REVIEW PAPER



Rubisco activity and regulation as targets for crop improvement

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Abstract

Rubisco (ribulose-1,5-bisphosphate (RuBP) carboxylase/oxygenase) enables net carbon fixation through the carboxylation of RuBP. However, some characteristics of Rubisco make it surprisingly inefficient and compromise photosynthetic productivity. For example, Rubisco catalyses a wasteful reaction with oxygen that leads to the release of previously fixed CO₂ and NH₃ and the consumption of energy during photorespiration. Furthermore, Rubisco is slow and large amounts are needed to support adequate photosynthetic rates. Consequently, Rubisco has been studied intensively as a prime target for manipulations to 'supercharge' photosynthesis and improve both productivity and resource use efficiency. The catalytic properties of Rubiscos from diverse sources vary considerably, suggesting that changes in turnover rate, affinity, or specificity for CO₂ can be introduced to improve Rubisco performance in specific crops and environments. While attempts to manipulate plant Rubisco by nuclear transformation have had limited success, modifying its catalysis by targeted changes to its catalytic large subunit via chloroplast transformation have been much more successful. However, this technique is still in need of development for most major food crops including maize, wheat, and rice. Other bioengineering approaches for improving Rubisco performance include improving the activity of its ancillary protein, Rubisco activase, in addition to modulating the synthesis and degradation of Rubisco's inhibitory sugar phosphate ligands. As the rate-limiting step in carbon assimilation, even modest improvements in the overall performance of Rubisco pose a viable pathway for obtaining significant gains in plant yield, particularly under stressful environmental conditions.

Key words: Chloroplast, photosynthesis, Rubisco, Rubisco activase, regulation, specificity, transformation.

Introduction

The primary determinant of crop biomass is the cumulative rate of photosynthesis over the growing season. A comprehensive analysis of free-air CO_2 enrichment experiments unambiguously demonstrated that increasing photosynthesis in C_3 plants increases yield (Ainsworth and Long, 2005). In C_3 photosynthesis, Rubisco (ribulose-1,5-bisphosphate (RuBP) carboxylase/oxygenase) initiates carbon assimilation through the carboxylation of RuBP. Despite the presence of a CO_2 -concentrating mechanism in C_4 , crassulacean acid metabolism, algal, and cyanobacterial species, the carboxylase activity of Rubisco plays a central role in CO_2 assimilation in all photosynthetic organisms. Even so, some characteristics of Rubisco, including constraints related to its complex reaction mechanism, make it surprisingly inefficient and compromise photosynthetic productivity. For example, Rubisco catalyses a wasteful side reaction with oxygen that leads to

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Fig. 1. Biotechnological strategies for improving photosynthetic carbon assimilation in crops. In addition to directly improving Rubisco catalysis, other strategies aim to enhance CO_2 levels around Rubisco to minimize photorespiratory expenses associated with recycling of Rubisco's oxygenase product, 2-phosphoglycolate (2PG, see dashed line). These strategies include: introducing assimilation characteristics from C_4 -physiology into C_3 cells (Covshoff and Hibberd, 2012); cyanobacteria inorganic carbon (C_i) pumps into chloroplast membranes (Price *et al.*, 2011); and novel catabolic by-pass pathways (Kebeish *et al.*, 2007). Other strategies include enhancing Calvin cycle RuBP regeneration by increasing sedoheptulose-1,7-bisphosphatase (SBPase) activity (Rosenthal *et al.*, 2011) and increasing the thermotolerance of Rubisco activase to sustain Rubisco activity under moderately elevated temperatures (Kureck *et al.*, 2007; Kumar *et al.*, 2009).

the release of previously fixed CO_2 , NH_3 , and energy during photorespiration (Fig. 1). Furthermore, Rubisco is slow, and large amounts of the enzyme (accounting for up to 50% of leaf soluble protein, 25% of leaf N) are needed to support adequate photosynthetic rates. In addition, Rubisco requires repeated conformational remodelling to stay active, a process that slows the apparent rate of catalysis.

Rubisco evolved 3 billion years ago in a high-CO₂ environment that contained very little molecular oxygen (Whitney et al., 2011a). As the earth's atmosphere slowly changed, Rubisco gradually evolved to its present-day forms, constrained by a complex reaction mechanism that originated under very different conditions. For over 500 million years, the evolution of Rubisco in land plants to its current L₈S₈ structure, comprising eight 52-kDa large and eight 14-15-kDa small subunits (Andersson and Backlund, 2008), has required multiple and concerted structural changes to both subunits. Given that photosynthetic carbon assimilation is frequently limited by Rubisco catalysis, the acquired evolutionary structural changes to both subunits have had to strike a balance between acquiring those conveying desired catalytic traits without compromising the enzyme's biogenesis or regulation by its ancillary activating protein Rubisco activase (Whitney et al., 2011a). As a result, considerable variation exits in the catalytic properties of Rubisco from diverse vascular plant sources (Fig. 2), based on kinetic measurements from only about 100 species. Even such a small sample has revealed sufficient variation, in principle, to confer superior characteristics to photosynthesis in specific crops and environments (Galmés et al., 2005; Zhu et al., 2010b; Parry *et al.*, 2011). These findings suggest that further variation in Rubisco turnover rate, affinity, or specificity for CO_2 is almost certainly present in the natural environment and awaits discovery by analysing Rubisco structure and function in plants adapted to more extreme growth conditions.

