

Amino acid oxidation of the D1 and D2 proteins by oxygen radicals during photoinhibition of Photosystem II

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The Photosystem II reaction center is vulnerable to photoinhibition. The D1 and D2 proteins, lying at the core of the photosystem, are susceptible to oxidative modification by reactive oxygen species that are formed by the photosystem during illumination. Using spin probes and EPR spectroscopy, we have determined that both $O_2^{\bullet-}$ and HO^{\bullet} are involved in the photoinhibitory process. Using tandem mass spectrometry, we have identified a number of oxidatively modified D1 and D2 residues. Our analysis indicates that these oxidative modifications are associated with formation of HO^{\bullet} at both the Mn_4O_5Ca cluster and the nonheme iron. Additionally, $O_2^{\bullet-}$ appears to be formed by the reduction of O_2 at either $Pheo_{D1}$ or Q_A . Early oxidation of D1:³³²H, which is coordinated with the Mn1 of the Mn_4O_5Ca cluster, appears to initiate a cascade of oxidative events that lead to the oxidative modification of numerous residues in the C termini of the D1 and D2 proteins on the donor side of the photosystem. Oxidation of D2:²⁴⁴Y, which is a bicarbonate ligand for the nonheme iron, induces the propagation of oxidative reactions in residues of the D-de loop of the D2 protein on the electron acceptor side of the photosystem. Finally, D1:¹³⁰E and D2:²⁴⁶M are oxidatively modified by $O_2^{\bullet-}$ formed by the reduction of O_2 either by $Pheo_{D1}$ or Q_A . The identification of specific amino acid residues oxidized by reactive oxygen species provides insights into the mechanism of damage to the D1 and D2 proteins under light stress.

photosynthesis | Photosystem II | reactive oxygen species | photo inhibition | mass spectrometry

Photosystem II (PSII) functions as a water-plastoquinone oxidoreductase (1, 2) and is a thylakoid membrane pigment-protein complex present in all oxygenic photosynthetic organisms (cyanobacteria, algae, and higher plants). Current high-resolution structures of thermophilic cyanobacterial PSII (3, 4), and lower resolution structures of the red algal (5) and higher plant photosystems (6), have been critically important in furthering our understanding of the molecular organization of PSII. Structurally, the PSII reaction center core is composed of five proteins: D1, D2, the α - and β -subunits of cytochrome b_{559} , and PsbI. These components bind all of the redox-active cofactors of PSII.

Excitation energy transfer and electron transport within PSII are unavoidably associated with production of reactive oxygen species (ROS) when the absorption of light by the chlorophyll antenna exceeds the capacity for energy utilization. Many mechanisms for ROS production have been proposed (for reviews, see refs. 7 and 8). Briefly, singlet oxygen (1O_2) may be formed by excitation energy transfer from triplet chlorophylls (formed either by the change in orientation of the spin of an excited electron in the PSII antenna complex, or via charge recombination of the primary radical pair $^3[P_{680}^{\bullet+}Pheo^{\bullet-}]$) to O_2 (9, 10). ROS production by electron transport involves either the two-electron oxidation of water or the one-electron reduction of O_2 on the PSII electron donor and acceptor sides, respectively. On the PSII electron donor side, a two-electron oxidation of water leads to the formation of hydrogen peroxide (H_2O_2), which may be oxidized to the superoxide anion radical

($O_2^{\bullet-}$) or reduced to the hydroxyl radical (HO^{\bullet}) (8). It has been proposed that H_2O_2 is oxidized either by the redox-active tyrosine residue $Tyr_Z^{\bullet+}$ (11) or the chlorophyll cation $Chl_Z^{\bullet+}$ (12). H_2O_2 may be reduced to HO^{\bullet} by free manganese released from damaged Mn_4O_5Ca clusters (13). On the PSII electron acceptor side, a one-electron reduction of O_2 forms $O_2^{\bullet-}$, which is known to initiate a cascade of reactions leading to the formation of both H_2O_2 and HO^{\bullet} (7). Redox-active cofactors known to reduce O_2 to $O_2^{\bullet-}$ are pheophytin ($Pheo^{\bullet-}$), the tightly bound plastoquinone at the Q_A site ($Q_A^{\bullet-}$), the loosely bound plastoquinone at the Q_B site ($Q_B^{\bullet-}$), free plastoquinone ($PQ^{\bullet-}$), and the ferrous heme iron in the low potential (LP) form of $cyt\ b_{559}$ (8). Free H_2O_2 is formed by dismutation of $O_2^{\bullet-}$, known to occur spontaneously or catalyzed by either $cyt\ b_{559}$ or the superoxide dismutase attached to the stromal side of the thylakoid membrane in the vicinity of PSII. Alternatively, bound peroxide may be formed by the interaction of $O_2^{\bullet-}$ with the nonheme iron (14). In this reaction, a ferric-peroxo species is formed, the protonation of which produces a ferric-hydroperoxo species. The reduction of free H_2O_2 or bound peroxide can form HO^{\bullet} via the Fenton reaction.

