



Minireview

The Calvin cycle revisited

Christine A. Raines

Department of Biological Sciences, University of Essex, Colchester CO4 3SQ, UK (e-mail: rainc@essex.ac.uk; fax: +44-1206-872592)

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Abstract

The sequence of reactions in the Calvin cycle, and the biochemical characteristics of the enzymes involved, have been known for some time. However, the extent to which any individual enzyme controls the rate of carbon fixation has been a long standing question. Over the last 10 years, antisense transgenic plants have been used as tools to address this and have revealed some unexpected findings about the Calvin cycle. It was shown that under a range of environmental conditions, the level of Rubisco protein had little impact on the control of carbon fixation. In addition, three of the four thioredoxin regulated enzymes, FBPase, PRKase and GAPDH, had negligible control of the cycle. Unexpectedly, non-regulated enzymes catalysing reversible reactions, aldolase and transketolase, both exerted significant control over carbon flux. Furthermore, under a range of growth conditions SBPase was shown to have a significant level of control over the Calvin cycle. These data led to the hypothesis that increasing the amounts of these enzymes may lead to an increase in photosynthetic carbon assimilation. Remarkably, photosynthetic capacity and growth were increased in tobacco plants expressing a bifunctional SBPase/FBPase enzyme. Future work is discussed which will further our understanding of this complex and important pathway, particularly in relation to the mechanisms that regulate and co-ordinate enzyme activity.

Abbreviations: ATP – adenosine triphosphate; FBPase – fructose-1,6-bisphosphatase; GAPDH – glyceraldehydes-3-phosphate dehydrogenase; LC-MS – liquid crystal-mass spectrometry; NADP – nicotinamide adenine phosphate; NMR – nuclear magnetic resonance; PGKinase – glycerate-3-phosphate kinase or phosphoglycerate kinase; PRKase – ribulose-5-phosphate kinase or phosphoribulokinase; RPI – ribose phosphate isomerase; RPE – ribulose phosphate epimerase; RuBP – ribulose-1,5-bisphosphate; Rubisco – ribulose-1,5-bisphosphate carboxylase/oxygenase; ssu – small subunit unit of ribulose-1,5-bisphosphate carboxylase/oxygenase; TPI – triose-3-phosphate isomerase

Introduction

The photosynthetic carbon reduction (Calvin) cycle is the primary pathway of carbon fixation and in higher plants is located in the chloroplast stroma. In the 1950s, Calvin and colleagues elucidated the sequence of reactions in this cycle. Following this, the enzymes catalysing the reactions in the pathway were identified and their kinetic properties studied *in vitro*. A major goal in photosynthetic research has been to identify limiting points in the process, in order to produce

plants with increased yield. Efforts to improve photosynthetic carbon fixation have been focussed on altering the catalytic properties of Rubisco, as this enzyme was believed to be the major limiting factor (Spreitzer 1993; Hartman and Harpel 1994). However, the emphasis of this research has now shifted, due in part to the lack of success in producing a Rubisco enzyme with reduced oxygenase activity. In addition, during the last decade DNA sequences for all the Calvin cycle enzymes have been isolated and sequenced and antisense transgenic plants with reduced levels of enzymes

have been produced and analysed. Data from these studies is challenging many of the previously held opinions on the importance of individual enzymes in determining the rate of carbon fixation. Previous reviews have considered the application of transgenic plants to the study of chloroplast metabolism (Furbank and Taylor 1995; Stitt and Sonnewald 1995). Two further articles discuss the earlier work on the antisense analysis of the Calvin cycle (Stitt and Schulze 1994; Quick and Neuhaus 1997) and the C4 photosynthetic pathway (Furbank et al. 1997). This review will focus on the interesting data that has emerged from the transgenic analysis of the Calvin cycle that has identified potential targets for manipulation to increase carbon fixation *in vivo*.

