA cassettes were cloned into the multiple cloning site of the basic chloroplast transformation vector pLD-CtV (16, 17) to yield pLDA10g10RbcS and pLDD410psbARbcS, respectively.

Chloroplast Transformation and Regeneration of Transgenic Plants. Seeds from nuclear RbcS antisense tobacco plants (12) were surface-sterilized and germinated on Murashige and Skoog salt
mixture without organic components (MSO)-kanamycin (50 mg/liter) media (18). All the germinating seedlings were resistant to kanamycin, indicating homozygous status of the transgene. Seedlings were transferred to small jars and maintained at 26°C under a 16-h light/8-h dark photoperiod. Leaves obtained from the nuclear RbcS antisense plants were used for particle bombardment, and these original mother plants were maintained in tissue culture or in soil to be used as controls for subsequent analysis.

Particle bombardment with the chloroplast transformation vectors pLDADg10RbcS and pLDADpsbARbcS was carried out as described (18). Putative chloroplast transgenic shoots were screened for site-specific integration of the transgene cassette by using PCR (detailed below). Positive shoots were subjected to another round of selection, and regenerating shoots were transferred to small jars containing Murashige and Skoog salt mixture without organic components (MSO)-spectinomycin (500 mg/liter) medium. After 3–4 weeks, plants were transferred to soil and maintained at 26°C under a 16-h light/8-h dark photoperiod in a growth chamber.

Continuous Illumination. Leaf samples of comparable age and morphology, grown under a normal photoperiod of 16-h light/8-h dark were harvested and frozen in liquid nitrogen for subsequent Northern and Western analyses (zero days (0D)). Light intensity was maintained at ~200 μE m−2 s−1 [1.5×105 erg cm−2 s−1] (E) is equal to 1 mol of photons [fluorescent lights]. Afterward, plants were kept under continuous light, and leaf tissue was harvested after 1, 3, or 5 days for Northern and Western analyses. The nuclear RbcS antisense line used for this study was the original mother plant from which the chloroplast transgenic plants were obtained.

PCR Screening and Southern Analysis. Total cellular DNA was isolated from 100 mg of leaf tissue by using DNeasy Plant Mini Kit (Qiagen, Valencia, CA). To investigate homoplasy, SmaI-digested total plant DNA was probed with the radiolabeled DNA fragment P1 (Fig. 1A). Prehybridization and hybridization were carried out per manufacturer protocol (Stratagene). The radiolabeled probe was prepared by using Ready-To-Go DNA labeling beads per manufacturer protocol (Amersham Pharmacia Biosciences). To confirm the presence of chloroplast-localized RbcS, total plant DNA from Nt-pLDADg10RbcS was digested with XbaI and that from Nt-pLDADpsbARbcS with SpeI. A radiolabeled 0.5-kb RbcS cDNA fragment was used as the probe to detect plastid-localized RbcS cDNA.

Northern Analysis. Total cellular RNA was isolated from leaves of similar developmental age by using RNeasy Plant Mini Kit (Qiagen). Northern blot analysis (5 μg of RNA per sample) was carried out as described (19). Northern blots were probed with a radiolabeled 0.5-kb RbcS cDNA fragment to detect relative RbcS transcript levels and a radiolabeled 0.9 Apal-digested fragment (P2) (Fig. 1A) representing 16S rRNA-encoding DNA. Relative transcript levels were measured by using spot densitometry (AlphaImager 3300, Alpha Innotech, San Leandro, CA). For the densitometric measurement of chloroplast transcripts, lane 1 (Fig. 2A and C) was used, and for determining the antisense and wild-type transcript ratio, lane 3 (Fig. 2A and C) was used. The measured values were plotted as a bar chart (Fig. 2B and D).