Light-induced production of ROS by PSII is accompanied by inevitable damage to the D1 and D2 proteins. This damage consists of initial protein oxidation events, which subsequently leads to cleavage and aggregation of the D1 subunit (15). Protein oxidation, cleavage, and aggregation have also been observed, although to a lesser extent, in the D2 protein, which degrades in a similar manner to the D1 protein but at a slower rate (16). Despite the fact

Significance

Reactive oxygen species (ROS) damage the D1 and D2 reaction center proteins of Photosystem II in a process known as photoinhibition. Photoinhibition is an unavoidable consequence of excitation energy transfer and electron transport. The ROS responsible for oxidative damage, the sites of ROS production, and the residues oxidatively modified have not been determined. In this work, we identify HO^{\bullet} as being produced on both the oxidizing and reducing sides of the photosystem. $O_2^{\bullet-}$ also appears to be produced at either $Pheo_{D1}$ or Q_A . Additionally, residues on the D1 and D2 proteins were identified that are oxidatively modified during a photoinhibitory timecourse. Finally, we propose plausible pathways for the propagation of protein oxidation events in the D1 and D2 proteins.

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Fig. 2C (top trace) shows the characteristic POBN-CH(CH₃)OH adduct EPR signal generated by using the Fenton reagent as a control. The time profile of the POBN-CH(CH₃)OH adduct EPR signal shows that HO[•] is produced throughout the illumination period (Fig. 2D). These results indicate that illumination of PSII membranes results in HO[•] production.

Effect of Antioxidants, Chloride, and Nonheme Iron on Hydroxyl Radical Formation. To explore the origin of HO[•] formation, the effects of antioxidants, chloride, and nonheme iron on the light-induced POBN-CH(CH₃)OH adduct EPR spectrum were examined. The addition of the enzymatic antioxidants of O₂^{•-} and H₂O₂, superoxide dismutase and catalase, respectively, suppressed the POBN-CH(CH₃)OH adduct EPR signal (Fig. S14). Additionally, when the chelator desferal, a potent inhibitor of the Fenton reaction (23), was used, the POBN-CH(CH₃)OH adduct EPR signal was also decreased. These results indicate that HO[•] is formed by reduction of H₂O₂ via Fenton reactions. Fig. S1B shows the effects of exogenous chloride, acetate, a chloride-binding inhibitor, and a chloride channel blocker, 4,4'-diisothiocyanatos-tilbene-2,2'-disulfonic acid (DIDS), on the formation of HO[•]. The POBN-CH(CH₃)OH adduct EPR signal was reduced significantly in the presence of chloride, acetate, and DIDS. This result indicates that chloride and reagents that modulate chloride binding decreased the POBN-CH(CH₃)OH adduct EPR signal. Fig. S1C shows the effect of a nonheme iron ligand, formate, a nonheme iron oxidant, ferricyanide (FeCN), and the exogenous electron acceptor, 2,6-dichlorophenolindophenol (DCPIP), on the formation of HO[•]. These all decreased the POBN-CH(CH₃)OH adduct EPR signal. These results indicate that both chloride and nonheme iron modulate HO[•] formation on the PSII electron donor and acceptor side, respectively.

