Molecular Characterization and Subcellular Localization of Protoporphyrinogen Oxidase in Spinach Chloroplasts

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Protoporphyrinogen oxidase (Protox) is the last common enzyme in the biosynthesis of chlorophylls and heme. In plants, there are two isoenzymes of Protox, one located in plastids and the other in the mitochondria. We cloned the cDNA of spinach (Spinacia oleracea) plastidial Protox and purified plastidial Protox protein from spinach chloroplasts. Sequence analysis of the cDNA indicated that the plastidial Protox of spinach is composed of 562 amino acids containing the glycine-rich motif GxGxxG previously proposed to be a dinucleotide binding site of many flavin-containing proteins. The cDNA of plastidial Protox complemented a Protox mutation in Escherichia coli. N-terminal sequence analysis of the purified enzyme revealed that the plastidial Protox precursor is processed at the N-terminal site of serine-49. The predicted transit peptide (methionine-1 to cysteine-48) was sufficient for the transport of precursors into the plastid because green fluorescent protein fused with the predicted transit peptide was transported to the chloroplast. Immunocytochemical analysis using electron microscopy showed that plastidal Protox is preferentially associated with the stromal side of the thylakoid membrane, and a small portion of the enzyme is located on the stromal side of the chloroplast inner envelope membrane.
acid residues (PPX-I), and the other a protein of 504 amino acid residues (PPX-II). The deduced amino acid sequences of PPX-I and PPX-II have only 27.3% conserved amino acid residues. Because the translation product of PPX-I cDNA could be translocated to plastids, and the translation product of PPX-II cDNA was targeted to mitochondria, PPX-I and PPX-II were termed as plastidal Protox and mitochondrial Protox, respectively (Lermontova et al., 1997). The 53-kD mature protein of plastidal Protox was detected in chloroplasts, suggesting that processing at a plastidial target sequence is needed to translocate into chloroplasts. Although much research has been done, the detailed mechanism of the transport of plastidal Protox is still uncertain.

We recently studied the molecular mechanism of herbicide resistance in tobacco cells (YZI-1S) that had been selected as an S23142-resistant line (Ichinose et al., 1995; Watanabe et al., 1998). Our data indicated that the primary target of the herbicide is plastidal Protox and its inhibition causes serious damage to chloroplast function in wild-type cells (Watanabe et al., 1998). In spinach (Spinacia oleracea) the activity of plastidal Protox has been detected entirely in thylakoid membranes and chloroplast envelopes (Matringe et al., 1992b). Protox-inhibiting herbicides such as S23142 and AF inhibited activity in envelope fractions as strongly as in thylakoid fractions. In addition, the binding constants of [3H]AF were similar for envelope membranes and thylakoids (Matringe et al., 1992b). From these data it is likely that the plastidal Protoxes of envelope membranes and thylakoids are the same and not isoenzymes.

Accurate examination of the transport and subcellular localization of chlorophyll and heme biosynthetic enzymes is important for a better understanding of the flux of tetrapyrrole precursors and the regulation of the synthesis of tetrapyrrole. This is particularly important for Protox because it is the last common enzyme of these two pathways (von Wettstein et al., 1995). The aim of this study is to obtain detailed information about plastidal Protox, including the transit sequence and processing sites, and to determine the precise location of plastidal Protox in chloroplasts. We report here the first cloning of spinach plastidal Protox cDNA and the analysis of the N-terminal sequence in mature plastidal Protox purified from spinach chloroplasts and discuss the mechanism of the transport of plastidal Protox into chloroplasts. In addition, we report the precise location of plastidal Protox by western-blot analysis and immuno-electron microscopy.

