

Effect of CO₂ Concentration on Carbonic Anhydrase and Ribulose-1,5-Bisphosphate Carboxylase/Oxygenase Expression in Pea¹

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The effect of external CO₂ concentration on the expression of carbonic anhydrase (CA) and ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) was examined in pea (*Pisum sativum* cv Little Marvel) leaves. Enzyme activities and their transcript levels were reduced in plants grown at 1000 μL/L CO₂ compared with plants grown in ambient air. Growth at 160 μL/L CO₂ also appeared to reduce steady-state transcript levels for *rbcS*, the gene encoding the small subunit of Rubisco, and for *ca*, the gene encoding CA; however, *rbcS* transcripts were reduced to a greater extent at this concentration. Rubisco activity was slightly lower in plants grown at 160 μL/L CO₂, and CA activity was significantly higher than that observed in air-grown plants. Transfer of plants from 1000 μL/L to air levels of CO₂ resulted in a rapid increase in both *ca* and *rbcS* transcript abundance in fully expanded leaves, followed by an increase in enzyme activity. Plants transferred from air to high-CO₂ concentrations appeared to modulate transcript abundance and enzyme activity less quickly. Foliar carbohydrate levels were also examined in plants grown continuously at high and ambient CO₂, and following changes in growth conditions that rapidly altered *ca* and *rbcS* transcript abundance and enzyme activities.

As atmospheric levels of CO₂ continue to increase, there is considerable research interest in the mechanisms by which plants respond to changes in CO₂ concentration, and, in particular, how these changes have an impact on photosynthetic processes (see reviews by Bowes, 1991; Stitt, 1991; Sage, 1994; Webber et al., 1994). Many laboratory studies using growth chamber- or glasshouse-grown plants have shown that some species experience a short-term stimulation followed by a decline in photosynthetic rate after prolonged exposure to high-CO₂ (Stitt, 1991; Webber et al., 1994). This decline in photosynthesis has been associated with a reduction in Rubisco activity, although the capacity of the plant for RuBP/Pi regeneration may also limit photosynthetic rate. Studies have shown that Rubisco protein levels are lower in high-CO₂-grown plants, particularly when additional factors such as nutrient limitation, developmental stage, or root-growth space inhibit effective carbohydrate translocation from leaves into sink tissues

(Sage et al., 1989; Besford et al., 1990; Rowland-Bamford et al., 1991). These additional factors are an important consideration, since some plant species grown in nonlimiting environments at high-CO₂ concentrations do not exhibit a reduction in photosynthetic capacity (Sage, 1994). Nonetheless, the observed reduction in photosynthetic capacity when source-to-sink translocation is constrained indicates that additional regulatory steps in photosynthesis are operating.

The enzyme CA (EC 4.2.1.1), which is localized primarily in the chloroplast stroma of C₃ higher plants, is thought to play a role in photosynthesis by facilitating diffusion into and across the chloroplast, as well as by catalyzing HCO₃⁻ dehydration to supply CO₂ for Rubisco (Badger and Price, 1994). Therefore, it would be anticipated that this enzyme would respond to changes in ambient levels of CO₂ in a manner similar to Rubisco. Previous studies have shown that CA activities are reduced in leaves of *Cucumis sativus* (Peet et al., 1986), *Avena sativa* (Cervigni et al., 1971), *Gossypium hirsutum* (Chang, 1975), and *Phaseolus vulgaris* (Porter and Grodzinski, 1984) grown at elevated CO₂ concentrations, although the mechanisms of regulation were not identified. Recently, in contrast with earlier studies showing a CO₂-induced reduction in CA activity, it was reported that chloroplast CA mRNA abundance increased during acclimation of *Arabidopsis thaliana* to elevated CO₂ levels; however, no measurements of CA or Rubisco activity were made in that study (Raines et al., 1992). In contrast to higher plant studies, the response of CA expression during acclimation to limiting levels of C_i is well documented in eukaryotic algae (Coleman, 1991; Badger and Price, 1992; Sultemeyer et al., 1993). Extracellular levels of C_i appear to regulate transcriptional activity of genes encoding various isoforms of CA, and transfer of cells from one CO₂ level to another results in rapid modification of *ca* mRNA abundance, protein level, and activity (Bailly and Coleman, 1988; Fukuzawa et al., 1990).