D1 Protein Oxidation, Cleavage, and Aggregation. Protein radicals (P[•]) are formed by hydrogen abstraction from amino acid residues and are located either on the protein backbone or residue side chains (24). To determine formation of P[•] in PSII membranes, the immuno-spin trapping technique using 5,5-dimethyl-1-pyrroline *N*-oxide (DMPO) was used (25). In this method, the DMPO spin trap interacts with P[•], forming a DMPO-P adduct, which is then detected by using immunological techniques with an antibody directed against the nitron of DMPO (anti-DMPO antibody). When PSII membranes were incubated with DMPO in dark, a 32-kDa band was detected with the anti-DMPO antibody (Fig. 3A). After illumination, the intensity of the 32-kDa band increased and an additional 68-kDa band appeared. These results demonstrate that illumination of PSII membranes induced the formation of P[•] located on the D1 protein.

Protein carbonyls can be introduced into oxidatively modified proteins by the β-scission of protein alkoxyl radicals, which leads to the formation of carbonyls and protein alkyl radicals (24). To monitor formation of protein carbonyl groups in PSII membranes, immunoblotting using an anti-2,4-dinitrophenylhydrazone (DNP) antibody was performed. In this method, carbonyl groups were first derivatized with 2,4-dinitrophenylhydrazine (DNPH) and the modified proteins were subsequently identified by using an anti-DNP antibody (26). PSII membranes incubated in the dark exhibited a single 32-kDa band. Illumination of the PSII membranes yields the appearance of an additional 68-kDa band (Fig. 3B). These results show that illumination of PSII membranes resulted in the formation of protein carbonyl groups located on the D1 protein.

The formation of carbonyls and P[•] is associated with protein backbone cleavage (fragmentation) and protein aggregation (protein-protein cross-linking), respectively. To monitor cleavage and aggregation of the D1 protein, immunoblot analysis using antibodies detecting the C terminus of the D1 protein (anti-C-terminal antibody) and the D-de loop of the D1 protein (anti-D-de loop antibody) was performed. When the anti-C-terminal antibody was

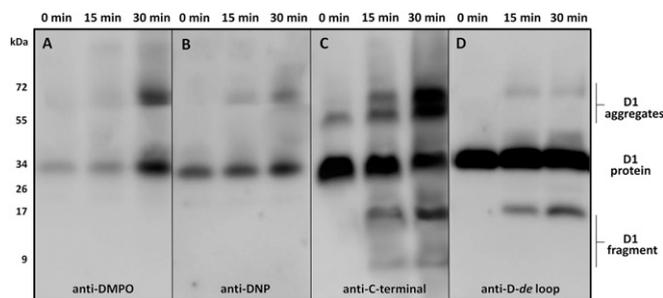


Fig. 3. Immunoblot identifying formation of protein radical, carbonyl group, fragment, and aggregates on the D1 protein. Immunoblot of dark-adapted and high intensity light illuminated PSII membranes labeled with DMPO and identified with an anti-DMPO antibody (A), labeled with DNP and identified with an anti-DNP antibody (B), identified with an anti-C-terminal antibody (C) and identified with an anti-D-de loop antibody (D). PSII membranes were exposed to high intensity red light for 15 and 30 min, separated by SDS/PAGE and blotted on nitrocellulose membrane and probed with an antibody. Representative blots from three independent experiments are presented. The duration of the high intensity illumination is shown above.

used, 32- and 52-kDa bands were observed in dark incubated PSII membranes. Illumination resulted in the appearance of new bands in the 9-, 18-, and 68-kDa molecular mass ranges (Fig. 3C) and an increase in the intensity of the 52-kDa band. The anti-D-de loop antibody detected a 32-kDa band in the dark, whereas the 9-, 18-, and 68-kDa bands appeared after exposure of PSII membranes to light (Fig. 3D). Our data demonstrate that, under our experimental conditions, the 18-kDa peptide arises from the C terminus of the D1 protein and includes the portions of the D-de loop bearing the antigenic determinants for the D-de loop antibody. A number of other laboratories, using a variety of experimental protocols, have observed a D1 fragment of similar apparent molecular mass (27–29). The higher molecular mass bands at 52 and 68 kDa are aggregates containing D1 and possibly other protein components. These results indicate that illumination of PSII membranes yields cleavage and aggregation of the D1 protein.