RESULTS

Isolation and Characterization of Plastidal Protox cDNA from Spinach

To identify cDNAs encoding plastidal Protox in spinach, one set of specific oligonucleotide primers (SCP-1F and SCP-2R) was synthesized based on conserved sequences in Arabidopsis and tobacco (Narita et al., 1996; Lermontova et al., 1997). PCR amplification of cDNA from spinach produced a product of 936 bp. The nucleotide sequence of the cDNA clone had high homology with the plastidal Protox of Arabidopsis (82%) and tobacco (75%), suggesting that this clone encodes part of the plastidal Protox cDNA of spinach. The full-length plastidal Protox cDNA, SO-POXI (accession no. AB029492), was obtained by 5'- and 3'-RACE PCR. Sequence analysis indicated that the plastid Protox of spinach is composed of 562 amino acids with a calculated molecular mass of 59,929 D (Fig. 1). The deduced amino acid sequence of its cDNA shows a very high identity to other plastidal Protoxes (Arabidopsis, 78%; tobacco, 71%; potato, 72%; Fig. 1), while the sequence identities to mitochondrial Protoxes of plants and other organisms (human, yeast, and Bacillus) are relatively low (20%–30%) (Hansson and Hederstedt, 1994; Nishimura et al., 1995b; Camadro and Labbe, 1996). In particular, the Gly-rich motif GxGxxG that had been
previously proposed as a dinucleotide binding site of many flavin-containing proteins (Wierenga et al., 1986; Bach et al., 1988; Lermontova et al., 1997; Dailey and Dailey, 1998) was also found in the sequence of spinach plastidal Protox (Fig. 1). Furthermore, the amino acid sequences from position 1 to 60 of spinach plastidal Protox were enriched for Ala, Arg, Gly, Leu, Ser, and Thr but included no Asp or Glu. Since these features have been found in several transit peptides for the transport to plastids (von Heijne et al., 1989; Cline and Henry, 1996), the existence of a transit peptide in the N terminus of plastidal Protox is expected.

To determine the copy number of the plastidal Protox gene in spinach we performed Southern-blot analysis by digesting spinach genome DNA with Bgl, Dra I, and Eco RI, which do not cut within the cDNA of plastidal Protox, and hybridized with a labeled DNA probe of the full length of the plastidal Protox cDNA. Hybridization patterns showed a single band in each lane, indicating that there is a single copy of the plastidal Protox gene in the spinach genome (Fig. 2).

**Purification and Determination of the N-Terminal Amino Acid Sequence of Plastidal Protox**

For characterization of mature plastidal Protox, localization of plastidal Protox was first examined by immunoblot using specific anti-plastidal Protox anti-

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**Figure 2.** Genomic Southern-blot analysis of plastidal Protox in spinach. Ten micrograms of spinach genomic DNA was digested with restriction enzymes (B, BglII; D, DraI; and E, EcoRI) and subjected to Southern-blot analysis. Hybridization was performed using full-length cDNA of spinach plastidal Protox labeled non-radioactively by random priming. The sizes (in kb) of standard DNA fragments obtained by digesting λ-DNA with HindIII are shown at left.

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body. A single band with a calculated molecular mass of approximately 60 kD was detected in leaf extracts and chloroplasts (Fig. 3, lanes 1 and 2). In contrast, no signal was detected in the mitochondrial fraction (Fig. 3, lane 3). These results suggest that the plastidal Protox is located only in the chloroplast.

To determine the precise cleavage site in the plastidal Protox precursor, we purified mature plastidal Protox protein from crude extracts by immunoprecipitation. Immunoprecipitation with specific antibodies against the plastidal Protox protein provided a single band except immunoglobulin with Coomasie Brilliant Blue staining (Fig. 4) and the N-terminal sequence analysis of this single band provided the 20-amino acid sequence STISTSNSAAAANYQNKN-. From this sequence, the N terminus of mature plastidal Protox was determined to be Ser-49 of plastidal Protox precursor (Fig. 1). This result suggests that plastidal Protox precursor is processed between Cys-48 and Ser-49. This is the first information about the cleavage site of the plastidal Protox precursor. The N-terminal domain (Met-1 to Cys-48) of the plastidal Protox precursor would contain the functional transit peptide sequence for targeting to chloroplasts.

It was reported that cDNAs encoding plastidal Protox of Arabidopsis (Narita et al., 1996) and of tobacco (Lermontova et al., 1997) were able to complement the hemG mutation in *E. coli*. The BT3 (ΔhemG:: Km') of *E. coli*, which is defective in the *hemG* gene, grows very poorly even in rich media. Full-length and
mature-type plastidal Protox cDNA were ligated into vector pCR 2.1 in-frame with LacZ. As a control experiment, hemG was ligated and introduced in the same manner. Mature plastidal Protox cDNA and hemG complements the mutation responsible for the poor growth (data not shown). The full-length cDNA also rescued the mutant cells but to a lesser extent (data not shown). The growth of both complemented strains was inhibited by Protox-inhibiting herbicides such as S23142 and AF at the submicromolar level (data not shown). The transformant introduced in the pCR 2.1 vector without any insert showed poor growth and formed a very small colony (data not shown). These data indicate that the mature-type cDNA of plastidal Protox in spinach can functionally complement the BT3 (ΔhemG::Km).