In this study we examined CA and Rubisco expression in pea (*Pisum sativum*) leaves acclimated to ambient, elevated, and below-ambient levels of CO₂. In addition, we have examined the capacity of the plants to modify CA and Rubisco activity and transcript abundance in response to rapid changes in CO₂ levels. The levels of soluble foliar

¹ Supported by a grant to J.R.C. from the Natural Sciences and Engineering Research Council of Canada.

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Abbreviations: CA, carbonic anhydrase; *ca*, gene encoding carbonic anhydrase; C_i, inorganic carbon; *rbcS*, gene encoding the small subunit of Rubisco; RuBP, ribulose-1,5-bisphosphate.

carbohydrates were also determined in an effort to correlate changes in gene expression with leaf carbohydrate abundance.

MATERIALS AND METHODS

Seeds of pea (*Pisum sativum* cv Little Marvel) were grown in growth chambers at the appropriate CO₂ concentration for 3 weeks in complete soil, with a daylength of 16 h, PPFD of 400 $\mu\text{mol m}^{-2} \text{s}^{-1}$, and a day/night temperature regime of 20/16°C. Plants were watered daily and fertilized weekly with a commercial preparation (PlantProd 20–20–20 with micronutrients, Plant Products, Brampton, Ontario, Canada). Pots were 20 cm in diameter with no more than three plants per pot. When required, plants were transferred to different CO₂ concentrations following 2.5 weeks of growth at high (1000 $\mu\text{L/L}$), ambient (350 $\mu\text{L/L}$), or low-CO₂ (160 $\mu\text{L/L}$) concentrations. Analyses were performed using the first set of fully expanded (mature) leaves or the set of developing (immature) leaves proximal to the apex.

Enzyme Activities

Leaves were excised from fully illuminated plants, their areas and fresh weights quickly determined, and then they were frozen in liquid nitrogen. When required, these frozen samples were ground with a mortar and pestle in extraction buffer (100 mM Bicine, pH 8.2, 20 mM MgCl₂, 5 mM DTT, 1 mM EDTA), and the samples were clarified by centrifugation for 10 min at 10,000g at 4°C. Total CA activity was determined electrometrically (Wilbur and Anderson, 1948). The rate of RuBP-dependent ¹⁴CO₂ incorporation at 25°C following full CO₂/Mg²⁺ activation of the enzyme was used to determine Rubisco activity (Hudson et al., 1992). Enzymes were assayed in triplicate and expressed on the basis of leaf area. Supernatant fractions were assayed for soluble protein (Bradford, 1976), and chlorophyll concentrations were determined (Porra et al., 1989).

Foliar Soluble Sugar Assays

Leaves from illuminated plants growing at the appropriate CO₂ concentrations were excised, their fresh weights and areas quickly determined, and then they were frozen in liquid nitrogen and ground in a mortar and pestle prior to perchloric acid extraction as described by Stitt et al. (1989). Foliar levels of Glc, Fru, and Suc were assayed using a coupled-enzyme system described previously (Stitt et al., 1989).

RNA Isolation and Northern Blot Hybridization

Isolation of total RNA from tissue harvested at the appropriate time was achieved using a previously described protocol (Majeau and Coleman, 1994). Equal aliquots of RNA (5 μg in each sample as determined spectrophotometrically) were denatured with formaldehyde:formamide (6.5:50%, v/v) and then immobilized on nitrocellulose using a slot-blot apparatus (Minifold II Slot-Blotter, Schlei-

cher & Schuell) (Fourney et al., 1988). Prehybridization, hybridization, and probe-labeling protocols were all as described previously (Majeau and Coleman, 1994). Gene probes used were a 0.95-kb pea chloroplast *ca* cDNA (Majeau and Coleman, 1991), a 0.68-kb pea *rbcS* cDNA (Coruzzi et al., 1983), and an 18S soybean rDNA sequence used for normalization of RNA loads. Quantification of hybridization to pea RNA by all probes was achieved by phosphorimaging of the blots (model 400S, Molecular Dynamics, Sunnyvale, CA).