Calvin cycle reactions

The Calvin cycle utilises the products of the light reactions of photosynthesis, ATP and NADPH, to fix atmospheric CO₂ into carbon skeletons that are used directly for starch and sucrose biosynthesis (Figure 1) (Woodrow and Berry 1988; Geiger and Servaites 1995; Quick and Neuhaus 1997). This cycle comprises 11 different enzymes, catalysing 13 reactions, and is initiated by the enzyme ribulose-1,5-bisphosphate carboxylase oxygenase (Rubisco) which catalyses the carboxylation of the CO₂ acceptor molecule, ribulose-1,5-bisphosphate (RuBP). The 3-phosphoglycerate (3-PGA) formed by this reaction is then utilised to form the triose phosphates, glyceraldehyde phosphate (G-3-P) and dihydroxyacetone phosphate (DHAP), via two reactions that consume ATP and NADPH. The regenerative phase of the cycle involves a series of reactions that convert triose phosphates into the CO₂ acceptor molecule, RuBP. The majority of the triose phosphate produced in the Calvin cycle remains within the cycle to regenerate RuBP. However, carbon compounds produced in this cycle are essential for growth and development of the plant and therefore triose phosphates exit from the cycle and are used to synthesise sucrose and starch. The Calvin cycle also supplies intermediates to an array of other pathways in the chloroplast, including the shikimate pathway for the biosynthesis of amino acids and lignin, isoprenoid biosynthesis and precursors for nucleotide metabolism and cell wall synthesis (Lichtenthaler 1999) (Figure 1). Clearly, the Calvin cycle occupies a central position in carbon metabolism and a full understanding of the mechanisms that control flux through this pathway, together

with those that control the allocation of carbon to intermediate and secondary metabolic pathways, is essential if genetic manipulation of plant metabolism is to be a realised.

Identifying enzymes that limit photosynthetic carbon flux

Traditionally, analysis of metabolic pathways focussed on the study of the kinetic properties of individual enzymes. This approach led to the identification of a number of 'key' enzymes in the Calvin cycle such as Rubisco, SBPase, FBPase and PRKase. This classification was based on the fact that the activity of these enzymes was regulated by a number of factors, including light, stromal pH [Mg²⁺], and that they catalysed reactions which were more or less irreversible (Portis et al. 1977; Woodrow and Berry 1988). The conclusion from this biochemical analysis was that these 'key' enzymes were likely to have the greatest importance in controlling the rate of CO₂ fixation. However, these *in vitro* studies provided no information on the extent to which any single Calvin cycle enzyme controlled the rate of carbon dioxide fixation *in vivo*.

Metabolic control analysis is an alternative approach that can be used to determine the relative importance of an individual enzyme in controlling the flux through a pathway (Fell 1997). To undertake metabolic control analysis of a pathway it is necessary to be able to reduce specifically the amount of an individual enzyme in that pathway; the effect of this reduction on flux can then be compared to the control with the normal level of enzyme activity (for fuller description of this approach, see Fell 1997). This analysis can provide a quantitative measure of the control exerted by a single enzyme over the flux through a pathway and can be defined mathematically:

$$C = \frac{\frac{\delta J}{J}}{\frac{\delta E}{E}}$$

where C is the flux control co-efficient; J the original flux through the pathway; δJ change in flux; E original enzyme activity; δE change in enzyme activity. The flux control coefficient can vary from 0, for an enzyme that makes no contribution to control, to 1, for an enzyme that exerts total control. The flux control value for any single enzyme is not a constant and can change depending on the conditions under which the