Transport into Chloroplasts

The sequence analysis of plastidal Protox cDNA isolated from spinach and the determination of the N-terminal sequence of the mature protein purified from chloroplasts showed that the N-terminal domain contains a possible transit peptide for targeting to plastids (Figs. 1 and 4). We used the reporter gene green fluorescent protein (GFP) to test if the putative transit peptide is functional. cDNA encoding the transit peptide plus partial mature protein (Met-1 to Asp-73) were fused with the GFP2 gene and each fusion placed under the control of cauliflower mosaic virus 35S promoter (M48C-GFP and M73D-GFP). These constructs were introduced into spinach leaves by bombardment, and transient expression was observed by fluorescence microscopy. Coincidence of green fluorescence with chloroplasts was observed in cells bombarded with either transit peptide constructs (Fig. 5, A–D). In the spinach leaf bombarded with control GFP the green fluorescence was spread out over the guard cells (Fig. 5E), indicating that the transit peptide (Met-1 to Cys-48) of spinach plastidal Protox is functional and sufficient to transport proteins to plastids.

**Figure 4.** SDS-PAGE analysis of plastidal Protox purified by immunoprecipitation and determination of the N-terminal sequence of the purified Protox from spinach chloroplasts. The protein was transferred to a polyvinylidene difluoride membrane and stained with Coomassie Brilliant Blue. The band of plastidal Protox was cut out and directly applied to a protein sequencer. The position of molecular mass markers (in kD) is given at left. The N-terminal sequence of purified protein is shown in the lower panel.

**Figure 5.** Transport of GFP fused to the N-terminal peptide of spinach plastidal Protox. GFP fused to the N-terminal peptide of spinach plastidal Protox (A and B, M48C-GFP; C and D, M73D-GFP) and GFP (E and F). The fluorescence of GFP was observed at excitation wavelength of 495 nm and emission wavelength of 530 nm (A, C, and E). The autofluorescence of chloroplasts was observed at excitation wavelength of 540 nm and emission wavelength of 600 nm (B, D, and F). Bar = 10 μm.
Organellar Location of Plastidal Protx

Since the plastidal Protx was only located in chloroplasts (Fig. 3), the location of mature plastidal Protx was further examined by immunoblot analysis using specific anti-plastidal Protx antibody. A plastidal Protx band of 60 kD was detected in envelope and thylakoid membrane fractions but not in the stromal fraction (Fig. 6, lanes 2, 3, and 5), suggesting that the plastidal Protx was associated with envelope and thylakoid membranes of chloroplasts. It seems that the mobilities of the Protx band in the envelope membrane fraction was slightly different from the thylakloid membrane fraction on the nitrocellulose membrane (Fig. 6, lanes 2 and 3). However, only one band was detected when the envelope and the thylakoid membrane fractions were loaded on the same lane, suggesting that the molecular mass of the thylakloid Protx was same as that of the envelope Protx.

To identify the spatial distribution of plastidal Protx in chloroplasts we performed an immunogold electron microscopic analysis. When ultra thin sections of leaf tissues from spinach were incubated with antibody against plastidal Protx and with gold-conjugated antiserum to rabbit immunoglobulins, gold particles were found in chloroplasts but not in mitochondria, cytoplasm, vacuoles, or plasma membrane (Fig. 7A). In chloroplasts most of the gold particles were on the stromal side of the thylakoid membrane, and a small number were present on the internal side of the inner envelope membrane (Fig. 7, B and C).

When preimmune serum was used there was no appreciable binding of gold particles (Fig. 7D). In addition, all other control tests, including the omission of primary antibody and pre-incubation of the primary antibody with the plastidal Protx before section labeling, yielded negative results (data not shown). These results clearly show that plastidal Protx is preferentially associated with the stromal side of the thylakoid membrane, and a small portion of plastidal Protx is located on the stromal side of the inner envelope membrane of chloroplasts.