RESULTS

Growth of pea plants at different CO₂ concentrations resulted in major changes in leaf area and fresh weight, Rubisco and CA activity, and soluble protein content (Table I). High CO₂ levels (1000 $\mu\text{L/L}$) increased individual leaf area, as well as leaf fresh weight. In contrast, plants grown under low-CO₂ conditions (160 $\mu\text{L/L}$) had smaller leaves (both area and fresh weight) than control plants. In vitro Rubisco activity in the youngest, fully expanded leaves was measured following full activation of the enzyme. A greater than 35% reduction in activity (expressed on a leaf area basis) was found in leaves grown at high levels of CO₂ compared with air-grown plants. Growth of plants at low-CO₂ concentrations resulted in no significant decline in total activity. CA activity in high-CO₂-grown plants was reduced by 30%, whereas low-CO₂-grown plants exhibited an increase in CA activity of approximately 50% relative to air-grown plants.

To investigate the effects of different CO₂ growth conditions on *ca* and *rbcS* transcript abundance, total RNA was extracted from mature leaves (pairs of youngest, fully expanded leaves, as described in "Materials and Methods") of plants germinated and grown for 3 weeks at 160, 350, and 1000 $\mu\text{L/L}$ CO₂. The results of the slot-blot analysis are shown in Figure 1. *ca* transcript levels for plants grown at high-CO₂ were reduced to less than 30% of that observed in plants grown in air; *rbcS* transcript levels were reduced in a similar fashion. Growth at 160 $\mu\text{L/L}$ CO₂ also resulted in a decline in *ca* and *rbcS* transcript abundance below that

Table I. Characteristics of the youngest, fully expanded leaves from pea plants grown at different CO₂ concentrations

Values represent means \pm SE of a minimum of six plant replicates from two separate experiments.

Characteristic	CO ₂ Concentration		
	High (1000 $\mu\text{L/L}$)	Ambient (350 $\mu\text{L/L}$)	Low (160 $\mu\text{L/L}$)
Leaf fresh weight (mg)	98 \pm 11	55 \pm 14	20 \pm 7
Leaf area (cm ²)	5.8 \pm 0.8	4.3 \pm 1.2	1.2 \pm 0.2
Chlorophyll (mg m ⁻²)	267 \pm 23	251 \pm 27	291 \pm 30
Soluble protein (mg m ⁻²)	2.05 \pm 0.13	2.47 \pm 0.44	3.09 \pm 0.37
CA activity (units m ⁻² 10 ⁻³)	7.87 \pm 1.18	11.39 \pm 0.97	17.43 \pm 1.22
Rubisco activity ($\mu\text{mol s}^{-1} \text{m}^{-2}$)	33.2 \pm 5.9	51.2 \pm 5.5	49.1 \pm 6.8

exhibited by the air-grown control plants, although the reduction in *ca* levels was less pronounced than that observed under high-CO₂ conditions (Fig. 1).

The effect on CA and Rubisco expression following transfer of pea plants from one CO₂ concentration to another was also examined. Plants grown for 2.5 weeks at high levels of CO₂ were transferred to ambient conditions, and their *ca* and *rbcS* transcript abundance in mature leaves determined (Fig. 2a). Both *ca* and *rbcS* transcript abundance exhibited a rapid increase following exposure to air, reaching maximum levels after 3 h. This was followed by a gradual decline, during which mRNA levels returned to the levels found in air-grown plants. Northern blot analysis of RNA isolated from immature leaves showed no changes in transcript abundance following transfer from high to air levels of CO₂ (data not shown); the effect on transcript abundance following transfer from air to high levels of CO₂ is shown in Figure 2b. Although the changes are less pronounced there appeared to be a decline in *ca* transcript abundance, with the lowest levels achieved at the 3-h time point, followed by a gradual increase to levels somewhat higher than those seen in high-CO₂-grown plants. Changes in *rbcS* transcript levels exhibited no discernible pattern, although the lowest value was obtained at the 3-h time point. Even after 12 h of exposure to 1000 $\mu\text{L/L}$ CO₂, *ca* and *rbcS* transcript levels were still somewhat higher than those observed in high-CO₂-grown plants. RNA blot analysis of immature leaves did not reveal any significant changes in