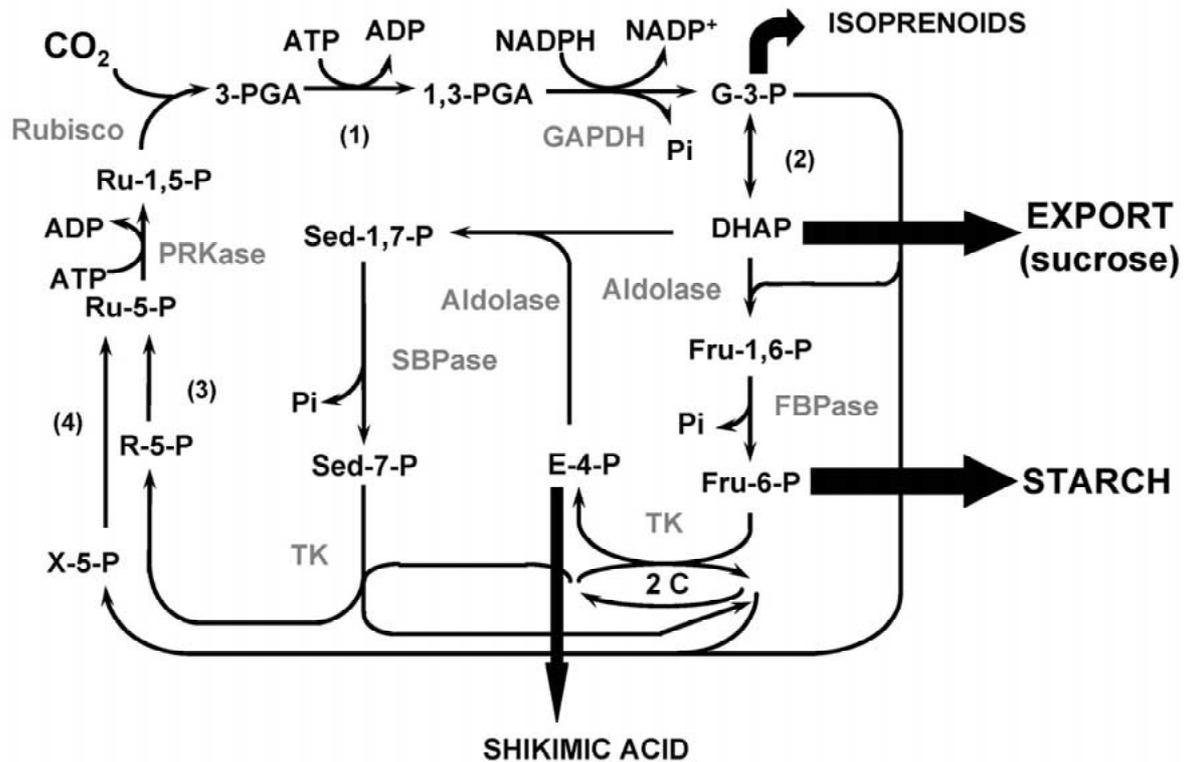


Figure 1. The Calvin cycle showing the intermediates from the first stable carbon compound, 3-PGA, to the carbon dioxide acceptor molecule, ribulose-1,5-bisphosphate and the exit points from the cycle into the pathways of sucrose, starch, isoprenoids and shikimic acid. The reactions catalysed by the enzymes whose levels have been manipulated in transgenic plants, are shown in grey. The site of function of the enzymes (1) 3-phosphoglycerate kinase (2) triose phosphate isomerase (3) ribose-5-phosphate isomerase and (4) ribulose-5-phosphate epimerase are also indicated.

analysis is carried out. However, the sum of the flux control co-efficients for the for all the enzymes in a single pathway should equal 1. Therefore, in order that this be maintained, when the control value for one enzyme in the system increases, then the control values for one or more of the other enzymes in the system must decrease. One fundamental difference between this approach and that of earlier studies based on the kinetics of individual enzymes, is that metabolic control analysis allows for all enzymes in a pathway to share control of flux in that pathway.

The contribution that individual enzymes make to the control of carbon flux through the Calvin cycle has been investigated using antisense plants with reduced levels of individual enzymes. The application of metabolic control analysis to address this problem was initiated by Stitt and co-workers using transgenic antisense Rubisco plants (Rodermeil et al. 1988). Presently, antisense plants for seven of the eleven enzymes in the Calvin cycle have been analysed using

this approach (Table 1). Although outwith the scope of this review it should be noted that antisense plants with reduced Calvin cycle enzyme levels have also been used extensively to study the interactions between electron transport processes and carbon assimilation (Ruuska et al. 1998, 2000a–c; Badger et al. 2000).

The enzymes Rubisco, sedoheptulose-1,7-bisphosphatase, aldolase and transketolase dominate control of photosynthetic carbon fixation and reduce carbohydrate accumulation and growth

Rubisco

An extensive analysis has been carried out using antisense plants with reduced levels of the enzyme Rubisco and much of this data has been reviewed previously (see the review by Stitt and Schulze 1994). For this

Table 1. Calvin cycle antisense plants; a summary of the plant species and promoters used, together with the photosynthetic flux control values