Whilst it may be possible to introduce novel Rubiscos by conventional breeding (e.g. wide crosses), it is most likely that this introduction will require biotechnological approaches. Some attempts to manipulate plant Rubisco by nuclear transformation have had limited success. Modifying Rubisco catalysis by targeted changes to its chloroplast encoded L-subunit gene (rbcL) via chloroplast transformation (Fig. 2) has been much more successful - albeit a technique still in need of development for the major food crops (i.e. maize, wheat, and rice). While bioengineering efforts to optimize the catalytic potential of Rubisco itself are pivotal to this approach, so too are several indirect targets for improving Rubisco performance in planta (von Caemmerer and Evans, 2011). These include improving the thermal tolerance of Rubisco's ancillary protein, Rubisco activase, and modulating the abundance or effects of naturally occurring sugar phosphate analogues that inhibit Rubisco activity. Ongoing fundamental research in model plant species (Arabidopsis, tobacco) and crop species (rice, wheat) are examining these and other strategies for improving photosynthetic carbon assimilation (Fig. 1). The inescapable fact is that the shared goal of almost all of these bioengineering strategies is to enhance CO₂ fixation by Rubisco.

To 'climate proof' crops for the future, innovative biotech approaches are required to go beyond the advances achieved



Fig. 2. Variation in L₈S₈ Rubisco catalysis and expression in *Escherichia coli* and in tobacco chloroplasts (^{tob}plastids). During the last 2–3 billion years different L₈S₈ Rubisco isoforms have selected for significant variations in their speed (v_{CO2}), CO₂ affinity (K_m^{CO2}), and specificity for CO₂ over O₂ ($S_{C/O}$) in response to increasing atmospheric O₂, diminishing CO₂, and other environmental and physiological stimuli. Identifying the structure–function detail to account for this variation has been hindered by variations in the extent to which the folding and assembly requirements of recombinant large (L) and small (S) Rubisco subunits can be met by *E. coli* and tobacco chloroplasts. Relative levels of expression are scaled incrementally from nil (–) to maximally expressed (+++). The range of each catalytic parameter for each L₈S₈ isoform summarizes the data from Whitney *et al.* (2011).

either by evolution or by empirical breeding. Rubisco is not optimal for current environmental conditions and agricultural practices, but there is enough variation present in nature to suggest that improvements in the catalytic properties of Rubisco or in its ancillary reactions can be achieved by rational design. Therefore, the goal is to provide a pathway for significantly boosting the CO_2 -fixing capability of a crop by introducing tailor-made changes to Rubisco and/or Rubisco activase function that are best suited to the particular crop and its growth environment.

The predicted major benefits include:

- Greater yield under current and future CO₂ levels. Improved Rubisco catalytic efficiencies of 5–25% would increase leaf photosynthetic rates and potentially increase dry matter yield by several-fold when integrated over the growing season in an appropriate crop with adequate nutrient and water supply (Zhu *et al.*, 2010b; Parry *et al.*, 2011).
- Improved tolerance to higher growing season temperatures and more frequent episodes of extreme heat. Enhancing the thermotolerance of Rubisco activase would increase

productivity in current and future climates by reducing inhibition of net CO_2 assimilation by heat stress and allow optimization for a warmer average temperature and/or less precipitation (Ainsworth and Ort 2010; Parry *et al.*, 2011).

• Enhanced nitrogen efficiency (more carbon fixed for the same amount of leaf protein; Reynolds *et al.*, 2012) and water use efficiency (more CO₂ flux for the same amount of water; Andrews and Whitney, 2003).

Many of the early limitations to Rubisco engineering have been overcome through significant technological advances in our capabilities to modify Rubisco in plant plastids. In this review we examine how these advances have unveiled the evolutionary restrictions that nature, and now bioengineers, face for discovering solutions that improve Rubisco catalysis in crops without hindering its biogenesis. The challenges faced necessitate concerted efforts to fully understand the molecular chaperone requirements of Rubisco biogenesis and improve our comprehension of the natural diversity in sequence-performance relationships among diverse Rubisco isoforms, including how influential the Rubisco small subunit is to catalysis. To meet these challenges requires plastome-transforming capabilities to be developed in key grain crops and the development of higher-throughput technologies involving in vitro, Escherichia coli, and/or transient plant expression systems. These advances will allow probing of structure-function relationships to identify solutions that benefit Rubisco and Rubisco activase catalysis and their integration into C₃ crops.

Overcoming Rubisco catalysis limitations

Altering leaf Rubisco content

Rubisco represents a major nitrogen investment in crops: it can exceed 25% of leaf nitrogen and comprise as much as 50% of soluble leaf protein (Parry *et al.*, 2003). Given that nitrogen is already a major limitation and an expensive nutrient in global agricultural systems, lowering the need for such an abundance of Rubisco is an obvious target for increasing crop nitrogen use efficiency. Modelling studies and data from growth experiments in elevated CO₂ suggest that in some environments there is an overinvestment in Rubisco (Ainsworth and Long, 2005). Evidence from antisense plants with decreased Rubisco content suggests that at low-to-moderate light intensities a reduction in Rubisco in the order of 15-20% would reduce nitrogen demand by as much as 10%without negatively impacting on the capacity for photosynthetic CO_2 fixation (Stitt and Schulze, 1994). This strategy would confer increasing benefit as atmospheric CO₂ concentrations continue to rise.