Effect of Antioxidants, Chloride, and Nonheme Iron on Protein Radical and Carbonyl Group Formation in the D1 protein. To explore the origin of P[•] and carbonyl group formation, the effects of antioxidants, chloride, reagents that modulate chloride binding with PSII, and reagents that interact with the nonheme iron were examined. The effects of these reagents on the formation of the DMPO-P adduct and DNP-carbonyl derivative were examined by immunoblotting (Fig. S2). The addition of the antioxidants superoxide dismutase, catalase, or mannitol (Fig. S2A) lowered the intensity of the 32- and 68-kDa bands labeled with both anti-DMPO and anti-DNP. Additionally, when samples were treated with desferal, a potent inhibitor of the Fenton reaction (23), the intensity of the 68-kDa band labeled with anti-DMPO and anti-DNP was nearly abolished (Fig. S2A). These results indicate that suppression of HO[•] production decreased the formation of both P[•] and protein carbonyl groups on the D1 protein. Fig. S2B shows the effects of chloride, acetate (a chloride-binding inhibitor), and DIDS (a chloride channel blocker), on the bands labeled with anti-DMPO and anti-DNP. The addition of chloride and acetate to PSII membranes during illumination lowered the labeling of the 32- and 68-kDa band with both anti-DMPO and anti-DNP. Incubation with DIDS during illumination completely abolished labeling of the 68-kDa band with both anti-DMPO and anti-DNP. These results demonstrate that chloride, and reagents that modulate chloride binding, influence the production of P[•] and carbonyl groups on the D1 protein. Fig. S2C shows the effects of formate (a nonheme iron ligand), ferricyanide (a nonheme iron oxidant), and DCPIP (an exogenous electron acceptor) on labeling with anti-DMPO and

anti-DNP. All three reagents lowered the intensity of labeling of the 32- and 68-kDa bands with anti-DMPO and anti-DNP. These results indicate that the nonheme iron influences in the formation of P[•] and carbonyl groups on the D1 protein.

Identification of Oxidized Amino Acid Residues on D1 and D2 Proteins During a Photoinhibitory Timecourse. To identify the oxidative modifications occurring within the D1 and D2 proteins during photoinhibition, samples were examined after 0, 15, and 30 min of illumination. These time-points corresponded to approximately 0, 45, and 60% inhibition of O₂ evolution. The quality of the tandem mass spectra used in this study is illustrated in Fig. S3. The results from these experiments are shown in Table S1 and Fig. 4. Initially, at 0 min, a number of residues were observed to be oxidatively modified, including the D1 residues ³¹⁶T, ³¹⁷W, ³¹⁹D, ³²⁸M, ³³¹M, and ³³³E and the D2 residues ¹⁸M, ²⁴⁶M, ²⁴⁷V, and ³²⁹M. Most of these residues (D1 residues ³¹⁶T, ³¹⁷W, ³¹⁹D, ³²⁸M, ³³¹M, and ³³³E and the D2 residue ³²⁹M) are located in the C-terminal domains of the D1 and D2 subunits and are in close proximity to the Mn₄O₅Ca cluster.

Comparison with this background of natively oxidized residues allows the identification of modifications that are directly the result of experimental photoinhibitory conditions. After 15 min of illumination, a number of additional residues were modified, including the D1 residue ³³²H and the D2 residues ³²⁸W, ³³³D, ³³⁴Q, and ³³⁶H. Most of the oxidatively modified residues that were identified at 0 min were also observed after 15 min of illumination. All of the additional residues observed to be modified after 15 min of photoinhibitory illumination are between 2.1 Å (D1:³³²H) and 32 Å (D2:³³⁶H) from the Mn₄O₅Ca cluster and located on the luminal side of PSII. These results indicate that under conditions where 45% of the O₂ evolution capacity of PSII has been lost, modifications of residues in the vicinity of the metal cluster were the first to be observed.