Protein Extraction and Western Analysis. Total soluble protein was extracted from 100 mg (fresh weight) of leaf tissue by using 2× Laemml buffer. Protein was quantified in three replicates by using the Bio-Rad RC-DC protein quantification kit per manufacturer protocol. An equal volume (10 μl) of the protein extract (qualitative analysis) or equal quantity (10 μg, quantitative analysis) of total soluble protein was subjected to 10% SDS/14% PAGE, and Western blot analysis was performed by using antibody against tobacco Rubisco (20). Alkaline phosphatase-linked secondary antibody was used to detect the Rubisco LSU and SSUs by using Lumi-Phos WB chemiluminescent reagent (Pierce). The SDS/PAGE gels were stained by using GelCode blue stain (Pierce). Relative SSU levels were measured by using spot densitometry (AlphaImager 3300, AlphaImager Corp.). The measured values were plotted as a bar chart (Figs. 3B and D and 4B and D).

Measurement of Photosynthetic CO2 Assimilation Rate. The photosynthetic CO2 assimilation rates were measured with an LI-6400 instrument (LI-Cor, Lincoln, NE). The following parameters were used: 28°C leaf temperature, 21% O2, 1,200 μmol m−2 s−1 light, 40% relative humidity, and CO2 concentration ranging from 0 to 1,200 μbar (1 bar = 100 kPa). Two leaves per plant of similar developmental age (~50 days old) were assayed.

Results and Discussion

Chloroplast Transformation Vectors. The tobacco chloroplast transformation vector pLD-CIV targets the transgene cassette to the 16S-rrn1/trnA-23S region of the chloroplast genome (Fig. 1A; see refs. 16 and 17 for details). To achieve enhanced transcription, the tobacco RbcS cDNA along with its transit peptide-coding sequence was cloned into the multiple cloning site of pLD-CIV downstream of two different 5′ UTRs. A psbA 3′ UTR is already present in pLD-CIV, which aids in transcript stability (21). The transit peptide sequence was retained for chloroplast expression in both the vectors, because it is probably involved in positively

**Fig. 1. (A) Schematic representation of the 16S-23S region of wild-type tobacco chloroplast genome. The BamHI/BglII restriction fragment, P1, was used as a probe to investigate homoplasy. The Apal restriction fragment, P2, was used as a probe to detect 16S RNA transcript levels in Northern analysis. Also shown are transgenic chloroplast genomes harboring pLDADg10RbcS (B) or pLDADpsbARbcS (C) as well as the annealing positions of primers 3P/3M and 5P/2M and expected ampiclon sizes. (D) PCR analysis with primer pair 3P/3M. Lane M, 1-kb DNA ladder; lanes 1 and 2, untransformed; lanes 3 and 4, Nt-pLDADg10RbcS; lanes 5 and 6, Nt-LDADpsbARbcS. (E) PCR analysis with primer pair 5P/2M. Lane M, 1-kb DNA ladder; lanes 1 and 2, untransformed; lanes 3 and 4, Nt-pLDADg10RbcS; lanes 5 and 6, Nt-pLDADpsbARbcS. (F) Southern blot analysis. Total DNA was digested with SmaI and probed with a radiolabeled BglII/BamHI fragment, P1. WT, untransformed; lanes 1 and 2, Nt-pLDADg10RbcS; lanes 3 and 4, Nt-pLDADpsbARbcS. (G) Southern blot analysis. Total DNA was probed with RbcS. Nt-pLDADg10RbcS was digested with XbaI (lanes 1 and 2) and Nt-pLDADpsbARbcS was probed with SpeI (lanes 3 and 4).**
affecting RbcS mRNA abundance and transcript stability in chloroplasts (11, 15).

In the chloroplast transformation vector pLDADg10RbcS, expression of the RbcS gene is regulated by a gene 10 5′ UTR (Fig. 1B). The gene 10 5′ UTR is derived from bacteriophage and is known to enhance translation in chloroplasts considerably when fused to endogenous promoters (22). In addition, it is free from developmental or light regulation, because it is derived from a foreign source. In this expression cassette, RbcS cDNA should be transcribed as a dicistron in the chloroplasts, because the upstream gene, aadA, is devoid of a 3′ UTR and the gene 10 5′ UTR is promoterless. In pLDADpsbARbcS, expression of the RbcS gene is regulated by the psbA promoter/5′ UTR (Fig. 1C). Because of the presence of a separate promoter, this expression cassette should produce an RbcS monocistron in addition to an aadA-RbcS dicistron.