A different approach may, however, be required in environments characterized by high light intensities, since any reduction in the amount (or activity) of Rubisco under these conditions is likely to decrease photosynthetic rates. A numerical simulation using an evolutionary algorithm that partitioned a fixed amount of protein-associated nitrogen among the enzymes of CO₂ fixation suggested that for optimal photosynthetic rate there was an underinvestment in Rubisco, sedoheptulose-1,7-bisphosphatase, and fructose-1,6-bisphosphate aldolase and an overinvestment in photorespiratory enzymes (Zhu *et al.*, 2007). In light of that study, rebalancing the investment in leaf proteins and increasing the amount (or activity) of Rubisco would be particularly beneficial, not only in conditions of high irradiance but also of high temperature when intercellular CO_2 concentrations are lower. Any additional investment in Rubisco would need to be offset by decreases in photorespiratory leaf proteins so that there was no overall increase in nitrogen requirement. Clearly, one strategy may not be suitable for all situations. Rather, a modelled optimization of photosynthetic metabolism may be required for specific crops and environments.

Modifying Rubisco performance

Natural variation in L₈S₈ Rubisco catalysis indicates that the enzyme has differentially evolved in response to environmental cues (Tcherkez et al., 2006). It is likely that the complex biogenesis requirements of Rubisco, its high level of expression, and its complex catalytic chemistry have restricted the rate at which beneficial changes have been, and can be, selected (Whitney et al., 2011a). This may explain the apparent slow catalytic adaptation of Rubisco to changing atmospheric CO₂ and O_2 levels. Indeed, many photosynthetic organisms have answered the selection pressure on Rubisco catalysis by preferentially adopting anatomical and biochemical changes that concentrate CO₂ around the enzyme. In C₄ plants, this compromise has led to the selection of coding sequence changes that increase Rubisco CO2 fixation rates, albeit at the expense of CO_2 affinity (Fig. 2). Using plastome transformation in the tobacco master line ^{cm}trL, the L-subunit Met309Ile substitution has recently been shown to be a trigger for converting Rubisco in *Flaveria* species from C₃- to C₄-like catalysis (Whitney et al., 2011b).

Some Rubisco isoforms in the 'red' L_8S_8 lineage have evolved further and faster than the 'green' L₈S₈ lineage in vascular plants. Compared with C3 crops, the Rubisco of some red algae has evolved 2-fold improvements in CO₂/O₂ specificity while sustaining adequate rates of carboxylation (v_{CO2}) and CO₂ affinity (Fig. 2). As the folding and assembly requirements of red algae Rubiscos cannot be met by higher plant chloroplasts (Whitney et al., 2001), the challenge is to identify the amino acids responsible for their catalytic properties and transpose these onto C_3 (and C_4) Rubiscos. Unfortunately for Rubisco bioengineers, despite high levels of L- and S-subunit expression, molecular chaperone incompatibilities hinder the production of most L₈S₈ Rubisco isoforms in E. coli, restricting use of this system to structure-function studies of certain cyanobacterial forms of Rubisco (Fig. 2). Much like the divergent catalytic properties of cyanobacteria Rubisco relative to other L_8S_8 enzymes, sequence-performance relationships in cyanobacteria Rubisco may also have limited translational relevance to higher plant Rubisco (e.g. Met309Ile mutation, Whitney et al., 2011b).

An expansion in Rubisco engineering capabilities came about with the development of chloroplast-transformation tools to modify the plastome-encoded *rbcL* gene in *Chlamydomonas reinhardtii* and tobacco plastids (Day and Goldschmidt-Clermont, 2011; Maliga and Bock, 2011). Research with *C. reinhardtii* has revealed much about the structure–function of the eukaryotic-type L_8S_8 Rubisco and its regulation by Rubisco activase (Spreitzer *et al.*, 2005). Rubisco engineering in this unicellular green alga is facilitated by the availability of an S-subunit deficient mutant, which enables the study of both L- and S-subunit changes in catalysis (Wostrikoff and Stern, 2009). By exploiting plastome transformation in *C. reinhardtii*, laboratory-directed protein evolution has confirmed that L-subunit amino acid substitutions can improve catalysis (i.e., better v_{CO2} , K_m^{CO2} , and $S_{C/O}$) and these improvements can be transferred to tobacco Rubisco (Zhu *et al.*, 2010a).

Plastome transformation in tobacco has also been used to delete, replace, and modify Rubisco with alternate and modified subunits (Andrews and Whitney, 2003). This pioneering work led to the development of tobacco lines specifically tailored for plastome engineering of Rubisco (Kode *et al.*, 2006; Whitney and Sharwood, 2008). Of these, the high transforming efficiency and non-denaturing PAGE screening simplicity of the ^{cm}trL tobacco master line (Fig. 3A) has emerged as a useful tool for introducing a variety of recombinant Rubiscos (Fig. 3B) and testing the accuracy of leaf photosynthesis assimilation models (see Whitney *et al.*, 1999, 2009, 2011b for examples). Overall, the chloroplast-transformation research in tobacco has shown that changes in L-subunit residues translate into changes in Rubisco catalysis, which directly correlate with plant photosynthesis and growth.