After 30 min of illumination, numerous additional residues on both the D1 and D2 proteins were observed to be oxidatively modified (Table S1). The D1 residues ¹M, ⁷R, ¹³⁰E, and ¹³¹W are located on the stromal side of the protein. D1:¹³⁰E and D1:¹³¹W are particularly interesting and are in close proximity to Pheo_{D1}. The D1 residues ³¹⁵N and ³²⁹E are located on the luminal side of the protein in the vicinity of the metal cluster. The additional D2 residues modified at 30 min include ²⁴²E, ²⁴⁴Y, and ²⁴⁵S, which are located on the stromal side of the protein in the D-de-loop region and are in the vicinity of both the nonheme iron and Q_A. The D2 residues

³⁴¹F, ³⁴²P, ³⁴³E, ³⁴⁴E, and ³⁴⁵V are located on the luminal side of the thylakoid membrane in the vicinity of the Mn₄O₅Ca cluster.

Discussion

During the light reactions of photosynthesis, water oxidation and plastoquinone reduction are associated with the accumulation of oxidizing and reducing equivalents on the PSII electron donor and acceptor sides, respectively. These redox equivalents have the ability to form ROS by either partial water oxidation or partial reduction of O₂ (8). It has been hypothesized that HO[•] is involved in D1 protein damage. This hypothesis was based on the observation that damage to the D1 protein could be initiated by the exogenous addition of H₂O₂ and prevented by exogenous HO[•] scavengers (27, 30). Similar oxidative modifications to the D2 protein occurs, however, with slower reaction kinetics (16). Oxidation of the D1 and D2 proteins by HO[•] is initiated by hydrogen atom abstraction from an amino acid residue forming P[•]. P[•] reacts with O₂, generating an oxygen-centered protein peroxy radical (POO[•]) that may subsequently oxidize other nearby residues as it is reduced to a protein hydroperoxide (POOH). Direct experimental evidence for the light-induced oxidation of specific amino acid residues on the D1 and D2 proteins by ROS is lacking. Early studies using electrospray ionization mass spectrometry revealed extensive oxidation of the D1 and D2 proteins in dark-treated PSII reaction centers (18). The use of tandem mass spectrometry recently allowed a more comprehensive identification of oxidized amino acids in PSII (31). Amino acids localized in the vicinity of the Mn₄O₅Ca cluster, Pheo_{D1}, and Q_A were identified as being oxidatively modified in PSII membranes isolated from field-grown spinach (17, 32). The aim of the present study was to investigate the role of HO[•] in oxidative damage to the D1 and D2 proteins during photoinhibition and to identify the oxidatively modified residues on these subunit proteins by using mass spectrometry. Our findings indicate that amino acid residues in close proximity to the Mn₄O₅Ca cluster were modified during the early stages of photoinhibition, whereas amino acids near Pheo_{D1}, Q_A, and the nonheme iron were modified later in the photoinhibitory timecourse.

PSII Electron Donor Side ROS Production by Incomplete Water Oxidation.

The addition of exogenous chloride to PSII membranes significantly suppresses the formation of HO[•] (Fig. S1B). This observation is in agreement with previous reports that chloride-depleted PSII membranes produced more HO[•] compared with control PSII membranes (33, 34). The involvement of chloride in HO[•] formation is supported by the observation that acetate and DIDS nearly

