A Perspective of Ribulose Bisphosphate Carboxylase/Oxygenase, the Key Catalyst in Photosynthesis and Photorespiration

BRUCE A. MCFADDEN

Institute of Biological Chemistry and Biochemistry/Biophysics Program, Washington State University, Pullman, Washington 99164

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In graduate school at UCLA, I learned about the elegant elucidation of the pathway of carbon in plant photosynthesis by M. Calvin, for which he received the Nobel Prize.[1] Simultaneously the fascinating diversity of chemosynthetic bacteria which could drive the utilization of CO_2 in the dark by catalyzing various inorganic chemical reactions became apparent. Indeed, my thesis in 1956 described the biochemistry of one of these, *Hydrogenomonas facilis*, an organism which coupled the exergonic reaction of H_2 with O_2 to the reduction of CO_2 by H_2.

Months later in Pullman I obtained the first evidence that these bacteria fix $^{14}CO_2$ by the same cyclic pathway as that described by Calvin and his colleagues.[2] Thus the unity of biochemistry was reinforced, but intriguing evolutionary questions were posed about the relationships between CO_2-assimilating bacteria and plants.[3-5] In this context, we discovered that broken cell preparations of *H. facilis* could fix CO_2 if a reducing agent and energy source were provided, thereby tightening the link between these bacteria and plants.[6-8]

Inevitably questions about comparative biochemistry centered upon two enzymes which function uniquely in the Calvin cycle as illustrated in Figure 1. Almost 20 years ago, we chose to investigate one of these, ribulose bisphosphate (RuBP) carboxylase, which has recently been described as the most abundant protein in Nature.[9] Studies focused initially upon the bacterial enzymes to determine whether variations in structure and function might reflect the evolutionary sequence of emergence of CO_2-fixing bacteria.

During our investigations, the function of RuBP carboxylase assumed special significance when it was reported that O_2 was competitive with the substrate CO_2.[10] In 1973 a rationale for this competition was provided through recognition that the carboxylase (from spinach) is also a monooxygenase which incorporates one atom from O_2 into the carboxylate of phosphoglycolate, one of the products of oxygenolysis.[11,12] Since then, it has been recognized that RuBP-derived phosphoglycolate is the main precursor of glycolate, the substrate for photorespiration,[13] a process which opposes photosynthesis in plants in that a fraction of the fixed CO_2 is released. Thus photorespiration ostensibly lowers the productivity of many commercially important plants such as barley, wheat, peas, soybeans, and potatoes.

Bruce McFadden received the A.B. in Chemistry at Whitman College in 1952 and, in 1978, a Sc.D (Hon.). He did graduate work to the Ph.D. in Biochemistry under D. E. Atkinson in the Chemistry Department at UCLA, and then joined the Chemistry Department at Washington State University. In 1958, he studied in microbiology under C. B. Van Niel at the Hopkins Marine Station of Stanford University. His research interests are in the areas of C_1 and C_2 metabolism by microorganisms, plants, and nematodes.

The enigma, then, is why the function of RuBP carboxylase/oxygenase may contribute to both photosynthesis and photorespiration, which are fundamentally opposed processes. This mode of function is unprecedented in biology and raises intriguing questions about the prospects and consequences of controlling RuBP carboxylase:oxygenase ratios in plants.

Catalysis by RuBP Carboxylase and Oxygenase

The RuBP carboxylase catalyzed reaction involving CO_2—the known substrate[14]—and the oxygenase-catalyzed reaction are summarized in Figure 2 which also stresses the fates of various substrate atoms. Much of the evidence has been summarized elsewhere[3] and supplemented recently.[15-17] The configuration of the bracketed, relatively unstable six-carbon intermediate[3] is postulated (Figure 2) on the basis of recent studies of the 1,5-bisphosphates of 2-*C*-carboxy-D-ribitol and 2-*C*-carboxy-D-arabinitol.[18] The latter behaves as a transition state analogue with a $K_d \sim$ or $< 10^{-11}$ M. If the postulated structure (Figure 2) is correct, inversion of configuration at C-2 is required to account for production of 2 molecules of 3-phospho-D-glycerate. In the oxygenase sequence, a refinement (not shown) is that the carbonyl oxygen of RuBP is known to exchange rapidly with H_2O.[12,15,16] Magnesium or manganese ions are required for overall activity.[3]