Confirmation of Transgene Integration and Determination of Homoplasmy. Both chloroplast transformation vectors were introduced into the chloroplasts of nuclear RbcS antisense leaves via particle bombardment. The presence of an origin of replication in the chloroplast transformation vector allows the vector to replicate independently and provide more copies for integration, thus expediting the process of achieving homoplasmy even in the first round of selection (16, 17). After 4–5 weeks, resistant shoots were obtained on RMOP-spectinomycin (500 mg/liter) medium. Putative chloroplast transgenic clones were screened initially for site-specific transgene integration by using primer pair 3P and 3M. Primer 3P anneals to the DNA sequence upstream of the flanking region used in the chloroplast transformation vector, and primer 3M anneals within the aadA coding sequence (Fig. 1B). True chloroplast transgenic shoots should produce an amplicon of 1.65 kb that should be absent in nuclear transgenic plants or mutants. PCR data from two clones, each of which has incorporated the transgene cassette, harboring pLDADg10RbcS and pLDADpsbARbcS are shown (Fig. 1D). The presence of a 1.65-kb PCR product in the chloroplast transgenic plants confirms site-specific integration of the transgene cassette. To verify the presence of the complete transgene cassette, primers 5P and 2M were used. Primer 5P anneals within the aadA coding region, and 2M anneals to the right flanking region of the chloroplast transformation vector (Fig. 1B and C). Shoots that have incorporated the pLDADg10RbcS cassette produced a 2.15-kb amplicon, whereas shoots successfully transformed with the pLDADpsbARbcS vector produced a 2.3-kb amplicon (Fig. 1E). These PCR-positive shoots were divided into small pieces and placed on RMOP-spectinomycin medium for a second round of selection to achieve homoplasmy.

Homoplasmy was investigated by Southern blot analysis. Restriction digestion of total plant DNA with Smal should produce a 4.01-kb fragment in the wild-type plastome when probed with a BamHI/BglII radiolabeled fragment P1 (Fig. 1A). Plants successfully transformed with the pLDADg10RbcS and pLDADpsbARbcS should produce a fragment of 6.0 and 6.15 kb, respectively (Fig. 1B and C). Southern blot analysis confirmed the presence of a transformed plastid genome in the selected lines. The wild-type sample generated the predicted fragment of 4.01 kb, whereas samples from the Nt-pLDADg10RbcS and Nt-pLDADpsbARbcS generated the predicted fragment of 6.0 and 6.15 kb, respectively (Fig. 1F). Absence of a wild-type fragment of 4.01 kb in the chloroplast transgenic plants confirmed the homoplasmy in these plants; i.e., all the chloroplast genomes were uniformly transformed with RbcS cDNA. To confirm the presence of RbcS cDNA, total plant DNA from Nt-pLDADg10RbcS plants was digested with XbaI, and that from Nt-pLDADpsbARbcS was digested with SpeI. The presence

Fig. 2. Analysis of transcript levels under normal photoperiod (0D) or continuous light for 1, 3, and 5 days. (A) Nt-pLDADg10RbcS, (B) Densitometry analysis of the Northern blot shown in A. (C) Nt-pLDADpsbARbcS. (D) Densitometry analysis of the Northern blot shown in C. Lanes 1–3 represent the Northern blot exposed for different durations. Cy-RbcS, cytosolic RbcS mRNA (900 nt); plastid (P1) 16S rRNA (1,490 nt) was used as a control for equal loading (lane 4). (E) Relative RbcS transcript levels in wild-type and RbcS antisense plant (v5). An equal amount of RNA (5 μg) was loaded per sample.
of 0.60-kb (Nt-pLDADg10RbcS) and 0.73-kb (Nt-pLDADps-bARbcS) fragments in the Southern blots probed with a radio-labeled RbcS cDNA fragment confirmed the presence of RbcS cDNA (Fig. 1G).