DISCUSSION

In this study we have isolated the plastidal Protx cDNA, SO-POX1, from spinach. The plastidal Protx of spinach has a highly conserved domain in its N terminus that contains the consensus sequence GxGxxG (Gly-89 to Gly-94), which is part of the $\beta\alpha\beta$-ADP binding fold found in many flavoproteins (Wierenga et al., 1986; Dailey and Dailey, 1998). Because the Gly residues in the $\beta\alpha\beta$-ADP binding fold are believed to interact with the phosphoryl groups of the adenosine moiety of FAD, the plastidal Protx of spinach would presumably require FAD as a cofactor. We have recently reported that Protx was purified from spinach chloroplasts, 1,600-fold (Watanabe et al., 2000). The activity of the purified Protx was stimulated about 1.4-fold by addition of 1 $\mu$M FAD, while NAD addition at the micromolar levels (1–10 $\mu$M) did not affect Protx activity (Watanabe et al., 2000). Such activation of Protx by FAD corresponds with the data of mammalian Protx purified from murine (Dailey and Karr, 1987). These data suggest that the plastidal Protx of spinach requires FAD as a cofactor and that FAD would presumably also bind Gly residues in the $\beta\alpha\beta$-ADP binding fold. However, we could not confirm the existence of FAD in purified Protx because the amount of purified Protx was too small to ascertain the presence of FAD.

Though our immunological studies indicate that plastidal Protx is a membrane-bound protein, no transmembrane domain has been confirmed in any known Protxes by sequence analysis using the TMAP software (EMBL Computational Services, Cambridge, UK) (Camadro et al., 1999). Therefore, we attempted to analyze the putative transmembrane motif of the plastidal Protx of spinach using another algorithm. The hydrophyt profile of the protein according to Kyte and Doolittle (1982) revealed that spinach plastidal Protx is a moderately hydrophobic protein with a putative transmembrane domain in the N-terminal region (data not shown). This transmembrane region was also predicted by PSORT (Genome NET Service, Osaka University, Japan; Nakai and Kaneshita, 1992), a commercially available subcellular localization predictor. PSORT software analysis suggested that plastidal Protx has a putative transmembrane domain at Val-81 to Ala-97 that contains the GxGxxG motif. The amino acid sequence of this predicted transmembrane domain was highly conserved among the other plant Protxes, suggesting that they may be bound to the membrane at this transmembrane domain.

It has been reported that the typical consensus sequence of the cleavage site, (Val/Ile) – 3 X 2 – (Ala/Cys) – 1 – Ala + 1, is found in the majority of

![Figure 6. Localization of plastidal Protx within chloroplast of spinach leaf. Proteins from the purified-chloroplast fraction (25 $\mu$g, lane 1), thylakoid fraction (10 $\mu$g, lane 2), envelope fraction (10 $\mu$g, lane 3), and mixed envelope and thylakoid fraction (5 $\mu$g each, lane 4) were stroma (10 $\mu$g, lane 5) separated on a SDS-PAGE (10% [w/v]). Proteins were transferred to a nitrocellulose membrane for immunodetection with specific antibody raised against the C-terminal region of the recombinant plastidal Protx of spinach. The position of molecular mass markers (in kD) is given at left.](image-url)
transit peptides (Gavel and von Heijne, 1990). However, this consensus sequence is not found in the deduced amino acid sequences of any known plastidal Protox precursors from higher plants, including spinach. Though the transit peptide sequences of plastidal Protoxes of various plants show no homology, three amino acids at the cleavage site are conserved in all known plastidal Protoxes (Arg-Cys-Ser; Fig. 1). Furthermore, the cleavage prediction generated by the ChloroP method (Emanuelsson et al., 1999) also revealed that the predicted cleavage site of plastidal Protoxes is within this conserved sequence, indicating that all other plastidal Protox precursors would also be cleaved between Cys and Ser.