The influence of S-subunits on Rubisco catalysis

Despite the precedence from plastome engineering in tobacco that the L-subunits primarily determine the catalytic prowess of plant L₈S₈ Rubisco (Sharwood et al., 2008; Whitney et al., 2011b), there is strong evidence that Rubisco catalysis can be modulated – possibly stimulated – by the S-subunits. C. reinhardtii has been extensively used to show the importance of the S-subunit on catalysis, in particular the important role of the structurally variable $\beta A - \beta B$ loop (Spreitzer *et al.*, 2005; Wostrikoff and Stern, 2009; Genkov et al., 2010). Recently, the introduction of a C4-Rubisco rbcS gene from sorghum into the nucleus of rice successfully produced chimeric L_8S_8 Rubisco - comprising both rice and sorghum S-subunits whose catalysis became more C_4 -like (i.e. a higher v_{CO2} and $K_{\rm m}^{\rm CO2}$, Ishikawa *et al.*, 2011). In contrast, introducing pea Rubisco S-subunits into Arabidopsis impeded Rubisco catalysis (Getzoff *et al.*, 1998). The basis for these conflicting results is unclear.

Recent computational analysis of natural and mutant Rubisco structures also tend to support the assertion that S-subunits can finetune the dynamic structure of the holoenzyme and influence catalysis (van Lun *et al.*, 2011). These properties might explain natural variation in the sequence and expression of different alleles in plant rbcS gene families but this has yet to be demonstrated experimentally.

Fully appreciating the extent to which L_8S_8 catalysis can be modulated by S-subunit engineering poses an exciting opportunity because, unlike plastome transformation,



A Plastid transformation and screening for recombinant Rubisco

Fig. 3. Plastome engineering of Rubisco in the tobacco master-line ^{cm}trL. (A) Using the homologous recombination route for transforming the chloroplast genome (plastome), the *Rhodospirillum rubrum* L₂ Rubisco encoding ^{cm}*rbcM* in the plastome of the ^{cm}trL tobacco master line (cell on left) can be efficiently replaced with candidate *rbcL* (± *rbcS*) (cell on right). In ^{cm}trL, the cytosolic-made tobacco S-subunits are not needed and therefore degraded (Whitney and Sharwood, 2008). Plastome-transformed (*trans*) ^{cm}trL plants producing alternative larger Rubsico isoforms are easily identified by non-denaturing PAGE of plant soluble protein. (B) Examples of the alternative Rubisco isoforms successfully expressed in tobacco chloroplasts using ^{cm}trL. [1] Whitney and Sharwood (2008); [2] Alonso *et al.* (2009); [3] Sharwood *et al.* (2008); [4] Whitney *et al.* (2011b); [5] Zhang *et al.* (2011); [6] Whitney *et al.* (2009).

nucleus-transforming capabilities are available for most crop species. By contrast, the suitability of testing recombinant *rbcS* genes by plastome transformation is hindered by the inability of S-subunits made in the plastid to effectively compete with the endogenous cytosolic S-subunits for assembly into L_8S_8 holoenzyme (Whitney and Andrews, 2001; Zhang *et al.*, 2002; Dhingra *et al.*, 2004).

The need to better understand Rubisco biogenesis

The inability of algal and some plant L-subunits to assemble into L_8S_8 complexes in recombinant hosts poses a significant hurdle to the detailed structure–function analysis of these Rubisco isoforms. This was first apparent when chaperone incompatibilities precluded successful replacement of plant Rubisco with a catalytically 'better' enzyme from red algae (Whitney *et al.*, 2001). Subsequent transplantation studies have shown that the chaperone requirements of the L-subunits from sunflower, tomato, and various *Flaveria* species Rubiscos can be met by tobacco chloroplasts, albeit to differing extents (Sharwood *et al.*, 2008; Whitney *et al.*, 2011b; Zhang *et al.*, 2011). In contrast, unknown sequence variations within the L-subunit of rice, wheat, and maize

Rubiscos preclude their synthesis, folding, and/or assembly with tobacco S-subunits into hybrid L_8S_8 enzymes in tobacco (S. M. Whitney and J. Galmés, unpublished). This is of little surprise when considering that single amino acid changes in *Flaveria* L-subunits significantly influence hybrid L_8S_8 biogenesis in tobacco (Whitney *et al.*, 2011b) and that tobacco L-subunit substitutions such as Ser112Phe or Gly322Ser prevent tobacco Rubisco biogenesis (Avni *et al.*, 1989; Shikanai *et al.*, 1996). Nevertheless, it is encouraging that the inability of some L-subunits to assemble in plastids may be reversed by only one or a few amino acid changes. In support of this is the finding that a number of single and complementary L-subunit mutations can enhance assembly of artificially evolved cyanobacterial Rubisco in *E. coli* by as much as 20-fold (Mueller-Cajar and Whitney, 2008a,b).