**Transcript Analysis of RbcS in Chloroplast Transgenic Plants.** The chloroplast-expressed RbcS cDNA is composed of the transit peptide sequence along with the coding sequence for the SSU of Rubisco. The nuclear RbcS transcript is ~900 nt long, and it encodes the SSU precursor (12). In Nt-pLDADg10RbcS plants, RbcS cDNA is expressed under the regulation of a promoterless gene 10 5’ UTR. The RbcS cDNA thus should be transcribed as a dicistron of ~1,630 nt. Total cellular RNA isolated from a nuclear RbcS antisense plant, an Nt-pLDADg10RbcS plant grown under normal photoperiod (0D) or exposed to continuous light for 1, 3, or 5 days, and a wild-type tobacco plant were probed with radiolabeled RbcS cDNA. From the autoradiogram, it is evident that the aadA/RbcS dicistron (1,630 nt) is highly abundant, whereas the nuclear transcript (900 nt) is barely detectable (Fig. 2A, lane 2). The blot had to be exposed for a longer duration to perform densitometry analysis (Fig. 2A, lanes 1 and 3). Densitometry analysis revealed that at 0D, the plastid- derived RbcS transcript was 143-fold more than the transcript levels in the nuclear RbcS antisense plant (Fig. 2B), which is in sharp contrast to an only 20-fold increase in plastid-derived RbcS transcript level observed in an earlier study in which the transgene was integrated into the single-copy region of the tobacco chloroplast genome (15). The RbcS transcript levels in the wild type were only 6.8-fold that of the antisense, similar to that derived wild-type tissue (100 mg) was subjected to SDS-PAGE. The large increase (20- to 25-fold) in steady-state RbcS transcript levels in chloroplast transgenic plants as compared with the wild type can be attributed partly to the high copy number (~20,000) of the chloroplast-engineered gene when integrated into the inverted repeat region. All the earlier efforts of manipulating the chloroplast genome for Rubisco engineering integrated the transgene into transcriptionally silent regions. The site of integration used here is the intergenic region between the trn-t-rnA genes in the rrn operon present in the inverted repeat regions of the tobacco chloroplast genome. This site is transcribed as a monocistron and the dicistron should be 890 and 1,760 nt long, respectively. The Northern blot had to be exposed for a longer duration to perform densitometry analysis (Fig. 2A, lanes 1 and 3). Densitometry analysis revealed that at 0D, the plastid-derived RbcS transcript was 143-fold more than the transcript levels in the nuclear RbcS antisense plant (Fig. 2B), which is in sharp contrast to an only 20-fold increase in plastid-derived RbcS transcript level observed in an earlier study in which the transgene was integrated into the single-copy region of the tobacco chloroplast genome (15). As expected, there was no increase in RbcS transcript duration exposure to light in the chloroplast-engineered plant. The Northern blot had to be exposed to observe the nuclear transcript in the nuclear RbcS antisense and wild-type plants.

In Nt-pLDADpsbARbcS line, RbcS is expected to be transcribed as a monocistron as well as an aadA/RbcS dicistron. The monocistron and the dicistron should be 890 and 1,760 nt long, respectively. (Fig. 2C). In this case also, the nuclear transcripts were undetectable after normal exposure of the blot (Fig. 2C, lane 2). Therefore, the blot was exposed for a longer duration to perform densitometry analysis. Based on densitometry analysis, the chloroplast-derived RbcS transcripts were 165-fold more than the transcript levels in the nuclear RbcS antisense plants (Fig. 2D). In an earlier study, RbcS was engineered into a transcriptionally silent region of the chloroplast genome, but the transcript abundance was only 5-fold more than the nuclear- derived wild-type RbcS transcript levels (6); no RbcS antisense plants were used in this study, and a direct comparison could not be made. However, we report here a 25-fold increase in RbcS transcript abundance over the wild-type nuclear transcript level. As expected, there was no discernible effect of continuous light exposure on transcription of RbcS cDNA (Fig. 1F). In an earlier study, SSU levels in Nt-pLDADg10RbcS plants were only 6.8-fold that of the antisense, similar to that derived wild-type nuclear transcript level. The Northern blot had to be exposed for a longer duration to perform densitometry analysis (Fig. 2A, lanes 1 and 3). Densitometry analysis revealed that at 0D, the plastid-derived RbcS transcript was 143-fold more than the transcript levels in the nuclear RbcS antisense plant (Fig. 2B), which is in sharp contrast to an only 20-fold increase in plastid-derived RbcS transcript level observed in an earlier study in which the transgene was integrated into the single-copy region of the tobacco chloroplast genome (15). As expected, there was no increase in RbcS transcript duration exposure to light in the chloroplast-engineered plant. The Northern blot had to be exposed to observe the nuclear transcript in the nuclear RbcS antisense and wild-type plants.