The results of immunogold electron microscopy showed that plastidal Protox was localized on the stromal side of the thylakoid and inner envelope. Chlorophyll and heme are synthesized from the intact carbon skeleton of Glu via the C5 pathway (Reinbothe and Reinbothe, 1996) with the initial steps of 5-aminolevulinic acid formation and the steps leading to Protogen IX likely to occur in the stroma (Smith and...
Rebeiz, 1979; Kruse et al., 1995; Mock et al., 1995). Plastidal Protox is the first enzyme in the chlorophyll synthetic pathway catalyzed by membrane-bound enzymes, and all subsequent steps are thought to be catalyzed by membrane-bound enzymes (von Wettstein et al., 1995). It is reasonable to assume that plastidal Protox is located on the stromal side of both membranes because this location is very convenient to receive the substrate of Protox from coproporphyrinogen oxidase located in stroma. It is not clear whether subsequent pathway membrane-bound enzymes such as Mg-chelatase (Walker and Weinstein, 1995) or ferrochelatase (Roper and Smith, 1997; Chow et al., 1998) are located on the stromal side of the membrane. However, it seems likely that these enzymes would also be located on the stromal side of the membrane because of the rapid enzymatic cascade reaction yielding chlorophyll or heme.

Since Protox is the last common enzyme in the biosynthesis pathway of chlorophyll and heme, Protox must play the important role of supplying and distributing Proto IX to the next two enzymes, Mg-chelatase and ferrochelatase. Mg-chelatase catalyzes the insertion of Mg$^{2+}$ into Proto IX to yield Mg-Proto IX, and the activity of this enzyme is detected in envelope membranes (Walker and Weinstein, 1995). Protoporphyril oxidase, which catalyzes the reduction of protoporphyrin to chlorophyllide $a$, is also located in an envelope membrane (Joyard et al., 1990). Thus, the envelope membrane is the major site of chlorophyll synthesis even though the final destination of chlorophyll is the thylakoid. In contrast, ferrochelatase, which catalyzes the insertion of ferrous ions into Proto IX, is associated with the thylakoid membrane (Matringe et al., 1994), suggesting that heme synthesis mainly takes place on the thylakoid membrane. Using immunoblot and immunogold electron microscopic analyses, we have shown in this work that plastidal Protox is located on the envelope and thylakoid membranes of chloroplasts. Such dual localization of plastidal Protox implies that the Protox located on the envelope membrane supplies Proto IX to the chlorophyll biosynthetic pathway, while the Protox on the thylakoid membrane supplies Proto IX to the heme biosynthetic pathway. The distribution of tetrapyrrole to chlorophyll and heme biosynthetic pathways would be controlled at the insertion step of magnesium and ferrous ions.

The information presented in this paper about the plastidal Protox insertion.

Characterization of Plastidal Protoporphyrinogen Oxidase

MATERIALS AND METHODS

Chemicals and Plant Materials

Spinach plants (Spinacia oleracea L. cv Tonic; Watanabe-Saiushujo Ltd., Japan) were grown in a greenhouse at 25°C for 8 weeks or in a growth chamber on a 16-h/8-h cycle (day/night) at 25°C for 4 weeks at a light intensity of 140 μmol m$^{-2}$ s$^{-1}$. The reagents used were of special or analytical grade from Wako Pure Chemicals (Osaka) and Nakarai Tesque Company (Kyoto). Herbicide S-23142 was a gift from Sumitomo Chemical Company (Takarazuka, Japan).

cDNA Cloning and Sequence Analysis

Total RNA was isolated using RNasy Plant Kits (Qiagen, Hilden, Germany) from 4-week-old spinach leaves. First-strand cDNA was synthesized from total RNA using a Ready-To-Go T-primed First-Strand Kit (Amersham Pharmacia Biotech, Piscataway, NJ). For PCR isolation of the plastidal Protox gene, one set of oligonucleotide primers was synthesized on the basis of the nucleotide sequences of Protox cDNAs conserved in Arabidopsis (Narita et al., 1996) and tobacco (Nicotiana tabacum cv Samsun NN; Lermontova et al., 1997). The sequences of the primer set were 5'-CTTGGTGCCGAAGTCTTGGAA-3' (SCP-1F) and 5'-CCAATGCTACACCTGACACATA-3' (SCP-1R). Taq-DNA polymerase and a buffer (Expand High Fidelity Plant Physiol. Vol. 124, 2000 65

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PCR system) were purchased from Boehringer Mannheim (Mannheim, Germany) and used for all PCR experiments (94°C for 5 min, 35 cycles of 30 s at 94°C, 30 s at 50°C, and 1 min at 72°C). PCR reactions were terminated with 10 min of incubation at 72°C and stored at 4°C. PCR fragments (0.9 kb) were cloned using a TA cloning kit (Invitrogen, Groningen, Netherlands), and five clones from each PCR reaction were sequenced with a DNA sequencer (model 377; Perkin-Elmer Applied Biosystems, Foster City, CA). PCR and cloning procedures were independently repeated twice to confirm DNA sequences.