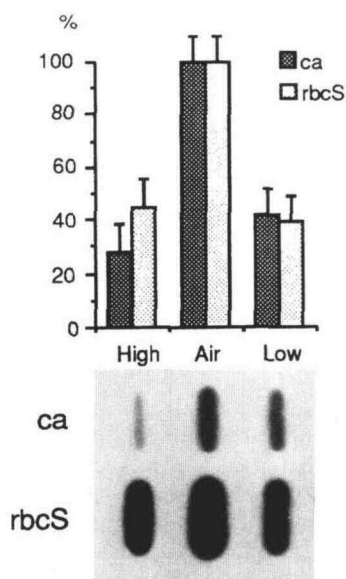


Figure 1. *ca* and *rbcS* transcript abundance of mature leaves grown at high (1000 $\mu\text{L/L}$), ambient (350 $\mu\text{L/L}$), and low (160 $\mu\text{L/L}$) concentrations of CO₂. Slot blots (5 μg of total RNA per slot) were probed with [³²P]dCTP-labeled cDNA encoding pea *ca* and *rbcS*. A radiolabeled soybean rDNA probe was used to ensure that each slot contained equal aliquots of pea RNA. The extent of probe hybridization was determined using phosphorimaging. Data are expressed as a percentage of the transcript level obtained for each gene from plants grown at air levels of CO₂ and represent the means \pm SE of six sample replicates from two individual experiments. Leaf samples for RNA analysis were taken at the midpoint of the illumination period.

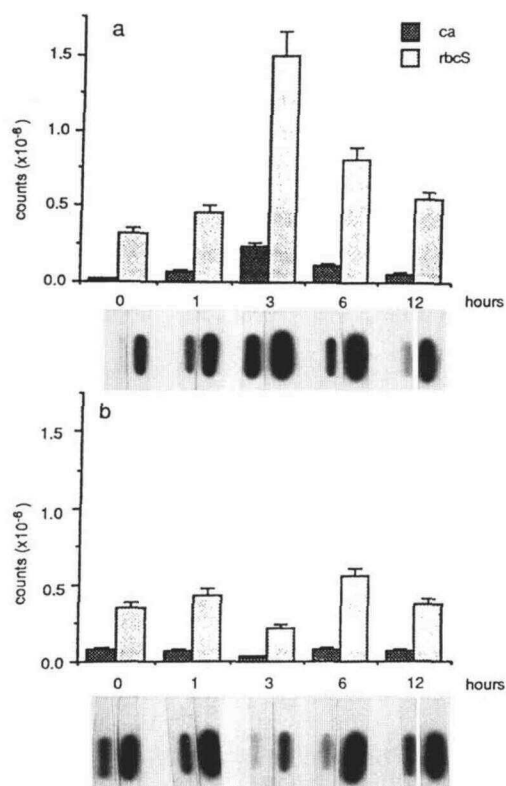


Figure 2. Time course of change in *ca* and *rbcS* transcript abundance following transfer of plants from 1000 to 350 $\mu\text{L/L}$ CO₂ (a), and from 350 to 1000 $\mu\text{L/L}$ CO₂ (b). Each slot contains 5 μg of total RNA and was probed with labeled cDNA encoding pea *ca* and *rbcS*, as well as with a soybean rDNA sequence for normalization of RNA loading. Data show the extent of probe hybridization (expressed as counts detected by phosphorimaging) to RNA in pooled extracts obtained from 15 individual plants and represent the means \pm SE of three sample replicates.

rbcS or *ca* transcript abundance during this time period (data not shown).

CA and Rubisco activities were also examined in mature leaves acclimated for 24 h following transfer to a different CO₂ concentration (Table II). Exposure of high-CO₂-grown plants to a lower CO₂ concentration resulted in an increase in the activity of both enzymes, with levels approaching those observed in air-grown plants. Transfer of air-grown

Table II. CA and Rubisco activities after transfer from high to ambient or low-CO₂ concentrations

The youngest, fully expanded leaves were analyzed after 24 h of exposure to a lower CO₂ concentration. Values represent means \pm SE of a minimum of four plant replicates from two experiments.

Characteristics	CO ₂ Concentration		
	High (1000 $\mu\text{L/L}$)	Ambient (350 $\mu\text{L/L}$)	Low (160 $\mu\text{L/L}$)
CA activity (units $\text{m}^{-2} 10^{-5}$)	7.17 \pm 0.45	9.49 \pm 1.79	10.65 \pm 0.74
Rubisco activity ($\mu\text{mol s}^{-1} \text{m}^{-2}$)	34.9 \pm 4.6	42.6 \pm 5.7	41.3 \pm 6.4

plants to high-CO₂ concentrations for 24 h did not change CA or Rubisco activities in mature leaves (data not shown).