Improvements in the assembly of some L_8S_8 Rubiscos in *E. coli* can be achieved by chaperonin overexpression and/or co-expression with the Rubisco-specific molecular chaperone RbcX (Goloubinoff *et al.*, 1989; Emlyn-Jones *et al.*, 2006; Mueller-Cajar and Whitney, 2008b). In contrast to the BSDII and newly identified RAF1 chaperones, whose functional roles in plastid Rubisco biogenesis remain unqualified (Brutnell *et al.*, 1999; Wostrikoff and Stern, 2007; Feiz *et al.*, 2012), significant

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functional detail has been resolved for RbcX (Saschenbrecker *et al.*, 2007; Bracher *et al.*, 2011). By interacting with postchaperonin folded L-subunits, RbcX directs their assembly into L_8 cores for holoenzyme assembly with S-subunits (Liu *et al.*, 2011). This level of understanding of the Rubisco chaperoneassembly mechanism and requirements is needed to expand our capabilities to bioengineer Rubisco in plastids, *E. coli*, and cell-free *in vitro* systems to fully explore sequence–performance relationships of different Rubisco isoforms. Progress in our Rubisco engineering capabilities will likely entail exploration and functional characterization of additional molecular chaperones involved in Rubisco biogenesis.

Maintaining Rubisco activity

Amelioration of Rubisco fallover and inhibition

A prominent feature of the evolution of L₈S₈ Rubisco of higher plants has been an increased specificity for RuBP carboxylation relative to oxygenation (the specificity factor; Jordan and Ogren, 1981). Since Rubisco does not bind either gaseous substrate prior to their reaction with the RuBPderived enediol acceptor (Cleland et al., 1998), discrimination in favour of carboxylation is likely to have been achieved through the selection of an active site configuration with high affinity for a carboxylation transition-state intermediate, in which the incoming CO_2 resembles a carboxylate group (Tcherkez et al., 2006). This strategy has the disadvantages of reducing the rate of catalytic turnover, due to the greater stability of the resulting enzyme-intermediate complex, as well as resulting in the tighter binding of phosphate analogues. These phosphate analogues include the naturally occurring inhibitor 2-carboxy-D-arabinitol 1-phosphate (CA1P; Gutteridge et al., 1986; Berry et al., 1987) and by-products of reaction intermediates, such as xylulose-1,5-bisphosphate (XuBP) formed by misprotonation of the enediol intermediate (Edmondson et al., 1990; Zhu and Jensen, 1991) and D-glycero-2,3-pentodiulose-1,5-bisphosphate (PDBP) formed by the abstraction of H_2O_2 from the peroxyketone intermediate of the oxygenase reaction (Chen and Hartman, 1995; Kim and Portis, 2004). Under some conditions, binding of these analogues and of RuBP itself (Laing and Christeller, 1976) to Rubisco is sufficiently tight to inactivate the enzyme by locking the active site in a closed conformation (Salvucci and Crafts-Brandner, 2004a).

Measurement of RuBP carboxylation *in vitro* reveals a significant decline in activity with time – a phenomenon known as fallover – caused by the progressive inhibition of Rubisco by the accumulation of XuBP and PDBP. This process also occurs *in vivo* during photosynthesis, necessitating the repeated intervention by Rubisco activase to reactivate Rubisco (see below). The autocatalytic inactivation of Rubisco, together with its energy-dependent reactivation, means that the activity of Rubisco can in principle be maintained at a level appropriate to the prevailing capacity to regenerate the co-substrate, RuBP.

A universal catalytic mechanism means that XuBP and PDBP inevitably arise during catalysis by all forms of Rubisco (Kim and Portis, 2004; Pearce, 2006). However, the L₈S₈ Rubisco of vascular plants shows far greater susceptibility to inhibition by these by-products than those from other evolutionary lineages (Pearce, 2006). The absence of fallover in Rubiscos from alternative lineages is accounted for either by increased rates of inhibitor release or by weaker inhibitor binding (Pearce, 2006). The potential for reducing the susceptibility of higher plant Rubisco to fallover has also been demonstrated for tobacco Rubisco incorporating a Leu335Val L-subunit substitution (Pearce and Andrews, 2003). Although posing an impediment to catalysis, the mutation reduced fallover by lowering the enzyme's sensitivity to XuBP inhibition and facilitating the rearrangement of PDBP to its apparently less-inhibitory isomer, carboxytetritol-1,4-bisphosphate. It is also anticipated that targeted improvements to S_{CO} will reduce fallover by plant Rubisco due to reduced rates of oxygenation and the associated formation of PDBP.

Both PDBP (Kim and Portis, 2004) and XuBP (Schrader *et al.*, 2006) production during catalysis by land plant Rubisco increase at elevated temperatures (35–45 °C). In spite of this, in the presence of excess CO₂ and Mg²⁺, the relative fall in Rubisco activity was less severe than in parallel experiments conducted at lower temperatures (Kim and Portis, 2006; Schrader *et al.*, 2006), implying that loss of Rubisco activity seen at similarly elevated temperatures. However, at lower, physiological concentrations of CO₂ and Mg²⁺, the extent of fallover at elevated temperatures was much greater, due in part to increased Rubisco inactivation by decarbamylation (Kim and Portis, 2006), re-emphasizing the relevance of Rubisco activity to photosynthetic performance across a range of temperatures.