Electron paramagnetic and nuclear magnetic resonance studies of the spinach enzyme suggested that saturating CO_2 favors one high affinity Mn^{2+}-binding site (K_D = 10 μM) and about ten weaker binding sites (K_D = 1–3 mM) per 70 000-dalton repeating unit.[19]

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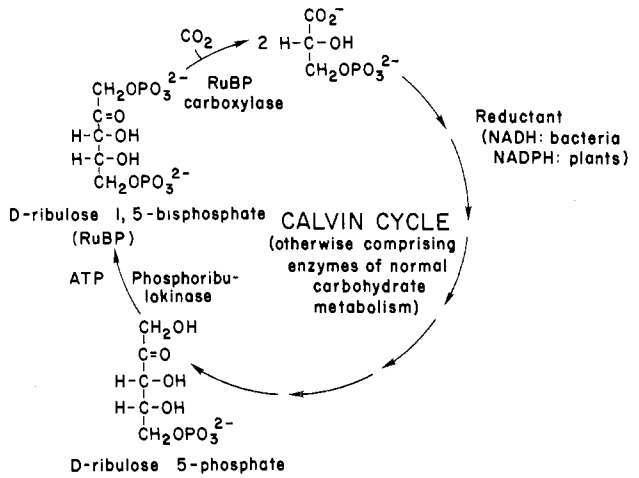


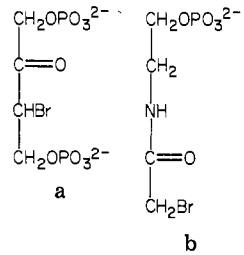
Figure 1. Unique reactions of the Calvin cycle.

Moreover, the Mn^{2+}–carbon distance established by NMR using $^{13}CO_2$ (provided as $H^{13}CO_3^-$) was 5.4 Å. 2-Carboxypentitol 1,5-bisphosphate (CPBP), a potent competitive inhibitor (now known to consist of the transition-state analogue 2-*C*-carboxy-D-arabinitol 1,5-bisphosphate, its diastereomer, and the two derived γ-lactones[18]), abolished all effects of Mn^{2+} on the ^{13}C relaxation rates, which is consistent with the displacement of CO_2 from the active site of the enzyme.[19] That the 2-carboxy group of the transition-state analogue was substituting for CO_2 at the active site was further indicated by the fact that bound CPBP also favored retention of Mn^{2+} at the high-affinity site. These findings were in consonance with the formation of a ternary complex in which the CO_2 is bound in the second sphere of Mn^{2+}. Presumably the RuBP (like the transition-state analogue) is bound in the inner sphere of Mn^{2+}.[19]

It is extremely likely that the oxygenolytic and carboxylative pathways catalyzed by RuBP carboxylase diverge after a common early RuBP-binding step. In the former path the spins of two unpaired electrons in triplet oxygen must each become paired in the course of the reaction. Unless the reaction mechanism is completely concerted, there must be one or more free-radical intermediates. In contrast to the postulated free-radical pathway for oxygenolysis, the carboxylative pathway is almost certainly polar and involves electrophilic addition of CO_2 to the bound RuBP. Enzymatic electrophilic addition (or elimination) of CO_2 is well documented.[20-22]

Active-Site Modification

The active site of RuBP carboxylase/oxygenase resides in the larger (L) of two peptides (L and S) found in the dominant form, L_8S_8, of RuBP carboxylase/oxygenase (see Subunit Structure). Hartman et al. have recently summarized their research on two compounds which meet most criteria as active-site directed reagents for the spinach enzyme:[23]



Reagent a, probably a racemate of 3-bromodihydroxybutanone 1,4-bisphosphate (provided with ^{14}C label), showed selectivity in reacting with either of two lysines/catalytic subunit with modification of either lysine being sufficient for inactivation. Curiously each lysine residue reacted to yield two presumably diastereomeric modifications with the racemic reagent as evidenced by the partial chromatographic separation of four ^{14}C-labeled peptides in tryptic digests. One pair was well separated from the other pair, and sequence analysis showed