The second chloroplast transformation vector has the psbA promoter/5’ UTR regulating the expression of RbcS cDNA. All plants were analyzed further for total protein and the level of SSUs and LSUs (Fig. 3A and C). On an equal fresh-weight basis, both transformed lines Nt-pLDADg10RbcS and Nt-pLDADps-bARbcS contained a higher level of total soluble protein when compared with nuclear antisense and the wild-type plants. This result is in contrast to observations made earlier in which RbcS cDNA was expressed under the regulation of the Shine–Dalgarno (GGAGG) sequence in the chloroplast genome of nuclear RbcS antisense plants. In that study, the total soluble protein on an equal leaf-area basis in the chloroplast transgenic plant was similar to the nuclear RbcS antisense plants and one third of wild type (15). In the present study, an equal volume (10 µl) of protein sample derived from equal fresh weight of leaf tissue (100 mg) was subjected to SDS-PAGE. The total protein content in leaves of Nt-pLDADg10RbcS under a normal photoperiod (0D) was 2.4- and 2.0-fold more when compared with the nuclear antisense and wild type, respectively (Fig. 3A). Furthermore, there was a 2.3-fold increase in the total protein content in these transgenic plants by the fifth day of continuous light exposure (Fig. 3A). The higher level of protein under a normal photoperiod (0D) was accompanied by an increased level of SSU, which was 102% when compared with the wild type by Western blot analysis (Fig. 3B). A corresponding increase in the level of LSU is clearly visible in the stained protein gel.

Similarly, the total soluble protein in leaves of Nt- pLDADpsbARbcS under a normal photoperiod (0D) was 1.6- and 1.3-fold more when compared with nuclear antisense and wild type, respectively (Fig. 3C). There was a 3.0-fold increase in the total soluble protein in these transformed plants on the fifth day of continuous light exposure. Western blot analysis revealed that SSU levels in Nt-pLDADpsbARbcS plant exposed to continuous light for 3 days were 107% of wild-type levels (Fig. 3D).

**Quantitative Analysis of SSU.** SDS gel electrophoresis and Western blots were carried out also by using an equal quantity of protein (i.e., 10 µg per sample). In the Nt-pLDADg10RbcS plant, the percentage SSU level was 58% greater under normal photope-
that the expression of \( RbcS \) and \( rbcL \) is coordinated by adjustments of subunit stoichiometries in response to the abundance of unassembled subunits (13, 29). The question that arises then is: Do the \( rbcL \) transcripts (10,000 copies in the large single-copy region) and LSU levels become limiting for SSU assembly?

The presence of abundant SSU in the chloroplast transgenic lines indicates that posttranslational cleavage of its transit peptide and assembly into the holoenzyme was achieved successfully inside the chloroplast. In light of this observation, most of the arguments put forth in an earlier, unsuccessful study regarding inefficient posttranslational modification of chloroplast-synthesized SSU (11) have been overcome in our investigations. Expression of foreign proteins from the transcriptionally active \( trnI-trnA \) intergenic region has resulted in the highest level of foreign protein accumulation ever reported in plants, i.e., 46.1% (30). Also, proteins ranging from 11 to 83 kDa in size have been expressed successfully (31, 32) at very high levels. The \( trnI-trnA \) intergenic region has also allowed for single-step multigene engineering for insect resistance and phytoremediation (30, 33, 34). Successful engineering of 11 biopharmaceutical proteins, vaccine antigens, and 6 agronomic traits (for herbicide, insect, disease resistance, drought/salt tolerance, phytoremediation, etc) at this intergenic site make it a preferred site for chloroplast genetic engineering in general (18, 35).

