

Rubisco small subunits from the unicellular green alga *Chlamydomonas* complement Rubisco-deficient mutants of *Arabidopsis*

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Summary

- Introducing components of algal carbon concentrating mechanisms (CCMs) into higher plant chloroplasts could increase photosynthetic productivity. A key component is the Rubisco-containing pyrenoid that is needed to minimise CO₂ retro-diffusion for CCM operating efficiency.
- Rubisco in *Arabidopsis* was re-engineered to incorporate sequence elements that are thought to be essential for recruitment of Rubisco to the pyrenoid, namely the algal Rubisco small subunit (SSU, encoded by *rbcS*) or only the surface-exposed algal SSU α -helices.
- Leaves of *Arabidopsis rbcS* mutants expressing 'pyrenoid-competent' chimeric *Arabidopsis* SSUs containing the SSU α -helices from *Chlamydomonas reinhardtii* can form hybrid Rubisco complexes with catalytic properties similar to those of native Rubisco, suggesting that the α -helices are catalytically neutral.
- The growth and photosynthetic performance of complemented *Arabidopsis rbcS* mutants producing near wild-type levels of the hybrid Rubisco were similar to those of wild-type controls. *Arabidopsis rbcS* mutants expressing a *Chlamydomonas* SSU differed from wild-type plants with respect to Rubisco catalysis, photosynthesis and growth. This confirms a role for the SSU in influencing Rubisco catalytic properties.

Introduction

Rubisco (EC 4.1.1.39) catalyses net CO₂ assimilation in all photosynthetic organisms. Despite this central role, Rubisco is an inefficient enzyme that limits photosynthetic productivity, particularly in plants with the C₃ photosynthetic pathway. Rubisco has a slow carboxylation rate (k_{cat}) and a relatively low affinity for CO₂, with a K_m for CO₂ at ambient O₂ (K_c^{air}) close to the CO₂ concentration in a C₃ leaf mesophyll cell (Galmés *et al.*, 2014). Rubisco also catalyses D-ribulose-1,5-bisphosphate (RuBP) oxygenation, resulting in the energetically expensive photorespiratory pathway where previously fixed CO₂ is lost (Sharkey, 1988). These features necessitate a large investment in the enzyme (up to 50% of leaf soluble protein) to support adequate rates of CO₂ assimilation (Parry *et al.*, 2013). Increasing the operating efficiency of Rubisco and reducing photorespiration are important approaches for improving yields in C₃ crop plants (Whitney *et al.*, 2011; Parry *et al.*, 2013; Carmo-Silva *et al.*, 2015; Long *et al.*, 2015; Ort *et al.*, 2015).

The operating efficiency of Rubisco in C₃ plants could be enhanced by elevating the CO₂ concentration in the

chloroplast by means of carbon concentrating mechanisms (CCMs). Possibilities include using components of biochemical CCMs (as in C₄ and CAM photosynthesis) and/or the biophysical inorganic carbon accumulation mechanisms from cyanobacteria and eukaryotic algae (von Caemmerer *et al.*, 2012; Price *et al.*, 2013; Meyer *et al.*, 2016). In algal CCMs, bicarbonate transporters and localisation of Rubisco and carbonic anhydrase within the chloroplast, and in most instances within the pyrenoid (a microcompartment commonly present in chloroplasts of microalgae), result in saturating CO₂ concentrations around Rubisco (Morita *et al.*, 1998; Giordano *et al.*, 2005; Wang *et al.*, 2015). Modelling approaches suggest that algal CCMs with a pyrenoid are likely to be more effective in maintaining elevated CO₂ concentrations around Rubisco than those without (Badger *et al.*, 1998). Modelling also reveals that the confinement of Rubisco to a microcompartment would be required for effective operation of a biophysical CCM in a higher plant (Price *et al.*, 2013; McGrath & Long, 2014). Recent work has shown that algal CCM components, including carbonic anhydrases and bicarbonate transporters, can be expressed in

appropriate subcellular locations in angiosperms (Atkinson *et al.*, 2016). To achieve a functional algal CCM in an angiosperm it will also be necessary to introduce a Rubisco capable of assembling into a pyrenoid-like structure.

Pyrenoid formation in the model green alga *Chlamydomonas reinhardtii* (hereafter *Chlamydomonas*) depends on the amino acid sequences of the small subunit of Rubisco (SSU, encoded by the *rbcS* nuclear gene family) and, more specifically, on two surface-exposed α -helices, which differ markedly between *Chlamydomonas* and higher plants (Meyer *et al.*, 2012). In *Chlamydomonas*, *rbcS* deletion mutants can be rescued with a SSU variant from angiosperms (*Arabidopsis*, spinach or sunflower) without compromising *in vitro* Rubisco catalysis (Genkov *et al.*, 2010). However, these hybrid Rubisco no longer assembled into a pyrenoid. Accordingly, lines expressing the hybrid Rubisco lacked a functional CCM, resulting in growth only at high CO₂. Pyrenoid formation and CCM function were restored by expression of a chimeric SSU, where a higher plant SSU was modified with the algal SSU α -helices (Meyer *et al.*, 2012). Thus, assembling a pyrenoid-like micro-compartment in chloroplasts would probably require the incorporation of *Chlamydomonas*-like α -helical sequence into the native angiosperm SSU, in addition to other proteins involved in pyrenoid formation such as the Rubisco-associated protein EPYC1 (Mackinder *et al.*, 2016).

Here we examine how the incorporation of SSUs with α -helices from *Chlamydomonas* SSU influences the biogenesis and catalysis of Rubisco in *Arabidopsis* leaves. The Rubisco large subunits (LSUs, encoded by *rbcL*) harbour the catalytic sites and are highly conserved between algae and angiosperms (*Arabidopsis* and *Chlamydomonas* LSUs are 88% identical at the level of amino acid sequences). By contrast, the SSU isoforms of *Arabidopsis* and *Chlamydomonas* are only 40–43% identical, even though their tertiary structures are extremely similar, including the positions of the α -helices (Spreitzer, 2003). Although located on the distal ends of the octameric LSU core of Rubisco and distant from the catalytic sites, the amino acid sequence of the SSUs can affect the catalytic properties of the enzyme (Genkov & Spreitzer, 2009).

In *Arabidopsis* the SSUs are encoded by four genes. *rbcS1A* on chromosome 1 accounts for ~50% of SSU transcript, the remainder being contributed by the *rbcS1B*, *rbcS2B* and *rbcS3B* genes located contiguously on chromosome 5 (Yoon *et al.*, 2001). An *Arabidopsis* double mutant lacking expression of *rbcS1A* and with strongly reduced expression of *rbcS3B* (the *1a3b* mutant) has a low Rubisco content (30% of wild-type plants) and slow growth (Izumi *et al.*, 2012). In this study the *1a3b* mutant was complemented with either the *Arabidopsis* *rbcS1A* (control), an *rbcS1A* variant encoding the *Chlamydomonas* α -helix sequences or the native *rbcS2* gene from *Chlamydomonas*. We compared the Rubisco content, catalytic properties, leaf photosynthesis and growth of multiple lines for each genotype produced. Our results show that the *1a3b* mutant is a valuable background for attempts to assemble an algal CCM in an angiosperm chloroplast, and for wider examination of the contribution made by SSU genetic diversity to Rubisco properties.

Materials and Methods

Plant material and growth conditions

Arabidopsis (*Arabidopsis thaliana* (L.) Heynh. Col-0) seeds were sown on compost, stratified for 3 d at 4°C and grown at 20°C, ambient CO₂, 70% relative humidity and 150 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ in 12 : 12 h light : dark. For comparisons of different genotypes, plants were grown from seeds of the same age and storage history, harvested from plants grown in the same environmental conditions. Tobacco (*Nicotiana benthamiana* L.) was cultivated in a glasshouse (minimum 20°C, natural light supplemented to give light periods of at least 12 h). An *Arabidopsis* *rbcS1a rbcS2b* mutant (double mutant *1a2b*) was generated by crossing T-DNA insertion lines GABI_608F01 (At1g67090) and GABI_324A03 (At5g38420). The *1a3b* mutant (GABI_608F01 (At1g67090); SALK_117835 (At5g38410)) was provided by Hiroyuki Ishida, Department of Applied Plant Science, Tohoku University, Japan.