Leu-Ser-Gly-Gly-Asp-His-Ile-His-Ser-Gly-Thr-Val-Gly-*Lys*-Leu-Glu-Gly-Glu-Arg

II

Tyr-Gly-Arg-Pro-Leu-Leu-Gly-Cys-Thr-Ile-*Lys*-Pro-Lys

I

Of interest were data obtained with b, *N*-bromoacetylethanolamine phosphate, an especially effective active-site reagent because acid hydrolysis of derivatized residues yields carboxymethylated amino acids, which are commercially available standards. Inactivation of RuBP carboxylase with ^{14}C-labeled reagent b in the absence of Mg^{2+} (inactive conformer of the enzyme; see next section) correlated with the modification of two cysteinyl residues, one of which was only three residues away from the lysine residue that was selectively modified in the presence of Mg^{2+} and CO_2 (active conformer of the enzyme). The sequence of the tryptic peptide containing these differentially labeled residues was

Tyr-Gly-Arg-Pro-Leu-Leu-Gly-*Cys*-Thr-Ile-*Lys*-Pro-Lys

$-Mg^{2+}$ $+Mg^{2+}$

L1

Because labeling of *Cys* ($-Mg^{2+}$) was greatly reduced by RuBP or of *Lys* ($+Mg^{2+}$) by competitive inhibitors like butanediol bisphosphate or CPBP, it was suggested that Mg^{2+} alters slightly the topology of a single binding site for RuBP (or reagent b). For example, in the reagent–enzyme complex formed from inactive conformer alkylation of an accessible sulfhydryl occurs, whereas in the reagent–active enzyme complex alkylation of an accessible nearby *Lys* occurs. While these interpretations are plausible, it is important to stress that modification of a second cysteinyl residue by reagent b also occurs in the absence of Mg^{2+} and is also greatly reduced by RuBP. The unique peptide arising from trypsin digestion has been sequenced and may include a region comprising a second or allosteric binding site for RuBP. Such a site has been inferred from recent fluorescence studies.[24]

Of considerable interest has been the finding of Hartman and colleagues that in the presence of Mg^{2+} (and CO_2) both reagents a and b label a common Lys

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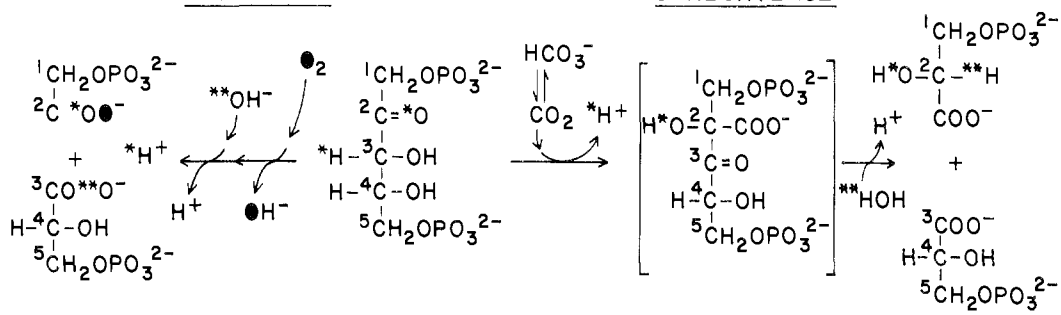

Figure 2. Reaction sequences catalyzed by RuBP carboxylase and RuBP oxygenase.