Levels of Fru/Glc and Suc were determined in the youngest, fully expanded leaf pairs obtained from plants grown at or transferred to various CO₂ concentrations (Table III). As expected, levels of Fru/Glc and Suc were highest in plants grown at 1000 $\mu\text{L/L}$ CO₂. Transfer from high to air levels of CO₂ resulted in a significant decline in foliar Suc. Leaves from plants grown at air levels of CO₂ contained lower amounts of Fru/Glc and Suc. Suc levels increased rapidly following transfer from air to high levels of CO₂.

DISCUSSION

In this study we examined the effect of long- and short-term exposure to varying CO₂ concentrations on the expression of CA and Rubisco in pea leaves. Transcript abundance and enzymatic activity of both proteins decreased in mature leaves when plants were grown at a CO₂ concentration of 1000 $\mu\text{L/L}$. As recently reviewed by Bowes (1991) and Webber et al. (1994), there are many examples of exposure to high-CO₂ concentrations lowering both CA and Rubisco activities in C₃ plants. Lowering of Rubisco activity in response to elevated CO₂ has been ascribed to enzyme inactivation, inhibition of translation, and modulation of transcript abundance. In this study we show that down-regulation of both Rubisco and CA activity is accompanied by a reduction in *rbcS* and *ca* transcript levels. Recent studies have also shown that growth at high-CO₂ concentrations results in a decline in Rubisco activity (Xu et al., 1994) and transcript abundance (Riviere-Rolland et al., 1996) in pea. The latter study also indicated that high-CO₂ repression of Rubisco expression occurred only during growth at limiting N conditions. Although the N status of plants was not monitored during our study, the fertilization regime should have provided sufficient N, and no symptoms of N deficiency were observed. Cultivar variation in N utilization or allocation may account for the differences between the two studies.

In contrast to pea, in the only other published study (to our knowledge) on the CO₂ regulation of *ca* gene expression, increased *ca* transcript abundance was observed when *A. thaliana* plants were grown at 660 $\mu\text{L/L}$ CO₂ (Rainey et al., 1992). No measurements of activity or protein levels were reported, however, and it is not known if increased transcript levels resulted in changes in activity. The results

from *Arabidopsis* may indicate that the control of CA expression by CO₂ concentration could vary between species, or that the lower CO₂ concentration used in the *Arabidopsis* study promotes CA expression. It has been reported that cotton grown at 660 $\mu\text{L/L}$ CO₂ exhibits increased CA activity compared with air-grown plants, but growth at 1000 $\mu\text{L/L}$ CO₂ represses CA activity (Chang, 1975). Plants grown at CO₂ concentrations below ambient also display a reduction in Rubisco activity, but have elevated levels of CA activity compared with air-grown plants. The decline in Rubisco activity, as well as modification of other leaf characteristics, are similar to those observed in the C₃ plant *Abutilon theophrasti* grown at 150 $\mu\text{L/L}$ CO₂ (Tissue et al., 1994). Although CA levels were not measured in the *Abutilon* study, chlorophyll, Rubisco content and activity, and leaf mass were all reduced in plants grown at 150 $\mu\text{L/L}$ compared with air-grown plants. In pea, *ca* transcript levels in mature leaves do not reflect enhanced enzyme activity, but are higher than those found in high-CO₂-grown plants. The difference between *ca* transcript abundance and activity may be a function of enhanced translational activity and/or a reduced rate of CA turnover under these growth conditions; these possibilities are under further study. Rubisco activity more closely parallels transcript abundance. Increased CA activity (which results in the CA/Rubisco ratio being enhanced) in plants grown at low-CO₂ levels may assist in the diffusion of C_i through the chloroplast and with HCO₃⁻ dehydration at the site of fixation.

Both *ca* and *rbcS* transcript levels of high-CO₂-grown plants increased significantly after a 3-h exposure to air levels of CO₂. There was also a significant increase in both CA and Rubisco activity 24 h after transfer from high-CO₂ to ambient or below-ambient levels of CO₂. It has recently been suggested that the modulation of nuclear-encoded photosynthetic gene expression by CO₂ is mediated by changes in the soluble carbohydrate concentration of the leaf (Stitt, 1991; van Oosten et al., 1994; van Oosten and Besford, 1995). High external CO₂ concentration results in the accumulation of elevated foliar levels of starch and soluble sugars when the rate of photosynthetic carbon fixation exceeds the translocation rate to sink tissues. Elevated levels of foliar carbohydrates are associated with reduced abundance of a number of transcripts encoding proteins required for carbon fixation (van Oosten et al., 1994). Similar results have been obtained by supplying

Table III. Soluble carbohydrate content in leaves exposed to high or ambient levels of CO₂

The youngest, fully expanded leaves were analyzed. Values represent means \pm SE of eight plant replicates from one experiment. Similar results were obtained in replicate experiments.