Enzyme	Antisense plants	Promoter used	Photosynthesis flux control values	Primary references
Rubisco	Tobacco	CaMV	0–1.0	Rodermal and Bogorad 1988 Stitt and Schulzel 1994 Hudson et al (1992)
PGKinase				No published data
GAPDH	Tobacco	CaMV	<0.2	Price et al. 1995
TPI				No published data
Aldolase	Potato	CaMV	0.07–0.55	Haake et al. 1998
Transketolase	Tobacco	CaMV	0.07–1.0	Henkes et al. 2001
FBPase	Potato	CaMV	<0.2	Kossman et al. 1994
SBPase	Tobacco	CaMV	0.3–0.75	Harrison et al. 1998
RPE				No published data
RPI				No published data
PRKase	Tobacco	Tobacco ssu	<0.28	Paul et al. 1995

reason only a brief summary of the most important findings will be included here. The most surprising observation was that halving the activity of Rubisco caused no significant decrease in photosynthesis. This finding applied regardless if the plants were grown in high or low light conditions; when photosynthesis was measured under the conditions in which the plants were grown and flux control co-efficient values obtained were below 0.2 (Stitt et al. 1991; Quick et al. 1991b; Hudson et al. 1992). However, if the tobacco Rubisco antisense plants were grown in ambient CO₂ and moderate light (350 $\mu\text{mol m}^{-2} \text{s}^{-1}$) and photosynthesis measured under saturating light and/or saturating CO₂, then the control exerted by Rubisco increased significantly, and control coefficient values could reach 0.8. Interestingly, when the antisense Rubisco plants were grown in a greenhouse with high irradiance, high temperature and low humidity, Rubisco had almost complete control of carbon fixation when photosynthesis was measured under the growth conditions (Krapp et al. 1994). The impact of reductions in Rubisco ssu protein on photosynthesis was also greater when the Rubisco antisense plants were grown in limiting nitrogen (Quick et al. 1991a; Fichtener et al. 1993; Masle et al. 1993). These results demonstrated that the flux control co-efficient varied dependent on both the conditions of growth and analysis and that the level of Rubisco protein does not limit photosynthetic capacity under a wide range of

conditions. However, it is clear that the biochemical characteristics of this enzyme severely limit the uptake of carbon from the atmosphere. This is evidenced by the high flux control co-efficient obtained in plants with reduced Rubisco content when the analysis is carried out under conditions where photorespiration is favoured, thereby reducing carboxylation efficiency. These results are in agreement with the model of von Caemmerer and Farquhar which predicts that, under high light and limiting CO₂ conditions, Rubisco is the single limitation on photosynthesis and would have a control co-efficient of 1 (von Caemmerer et al. 1981; von Caemmerer 2000).

In keeping with the insensitivity of photosynthesis to reductions in Rubisco activity, when the Rubisco antisense plants were grown in low light (300 $\mu\text{mol m}^{-2} \text{s}^{-1}$) and nitrogen-sufficient conditions, little or no effect, on growth, or carbohydrate accumulation were observed. However, plants with less than 50% of wild-type Rubisco activity had decreased starch and sucrose levels, increased shoot to root ratio and when only 20% Rubisco activity remained, an increase in specific leaf area was observed (Quick et al. 1992; Fichtener et al. 1993). These results suggested that carbon allocation was being shifted in an attempt to maximise photosynthetic capacity in response to reduced Rubisco activity. Further analysis of growth and development in these antisense plants with only 20% of normal Rubisco activity revealed that the timing

of shoot development was altered, possibly due to reduced source strength or to changes in the sink-source balance (Jiang and Rodermel 1995; Tsai et al. 1997).

Sedoheptulose-1,7-bisphosphatase

Photosynthetic carbon fixation was reduced in antisense tobacco plants with small decreases in SBPase activity. This was reflected in the control co-efficient values for SBPase of between 0.3 and 0.5 when photosynthesis was measured in greenhouse grown plants (irradiance of between 600–1500 $\mu\text{mol m}^{-2} \text{s}^{-1}$) under saturating light (Harrison et al. 1998; Raines et al. 2000; Olcer et al. 2001). Even higher flux control values, in the range 0.6–0.75, were obtained when the SBPase antisense plants were grown in controlled environment conditions with a constant high irradiance (800 $\mu\text{mol m}^{-2} \text{s}^{-1}$). These results provide convincing evidence that the activity of SBPase *in vivo* is a major determinant of photosynthetic capacity in tobacco.