DNA and RNA extraction, PCR and RT-qPCR

Genomic DNA was extracted from rosettes according to Li & Chory (1998). PCRs were performed as in McCormick & Kruger (2015) using gene-specific primers (Supporting Information Table S1). Insertion copy numbers were obtained by quantification of 35S promoter copies (performed by iDNA Genetics, www.idnagenetics.com). mRNA was isolated from the sixth and seventh leaves of 28-d-old rosettes and complementary DNA was synthesized with oligo(dT) primers. Reverse transcription quantitative PCR (RT-qPCR) was carried out as in Andriotis *et al.* (2010). Primers to test for expression of SSU genes were designed to amplify the unique 3' region of the transcripts (Table S1). Amplification efficiency was determined with a calibration curve for each primer set. Three reference genes (At4g05320 (*UBQ10*), At1g13320 (*PP2A*) and At4g26410 (*RHIP1*) (Czechowski *et al.*, 2005)) were used for normalisation. Calculations of relative expression ratios were performed according to Pfaffl (2001).

Expression of *rbcS* genes in *N. benthamiana* and *Arabidopsis* *1a3b* mutants

The α -helices of *rbcS1A* (At1g67090) were replaced with those from the *Chlamydomonas* *rbcS* family (Fig. 1) using overlapping PCR with Phusion[®] High-Fidelity DNA polymerase (as per the manufacturer's instructions; New England BioLabs). The promoter region (2 kb) upstream of *rbcS1A* was fused to the complete cDNA sequences of native or modified SSUs. The *rbcS1A* chloroplast transit peptide (TP) sequence was fused to the mature *Chlamydomonas* *rbcS2* (Cre02.g120150) (Goldschmidt-Clermont & Rahire, 1986) cDNA before promoter addition. Promoter–cDNA fusions were cloned into Gateway Entry vectors (pCR[®]8/GW/TOPO[®]TA Cloning[®] Kit; Thermo Fisher Scientific), then into the binary destination vector pGWB4 (Nakagawa *et al.*, 2009) or pB7WG (Karimi *et al.*, 2002) (Notes S1). Stop codons were removed to allow in-frame C-terminal

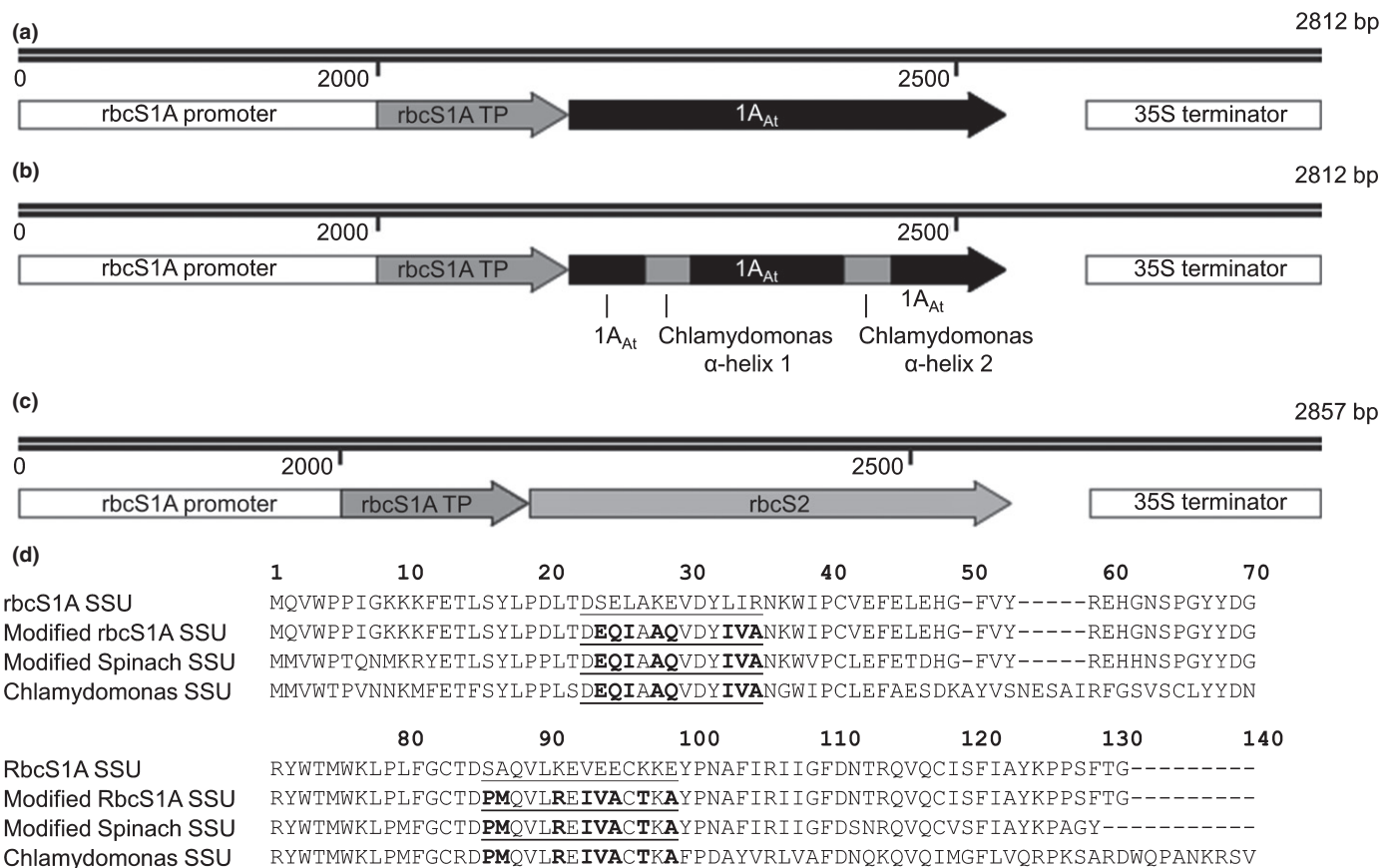


Fig. 1 Gene expression cassettes for native and heterologous Rubisco small subunits. *rbcS1A* from *Arabidopsis thaliana* (1A_{At}) (a), *rbcS1A* with α -helices from the *Chlamydomonas reinhardtii* *rbcS* family (1A_{At}/MOD) (b), and mature *rbcS2* from *Chlamydomonas* (S2_{Ct}) (c) were expressed using the *rbcS1A* promoter (not drawn to scale) and 35S terminator. For S2_{Ct}, the chloroplast transit peptide (TP) of *Chlamydomonas rbcS2* (45 amino acids) was replaced with the *rbcS1A* TP (55 amino acids) from *Arabidopsis* to facilitate localisation of the mature *rbcS2* to the chloroplast. (d) Alignments of the mature SSU peptides generated in this study. Numbering is relative to the *Chlamydomonas rbcS2* sequence. Residues that comprise the two α -helices A and B are underlined, and those different from *rbcS1A* are in bold. For comparison with 1A_{At}/MOD, the modified spinach SSU generated by Meyer *et al.* (2012) is included.

fusion to a sequence encoding green fluorescent protein (GFP) in pGWB4. Binary vectors were transformed into *Agrobacterium tumefaciens* (AGL1) for transient gene expression in tobacco (Schöb *et al.*, 1997) or stable insertion in *Arabidopsis* plants by floral dipping (Clough & Bent, 1998). Homozygous insertion lines were identified in the T₃ generation by seedling segregation ratios on Murashige & Skoog (MS) medium (half-strength) plates containing phosphinothricin (BASTA[®], final concentration 10 ng μ l⁻¹) as a selectable marker. Lines used for subsequent analysis were checked for the presence of T-DNA insertions at the *rbcS1A* and *rbcS3B* loci.

Protein quantification and Rubisco content

For determination of leaf protein and Rubisco contents on an area basis, soluble protein was extracted from 2 cm² of snap frozen leaf material from 32-d-old plants (sixth and seventh leaf) in 500 μ l of 50 mM Tricine-NaOH (pH 8.0), 10 mM EDTA, 1% (w/v) PVP₄₀, 20 mM 2-mercaptoethanol, 1 mM phenylmethylsulfonyl fluoride and 10 μ M leupeptin. Following

centrifugation at 2380 g for 5 min at 4°C, soluble protein was quantified using a Bradford-based assay (Bio-Rad) against BSA standards (Thermo Fisher Scientific). Rubisco content was determined in an aliquot of the extract via ¹⁴C-CABP (carboxy-D-arabinitol 1,5-bisphosphate) binding following incubation with 10 mM NaHCO₃, 20 mM MgCl₂ and the addition of 3 μ l 12 mM ¹⁴C-CABP (37 MBq mmol⁻¹) for 25 min at room temperature (Whitney *et al.*, 1999).