Carbohydrate Concentration (mmol m ⁻²)	High ^a (1000 $\mu\text{L/L}$)	CO ₂ Concentration				
		Ambient ^a (350 $\mu\text{L/L}$)	High to ambient ^b		Ambient to high ^b	
			(3 h)	(24 h)	(3 h)	(24 h)
Glc and Fru	10.2 \pm 3.6	6.6 \pm 1.8	5.6 \pm 1.3	6.4 \pm 0.9	10.7 \pm 1.3	9.7 \pm 3.1
Suc	7.0 \pm 1.5	1.7 \pm 0.3	4.1 \pm 1.1	2.8 \pm 0.4	3.0 \pm 0.5	7.5 \pm 1.0

^a Grown continuously at the indicated CO₂ concentration.

^b Transferred from growth CO₂ concentration to indicated CO₂ concentration and carbohydrate levels assayed after 3 or 24 h.

detached leaves with external sources of hexoses (Krapp et al., 1991, 1993; van Oosten et al., 1994). Convincing evidence for specific and coordinated hexose-dependent repression of transcription was provided in studies using reporter sequences fused to promoter regions obtained from maize photosynthetic genes (Sheen, 1990, 1994). In our study, the transfer of plants from high to air levels of CO₂ rapidly reduced the foliar levels of carbohydrates by decreasing photosynthesis but permitting continued translocation. The rapid increase in *ca* and *rbcS* mRNA levels could be a response to the removal of carbohydrate repression of transcriptional activity. The changes in *ca* and *rbcS* transcript abundance result in increases in enzyme activity following a 24-h exposure to air levels of CO₂.

The transfer of plants from air to high levels of CO₂ did not result in definitive changes in transcript abundance within the 12-h time course of the experiments. In our studies, it was only after long-term exposure to high levels of CO₂ that decreased CA and Rubisco expression was observed.

Immature pea leaves failed to down-regulate *ca* and *rbcS* transcript levels in response to elevated CO₂ concentrations. This observation is in agreement with the carbohydrate model of transcriptional regulation, as these immature tissues are effective sinks for carbohydrate reserves. In addition, the developmental stage of the nascent leaf may preclude modulation of gene expression by carbohydrate levels. In a recent publication by Nie et al. (1995), high-CO₂ (550 μL/L) field-grown wheat exhibited a similar down-regulation of a number of nuclear-encoded photosynthetic genes, but CO₂ modulation of gene expression was highly dependent on the stage of leaf and crop development. These data show that a number of additional factors, both environmental and developmental, may override carbohydrate regulation of gene expression in the field.

In our studies with pea, if we assume that elevated levels of foliar carbohydrates were responsible for the down-regulation of CA and Rubisco expression in high-CO₂-grown plants, this suggests that the source-to-sink allocation of photosynthate was limiting during these experiments. Although we attempted to maximize growth space (few plants per pot) and maintained the plants in a well-watered and fertilized environment, it is still possible that resource allocation to sinks such as roots was restricted by the physical environment. Further studies will be required to determine if pea translocation capacity is limited by biotic or abiotic factors when plants are grown at high-CO₂ concentrations.

In earlier studies we suggested that the expression of Rubisco and CA was coordinated and presumably controlled by similar mechanisms (Majeau and Coleman, 1994). Although this may be true with respect to developmental timing of expression, light regulation, and tissue specificity, it is apparent that in at least low-CO₂-grown plants, this coordination of expression can be broken. Although the mechanisms are dissimilar, these data are in agreement with antisense studies in which reductions in CA were not accompanied by a decline in Rubisco (Majeau et al., 1994; Price et al., 1994).

In conclusion, the data presented in this paper are generally consistent with the proposed model for carbohydrate regulation of photosynthetic gene expression in higher plants. It is also interesting to note that CA expression responds to below-ambient levels of CO₂ in a manner somewhat analogous to that observed in eukaryotic algae. The ability of the plant to rapidly modulate *ca* and *rbcS* transcript abundance in response to external CO₂ concentrations suggests that regulation of gene expression may be an important general mechanism in the acclimation of photosynthesis to changing environmental parameters.

Received March 12, 1996; accepted July 5, 1996.

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