Carbohydrate levels in the source leaves of the SBPase antisense plants were also sensitive to small decreases in SBPase activity. Starch levels declined linearly as SBPase activity was reduced and flux control values for starch accumulation were as high as 0.6 in plants grown in high light (800 $\mu\text{mol m}^{-2} \text{s}^{-1}$). In plants with less than 20% of wild-type SBPase activity, starch was barely detectable (Raines et al. 2000). Growth analysis of SBPase antisense plants revealed that shoot, leaf and floral biomass declined linearly in response to reductions in SBPase activity. An interesting feature observed in these plants was a biphasic response of leaf and stem morphology to reductions in SBPase activity (Bryant 2000). Plants with large reductions in SBPase activity were the same height or taller than wild-type plants, with thin stems and increased specific leaf area. In contrast, small reductions in SBPase activity resulted in plants that were shorter, had thicker stems and reduced specific leaf area when compared to wild type plants. Similar changes in leaf and stem morphology occur in some species in response to the light environment (Björkman 1981; Evans 1996). It is possible that the reductions in source capacity in the antisense plants mimic the metabolic signals that invoke the acclimatory responses to different light environments.

Plastid aldolase

In the first report on the analysis of antisense potato with reduced aldolase levels, photosynthesis did not decrease until aldolase activity was reduced to less than 60% of normal wild-type levels, in plants grown in low light (250 $\mu\text{mol m}^{-2} \text{s}^{-1}$) and ambient CO_2 . In this analysis flux control co-efficient values for aldolase of between 0.18 (measured in ambient conditions) and 0.32 (measured in saturating light and saturating CO_2 conditions) were obtained (Haake et al. 1998).

In a subsequent more extensive analysis antisense aldolase plants were grown in three different environmental conditions and photosynthetic carbon fixation measured (Haake et al. 1999). Under very low light and ambient CO_2 (70 $\mu\text{mol m}^{-2} \text{s}^{-1}$ light and 350 ppm CO_2) a flux control co-efficient of 0.15 was obtained; increasing both the growth and measuring light level (390 $\mu\text{mol m}^{-2} \text{s}^{-1}$ light and 400 ppm CO_2) resulted in a flux control value of aldolase of 0.21 which increased even further to 0.55 at saturating CO_2 (390 $\mu\text{mol m}^{-2} \text{s}^{-1}$ light and 800 ppm CO_2). These results were surprising as they showed for the first time that a non-regulated enzyme, catalysing a freely reversible reaction, had a significant share of control over photosynthetic carbon flux.

Carbohydrate accumulation was reduced in the aldolase antisense plants and, as with photosynthetic capacity, the extent of this was dependent on growth conditions. In general, reductions in aldolase activity had a greater effect on starch than sucrose and, in light conditions of 400 $\mu\text{mol m}^{-2} \text{s}^{-1}$, the flux control co-efficient for aldolase over starch accumulation could be as high as 0.45. In contrast, little effect on sucrose levels was seen until only 30% of normal wild type aldolase activity remained. The changes in sugar levels correlated with the finding that no major decrease in the fresh weight of leaves, stem, root or tubers were evident, regardless of the growth conditions until aldolase activity was less than 50% of wild type (Haake et al. 1999).

Transketolase

The unexpected result obtained from analysis of antisense aldolase plants, showing that non-regulated enzymes could exert control over carbon fixation, was reinforced by results obtained from tobacco plants with reduced levels of plastid transketolase (Henkes et al. 2001). When these antisense tobacco plants

were grown in greenhouse conditions (daily irradiance levels were between $170 \mu\text{mol m}^{-2} \text{s}^{-1}$ to $600 \mu\text{mol m}^{-2} \text{s}^{-1}$). The flux control value for transketolase over carbon fixation, in ambient CO_2 and low light ($170 \mu\text{mol m}^{-2} \text{s}^{-1}$), was 0.07. This value increased to 0.32 when photosynthesis was measured at high irradiance ($700 \mu\text{mol m}^{-2} \text{s}^{-1}$) and ambient CO_2 .

Reductions in transketolase activity had dramatic effects on carbon partitioning between the sucrose and starch biosynthetic pathways. Sucrose levels declined linearly with reductions in transketolase activity and, even in plants with 75% of wild-type transketolase activity a 25% reduction in the levels of sucrose was evident. In contrast, starch accumulation was unaffected until transketolase activity was reduced to below 60% of wild-type activity. These results were particularly interesting as they are unique when compared to all the other Calvin cycle antisense plants where sucrose levels were maintained at the expense of starch. Another interesting consequence of reduction in transketolase activity was a decrease in aromatic amino acid biosynthesis and intermediates of the shikimic acid pathway, indicating that the availability of carbon skeletons from the Calvin cycle could control the flux of carbon into phenylpropanoid metabolism. Although photosynthetic capacity and sucrose accumulation were sensitive to small reductions in transketolase, the total biomass (fresh weight) of these antisense plants did not change until transketolase activity was below 60% of wild-type. However, further reductions in the levels of this enzyme results in a linear decline in total fresh weight of these plants.