Subunit ratios were estimated by immunoblotting. Extracts were subjected to sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE) on a 4–12% (w/v) polyacrylamide gel (Bolt[®] Bis-Tris Plus Gel; Thermo Fisher Scientific), transferred to polyvinylidene fluoride (PVDF) membrane then probed with rabbit serum raised against wheat Rubisco at 1 : 10 000 dilution (Howe *et al.*, 1982) followed by Li-Cor IRDye[®] 800CW goat anti-rabbit IgG (Li-Cor Inc.) at 1 : 10 000 dilution, then viewed on a Li-Cor Odyssey CLx Imager. The contributions of LSU and SSUs were estimated from a five-point standard curve of a wild-type sample of known Rubisco content (0.1–2.4 μ g Rubisco).

Rubisco catalytic properties

Whole 45-d-old rosettes (20–30 cm²) were rapidly frozen in liquid nitrogen (N₂) and Rubisco was extracted as described by Prins *et al.* (2016), then activated for 45 min on ice before assays were conducted at 25°C. Catalytic properties of Rubisco from wild-type and transgenic lines were determined from ¹⁴CO₂ consumption, essentially as described by Prins *et al.* (2016) with alterations as per Orr *et al.* (2016), using 40 µl of extract. Six CO₂ concentrations were used with O₂ concentrations of 0 and 21%.

Rubisco specificity factor was determined on Rubisco purified from each genotype from *c.* 300 cm² rosette tissue using the method described by Prins *et al.* (2016), with the omission of the final Sephacryl S-200 step, which was found to be unnecessary for obtaining a clean extract (Orr *et al.*, 2016). Rubisco CO₂/O₂ specificity ($S_{C/O}$) was determined using the method of Parry *et al.* (1989). At least 10 measurements were made on the Rubisco purified from each genotype. Values were normalised based on measurements made in the same experiment on purified wheat (*Triticum aestivum*) Rubisco, which has an established $S_{C/O}$ of 100 (Parry *et al.*, 1989).

Chlorophyll quantification

Leaf discs (*c.* 10 mg fresh weight) were frozen in liquid N₂, powdered, and then mixed with 100 volumes of ice-cold 80% (v/v) acetone, 10 mM Tris–HCl. Following centrifugation at 17 200 g for 10 min, chlorophyll was quantified according to Porra *et al.* (1989).

Measurement of photosynthetic parameters

Gas exchange and chlorophyll fluorescence were determined using a Li-Cor LI-6400 portable infra-red gas analyser with a 6400-40 leaf chamber on either the sixth or the seventh leaf of 35- to 45-d-old nonflowering rosettes grown in large pots to generate leaf area sufficient for gas exchange measurements (Flexas *et al.*, 2007). For all gas exchange experiments, leaf temperature and chamber relative humidity were 20°C and *c.* 70%, respectively. Gas exchange data were corrected for CO₂ diffusion from the measuring chamber as in Bellasio *et al.* (2016). Light response curves for net photosynthetic CO₂ assimilation (*A*) were generated at ambient CO₂ (400 µmol mol⁻¹). A nonrectangular hyperbola was fitted to the light response (Marshall & Biscoe, 1980; Thornley, 1998). The response of *A* to varying substomatal CO₂ concentration (*C*_i) was measured at 1500 µmol photons m⁻² s⁻¹. To calculate the maximum rate of Rubisco carboxylation (*V*_{c,max}) and the maximum photosynthetic electron transport rate (*J*_{max}), the *A/C*_i data were fitted to the C₃ photosynthesis model as in Ethier & Livingston (2004) using the catalytic parameters *K*_{c^{air}} and affinity for O₂ (*K*_o) values for wild-type Arabidopsis Rubisco at 20°C as reported in Walker *et al.* (2013). For estimates of the ratio of Rubisco oxygenase to carboxylase activity (*V*_o/*V*_c), leaves were measured under

photorespiratory (ambient oxygen (O₂), 21% (v/v)) or low-photorespiratory (low O₂, 2% (v/v)) conditions (Bellasio *et al.*, 2014).

Maximum quantum yield of photosystem II (PSII) (*F*_v/*F*_m) was measured using a Hansatech Handy PEA continuous excitation chlorophyll fluorimeter (Hansatech Instruments) (Maxwell & Johnson, 2000). Nonphotochemical quenching (NPQ) analyses were performed using a Hansatech FMS1 pulse-modulated chlorophyll fluorimeter. Rapid light response curves were generated by measuring the fluorescence response to a saturating pulse (applied every 30 s) under increasing levels of actinic light (0–1500 µmol photons m⁻² s⁻¹). Quenching parameters, including NPQ_s and NPQ_f, were derived as in Griffiths & Maxwell (1999).

Confocal laser scanning microscopy

Leaves were imaged with a Leica TCS SP2 laser scanning confocal microscope (Leica Microsystems) as in Atkinson *et al.* (2016).

Results

The *1a3b* mutant of Arabidopsis provided a suitable genotype for examining the influence of heterologous SSUs on leaf photosynthesis and growth. Some aspects of the *1a3b* mutant phenotype may reflect loss of distinct Rubisco isoforms (i.e. forms with different SSU compositions), as well as loss of total Rubisco activity. As a first step to evaluate this possibility, a second mutant, lacking expression of *rbcS1A* and a different minor SSU, *rbcS2B* (the *1a2b* mutant) was included in some of the analyses. Quantification of T-DNA copy numbers indicated that neither double mutant contained T-DNA insertions other than those at their respective *rbcS* loci.

Design and targeting of native and heterologous SSUs

Binary vectors were generated to express either the full-length native Arabidopsis *rbcS1A* (1A_A), the mature Chlamydomonas *rbcS2* N-terminally fused to the chloroplast TP sequence from Arabidopsis *rbcS1A* (S2_C), or the full-length Arabidopsis *rbcS1A* modified to contain α-helices matching the amino acid sequence as those of the Chlamydomonas SSU family (1A_AMOD) (Fig. 1; Notes S1). Chlamydomonas and Arabidopsis SSU α-helices have the same number of amino acids, but differ in terms of chemical composition. Expression of the introduced proteins was driven by the promoter of Arabidopsis *rbcS1A*, which has the highest expression level of the Arabidopsis *rbcS* genes (Izumi *et al.*, 2012).

To check the subcellular locations of introduced SSUs, they were initially generated as C-terminal fusions to GFP and transiently expressed in leaves of *N. benthamiana*. Fluorescence microscopy revealed that all three fusion proteins were located in the chloroplast stroma (Fig. S1). Untagged SSUs were then stably expressed in the Arabidopsis *1a3b* mutant.

Expression levels, leaf protein and Rubisco content of native and heterologous SSU isoforms

In wild-type plants, *rbcs1A* transcripts were the most abundant (43% of the *rbcs* pool), followed by *rbcs3B* (28%), *rbcs2B* (21%) and *rbcs1B* (8%) (Fig. 2; Table S2). The *1a3b* mutant had no detectable transcript for *rbcs1A* and much reduced levels of transcript for *rbcs3B* (c. 10% of wild-type levels). Both *rbcs1A* and *rbcs2B* transcripts were below the level of detection in the *1a2b* mutant. In the *1a3b* mutant, transcript levels for the two undisrupted *rbcs* genes, *rbcs1B* and *rbcs2B*, were 50 and 170% of those in wild-type plants, respectively. In the *1a2b* mutant, *rbcs1B* and *rbcs3B* transcript levels were 120 and 140% of those in wild-type plants, respectively. For both mutants, transcript levels for *rbcl* (ATCG00490) and for the overall *rbcs* pool were 50% of those in wild-type plants.

For each of the three transgenic genotypes expressing native or heterologous SSUs in the *1a3b* mutant background, at least six independent lines segregated in the T₂ generation. Transgenic plants were screened for faster growth rates and maximum quantum yield of PSII (measured by dark-adapted leaf fluorescence; F_v/F_m) compared to the *1a3b* mutant (Fig. S2). For further analysis, homozygous T₃ lines for each genotype were selected from the three best-performing T₂ segregating lines.

For each line of each transgenic genotype, transcript levels for the inserted transgene were comparable to those of the native *rbcs1A* gene in wild-type plants (Fig. 2; Table S2). Levels of transcript of the undisrupted native Rubisco genes were altered in these lines relative to wild-type plants. For *rbcl*, transcript levels were higher in transgenic than in *1a3b* mutant plants, and in at least one independent line for each construct they were as high as in wild-type plants. As in *1a3b* mutants, transcript levels for *rbcs2B* in transgenic plants were generally higher than those in wild-type plants (Fig. 2; Table S2).