(cf. peptide I and L1) at the catalytic site of the active spinach enzyme.[25]

To recapitulate, two lysines are labeled with reagent a at the active site of the spinach enzyme. Analogous results have been obtained with the dimeric enzyme from *Rhodospirillum rubrum* (an enzyme lacking small subunits), although the stoichiometry of modification suggested half-of-the-sites reactivity.[25] It will be of interest to determine whether one of these lysines is identical with the lysyl residue(s) modified by pyridoxal phosphate,[26-28] a reagent that also show half-of-the-sites reactivity with *R. rubrum* RuBP carboxylase.[28]

Our studies have suggested that arginine is at the active site of enzymes from chemosynthetic[29] and photosynthetic bacteria[30] and higher plants,[29] presumably to facilitate binding of the polyanionic substrate RuBP. Quite recently, we have inferred the presence of histidine at the active site of the spinach enzyme from protection against histidine modification[31] by RuBP, 3-phosphoglycerate, or the competitive inhibitors 2-carboxy-D-hexitol bisphosphate[32] and D-sedoheptulose 1,7-bisphosphate.[33] Other workers have described the inactivation of one of the bacterial enzymes by tetranitromethane which is correlated with the modification of tyrosine (without oxidation of thiols).[34] However, criteria to establish active-site modification by tetranitromethane must still be met.

In the future, it will be crucial to probe the three-dimensional structure of the catalytic site of RuBP carboxylase with a greater array of active-site reagents. Of special interest will be tests of the modification of both catalytic activities (the carboxylase and oxygenase) of this dual-function enzyme. Parallel studies should be conducted to ascertain which residues function in catalysis.

Activation of RuBP Carboxylase and RuBP Oxygenase

It is now well established that both activities of plant RuBP carboxylase/oxygenase are dependent upon prior sequential binding of CO_2 and Mg^{2+}.[35,36] The activator and catalytic sites which bind CO_2 are probably different.[37-39] Binding of CPBP traps the activating CO_2.[37-39] Mg^{2+}, Mn^{2+}, or Co^{2+} support stoichiometric binding of activator CO_2 to the spinach enzyme in the presence of CPBP. When the quaternary complex is formed in the presence of saturating CO_2, stoichiometric amounts of metal ion are nonexchangeably bound.[39] The conclusion that activator CO_2 forms a carbamate with an enzymatic amino group[40] must await confirmation from NMR studies done on the enzyme in the presence of both $^{13}CO_2$ and 2-*C*-carboxy-D-arabinitol 1,5-bisphosphate.

Recently it has become evident that the metal ion specificity of the carboxylase and oxygenase activities is different. When assayed at saturating CO_2 but subsaturating O_2 (0.25 mM, which approximately equals K_m)[41] the RuBP carboxylase:oxygenase ratio is 11 if 10 mM Mg^{2+} [42] is present during both activation and catalysis. Under analogous conditions the ratio is 1 when 5 mM Mn^{2+} (a saturating concentration) is employed during activation and catalysis.[42a]

Magnesium-depleted RuBP carboxylases from some sources show dependence upon Co^{2+}.[3] This has raised the question as to whether Co^{2+} can be oxidized on the enzyme to exchange-inert Co^{3+} resulting in inactivation. Our data establish that time-dependent inactivation of the enzyme from *Pseudomonas oxalaticus* occurs using a mixture (mole ratio 10:1) of (carbonato)bis(1,10-phenanthroline)cobalt(III) and a cobalt(II) complex prepared by mixing equimolar quantities of $CoSO_4$ and 1,10-phenanthroline.[42b] The latter Co(II) complex was used in 10-fold excess to the concentration of enzyme active sites. The Co(III) complex alone does not inactivate, and the addition of EDTA rapidly quenches but does not reverse the inactivation.

On the basis of research on myosin,[43] the most plausible interpretation of our results is that the Co(II) complex is bound at metal ion binding sites that are essential for activation or catalysis and is oxidized by

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the Co(III) complex. As a consequence, the bound Co(III) becomes exchange inert and the enzyme is progressively inactivated. As with myosin,[43] the inactivation can be fully reversed by addition of a thiol, which probably reduces the Co(III) to exchange-labile Co(II). The inactivation of RuBP carboxylase has a half-time of 124 min (2 °C) which is prolonged to 240 min in the presence of CO_2 or Mg^{2+} and is greatly prolonged in the presence of CO_2 plus Mg^{2+} with or without the competitive inhibitor 2-carboxyhexitol 1,6-bisphosphate.[32] These observations suggest that the generation of Co(III) may be occurring at the activation site. Inactivation of the *R. rubrum* enzyme by H_2O_2-dependent Co^{2+} oxidation has also been reported with attendant trapping of HCO_3^-,[44] but in the absence of free-radical scavengers. In the future, it will be important in all analogous experiments to realize good concordance between Co(III) incorporation and inactivation as well as reversibility by virtue of reduction of Co(III) to Co(II). Only when these criteria have been met can conclusive trapping experiments be designed.