Glyceraldehyde-3-phosphate dehydrogenase, fructose-1,6-bisphosphatase or phosphoribulokinase have little control over photosynthetic carbon fixation

The antisense analysis described above has provided a picture of the distribution of control that has overturned the preconception that highly regulated enzymes ('key') had most control. Further support for this came from the finding that some highly regulated enzymes had almost no control over carbon fixation. In antisense tobacco plants with reduced levels of GAPDH were grown in high light greenhouse conditions (maximum irradiance of $900 \mu\text{mol m}^{-2} \text{s}^{-1}$) no effects on photosynthesis were observed until GAPDH activity was reduced to below 35% of

wild type, even when photosynthetic carbon assimilation was measured under saturating light (irradiance of $1500 \mu\text{mol m}^{-2} \text{s}^{-1}$) (Price et al. 1995). Similar results were obtained with FBPase antisense potato plants where no effect on photosynthesis occurred until FBPase activity was less than 34% of wild type (Kossman et al. 1994). These plants were grown in low light ($250 \mu\text{mol m}^{-2} \text{s}^{-1}$) and photosynthesis measured as oxygen evolution with saturating light ($1000 \mu\text{mol m}^{-2} \text{s}^{-1}$) and CO_2 . The flux control coefficients for GAPDH and FBPase were less than 0.2 in most conditions.

Photosynthetic carbon fixation was also insensitive to reductions in the levels of PRKase activity. Analysis of antisense PRKase tobacco plants that had been grown in low light conditions ($330 \mu\text{mol m}^{-2} \text{s}^{-1}$), or in nitrogen deficient conditions, showed that PRKase activity could be reduced to less than 20% of wild-type levels before any decrease in photosynthesis was evident (Paul et al. 1995; Banks et al. 1998). The maximum flux control coefficient for carbon flux through the Calvin cycle obtained for PRKase was 0.25, in plants grown at $330 \mu\text{mol m}^{-2} \text{s}^{-1}$ and photosynthesis measured under saturating light of between $800\text{--}1400 \mu\text{mol m}^{-2} \text{s}^{-1}$. (Paul et al. 2000). Measurements of *in vivo* PRKase activity revealed that reductions in levels of this enzyme in transgenic plants were compensated for by activating a higher percentage of the remaining PRKase (Banks et al. 1999).

Can photosynthetic carbon fixation and plant growth rates be increased?

Analyses of antisense plants have provided direct experimental evidence that control over the rate of carbon fixation in the Calvin cycle is shared between a restricted number of enzymes. Two enzymes, Rubisco and SBPase, appear to dominate, however, two non-regulated enzymes, transketolase and aldolase, were also shown to have the potential to contribute significantly to carbon flux through the Calvin cycle (Hudson et al. 1992; Stitt and Schulze 1994; Harrison et al. 1998; Haake et al. 1998, 1999, Henkes et al. 2001; Raines et al. 2000). In contrast, there was no evidence that GAPDH, FBPase or PRKase had any significant control over carbon fixation. Although the level of control exerted by any single enzyme in the cycle varied dependent on environmental conditions and developmental status, the data from the transgenic plants strongly indicated that carbon flux

was co-limited by the enzymes at the branch point in the cycle, between regeneration and export, and the carboxylation reaction of Rubisco.