The leaf Rubisco content in the *1a3b* and *1a2b* mutants was reduced by 70 and 50%, respectively, relative to wild-type plants (Fig. 3a). Total soluble protein content in leaves of the mutants was also c. 60% of wild-type values in both cases. This reduction

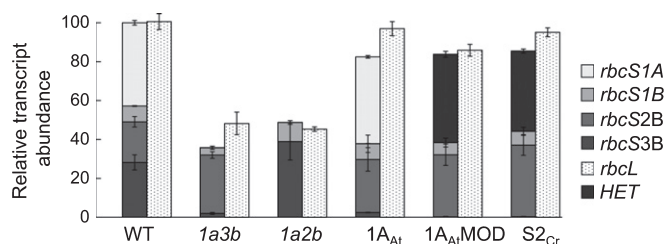


Fig. 2 Transcript abundances of the Rubisco gene family in *rbcs* mutants and transgenic lines of *Arabidopsis thaliana*. Abundances of *rbcs1A* (At1g67090), *rbcs1B* (At5g38430), *rbcs2B* (At5g38420), *rbcs3B* (At5g38410) and *rbcl* (Atcg00490) transcripts were quantified relative to wild-type levels (set at 100) from 28-d-old rosettes using RT-qPCR with gene-specific primers (Supporting Information Table S1). For wild-type, *1a3b* and *1a2b* values are the means \pm SE of measurements made on three individual 28-d-old rosettes. For transgenic lines values are means \pm SE of measurements made on nine rosettes, three from each of the three lines. Full expression data are shown in Table S2. HET, heterologous *rbcs*.

was larger than could be accounted for by the reduction in Rubisco content alone (Fig. 3b; Table S3).

Complementation of the *1a3b* mutant restored total Rubisco to 75% of wild-type levels for 1A_{At} and 1A_{At}MOD lines, and to 65% of wild-type levels for S2_{Cr} lines. Immunoblotting revealed that the heterologous SSUs 1A_{At}MOD and S2_{Cr} had different mobilities on SDS-PAGE gels from the native SSUs (Fig. 3c). This enabled quantification of the relative contributions of the LSU, the native SSUs and the heterologous SSUs to total Rubisco content (Fig. 3a). There were no significant differences in the ratio of LSU to SSU protein between any of the lines tested (Table S3). The 1A_{At}MOD and S2_{Cr} transgenic lines retained the same amount of native SSU (i.e. products of the *rbcs1B* and *rbcs2B* genes) as the *1a3b* mutant. Heterologous SSU levels were 2.4-fold higher than native SSU levels in 1A_{At}MOD. By contrast, heterologous SSU levels were 1.4-fold lower than native SSU levels in S2_{Cr} lines.

Rubisco activity in mutant and transgenic plants

The *in vitro* catalytic properties of Rubisco from wild-type plants (Table 1) were in good agreement with those of Galmés *et al.* (2014). The catalytic properties of Rubisco from *1a3b* and *1a2b* mutants were comparable to values for Rubisco from wild-type plants. Rubisco from 1A_{At} lines had the same catalytic properties as Rubisco from wild-type plants. This was also true for 1A_{At}MOD lines, despite the modification to the Rubisco SSU in these plants. However, k_{cat}^c and $S_{C/O}$ values were significantly lower for Rubisco from S2_{Cr} lines than for Rubisco from wild-type plants.

Growth phenotypes

Growth of transgenic lines was compared with that of (1) wild-type plants, (2) the parental *1a3b* mutant and (3) representative nontransgenic *1a3b* mutant lines selected as out-segregants from the T₂ populations (Fig. 4). Fresh and dry weights of the out-segregant mutant lines were the same as those of the parental *1a3b* mutant at 28 d (Fig. 4c; Table S4). Out-segregant lines had lower rates of rosette expansion than the parental *1a3b* mutant (Fig. 4b), but this did not affect interpretation of the effects of the transgenes on growth.

As reported previously, *1a3b* mutants had very low growth rates (Izumi *et al.*, 2012). All three transgenic genotypes had greater rates of rosette expansion than *1a3b* lines, with 1A_{At} and 1A_{At}MOD having higher expansion rates than S2_{Cr} (Fig. 4b). The dry weight of 1A_{At} rosettes at 28 d was on average 84% of that of wild-type plants, and was not significantly different from the wild-type for two of the three lines. For 1A_{At}MOD and S2_{Cr} lines, dry weight was on average 75 and 56%, respectively, of that of wild-type plants. There was no significant difference in the ratio of dry weight to fresh weight between wild-type plants and transgenic lines. All three transgenic genotypes had higher leaf area to weight ratios (rosette area per unit fresh or dry weight) than *1a3b* mutants, and were not significantly different in this respect from wild-type plants (Table S4).

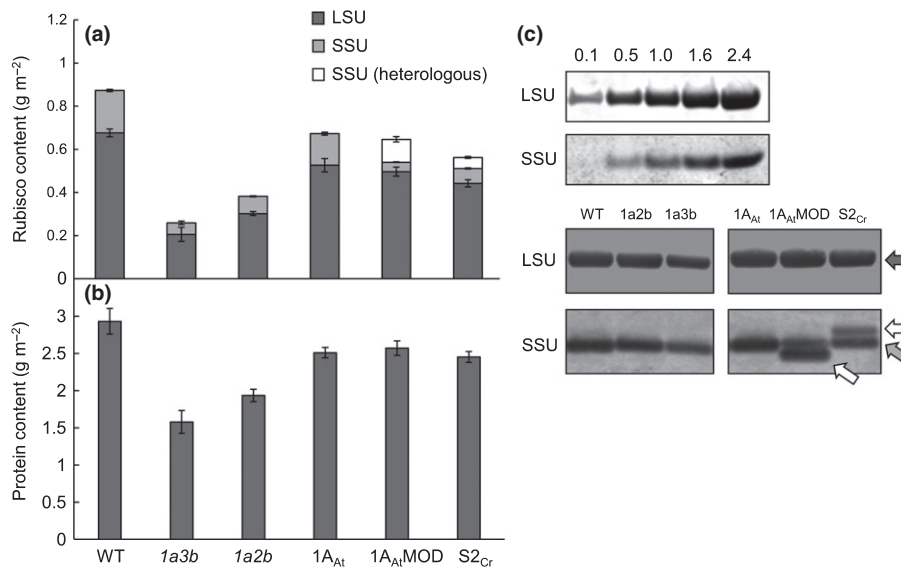


Fig. 3 Rubisco and protein contents in *rbcS* mutants and transgenic lines of *Arabidopsis thaliana*. Rubisco (a) and total protein contents (b) are shown for 32-d-old plants. Rubisco content was determined via ^{14}C -CABP binding, and subunit ratios were estimated by immunoblotting. For wild-type, *1a3b* and *1a2b* values are the means \pm SE of measurements made on three individual rosettes. For transgenic lines values are means \pm SE of measurements made on nine rosettes, three from each of the three lines. (c) Representative immunoblots for wild-type plants and transgenic lines, probed with a serum containing polyclonal antibodies against Rubisco. Standard curves (0.1–2.4 μg Rubisco) are shown for wild-type large subunit (LSU, 55 kDa) and small subunits (SSUs, 14.8 kDa), followed by protein amounts in different lines. Native LSU, SSU and heterologous SSUs (15.5 and 14 kDa, respectively) are indicated by dark grey, light grey and white arrows, respectively. Quantification of soluble protein and Rubisco is shown in Supporting Information Table S3.