The 5′ end of Protox cDNA was amplified by RACE using a 5′/3′ RACE kit (Boehringer Mannheim). First-strand cDNA synthesized from mRNA was dA-tailed with terminal deoxytransferase, and second-strand cDNA was synthesized using a poly(T) cassette primer (5′-ACTCTGAATTCCGGCGCCGAT15-3′). A first 5′-RACE PCR was performed using specific primer I (5′-CCTGCCAAAGCCAGCTTTTACAT-3′) and cassette primer I (5′-ACTCTGATTCACCCGGCGCCA-3′) with the recommended PCR condition. After the first reaction the PCR product was diluted 2,000-fold and subjected to secondary PCR amplification. The second amplification was performed using specific primer II (5′-ACTTCCAGCACAATTCTCTT-3′) and cassette primer I. For 3′-RACE, cDNA was synthesized from mRNA with a poly(T) cassette primer (5′-TGGAAATTCGCGGCGAGT16–3′). 3′-RACE PCR was performed using specific primer III (5′-ATCTGCCCAACATTCCCGAG-3′) and cassette primer II (5′-TGGAAATTCGCGGCGAG-C-3′). The amplified fragments for 3′ RACE (0.65 kb) and for 5′ RACE (0.8 kb) were cloned with a TA cloning kit (Invitrogen), and five independent clones from each PCR reaction were sequenced as described above. PCR and cloning procedures were independently repeated twice, and DNA inserts were sequenced on both strands to ensure that no mutation had been introduced during PCR amplification.

Southern-Blot Analysis

Genomic DNAs were isolated from young spinach leaves by Nucleon plant-DNA extraction kits (Amersham Pharmacia Biotech) according to the standard protocol. The DNAs (10 μg) were digested with BglII, DraI, or EcoRI and then electrophoresed on a 0.7% (w/v) agarose gel. Fractionated DNA was transferred onto a Hybond N+ membrane (Amersham Pharmacia Biotech). Plastidal Protox cDNA (1.8 kb) was labeled with an AlkPhos Direct labeling kit (Amersham Pharmacia Biotech) according the manufacturer’s instructions. Hybridization was performed at 65°C, and the signals were detected by a chemiluminescent developer (model 377; Perkin-Elmer Applied Biosystems, Foster City, CA). PCR and cloning procedures were independently repeated twice to confirm DNA sequences.

Inmunoblot Analysis

For immunoblot analysis, intact chloroplasts and mitochondria were isolated from 4-week-old spinach leaves by centrifugation on a Percoll linear gradient according to the method of Gualberto et al. (1995). Intactness of chloroplasts and mitochondria was judged by the activity of ferricyanide reduction (Lilley et al., 1975) and by the latency of cytochrome c oxidase activity (Krömer and Heldt, 1991). For purification of the stroma, envelope, and thylakoid fractions from intact chloroplasts, 15 mL of two sets of discontinuous Suc gradients (0.6 and 0.98 M) dissolved in hypotonic buffer (10 mM Tricine [N-(2-hydroxy-1,1-bis[hydroxymethyl]ethyl)glycine]-KOH, pH 7.8, 4 mM MgCl₂, and 1 mM phenylmethylsulfonyl fluoride [PMSF]) were prepared (Joyard et al., 1982). A 5-mL suspension of intact chloroplasts osmotically lysed in hypotonic buffer was layered onto the gradients, and the tubes were ultracentrifuged at 90,000g for 90 min at 4°C. After centrifugation, three fractions were clearly separated: a dark green pellet at the bottom of the tube (thylakoid fraction); a yellow band at the interface of the two Suc layers (envelope fraction); and a slightly yellow supernatant (stroma fraction). These samples were separated by SDS-polyacrylamide gels (12.5%) as described by Laemmli (1970). Separated proteins were electrophoretically transferred to a nitrocellulose membrane (Millipore, Bedford, MA) with a semidry blotter (Bio-Rad Laboratories, Hercules, CA). Non-specific binding was blocked with 3% (w/v) bovine serum albumin (BSA) in PBS buffer for 1 h at room temperature. Immunoreactive polypeptides were detected using an alkaline phosphatase-conjugated goat antibody raised against rabbit immunoglobulin G (Jackson ImmunoResearch Laboratories, West Grove, PA) and visualized by reaction with nitroblue tetrazolium chloride and bromochloroindolyl phosphate.