A model of CO₂ uptake developed by Farquhar and colleagues partitioned the limitation of photosynthesis between Rubisco activity and the capacity for RuBP regeneration (von Caemmerer et al. 1981, 2000). This model predicts that, under light saturating, CO₂ limiting conditions, Rubisco activity is the major determinant of carbon fixation. Application of this model demonstrated that the balance of co-limitation of photosynthetic carbon fixation is poised between carboxylation and regeneration, under a wide range of environmental conditions (von Caemmerer and Farquhar 1984) in a large number of plant species (Evans 1986; Evans and Farquhar 1991; Wullschleger 1993; Leuning 1997). The balance between regeneration and carboxylation capacities is normally maintained such that they co-limit photosynthesis and neither of these capacities dominate control of carbon dioxide flux in the Calvin cycle. This implied that in order to increase photosynthetic capacity both of these parameters would have to be increased simultaneously. A kinetic model of the Calvin cycle, developed by Fell and Poolman, has also predicted that the control of photosynthetic carbon flux is likely to be co-limited by Rubisco and regeneration, with the enzyme SBPase being the major controlling enzyme in this phase of the cycle. Interestingly, this model also predicted that share of control between Rubisco and SBPase was balanced, however, these authors suggested that this co-limitation could be shifted dependent on conditions within the cell (Poolman et al. 2000, 2001). Analysis of the Calvin cycle antisense plants has shown clearly that it is possible to disrupt this balance, such that either regenerative capacity or Rubisco activity dominates control. In addition, this transgenic approach has identified individual enzymes that have significant control of flux through the cycle. These results are highly significant as they provide evidence to suggest that by using genetic manipulation that it might be possible to increase carbon assimilation without changing Rubisco activity (Stitt and Schulze 1994; Ruuska et al. 1998; Harrison et al. 2001).

The information obtained from the analysis of the antisense Calvin cycle plants suggested that increasing the levels of SBPase and, to a lesser extent, transketolase or aldolase, may lead to an increase in photosynthetic carbon fixation and growth rates. In support of this hypothesis, expression of a bi-functional cyanobacterial FBPase/SBPase in transgenic tobacco

plants has resulted in a stimulation in photosynthetic capacity and in an increase in height and dry weight (Miyagawa et al. 2001). This dramatic effect maybe due to differences in regulatory properties between the bifunctional cyanobacterial FBPase/SBPase, and the plant FBPase and SBPase enzymes. Transgenic tobacco plants have been produced using a full-length *Arabidopsis* SBPase cDNA clone expressed under the control of the CaMV35S promoter. Interestingly, photosynthetic capacity and plant biomass were also increased in these tobacco plants with increased SBPase protein levels (Lefebvre, Lloyd and Raines, unpublished data). This work suggested that an increase in SBPase activity alone may be sufficient to stimulate carbon fixation capacity and plant growth in tobacco (Figure 2). These findings are remarkable and show for the first time that photosynthetic carbon fixation can be improved by increasing the activity of one enzyme in the Calvin cycle. Of particular significance is the clear demonstration that carbon fixation can be improved without any direct manipulation of Rubisco activity or content. It has also overturned earlier assumptions that changing the activity of only one enzyme in the cycle would be likely to have no effect on photosynthetic capacity and be even less likely to impact on yield (see reviews in Paul and Lawlor 2000).

Future directions

Regulation of the Calvin cycle

Transgenic plants will continue to be excellent tools to use to further our understanding of the regulatory mechanisms which, not only control the flux of carbon within the Calvin cycle, but may also determine the rate of carbon flow into intermediate and secondary metabolism. Although it has been known for over 20 years that thioredoxin regulates the activity of four enzymes within the Calvin cycle, the importance of thioredoxin in controlling flux of carbon *in vivo* is still unknown (Buchanan et al. 1980). The availability of fully active deregulated mutants of FBPase and SBPase enzymes in the cycle together with plants with altered thioredoxin levels will allow these questions to be addressed *in vivo* (Jacquot et al. 1995; Dunford et al. 1998; Raines et al. 2000). Using mutant *Arabidopsis* plants lacking Rubisco activase, together with mutated activase protein sequences, a role for Rubisco activase in the redox modulation of Rubisco activity in light limiting conditions has been demonstrated