**Plant Growth and Photosynthetic CO\(_2\) Assimilation Rate.** The nuclear \( RbcS \) antisense plants are easily distinguishable from wild-type
plants, because they have retarded growth and delayed flowering (14). Expression of a promoterless gene 10 5'-UTR-regulated RbcS cDNA in the chloroplasts of nuclear RbcS antisense plant (Nt-pLDADg10RbcS line) resulted in a phenotype that was similar to the wild-type plants under the growth conditions used. However, these plants started flowering ~27–35 days earlier than the wild-type plants (data not shown) for reasons that remain to be determined. A similar observation was made for five different Nt-pLDADg10RbcS transgenic lines. Comparison between the 29-day-old (after transfer to soil) Nt-pLDADg10RbcS line and wild-type plant is shown in Fig. 5A. Expression of psbA 5'-UTR-regulated RbcS cDNA in the Nt-pLDAD-psbARbcS plants also resulted in the restoration of normal growth and flowering time.

Young, fully expanded leaves were subjected to gas-exchange measurements for determining photosynthetic CO2 assimilation. Photosynthesis of the Nt-pLDADpsbARbcS plants was nearly restored to the wild-type level (Fig. 5B), indicating increased Rubisco activity in the chloroplast transgenic line derived from nuclear RbcS antisense plant. The initial slope of the CO2 response curve, which is determined by the amount and activity of Rubisco, in the Nt-pLDADg10RbcS line, is comparable with the wild type. Photosynthesis of the Nt-pLDADg10RbcS line was not restored completely, but it was ~2-fold greater than that of the nuclear RbcS antisense plant as determined by comparison of the initial slope of CO2 assimilation.

Conclusions

Successful complementation of the SSU deficiency in a nuclear RbcS antisense line by chloroplast-derived SSU opens avenues for additional research in this field, which has been seriously limited by our inability to engineer RbcS genes via the chloroplast genome. Genetic engineering of Rubisco has been complicated by the separate location of its genes, mechanisms that integrate gene expression in the chloroplast and nucleus, and the low catalytic ability of hybrid Rubisco proteins obtained previously with chloroplast or nuclear transformation. Existing eu-karyotic Rubiscos with kinetic properties that can result in greater photosynthesis if introduced into C3 crop plants are being identified by biochemical analysis and improved modeling of photosynthesis, which takes into account the crop canopy structure (36). However, demonstrating that a foreign Rubisco will undergo possibly essential posttranslational modifications and whether it can be properly assembled and expressed at a high level in a foreign host has not been feasible yet. The ability to express the SSU gene successfully from the chloroplast genome, as we have demonstrated here, will facilitate the expression and analysis of foreign Rubisco genes, because only chloroplast transformation will be required and both genes can be engineered simultaneously in a single compartment. Then, the ability of a selected foreign Rubisco to increase photosynthesis and crop productivity can be evaluated further in planta. Use of a nuclear rbcS antisense line to hyperexpress mutant or foreign RbcS genes in the chloroplast genome also can serve as a model system to study the dynamics of Rubisco assembly. For example, continued study of the transformed plants created here should provide additional insights into the mechanisms controlling Rubisco expression, because nuclear control via the regulation of SSU expression has been short-circuited. Specifically, consequences of the physical relocation of the RbcS gene into its pre-evolutionary state on the processing of SSU and effect of light and developmental cues on the expression of RbcS gene can be elucidated. It will be vital to determine whether nuclear control of Rubisco expression is necessary for a proper response to external signals in the environment and thus maximal growth. Consequently, the approach and methods developed here should greatly facilitate future Rubisco engineering to achieve the long-cherished goal of increasing plant productivity.

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