Purification and Determination of the N-Terminal Sequence

Spinach leaves (2.4 kg) were harvested and kept in a cold room for 2 d in the dark. The leaves were subsequently irradiated with light (120 μmol m⁻² s⁻¹) for 2 h before extraction of chloroplasts. Spinach chloroplasts were isolated by the method of Wang et al. (1993) with slight modifications. Spinach leaves were cut into small pieces, directly immersed in an ice-cold extraction medium (330 mM Suc, 1 mM EDTA, 1 mM MgCl₂, 0.1% [w/v] BSA, 5 mM Cys hydrochloride monohydrate), 20 mM TES [N-Tris(hydroxy-
methyl)-2-aminoethanesulfonic acid], and 10 mM HEPES [4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid] adjusted to pH 7.9 with KOH) and homogenized for 5 s with a Polytron (PT 10/35; Kinematica, Westbury, NY). After filtration through four layers of gauze, the chloroplasts were pelleted by centrifugation at 2,500g for 3 min. The pellet was gently resuspended and centrifuged at 150g for 2 min, and then the supernatant was centrifuged at 2,000g for 1 min. Intact chloroplasts were osmotically broken by resuspension in a 1:13 dilution of a chloroplast extraction buffer plus 0.8 mM PMSF and centrifuged at 10,000g for 30 min. The resulting pellets contained chloroplast membranes (thylakoids and envelope). Protox activity was solubilized by diluting the membrane fraction to a protein concentration of 5 mg/mL in a 1:13 dilution of a chloroplast extraction buffer plus 0.8 mM PMSF and 0.1% (w/v) Triton X-100. The membrane suspension was gently stirred for 1 h, and then the insoluble material was removed by ultracentrifugation at 105,000g for 1 h. Protox activity was recovered in the soluble fraction, and the resultant soluble extract was used as crude extract.

Additional purification of plastidal Protox was performed by the immunoprecipitation method. The crude extract was incubated with 15 μg of specific antibody against Protox at room temperature for 3 h and further incubated with 50 μL of Protein A-beads (Pierce Chemical, Rockford, IL) at 4°C overnight. The complex of Protein-A beads and antibody protein was collected by centrifugation and then washed with cold Tris-HCl, pH 7.4, 0.15 M NaCl, 0.05% (w/v) Triton X-100 and further washed with cold distilled water. The bead complex was suspended in 50 μL of the sample buffer for SDS-PAGE and analyzed on a 10% (w/v) gel according to the method of Laemmli (1970). The proteins in the gel were electrophoretically transferred onto a polyvinylidene difluoride membrane (Millipore) using Transblot SD (Bio-Rad Laboratories) at 10 V for 2 h. After staining with 0.1% (w/v) Coomassie Brilliant Blue R-250 in 50% (v/v) methanol, the visualized band (60 kD) was excised and the N-terminal sequence was determined with a pulse liquid-phase protein sequencer (Perkin-Elmer Applied Biosystems, model 492A). Protein contents were analyzed with a pulse liquid-phase protein sequencer (Perkin-Elmer Applied Biosystems, model 492A). Protein contents were determined by a Protein assay kit (Bio-Rad Laboratories) using BSA as a standard.