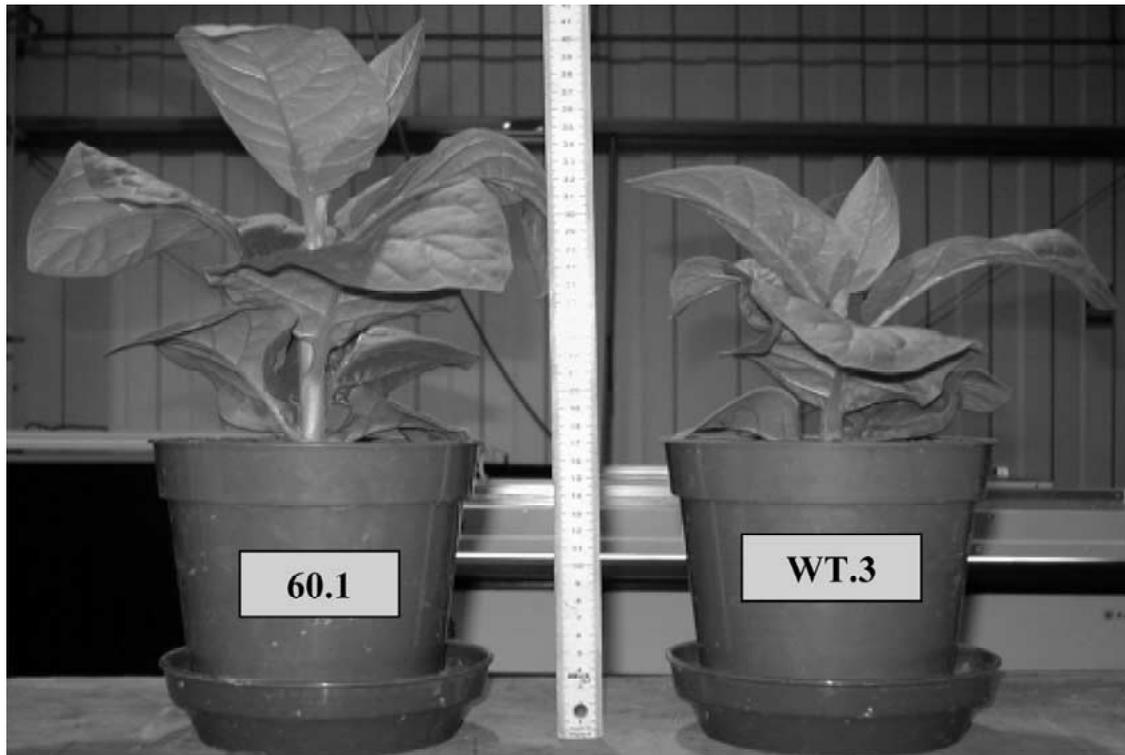


Figure 2. Growth of wild type and transgenic *Nicotiana tabacum* plants over-expressing *Arabidopsis* SBPase. Wild type and T1 progeny were analysed after 6 weeks of growth in soil in greenhouse conditions, at an irradiance of between $600\text{--}1500 \mu\text{mol m}^{-2} \text{s}^{-1}$ and 340 ppm CO_2 .

(Zhang et al. 2002). Recently, a novel chloroplast protein, CP12, was identified that binds to PRKase and GAPDH in a NADPH-dependent manner, possibly regulating the activity of these enzymes (Wedel et al. 1997; Wedel and Soll 1998). Clearly we still have much to learn about the regulatory processes that operate *in vivo* to modulate Calvin cycle enzyme activity, and of the role that they play in controlling the rate of carbon fixation.

Novel modelling approaches

Although transgenic analysis has proved to be a powerful approach to determine the control that specific enzymes exert over carbon fixation, it will not be possible to analyse every step in the photosynthetic process, under every environmental variable, in every species. For these reasons modelling of photosynthesis will continue to be a desirable goal. The application of analytical techniques such as LC-MS and NMR will make it possible to obtain accurate measurements of fluxes through the Calvin cycle in both wild type and transgenic plants. Using these data, together with state-of-the-art computing technology it may be pos-

sible to produce a dynamic model of these processes (Giersch 2001). This type of model is predictive and would have the potential to identify likely targets for further manipulation, in a wide range of species and environmental conditions.

Increasing carbon assimilation

The transgenic over-expression studies carried out using SBPase/FBPase represent a significant step forward in the attempt to identify targets that may be manipulated to increase photosynthesis. However, it remains to be seen if this technology can be applied to crop species or be maintained in field conditions. This notwithstanding, these preliminary studies pave the way for biotechnological applications using genetic manipulation of photosynthetic carbon fixation to increase plant growth and yield. At present there is no data available from over-expression studies involving any other Calvin cycle enzymes but, given the impact of reductions in transketolase on photosynthesis and growth, it will be of great interest to see if over-expression of this enzyme will also increase photosynthetic capacity and yield.

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