The naturally occurring Rubisco inhibitor CA1P binds tightly to the carbamylated form of Rubisco during periods of low light or darkness. CA1P is subsequently released from Rubisco and rendered non-inhibitory by the concerted action of the light-activated enzymes, Rubisco activase (elaborated below) and CA1P phosphatase (CA1Pase; Parry et al., 2008). Details of the biosynthesis of CA1P from CO₂ via the Calvin cycle intermediate fructose-1,6-bisphosphate (FBP) have been elucidated through a combination of in vitro radiotracer (Andralojc et al., 1994, 1996; Martindale et al., 1997) and in vivo pulse-chase experiments in combination with the demonstration that intermediates of CA1P biosynthesis accumulate in transgenic potato expressing the gene for chloroplast FBP phosphatase in the antisense orientation (Andralojc et al., 2002). The Rubisco-CA1P complex is likely to resemble that between Rubisco and the closely related substrate analogue 2-carboxy-D-arabinitol 1,5-bisphosphate (CABP; Knight et al., 1990), having a closed conformation which is resistant to proteolysis (Mulligan et al., 1988; Khan et al., 1999). It is likely that the tight binding of either PDBP or XuBP to Rubisco also confers resistance to proteolysis.

The sequence and functional characterization of CA1Pase from wheat was recently published (Andralojc *et al.*, 2012), presenting the opportunity not only to manipulate the



Fig. 4. Activation of CA1P-inhibited Rubisco in the presence and absence of CA1Pase. Activated Rubisco was preincubated for 10 min with a 3-fold excess of CA1P, after which aliquots were taken for measurement of carboxylase activity in the presence and absence of CA1Pase. The total assay volume was 500 μ l containing 12.5 μ g of Rubisco and 2.5 μ g CA1Pase. The reactions were acid-quenched at the indicated times and the remaining ¹⁴C (i.e. PGA) determined. Assay buffers and all other details were as described previously (Andralojc *et al.*, 2012). All assays were performed in triplicate.

abundance of CA1P but also to investigate the interactions between Rubisco, Rubisco activase, and CA1Pase from the same species. Unexpectedly, the cloned CA1Pase was found to diminish PDBP inhibition of Rubisco (fallover), indicating that the phosphatase may play a broader role in Rubisco regulation by removing PDBP generated non-enzymically within the chloroplast (Andralojc et al, 2012). CA1Pase has also been found to accelerate the in vitro activation of CA1P-inhibited Rubisco (Fig. 4), although the relative contribution of CA1P dephosphorylation and the removal of inhibitory contaminants in the RuBP to this process is unknown. The ability of CA1Pase to remove inhibitors other than CA1P is consistent with the widespread occurrence of putative coding sequences for CA1Pase in plant species, including those that produce little or no detectable levels of CA1P (Andralojc et al., 2012). Therefore, altered expression of CA1Pase may impact on Rubisco activity in the light but, like Rubisco activase, CA1Pase has also been shown to be inactivated at moderately elevated temperatures (Holbrook et al., 1991).

Activation of Rubisco by Rubisco activase

Reactivation of Rubisco active sites that have been locked in closed conformation by the unproductive binding of sugar phosphates requires conformational remodelling by Rubisco activase (Portis, 2003). Rubisco activase is an AAA+ ATPase, which uses the energy from the hydrolysis of ATP to power the remodelling reaction and thereby facilitates the release of the tightly binding sugar phosphate. Because of this dependence on ATP hydrolysis and the inhibition of this activity by ADP (Robinson and Portis, 1989), the activation of Rubisco by Rubisco activase serves an important regulatory function



Fig. 5. Temperature response of net CO_2 assimilation rate (filled circles) and Rubisco activation state (open squares) in plants of *Camelina sativa* (L.) Crantz cv. Robinson. Gas exchange was measured in attached leaves at the indicated leaf temperatures using a PPFD of 1800 μ mol m⁻² s⁻¹, a reference CO_2 concentration of 380 μ mol mol⁻¹, and 21% (v/v) O_2 . Rubisco activation state [(initial activity/total activity) × 100] was determined by measuring Rubisco activities in extracts prepared from leaf discs that were exposed to the same conditions used for the gas-exchange measurements. Data from Carmo-Silva and Salvucci (2012).

in linking the rate of CO_2 fixation to the rate of electron transport activity via the production of ATP.

Rubisco is typically fully activated in leaves under steadystate conditions and high light, except at high temperatures. As leaf temperatures increase above the optimum for photosynthesis, the activation state of Rubisco decreases in concert with the decrease in CO₂ assimilation rate (Fig. 5). The responses of Rubisco activation state and photosynthesis to supra-optimal temperatures are closely correlated, both qualitatively and quantitatively. Species from warm environments exhibit a higher temperature optimum of activation and CO₂ assimilation than species from colder environments (Feller *et al.*, 1998; Crafts-Brandner and Salvucci, 2000; Haldimann and Feller, 2004; Yamori *et al.*, 2006; Carmo-Silva and Salvucci, 2012; Scafaro *et al.*, 2012).