Table 1 Catalytic parameters of Rubisco in *rbcS* mutants and transgenic lines of *Arabidopsis thaliana*

	Wild-type	<i>1a3b</i>	<i>1a2b</i>	1A _{At}	1A _{At} MOD	S2 _{Cr}
$k_{\text{cat}}^{\text{c}}$ (s^{-1})	4.1 \pm 0.1	4.2 \pm 0.1	4.1 \pm 0.2	4.0 \pm 0.1	4.1 \pm 0.1	3.6 \pm 0.1*
K_{c} (μM)	10.7 \pm 0.7	9.5 \pm 0.7	9.4 \pm 1.1	10.4 \pm 1.1	11.5 \pm 0.9	9.6 \pm 1.0
$K_{\text{c}}^{\text{air}}$ (μM)	15.8 \pm 1.0	14.3 \pm 0.5	15.4 \pm 1.5	16.9 \pm 1.8	17.1 \pm 1.0	16.4 \pm 1.2
$k_{\text{cat}}^{\text{c}}/K_{\text{c}}^{\text{air}}$	0.25 \pm 0.01	0.3 \pm 0.02	0.27 \pm 0.02	0.25 \pm 0.03	0.24 \pm 0.02	0.22 \pm 0.03
$S_{\text{C/O}}$	92.5 \pm 1.0 (27)	96.3 \pm 1.7 (11)	93.4 \pm 1.7 (10)	91.8 \pm 1.0 (17)	92.7 \pm 0.8 (18)	87.8 \pm 0.9* (14)

Rubisco specificity was determined from at least 10 replicate measurements for the enzyme purified from each line. Other catalytic parameters are calculated using the Michaelis–Menten model as described in Prins *et al.* (2016). The table shows mean \pm SD values for three biological replicates, except for Rubisco specificity, which is the mean \pm SD of the numbers of technical replicates shown in parentheses. All values were measured at 25°C. K_{c} , K_{m} for CO_2 at 0% O_2 ; $K_{\text{c}}^{\text{air}}$, K_{m} for CO_2 at 21% O_2 ; $k_{\text{cat}}^{\text{c}}$, turnover number (mol carboxylation product mol $^{-1}$ active site s $^{-1}$); $k_{\text{cat}}^{\text{c}}/K_{\text{c}}^{\text{air}}$, Rubisco carboxylation efficiency at 21% O_2 ; $S_{\text{C/O}}$, Rubisco specificity factor.

*Significant difference ($P < 0.05$) as determined by ANOVA followed by Tukey's HSD tests.

Rosette expansion rates and fresh and dry weights in the *1a2b* mutant were greater than in the *1a3b* mutant, but lower than those of wild-type and transgenic lines (Fig. 4c). The *1a2b* mutant had a lower ratio of fresh to dry weight than the *1a3b* mutant (Table S4). Although the specific leaf areas (rosette area per unit dry weight) of *1a2b* and *1a3b* mutants were comparable, rosette area per unit fresh weight was significantly higher in *1a2b* than in *1a3b* mutants.

Photosynthetic characteristics

At ambient CO_2 and saturating light, all three transgenic genotypes had much higher rates of CO_2 assimilation (A_{max}) than the *1a3b* mutant (A /photosynthetically active radiation (PAR) curves, Fig. 5a). A_{max} was similar to that of wild-type plants in

1A_{At} and 1A_{At}MOD lines but lower in S2_{Cr} lines (Table 2). A_{max} was higher in the *1a2b* than in the *1a3b* mutant, and was comparable in *1a2b* and S2_{Cr} lines. The apparent quantum efficiency (Φ) for all three transgenic lines was higher than in the *1a3b* mutant and comparable with the wild-type value. Light compensation point and respiration rate in the dark (R_{d}) were the same in all lines.

There were substantial differences between the *1a3b* mutant and the transgenic genotypes in the response of CO_2 assimilation to changing external CO_2 concentrations under saturating light (A/C_i curves, Fig. 5b). Several photosynthetic parameters can be derived from A/C_i curves (Table 2). The maximum rate of Rubisco carboxylation ($V_{\text{c,max}}$) and maximum photosynthetic electron transport rate (J_{max}) were not significantly different between wild-type, 1A_{At} and 1A_{At}MOD plants, but were lower

in $S2_{Cr}$ plants than in wild-type plants. The initial linear slope of the A/C_i curve (a measure of the carboxylation efficiency and activation state of Rubisco) was lower for transgenic genotypes than for wild-type plants due to reduced Rubisco content in the transgenic lines (Fig. 3a). In the $1a2b$ mutant, $V_{c,max}$, J_{max} , the substomatal CO_2 compensation point (Γ) and the initial slope of the A/C_i curve were different from those of the $1a3b$ mutant, but similar to values for the $S2_{Cr}$ lines.

Gas exchange rates and chlorophyll fluorescence measurements under photorespiratory (ambient O_2 (21%)) and nonphotorespiratory (low O_2 (2%)) conditions were used to derive information about photorespiration (Table 3). Gross CO_2 assimilation rates (GA , CO_2 assimilation in the absence of respiration) and NADPH production (estimated from the photosynthetic electron transport rate, J_{NADPH}) can together be used to estimate the ratio of Rubisco oxygenase to carboxylase activity (V_o/V_c) (Bellasio *et al.*, 2014).

The transgenic genotypes had higher GA and J_{NADPH} values than the $1a3b$ mutant. Values for $1A_{At}$ and $1A_{At}MOD$ lines were similar to those of wild-type plants, but values for $S2_{Cr}$ lines were lower. GA and J_{NADPH} in the $1a2b$ mutant were higher than in the $1a3b$ mutant, and comparable with values for the $S2_{Cr}$ lines. There were no significant differences in V_o/V_c values between any of the lines, indicating that relative photorespiratory rates were similar across genotypes under the conditions used.

Chlorophyll content and dark-adapted F_v/F_m values in the transgenic lines and the $1a2b$ mutant were higher than in the

$1a3b$ mutant, and were not significantly different from those of wild-type plants (Table S5). The $1a3b$ mutants had higher levels of NPQ than wild-type plants, but NPQ in transgenic genotypes was comparable with that of wild-type plants (Fig. 6). By contrast, the NPQ value for the $1a2b$ mutant was lower than that of wild-type plants. NPQ has two components: fast relaxing quenching (qE: NPQ_{fast}) associated with photoprotection, and slow relaxing quenching (qI: NPQ_{slow}) associated with chronic photoinhibition (Walters & Horton, 1991). To calculate the contribution of these components in the mutant lines, NPQ was tracked following a period of high light ($600 \mu mol photons m^{-2} s^{-1}$ for 1 h) and subsequent recovery in darkness (1 h). qI was lower in both transgenic genotypes than in wild-type plants, but qE was elevated in the $1a3b$ mutant and reduced in the $1a2b$ mutant. The qE:qI ratio was higher in the $1a3b$ mutant but lower in the $1a2b$ mutant than in wild-type plants (Table S6).

Discussion

Our results illustrate the impact of varying Rubisco content and native SSU composition on plant performance in *Arabidopsis*. Furthermore, we have shown that heterologous, pyrenoid competent SSUs assemble with the native LSU to produce a functional hybrid Rubisco with catalytic properties similar to the native Rubisco. This is a significant step towards the introduction of a functional algal CCM into higher plants.