Results to date suggest very different requirements for activation and catalysis by RuBP carboxylase. At least 10-fold higher concentrations of CO_2 are required for optimal activation than for catalysis.[41,45] Analogously, we and others have established that at least 30-fold higher concentrations of Mg^{2+} are required for activation.[45,46] The latter is also the case for RuBP oxygenase.[46] Unfortunately, little is known about the relative requirements for activation and catalysis with respect to other metal ions.

Of significance is our observation that the metabolite 6-phosphogluconate, which at low concentrations is a positive effector for RuBP carboxylase, lowers the requirement for half-maximal activation by 3- and 4.5-fold in terms of CO_2 and Mg^{2+}, respectively.[47,48] In these kinds of experiments, it is crucial to distinguish between the action of effectors upon activation and catalysis. It is also critical to recognize the effect of enzyme storage on activation parameters.[47]

Subunit Structure

RuBP carboxylase occurs in a variety of CO_2-assimilating bacteria as well as in lower and higher plants. Many bacteria are difficult to grow, however, on CO_2 as the sole carbon source. For this reason, studies in our laboratory of the regulation of RuBP carboxylase in cells grown on organic carbon sources have defined conditions resulting in enzyme-enriched cells[8,49-55] enabling the facile isolation of this enzyme from a variety of bacteria.

The dominant form of the enzyme in Nature has a molecular weight of ca. 550000 and can often be isolated in one step in a homogeneous or nearly pure state by centrifugation of cell-free preparations from plants[56] or microorganisms[57,58] into a density gradient. Subunit structures have been tabulated elsewhere[59] and are summarized in Table I. One category, O enzymes, comprises only large subunits (ca. 55000 daltons), whereas a second category, T enzymes, comprises both large and small (ca. 15000 daltons) subunits in a mole ratio of 1:1. All highly purified RuBP carboxylases examined also apparently have RuBP oxygenase activity (Table I), although future studies should be conducted with more rigorous assays for the oxygenase. A recent report describing the separation of the RuBP carboxylase and oxygenase activities from parsley[60] could not be confirmed in subsequent experiments.[61]

Quantitative comparisons[62] of the amino acid compositions of large subunits suggest that these polypeptides may be homologous from all sources examined.[4,63] The evolutionary conservation of this structure is in harmony with the fact that the large subunits harbor the catalytic potential in T enzymes (for a review, see ref 59). On the other hand, the small subunits from *Halimeda*, *Chlorella*, spinach, and *Alcaligenes eutrophus* are very dissimilar in composition. Even among different genera of higher plants, the small subunits are quite variable in composition.[59] The primary structures of small subunits from several higher plants have been partially determined, revealing sequence variability although large regions are homologous.[64] Recently the sequence of the spinach small subunit has been elucidated.[65] Less variability has been found in limited comparisons of the sequence of barley and spinach large subunits.[64] Progress on the primary structure of the barley large subunit has been excellent, placing 210 of approximately 490 residues.[66] Studies of primary and three-dimensional structure[67,68] will be essential in comprehending structure–function relationships for RuBP carboxylase/oxygenase.

The immunogenicity of large (L) and small (S) subunits of the higher plant enzymes has been discussed.[59] Basically the limited information suggests that antibodies to S will precipitate but not inhibit the native L_8S_8 enzyme whereas antibodies to L both precipitate and inhibit native RuBP carboxylase.