Inhibition of photosynthesis by heat stress is of practical concern for agriculture since climate change scenarios predict that global temperatures will increase by 2–5 °C by the end of the century (IPCC, 2007), if not sooner (Rowlands et al., 2012). Accompanying this rise, an increased frequency of periods of elevated temperatures is expected. Moreover, these analyses also predict marked changes in water availability in some areas that could exacerbate the general warming trend by reducing the hydration status of the plants and thereby limiting the capacity for leaf cooling via transpiration (Radin et al., 1994; Haldimann et al., 2008; Carmo-Silva et al., 2012). Fig. 6 illustrates this point by showing that Rubisco activation decreases in field-grown cotton cultivars under drought because their lower stomatal conductance reduces evaporative cooling, leading to warmer leaf temperatures. The individual and combined effects of heat and drought on the relationship between the net CO_2 assimilation rate and intercellular CO₂ concentration (C_i) are shown in Fig. 7. Drought-induced stomatal closure lowers



Fig. 6. Relationships between leaf temperature, stomatal conductance and Rubisco activation state in four cotton (*Gossypium* barbadense L.) cultivars grown in a semi-arid environment under well-watered and water-limited conditions. The cultivars measured in the study were: Monseratt Sea Island (MS), Pima 32 (P32), Pima S-6 (S6), and Pima S-7 (S7). Measurements were taken near midday on several occasions throughout the growing season. Conditions for infra-red gas analysis were: reference $CO_2 = 380 \,\mu\text{mol}\,\text{mol}^{-1}$, PPFD =1800 $\mu\text{mol}\,\text{m}^{-2}\,\text{s}^{-1}$, and block temperature = 32 °C. Frozen samples were assayed for Rubisco activity and the activation state was calculated as (initial activity/total activity) × 100. Data from Carmo-Silva *et al.* (2012).



Fig. 7. Individual and combined effects of drought and heat stress on the net CO_2 assimilation rate (A) at a given intercellular CO_2 concentration (C_i). The A–C_i response of cotton Monseratt Sea Island plants under well-watered conditions (data from Carmo-Silva *et al.*, 2012) was modelled. Drought-induced diffusional limitations lower the C_i and heat-induced metabolic limitations caused by Rubisco deactivation decrease the slope of the A–C_i response. In semi-arid environments, drought and heat stress can combine to severely inhibit photosynthesis. Stars denote the values of A and corresponding C_i under each circumstance.

 C_i , thereby causing a diffusional limitation to photosynthetic CO_2 assimilation by Rubisco. Heat-induced Rubisco deactivation, on the other hand, causes a metabolic limitation to photosynthesis, reducing the slope of the A–C_i response due to increased restriction to Rubisco activity. When combined, the inhibitory effects of drought and heat stress on photosynthetic performance are additive.

Considerable effort has been made recently on elucidating the biochemical basis for the decrease in Rubisco activation state under heat stress (Salvucci and Crafts-Brandner, 2004a; Sage *et al.*, 2008). Extensive evidence supports the finding that thermal inactivation of Rubisco activity arises primarily from temperature-dependent inactivation of Rubisco activase (Spreitzer and Salvucci, 2002; Portis, 2003). Rubisco activase is exceptionally sensitive to heat inactivation, exhibiting a temperature optimum for activity below 40 °C (Salvucci and Crafts-Brandner, 2004b; Barta *et al.*, 2010; Carmo-Silva and Salvucci, 2011). The optimum temperature varies among plant species in relation to their thermal environment (Fig. 8), within about the same range as photosynthesis (Salvucci and Crafts-Brandner, 2004b). *In planta*, activase stability could be influenced by heat-induced changes either in redox state (Schrader *et al.*, 2007; Zhang *et al.*, 2009; Sharkey and Zhang, 2010) or the concentrations of ions, nucleotides, or other chloroplast constituents (Sage *et al.*, 2008).

The conformational flexibility required to remodel Rubisco at ambient and low temperatures is likely to limit the thermostability of Rubisco activase. It has even been proposed that the thermotolerance of Rubisco activase might even be responsible for restricting the distribution of certain plant species (Sage *et al.*, 2008). The response of Rubisco activase activity to temperature for cotton, a warm-season species, and *Camelina sativa*, a cool-season species, clearly demonstrates this trade-off between thermostability and performance at low temperature (Fig. 8).

Another aspect of photosynthesis affected by the activity of Rubisco activase is the rate of photosynthetic induction during transitions in irradiance level (Woodrow *et al.*, 1996; Mott *et al.*, 1997; Mott and Woodrow, 2000). Compared with electron transport activity, the rate of CO_2 assimilation increases slowly after increasing the irradiance, primarily because of the slow rate of Rubisco activation. Following an abrupt increase in irradiance, slow induction might prevent photoinhibition by allowing stomata time to open. However, a faster response to the transition would increase the amount of CO_2 fixed during sunflecks and in environments where irradiance levels are variable (Roden and Pearcy, 1993; Ögren and Sundin, 1996). Recently, Yamori *et al.* (2012) showed that photosynthetic induction was faster in transgenic rice plants that overexpressed Rubisco activase from



Fig. 8. Temperature response of Rubisco activase activity in leaf extracts of *Camelina sativa* (L.) Crantz cv. Robinson, a cool-season crop species, and *Gossypium hirsutum* L. cv. Coker 100A, a warm-season crop species. Data from Carmo-Silva and Salvucci (2011).

a maize transgene. The performance of these plants under fluctuating irradiance was not analysed in this or a previous study (Fukayama *et al.*, 2012).