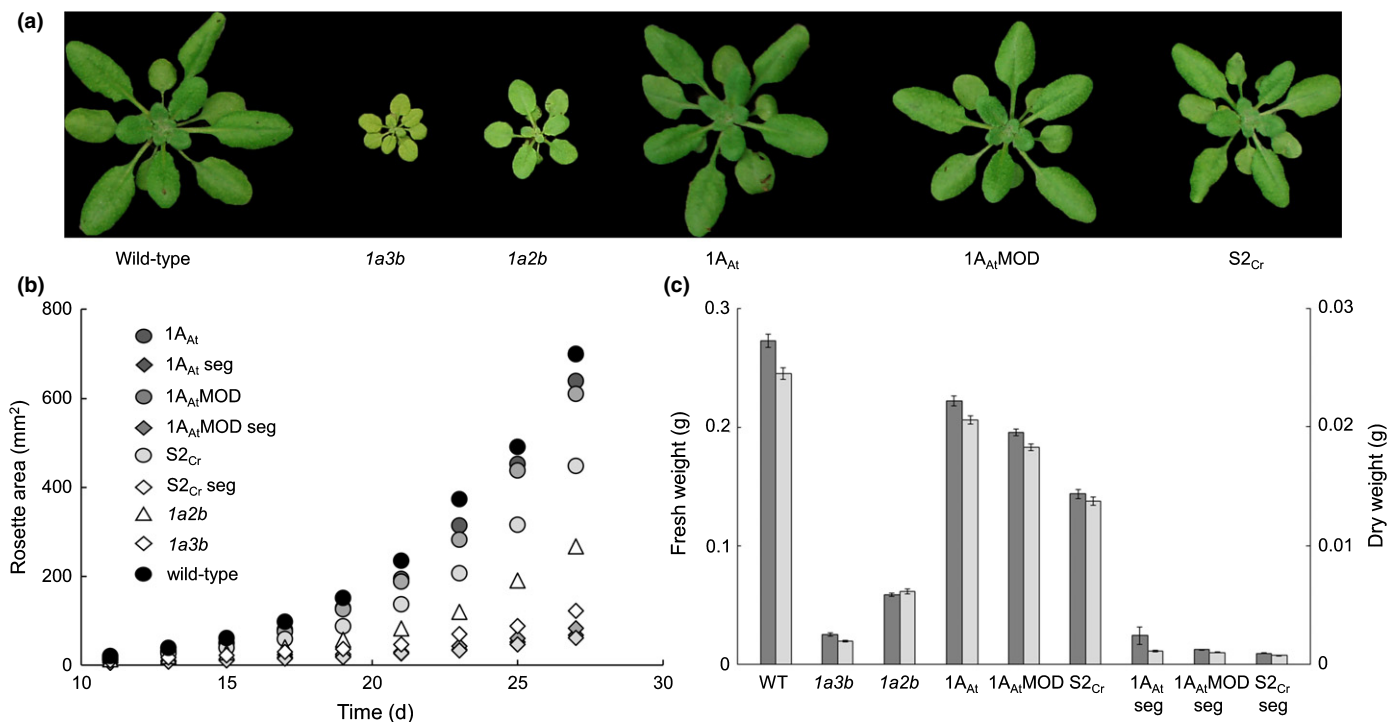


Fig. 4 Growth analysis of *rbcS* mutants and transgenic lines of *Arabidopsis thaliana*. (a) Representative examples of 28-d-old rosettes (T_3) for mutants and transgenic genotypes. (b) Rosette expansion of homozygous transgenic and $1a3b$ out-segregant plants compared to that of wild-type and $1a3b$ mutant plants. (c) Fresh and dry weights were compared after 28 d. For wild-type (WT), $1a3b$ and $1a2b$ values are the means \pm SE of measurements made on 10 individual rosettes. For transgenic lines values are means \pm SE of measurements made on 30 rosettes, 10 from each of the three lines. See Supporting Information Table S4 for full dataset. seg, segregating T_3 wild-type.

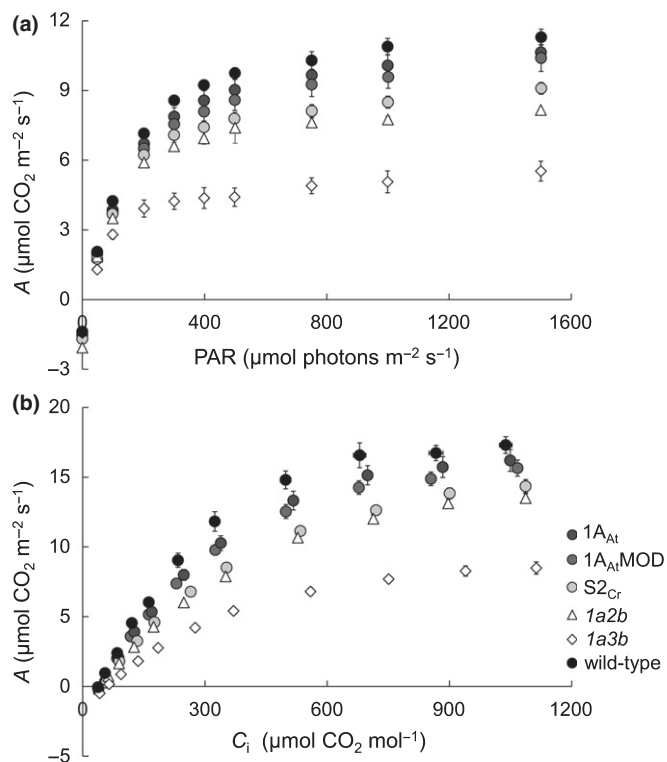


Fig. 5 Photosynthesis response curves of *rbcS* mutants and transgenic lines of *Arabidopsis thaliana*. Measurements were made on the sixth or seventh leaf of 35- to 45-d-old nonflowering rosettes. (a) A/PAR curves show the response of CO_2 assimilation rates to different light levels at ambient CO_2 levels of $400 \mu\text{mol mol}^{-1}$. (b) A/C_i curves showing the response of net CO_2 assimilation to different sub-stomatal concentrations of CO_2 (C_i) under saturating light ($1500 \mu\text{mol photons m}^{-2} \text{s}^{-1}$). For wild-type, *1a3b* and *1a2b* values are the means \pm SE of measurements made on individual leaves from four different rosettes. For transgenic lines values are means \pm SE of measurements made on 12 rosettes, four from each of the three lines.

Differences in native SSU composition of Rubisco have only minor implications for plant performance in *Arabidopsis*

The data presented here suggest that the four native SSUs in *Arabidopsis* are largely equivalent in the properties they convey to the Rubisco enzyme under the growth conditions tested. Four genotypes provided data that lead to this conclusion: (1) wild-type plants, with the highest Rubisco content and with Rubisco containing almost exclusively *rbcS1A*, *rbcS2B* and *rbcS3B* SSUs (because of its very low transcript levels it is assumed that *rbcS1B* makes a very minor contribution to the SSU population); (2) *1A_{At}* plants, with *c.* 78% of wild-type Rubisco content and with Rubisco containing mainly *rbcS1A* and *rbcS2B*; (3) the *1a2b* mutant, with 45% of wild-type Rubisco content and with Rubisco containing mainly *rbcS3B*; and (4) the *1a3b* mutant, with 30% of wild-type Rubisco content and with Rubisco containing *rbcS2B*. The catalytic properties k_{cat}^c , K_c^{air} and $S_{C/O}$ of Rubisco at 25°C were similar in these four genotypes (Table 1), and thus they are largely independent of the native SSU composition of Rubisco in *Arabidopsis*.

Nearly all the phenotypic differences between the four genotypes with different native SSU compositions can be explained by the differences in total Rubisco content alone. Across these four genotypes, parameters including leaf protein content (Fig. 3; Table S3), the response of photosynthesis to light and to CO_2 (Fig. 5), Γ and J_{max} (Table 2), and the rates of biomass accumulation and rosette expansion (Fig. 4; Table S4) responded to decreasing Rubisco activity in the manner expected for a single enzyme exercising a moderate degree of control over CO_2 assimilation (Stitt & Schulze, 1994). Additionally, the responses were broadly in line with those observed for tobacco plants with varying amounts of Rubisco activity of probably constant SSU composition (Quick *et al.*, 1991; Fichtner *et al.*, 1993; Lauerer *et al.*,

Table 2 Variables derived from photosynthetic response curves, based on gas exchange analysis of 35- to 45-d-old *Arabidopsis thaliana* plants

	Wild-type	<i>1a3b</i>	<i>1a2b</i>	<i>1A_{At}</i>	<i>1A_{At}MOD</i>	<i>S2_{Cr}</i>
A_{amb} ($\mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$)	5.7 ± 0.1^a	3.4 ± 0.3^c	4.7 ± 0.1^b	5.3 ± 0.2^{ab}	5.1 ± 0.2^{ab}	5.0 ± 0.1^{ab}
A_{max} ($\mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$)	13.5 ± 0.5^a	6.8 ± 0.5^c	10.4 ± 0.2^b	12.8 ± 0.6^{ab}	12.3 ± 0.7^{ab}	10.9 ± 0.4^{bc}
g_s ($\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$)	0.34 ± 0.06^a	0.42 ± 0.06^a	0.33 ± 0.02^a	0.3 ± 0.02^a	0.36 ± 0.03^a	0.41 ± 0.03^a
Φ ($\text{mmol CO}_2 \text{ mol}^{-1} \text{ photons}$)	55.9 ± 1.9^a	42.2 ± 2.3^b	55.3 ± 1.4^a	53.5 ± 3.3^a	51.5 ± 1.8^a	53.6 ± 0.4^a
LCP ($\mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$)	16.6 ± 1.3^a	18.8 ± 0.7^a	22.7 ± 0.8^a	18.0 ± 2.6^a	17.0 ± 1.5^a	20.9 ± 1.6^a
$V_{c,\text{max}}$ ($\mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$)	31.4 ± 1.4^a	14.6 ± 0.4^d	20.9 ± 0.4^c	27.1 ± 1.3^{ab}	26.1 ± 1.1^{ab}	22.2 ± 0.6^{bc}
J_{max} ($\text{mmol e}^- \text{ m}^{-2} \text{ s}^{-1}$)	73.3 ± 2.8^a	32.8 ± 1.3^d	53.7 ± 0.9^c	66.6 ± 3.0^{ab}	63.7 ± 2.1^{ab}	56.3 ± 1.6^{bc}
Γ ($\mu\text{mol CO}_2 \text{ mol}^{-1}$)	39.4 ± 2.2^b	60.0 ± 3.9^a	42.8 ± 1.6^b	39.1 ± 0.9^b	41.4 ± 0.5^b	43.2 ± 0.8^b
R_d ($\mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$)	1.9 ± 0.2^a	1.8 ± 0.1^a	2.0 ± 0.1^a	1.8 ± 0.1^a	1.9 ± 0.1^a	1.8 ± 0.1^a
Initial slope (A/C_i)	0.055 ± 0.003^a	0.024 ± 0.007^d	0.034 ± 0.006^c	0.045 ± 0.002^b	0.044 ± 0.002^b	0.036 ± 0.001^{bc}