Catalysis or catalytic potential resides in the L subunits.[3,4] Although the variation of catalytic activity with

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Table I
Comparisons of RuBP Carboxylases Isolated from Bacteria, Green Algae, and Higher Plants[a]

enzyme source, (M_r or $s_{20,w}$)	quaternary structure	oxygenase	inhibition by 1 mM 6PGN	ref[b]
photosynthetic bacteria (classical)				
Rhodospirillum rubrum (112 000)	2L	yes	no	*c*
Chlorobium thiosulfatophilum (360 000)	6L	-	yes	
Rhodomicrobium vannielii	6L, 6S	-	-	*d*
Chromatium D (550 000)	8L, 8S	yes	yes	*e*
Ectothiorhodospira halophilia (600 000)	8L, 8S	-	yes	
Thiocapsa roseopersicina (ca. 18 S)	8L, 8S	yes	yes	
Rhodopseudomonas sphaeroides (360 000)	6L	-	no	
Rhodopseudomonas sphaeroides (550 000)	8L, 8S	-	yes	
chemosynthetic bacteria				
Pseudomonas oxalaticus (436 000)	6L, 6S	-	yes	47
Thiobacillus intermedius (455 000)	8L	-	yes	
Thiobacillus novellus (498 000)	-	-	yes	
Thiobacillus A2 (512 000)	8L, 8S	-	yes	
Thiobacillus neopolitanus (500 000)	8L, 8S	-	yes	*f*
Alcaligenes eutrophus (516 000)	8L, 8S	yes	yes	*g*, *h*
Pseudomonas facilis (551 000)	-	-	-	*g*
Nitrobacter agilis (500 000)	8L, 8S	-	-	*i*
Paracoccus denitrificans (525 000)	8L, 8S	-	yes	*j*
blue-green bacteria				
Aphanothece halophytica (237 000)	4L	-	-	*k*
Agmenellum quadruplicatum (456 000)	8L	-	-	
Anabaena cylindrica (452 000)	8L (8S)	-	-	
Anabaena variabilis (18S)	8L, 8S	-	-	
Plectonema boryanum (18 S)	8L, 8S	-	-	
Aphanocapsa (525 000)	8L, 8S	yes	yes	
Microcystis aeruginosa (518 000)	8L, 8S	-	-	*l*
green algae				
Euglena gracilis	8L, 8S	yes	yes	
Chlamydomonas reinhardi (530 000)	8L, 8S	-	-	
Chlorella fusca (530 000)	8L, 8S	yes	yes	
Chlorella ellipsoidea (18 S)	8L, 8S	-	-	
Halimeda cylindracea (18 S)	8L, 8S	yes	-	
higher plants				
spinach (560 000)	8L, 8S	yes	yes	
spinach beet (560 000)	8L, 8S	-	-	
tobacco (525 000)	8L, 8S	yes	-	
french bean (17.9 S)	8L, 8S	-	-	

[a] L = large (M_r 50 000 to 58 000); S = small (M_r 12 000 to 18 000). A dash indicates not determined. [b] Where no citation is given in this column, primary references can be found in ref 59. Data not summarized there can be found in the following citations. [c] B. A. McFadden, *Biochem. Biophys. Res. Commun.*, **60**, 312 (1974). [d] S. C. Taylor and C. S. Dow, *J. Gen. Microbiol.*, **116**, 81 (1980). [e] T. Takabe and T. Akazawa, *Biochem. Biophys. Res. Commun.*, **53**, 1173 (1973). [f] R. M. Snead and J. M. Shively, *Current Microbiol.*, 1, 309 (1978). [g] B. A. McFadden, F. R. Tabita, and G. D. Kuehn, *Methods Enzymol.*, **42**, 461 (1975). [h] K. Purohit and B. A. McFadden, *J. Bacteriol.*, **129**, 415 (1977). [i] D. Harrison, L. J. Rogers, and A. J. Smith, *FEMS Microbiol. Lett.*, **6**, 47 (1979). [j] J. M. Shively, A. Saluja, and B. A. McFadden, *J. Bacteriol.*, **134**, 1123 (1978). [k] G. A. Codd, C. M. Cook, and W. D. P. Stewart, *FEMS Microbiol. Lett.*, **6**, 81 (1979). [l] R. Stewart, C. C. Auchterlonie, and G. A. Codd, *Planta*, **136**, 61 (1977).

aggregation state has not been established, recent evidence in our laboratory suggests that monomeric L subunits may have unusually high catalytic activity under certain conditions.[59] On the other hand, the function of S subunits remains an enigma. Evidence that the enzyme from *Rhodospirillum rubrum* lacking small subunits is unusual in its response to activation by CO_2[69,70] requires reexamination in light of the recent finding that storage at 2 °C of the pure enzyme from *Pseudomonas oxalaticus* (of L_6S_6 structure) markedly alters its response to CO_2 during activation.[47] Certainly, the presence of small subunits is not required for RuBP oxygenase, an activity that can even be found in the enzyme from anaerobic bacteria (Table I, footnotes *c* and *e*).