Opportunities and limitations for manipulating Rubisco activase

The best evidence for a causal relationship between the thermal instability of Rubisco activase and the inhibition of photosynthesis by heat stress comes from two separate studies with Arabidopsis, showing that replacement of the native Rubisco activase with a more thermostable Rubisco activase increased plant tolerance to heat stress (Kurek et al., 2007; Kumar et al., 2009). Moreover, the improvements in photosynthetic performance under heat stress translated into a significant increase in seed yield, showing that assimilate supply from photosynthesis is a primary cause of yield penalty under moderate heat stress. These proof-of-concept experiments with Arabidopsis (Kurek et al., 2007; Kumar et al., 2009) demonstrated that improvement of the thermal stability of Rubisco activase by a few degrees would be sufficient in itself to increase photosynthetic performance and yield under moderate heat stress. However, the experiments in these studies were performed with a model plant (Arabidopsis) containing no endogenous Rubisco activase (i.e. the null rca mutant) that was transformed with constructs that encoded for a more thermostable, but nonregulated, form of Rubisco activase. Thus, it is uncertain if introduction of a more thermostable Rubisco activase will improve the thermotolerance of photosynthesis in a background containing endogenous Rubisco activase. It is also not clear which of the isoforms, regulatory or non-regulatory, would be more effective, particularly under natural conditions of fluctuating irradiance.

Yamori *et al.* (2012) recently showed that the thermal stability of photosynthesis was increased slightly when maize Rubisco activase was overexpressed in the presence of endogenous rice Rubisco activase. Based on the temperature optimum for photosynthesis for these plant species, the introduced Rubisco activase from maize should have a similar temperature optimum to the endogenous Rubisco activase in rice. Thus, as the authors conclude, the improvement in thermal tolerance was probably related to the increased amount of Rubisco activase relative to Rubisco in the transgenic plants (Yamori *et al.*, 2012).

Rubisco activase is a relatively abundant protein representing about 5% of the soluble leaf protein (He et al., 1997), and possibly more (Piques et al., 2009). To lower the investment in nitrogen and thereby avoid reductions in Rubisco amount (Mott and Woodrow, 2000; Fukayama et al., 2012; Yamori et al., 2012), we favour a different engineering strategy involving introduction of a significantly more thermostable Rubisco activase. For example, based on the temperature response shown in Fig. 8, introduction of the Rubisco activase from cotton into a cool-season species like Camelina should improve the thermotolerance of photosynthesis by as much as 5 °C (Carmo-Silva and Salvucci, 2012). Expressing cotton Rubisco activase in the presence of endogenous Camelina Rubisco activase should broaden the temperature range for activity, avoiding problems with Rubisco activase performance at low temperatures. Improving the thermotolerance of photosynthesis in warm season plants will require engineering new Rubisco activases since these plants already contain the most thermostable Rubisco activase. Recently resolved structural information for Rubisco activase (Blayney et al., 2011; Henderson et al., 2011; Stotz et al., 2011) and its CbbX homologue (that regulates 'red' L₈S₈ Rubisco activity; Mueller-Cajar et al., 2011) provide key advances in understanding the enzyme's structure and interactions with Rubisco - information that is essential for improving Rubisco activase catalysis by rational design.

Conclusions

The central role of Rubisco as the limiting step in CO₂ assimilation under ambient conditions of CO₂ and high light continues to make it the most attractive target for improving photosynthetic activity. Twenty years ago, the thought of modifying Rubisco catalysis in chloroplasts seemed an immense challenge. This changed with the development of plastome-transformation systems that have successfully expanded our Rubisco engineering capabilities. The new challenges include understanding the intricacies of Rubisco biogenesis in plastids to remove the existing constraints on the range of Rubisco isoforms that can be bioengineered in vitro, in E. coli, and in plastids. Equally important are the needs to measure catalysis from a larger number and greater variety of Rubiscos to identify useful sequence-performance relationships and to fully evaluate the potential of altering catalysis via modification of the S-subunits. These challenges require the development of existing and new higher-throughput recombinant technologies to systematically identify, test, and possibly improve upon Nature's solutions for improving Rubisco catalysis. Unfortunately, efficient and stable plastome transformation is only available for a limited number

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of plants (Maliga and Bock, 2011), although recent evidence of horizontal plastome transmission between plant species using grafting approaches may prove beneficial for developing alternative plastome-transforming approaches for crops (Stegemann *et al.*, 2012, Thyssen *et al.*, 2012).

Discovering solutions for enhancing catalysis that can then be tailored into a target Rubisco will therefore likely continue to take advantage of the customized Rubisco-transformation systems available in tobacco (Kode *et al.*, 2006; Whitney and Sharwood, 2008). Being able to take full advantage of such improvements in crops will require co-integration with other biotechnological strategies for improving photosynthetic carbon assimilation (Fig. 1), including the adaptation of Rubisco activase function to meet the temperature changes associated with global climate change. The successful manipulation of the kinetics and regulation of Rubisco play a major role in improving crop photosynthesis and yield and thereby contribute to the challenge of ensuring food security (Parry and Hawkesford, 2010; Parry, 2012; Tiffin, 2012),

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