Functional Complementation of hemG-Deficient Mutant of E. coli

The full-length (Met-1 to Lys-563) and mature forms (Ser-49 to Lys-563) of plastidial Protox cDNA clones were amplified by PCR using two sets of specific primers, (5'-ATGTGAGTTACCAATTCG-3') and (5'-TTCAAATCACCTATCCCTTCA-3'), respectively. Amplified fragments were cloned into a pCR 2.1 plasmid vector (Invitrogen). The targeting sequences corresponding to the upstream region of the processing point (Met-1 to Cys-48) and the flanking 25 amino acid residues (Met-1 to Asp-73) upstream region of the processing point (Met-1 to Cys-48) and the flanking 25 amino acid residues (Met-1 to Asp-73) were PCR-amplified from the Protox cDNA using pairs of primers as follows: Met-1 to Cys-48, 5'-AGGCTTATGGAATTTGCTAG-3' and 5'-GAGCTTATGGAATTTGCTAG-3'; and Met-1 to Asp-73, 5'-AC CAGTATGTAAGGGAGAG-3' and 5'-CAGTATGTAAGGGAGAG-3'. Amplified fragments were digested with Ncol and SpeI and cloned in-frame into the Ncol and SpeI sites of the pCR 2.1 vector contained with GFP2 gene. The plasmid was further digested with Ncol and SacI and cloned into the Ncol and SacI sites of the expression vector pBI221 (Novagen). Gold particles (2.5 μg of 1-μm gold particles) were coated with 2.5 μg of the constructed plasmid DNAs by CaCl2/spermidine precipitation as previously described (Cao et al., 1992). Spinach leaves were bombarded with the gold particles using a particle gun (Bio-Rad Laboratories PDS-100/He). The distance between the loaded DNA and the target leaves was 8 cm, and the pressure used was 1,100 psi. After overnight incubation at 25°C, transient expression was observed using a fluorescence microscope (Leica Microsystems, Wetzlar, Germany) with Micro Mover-W (Photometrics, Tucson, AZ) fitted with a triple-band filter (no. 81 series PINKEL no. 1 Filter SET, Chroma Technologies, Brattleboro, VT). Autofluorescence was observed in chloroplasts at excitation wavelength of 540 nm and emission wavelength of 600 nm, and the fluorescence of GFP was observed at excitation wavelength of 495 nm and emission wavelength of 530 nm. Two images were acquired separately in the IF Lab/PV-CAM system through a cooled CCD camera (Photometrics) and pseudocolored.
based on the original emission fluorescence. The composite images were printed with Pictography (Fuji, Tokyo).

**Immunogold Electron Microscopy**

For immunogold electron microscopy of plastidal Protox distribution, spinach leaves of 1-month-old seedlings were fixed with 0.6% (v/v) glutaraldehyde and 4% (v/v) paraformaldehyde in a 0.05 M sodium cacodylate buffer (pH 7.4) for 5 min at 4°C under a vacuum and stored at 4°C for 1 h. The tissues were rinsed with a 0.05-M sodium cacodylate buffer (pH 7.4) for 2 h at 4°C. The fixed materials were then dehydrated in an ethanol series at 4°C, embedded in LR White resin (The London Resin Co., London), and polymerized by UV irradiation at room temperature (Suzaki and Kataoka, 1992; Tomoyasu et al., 1993). Ultrathin sections were cut with a diamond knife and mounted on uncoated nickel grids.

Prior to incubation in the primary antibody, the sections were blocked with 5% (w/v) BSA in PBS for 30 min. Specific antibody against plastidal Protox was diluted in PBS supplemented with 1% (w/v) BSA. Incubation with the primary antibody was performed overnight at 4°C followed by washing with 0.05% (w/v) Tween 20 in PBS (PBST, pH 7.4). The secondary antibody, goat anti-rabbit immunoglobulin G conjugated to 15-nm gold particles (Biocell Research Laboratories, Cardiff, UK), was diluted in PBST. Sections were incubated in the secondary antibody for 30 min at 37°C. The sections were then washed in PBST and in distilled water, followed by staining with uranyl acetate for 15 min. The sections were observed under a transmission electron microscope (H-7100; Hitachi, Tokyo) at an accelerating voltage of 75 kV.

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**LITERATURE CITED**


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Characterization of Plastidal Protoporphyrinogen Oxidase


Hansson M, Hederstedt L (1994) Bacillus subtilis HemY is a peripheral membrane protein essential for protoheme IX synthesis which can oxidize coproporphyrinogen III and protoporphyrinogen IX. J Bacteriol 176: 5962–5970