For measurements of net photosynthetic CO_2 assimilation (A)/photosynthetically active radiation (PAR), relative humidity was maintained at $68 \pm 4\%$ and ambient CO_2 levels at $400 \mu\text{mol mol}^{-1}$. For measurements of A /sub-stomatal CO_2 concentration (C_i), relative humidity was maintained at $73 \pm 1\%$ under a constant illumination of $1500 \mu\text{mol photons m}^{-2} \text{s}^{-1}$. All measurements were performed at 20°C . Values are the mean \pm SE of measurements made on four leaves, each from a different plant (as shown in Fig. 5) followed by letters indicating significant differences ($P < 0.05$) as determined by ANOVA followed by Tukey's HSD tests. Values followed by the same letter are not significantly different. A_{amb} , net photosynthesis measured at ambient CO_2 and growth chamber light levels; A_{max} , light-saturated CO_2 assimilation rate at ambient CO_2 ; g_s , stomatal conductance to CO_2 (at ambient CO_2); Φ , apparent quantum efficiency; LCP, light compensation point; $V_{c,\text{max}}$, maximum rate of Rubisco carboxylation; J_{max} , maximum electron transport rate; Γ , CO_2 compensation point ($C_i - A$); R_d , respiration in the dark.

Table 3 Estimates of *in vivo* Rubisco oxygenase and carboxylase activities made from measurements of gas exchange and chlorophyll fluorescence under ambient (21%) or low (2%) O₂

	Wild-type	1a3b	1a2b	1A _{At}	1A _{At} MOD	S2 _{Cr}
GA _{Low} (μmol m ⁻² s ⁻¹)	9.48 ± 0.56 ^a	4.58 ± 0.4 ^c	5.69 ± 0.53 ^c	8.73 ± 0.09 ^{ab}	8.57 ± 0.64 ^{ab}	6.72 ± 0.49 ^{bc}
GA _{amb} (μmol m ⁻² s ⁻¹)	6.17 ± 0.36 ^a	2.98 ± 0.25 ^d	3.67 ± 0.36 ^{cd}	5.6 ± 0.15 ^{ab}	5.49 ± 0.42 ^{ab}	4.36 ± 0.38 ^{bc}
J _{NADPH_{low}} (μmol m ⁻² s ⁻¹)	18.9 ± 1.1 ^a	9.1 ± 0.8 ^c	11.4 ± 1.1 ^c	17.5 ± 0.2 ^{ab}	17.1 ± 1.3 ^{ab}	13.4 ± 0.9 ^{bc}
J _{NADPH_{amb}} (μmol m ⁻² s ⁻¹)	19.9 ± 0.9 ^a	9.2 ± 0.7 ^c	11.9 ± 0.9 ^{bc}	18.4 ± 0.2 ^a	18.2 ± 1.4 ^a	14.1 ± 1 ^b
V _o (μmol m ⁻² s ⁻¹)	2.21 ± 0.13 ^a	1.06 ± 0.11 ^b	1.34 ± 0.12 ^b	2.09 ± 0.06 ^a	2.06 ± 0.17 ^a	1.57 ± 0.07 ^{ab}
V _c (μmol m ⁻² s ⁻¹)	7.27 ± 0.43 ^a	3.52 ± 0.29 ^d	4.35 ± 0.41 ^c	6.64 ± 0.12 ^{ab}	6.52 ± 0.49 ^{ab}	5.15 ± 0.42 ^{bc}
V _o /V _c	0.304 ± 0.002 ^a	0.302 ± 0.013 ^a	0.307 ± 0.008 ^a	0.313 ± 0.015 ^a	0.316 ± 0.012 ^a	0.307 ± 0.011 ^a

Arabidopsis thaliana plants (35–40 d old) were measured under 300 μmol photons m⁻² s⁻¹, and ambient CO₂ of 300 μmol mol⁻¹ as in Bellasio *et al.* (2014). For wild-type, 1a3b and 1a2b values are the means ± SE of measurements made on individual leaves from five different rosettes. For transgenic lines, values are means ± SE of measurements made on 15 rosettes, five from each of the three lines. Values are followed by letters indicating significant difference (*P* < 0.05), as determined by ANOVA followed by Tukey's HSD tests. Values followed by the same letter are not significantly different. GA_{low}, gross photosynthetic rate (A+R_d) under 2% O₂ (2%); GA_{amb}, gross photosynthetic rate under 21% O₂; J_{NADPH_{low}}, NADPH produced for photosynthesis (derived from electron transport rate) under 2% O₂; J_{NADPH_{amb}}, NADPH produced for photosynthesis under 21% O₂; V_o, Rubisco oxygenation rate; V_c, Rubisco carboxylation rate.

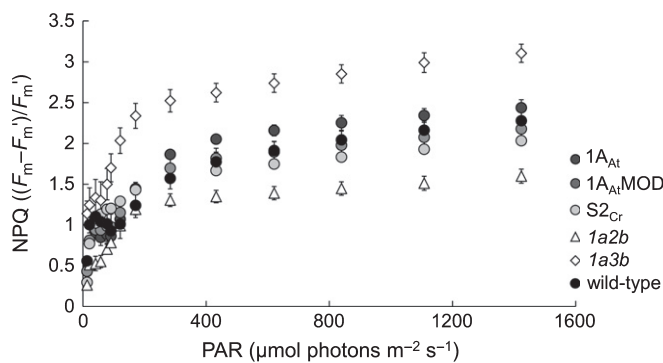


Fig. 6 Nonphotochemical quenching response to light in leaves of *rbcS* mutants and transgenic lines of *Arabidopsis thaliana*. All plants were 28 d old. For wild-type, 1a3b and 1a2b values are the means ± SE of measurements made on individual leaves from four different rosettes. For transgenic lines values are means ± SE of measurements on leaves from 12 plants, four from each of the three lines.

1993; Stitt & Schulze, 1994), and *Arabidopsis* plants with strong suppression of expression of all four SSU genes (Zhan *et al.*, 2014).

Some features of the four genotypes did not vary consistently with Rubisco content. For example, chlorophyll content, *F_v/F_m* and Φ were strongly affected only in the genotype with the lowest levels of Rubisco, 1a3b (Tables 2, S5). Other parameters including leaf soluble protein content and specific leaf area were affected only in genotypes with less than 50% of wild-type Rubisco levels (Fig. 3; Table S4). Our data in these respects are reminiscent of those obtained for tobacco under limiting light in which Rubisco activity was varied by expression of antisense RNA that targeted all of the SSUs (Quick *et al.*, 1991; Fichtner *et al.*, 1993; Lauerer *et al.*, 1993; Stitt & Schulze, 1994). Reductions of *c.* 40% or less in Rubisco activity in tobacco plants under limiting light (as in our experiments) had relatively little effect on the rate of photosynthesis and few pleiotropic consequences. Greater reductions progressively affected photosynthesis and downstream processes, different processes being affected at different levels of Rubisco reduction (Quick *et al.*, 1991; Stitt &

Schulze, 1994). Future experiments will investigate which phenotypic differences between the lines are exaggerated when plants are grown in saturating light.

For processes associated with photoprotection, qualitatively different phenotypes were observed in the 1a3b and 1a2b mutants. NPQ was elevated in the 1a3b mutant. NPQ was also elevated in tobacco and rice with reduced levels of Rubisco (Quick *et al.*, 1991; Lauerer *et al.*, 1993; Ruuska *et al.*, 2000; Ushio *et al.*, 2003; von Caemmerer *et al.*, 2004): this effect may result from reduced ATP consumption for CO₂ assimilation, and hence a higher Δ pH across the thylakoid membrane. Lumen acidification promotes activity of the energy-dissipating xanthophyll cycle (Ruuska *et al.*, 2000; Johnson *et al.*, 2009; Zaks *et al.*, 2012). By contrast, with 1a3b plants and other plant species with reduced Rubisco, NPQ was reduced in 1a2b mutants. In particular, 1a2b plants had a much reduced rate of relaxation of NPQ immediately following the onset of darkness (the qE or fast component of NPQ). The exact mechanism underlying qE is not known (e.g. Johnson *et al.*, 2009; Zaks *et al.*, 2012). However, as mature *rbcS2B* and *rbcS3B* have identical amino acid sequences, the difference in NPQ between the 1a2b and 1a3b mutants is likely to stem from the pleiotropic effects of the different degrees of reduction of Rubisco activity in the two mutants, rather than from the different SSU compositions of their Rubiscos.