Observations have been summarized which suggest that the higher plant enzymes, especially those from tobacco, consist of heterogeneous L and heterogeneous S subunits (see, for example, ref 9). Indeed, the implications of these results in the evolution of higher plants have been discussed.[9] It is crucial to stress, however, that proteolysis after cell rupture may explain the observed heterogeneity. It was recently reported that several proteinases from wheat leaves catalyze the rapid degradation of RuBP carboxylase[71] and that one or more are present not only in aging leaves but also in immature or rapidly growing tissue.[72] Although these proteinases exhibit a distinctly acid pH optimum, they may contribute to limited proteolysis of RuBP carboxylase/oxygenase during storage. These obser-

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vations establish the need for cautious interpretation of the finding of multiple L and S subunits in this enzyme.

Assembly of RuBP Carboxylase/Oxygenase in Eukaryota

In eukaryotic organisms, RuBP carboxylase/oxygenase is found in the chloroplasts. Evidence summarized recently[59] suggests that a 20 000-dalton precursor of the small (S) subunits is synthesized in the cytoplasm and trimmed by an endopeptidase prior to combining with large subunits, which are encoded and synthesized in chloroplasts. Indeed, the amino acid sequence of this precursor from a green alga has been recently determined.[73] Whether the precursor of S is processed during or after transfer across chloroplast membranes remains to be established.

Concluding Remarks

Ribulose bisphosphate (RuBP) carboxylase catalyzes two reactions of opposing consequences. One (the carboxylase) leads to assimilation of carbon dioxide and photosynthesis whereas the other (an oxygenase) opposes photosynthesis by initiating photorespiration. Mechanistic considerations and recent experiments suggest that it should be possible to increase the RuBP carboxylase:oxygenase ratio by mutation and that this may lead to higher plant productivity. The design of such experiments, however, is complicated because the synthesis of large (L), catalytically competent subunits is chloroplast DNA encoded and because each cell contains multiple chloroplasts. Nevertheless, suitable selection pressure may result in chloroplasts enriched in the ratio of RuBP carboxylase to RuBP oxygenase. The feasibility of this approach to increase plant productivity will be greatly enhanced by a better understanding of the catalytic mechanisms for these activities. Moreover, the use of bacteria as photorespiratory models is feasible and important because of the relative ease of producing and selecting for mutants altered in the ratio of RuBP carboxylase:oxygenase.

Ultimately this experimental approach will depend also upon an understanding of the function of the nucleus-encoded small (S) subunits found in the higher plant enzyme. Although the structure of this enzyme, L_8S_8, can be found in many microorganisms, a simple L_2 structure and various intermediate species have also been isolated. Detailed comparisons of these diverse RuBP carboxylase/oxygenases will certainly contribute to our understanding of structure–function relationships for this important enzyme.

Elsewhere, we have proposed that evolutionarily conserved large subunits were established first in ancient organisms and that small subunits were added in descendents during evolution.[3-5,74] More compelling evolutionary inferences will require complete knowledge of the primary structures of the subunits or of the related DNA base sequences. Information about the latter will be powerful and experimentally accessible in deducing the amino acid sequences of large (and small) subunits of bacterial enzymes. Thus the vista is promising, yet in this regard we are scarcely beyond where we were almost 20 years ago.

In conclusion there is much yet to be learned about catalysis by and the structure and activation of RuBP carboxylase/oxygenase. The control of activation of this dual-function enzyme is poorly understood and probably critically depends upon chloroplast metabolites as well as metal ions. Advances in our understanding of activation and catalysis will greatly buttress our knowledge of photosynthesis—a process vital to human survival.

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