It is clear from previous work that SSUs can influence Rubisco catalysis. For example, overexpression of specific native or heterologous SSU proteins altered the catalysis of Rubisco in rice leaves, resulting in properties that are more like those of C₄ plants (i.e. higher *k_{cat}*, but also higher *K_c* (lower CO₂ affinity) than for native rice Rubisco) (Ishikawa *et al.*, 2011; Morita *et al.*, 2014). Over-expression in *Arabidopsis* of a pea SSU, differing from *Arabidopsis* SSUs by 40 amino acids, resulted in Rubisco with slightly reduced carboxylase activity and capacity for activation (Getzoff *et al.*, 1998). Similarly, Rubisco properties were changed by introduction of a sorghum SSU into rice (Ishikawa *et al.*, 2011). However, except in the case of the rice SSU above, little is known about the functional importance of sequence variation between SSUs within a species. SSU isoforms in a single species

are typically very similar. In *Chlamydomonas*, for example, the two SSUs differ by only four amino acid residues (all outside the α -helices) and appear to be functionally equivalent (Rodermel *et al.*, 1996; Genkov *et al.*, 2010). In *Arabidopsis*, the mature *rbcS1A* differs from *rbcS1B*, *rbcS2B* and *rbcS3B* by only eight amino acids, six of which are conserved between the three B-class SSUs (Fig. S3). Two of these are located in the first α -helix.

Chlamydomonas-like SSUs generate a functional hybrid Rubisco in *Arabidopsis*

Introduction of either a *Chlamydomonas* SSU ($S2_{Cr}$) or a modified version of *rbcS1A* ($1A_{At}MOD$) into the *Arabidopsis 1a3b* mutant substantially complemented several aspects of the *1a3b* phenotype. In a previous study, a *Chlamydomonas* SSU introduced into pea chloroplasts was not processed to the mature, active form, probably due to differences in chloroplast import machinery between *Chlamydomonas* and higher plants (Su & Boschetti, 1994). In this study, replacing the *Chlamydomonas* SSU TP with the *rbcS1A* TP directed the mature protein to the chloroplast stroma (Fig. S1). Expression of $S2_{Cr}$ or $1A_{At}MOD$ increased Rubisco content in the *1a3b* mutant without significantly enhancing levels of the remaining native SSUs, and thus both introduced proteins promoted expression of the native LSU and assembled into catalytically active hybrid Rubiscos. These results are consistent with the idea that *rbcL* transcription and LSU synthesis adjust according to the availability of SSU (Wollman *et al.*, 1999; Wostrikoff & Stern, 2007; Wostrikoff *et al.*, 2012; Zhan *et al.*, 2014).

Photosynthesis was restored almost to wild-type levels in $1A_{At}MOD$ (Fig. 5). Furthermore, the catalytic characteristics of Rubisco in $1A_{At}MOD$ plants, where *c.* 70% of the SSU pool was heterologous, were comparable to those of $1A_{At}$ and wild-type plants (Table 1). This suggests that the SSU α -helix regions alone do not affect Rubisco biogenesis or catalysis, and that Rubisco in higher plants can be made compatible with the requirements of the algal CCM without affecting enzyme performance.

Rubisco in $S2_{Cr}$ plants had lower k_{cat}^c and $S_{C/O}$ values than those of wild-type and $1A_{At}MOD$ Rubisco, even though the $S2_{Cr}$ SSU pool contained only *c.* 40% *Chlamydomonas* SSU. $S2_{Cr}$ lines generally performed less well than $1A_{At}MOD$ lines. Neither $S2_{Cr}$ nor $1A_{At}MOD$ lines are likely to be Rubisco-limited because they both have *c.* 70% of the Rubisco content of wild-type plants (Quick *et al.*, 1991). Differences in photosynthesis and growth between $S2_{Cr}$ and $1A_{At}MOD$ lines are thus likely to result largely from SSU-dependent differences in Rubisco catalytic properties. In *Chlamydomonas*, expression of a higher plant SSU can impart improved catalysis and $S_{C/O}$ (Genkov *et al.*, 2010). The data shown here demonstrate that the reverse is also true: an algal SSU can negatively affect catalytic properties of the hybrid Rubisco in a higher plant. Since the $1A_{At}MOD$ and $S2_{Cr}$ SSUs have the same α -helices, differences in catalytic properties of the hybrid enzyme must arise from sequence differences in regions of the SSU outside of these helices.

The *Chlamydomonas* SSU protein differs in several respects from the *Arabidopsis* SSUs, including the presence of additional

amino acid residues at the C-terminus and in the loop between β -strands A and B (Spreitzer, 2003). The latter forms the entrance of the solvent channel and may be important for carboxylation rates and $S_{C/O}$ (Karkehabadi *et al.*, 1995; Esquivel *et al.*, 2013). Hybrid Rubisco enzymes with SSUs that diverge significantly in amino acid sequence from the native SSU frequently have altered stability and properties, and a lower capacity for assembly with the native LSU. The poor complementation of *Arabidopsis* Rubisco in $S2_{Cr}$ warrants further study to expand upon existing knowledge in this area, including the functional capacity of the chaperone Rubisco activase when presented with hybrid Rubiscos.

rbcS mutants of *Arabidopsis* are a useful platform for Rubisco analyses and the assembly of an algal CCM

This study shows that *Arabidopsis* mutants lacking SSU isoforms are a useful platform for attempts to assemble a functional algal CCM in higher plants. Introduction of $1A_{At}MOD$, containing α -helices believed to be necessary for pyrenoid assembly, had no apparent effect on Rubisco function and assembly, and plant performance was generally close to wild-type levels under our growth conditions.

For aggregation of Rubisco into a pyrenoid, additional algal CCM components will be required. Cryo-electron tomography of *Chlamydomonas* pyrenoids showed that Rubisco proteins are not randomly arranged, and periodicity is consistent with hexagonal close packing, with a space of 2–4.5 nm between each protein depending on their relative orientations (Engel *et al.*, 2015). Other factors, such as linker proteins, are probably needed. Recently, a multiple repeat linker-protein, EPYC1 (formerly known as LCI5), has been identified in *Chlamydomonas* that is associated with Rubisco during aggregation within the pyrenoid (Mackinder *et al.*, 2016). The $1A_{At}MOD$ and $S2_{Cr}$ *Arabidopsis* lines are ideal backgrounds in which to test candidates for these other factors as they emerge, to clarify the nature of SSU-associated interactions, and to integrate other essential algal CCM components (Atkinson *et al.*, 2016).

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Author contributions

A.J.M. and N.A. planned and designed the research and wrote the manuscript. A.M.S., D.J.O., M.T.M., H.G. and E.C.S. assisted in experimental design, data analysis and writing of the

manuscript. A.J.M., N.A. and N.L. performed the research, data analysis, collection, and assisted with data interpretation and writing.

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Supporting Information

Additional Supporting Information may be found online in the Supporting Information tab for this article:

Fig. S1 Transient expression of Rubisco small subunit–GFP fusion proteins in tobacco.

Fig. S2 Impact of native and heterologous SSUs on photosynthesis and growth in the *Arabidopsis* mutant *1a3b* background.

Fig. S3 Alignments of the mature *Arabidopsis* SSU amino acid sequences.

Table S1 Sequences of synthetic oligonucleotides used in this study

Table S2 Transcript abundances of the Rubisco gene family in *rbcS* mutants and transgenic lines

Table S3 Rubisco and soluble protein contents for *rbcS* mutants and transgenic lines

Table S4 Rosette area and biomass for *rbcS* mutants and transgenic lines

Table S5 Chlorophyll characteristics and maximum quantum yield of PSII (F_v/F_m) for *rbcS* mutants and transgenic lines

Table S6 Photosynthetic nonphotochemical quenching capacity for *rbcS* mutants

Notes S1 Expression vectors for Rubisco small subunit (*rbcS*) cassettes.

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