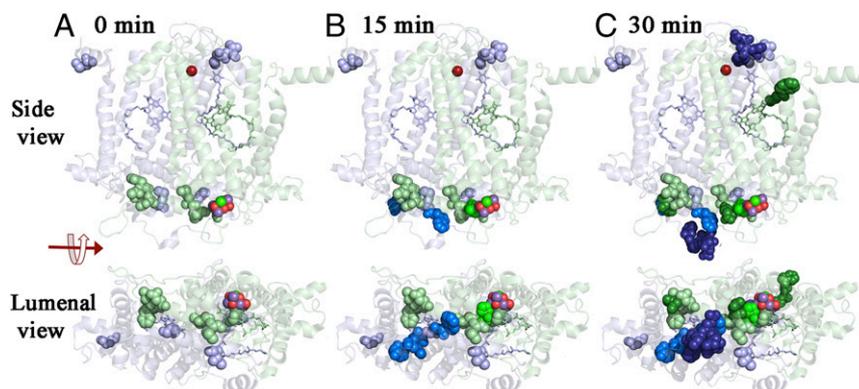


Fig. 4. Oxidative modifications of the D1 and D2 proteins. Time course for the appearance of oxidative modifications of the D1 and D2 proteins presented as side and luminal views. The D1 protein is shown in pale green and the D2 protein is shown in pale blue. Oxidized residues are shown as spheres. Those present at 0 min are shown as pale green (D1) and pale blue (D2). Residues oxidatively labeled at 15 and 30 min are shown in progressively darker shades of green (D1) and blue (D2), respectively. The Mn₄O₅Ca cluster and the nonheme iron are shown as spheres. Pheo_{D1} and Q_A are rendered as pale green and Pheo_{D2} as pale blue sticks, respectively. The protein structure is from spinach PSII (PDB ID code 3JCU; ref. 6) as rendered in PYMOL (51).

abolished detectable HO[•] production (Fig. S1B). It is possible that a water channel plays a crucial role in HO[•] formation. One hypothesis is that the removal of chloride from a water channel results in the uncontrolled delivery of water to the Mn₄O₅Ca cluster, resulting in the formation of H₂O₂ by incomplete water oxidation. Subsequently, H₂O₂ is reduced to HO[•] by the Fenton reaction mediated by Mn. Previously, it was demonstrated that removal of chloride during moderate heat treatment of PSII membranes in the dark resulted in the formation of H₂O₂ and, subsequently, HO[•] production via Fenton reaction (35). One should note that chloride depletion leads to the formation of protein-bound Mn²⁺ (36) possibly facilitating this reaction. Additionally, it is possible that chloride depletion perturbs a proton exit pathway (37). Such disruption could give rise to long-lived higher S states (38, 39) that may increase the probability of the release of partially oxidized water intermediates. These possibilities are not mutually exclusive.

Oxidation of C-Terminal Residues of D1 and D2 Proteins by the Hydroxyl Radical. Oxidized amino acids identified on the PSII electron donor side are located at the C termini of the D1 and D2 proteins and are in close proximity of the Mn₄O₅Ca cluster. D1:³³²H was identified as being oxidatively modified early in the photoinhibitory time-course (Fig. 4 and Table S1). This residue is a ligand to Mn1 of the metal cluster (3) and may be associated with a water ingress channel to the oxygen-evolving site (40). We hypothesize that HO[•] formed by the reduction of H₂O₂ by Mn1, which may partially dissociate from the metal cluster, leads to hydrogen abstraction from D1:³³²H with subsequent propagation of amino acid oxidation events in the C termini of the D1 and D2 proteins (Fig. S44).

ROS Production by the Reduction of O₂. The one-electron reduction of O₂ on the PSII electron acceptor side leads to O₂^{•-} formation (Fig. 2A). Earlier it was shown that interaction of O₂^{•-} with the nonheme iron forms an iron-peroxo intermediate (14). The observation that replacement of bicarbonate by formate suppressed HO[•] formation supports the hypothesis that nonheme iron is involved in HO[•] formation. Additionally, when the nonheme iron was oxidized by ferricyanide, HO[•] formation was essentially eliminated. The artificial electron acceptor DCPIP, which accepts electrons from Q_A^{•-}, also significantly suppressed HO[•] formation (Fig. S1C). These data are consistent with the hypothesis that electron transfer from Q_A^{•-} may reduce the bound ferric iron-peroxo intermediate forming HO[•]. HO[•] generated at the nonheme iron can abstract hydrogen from nearby residues. In the presence of O₂, subsequent propagation of amino acid oxidation reactions may occur in the D-de loop of the protein (Fig. S4B). It should be noted that O₂^{•-}, formed by the reduction of O₂ by Pheo_{D1}^{•-} or Q_A^{•-}, may directly modify nearby amino acid residues without first forming the ferric iron-peroxo intermediate (Fig. S4B). These mechanisms are not mutually exclusive.

Conclusions

Our results significantly enhance our understanding of the mechanisms of photoinhibition. We have identified specific amino acid residues of the D1 and D2 proteins that are oxidized by HO[•], and, possibly O₂^{•-}, during illumination. Early in the process, HO[•] is produced by reduction of H₂O₂ formed by incomplete water oxidation, possibly due to uncontrolled water accessibility to the Mn₄O₅Ca cluster or defects in the proton exit pathway. Hydrogen abstraction from D1:³³²H, coordinated to the Mn₄O₅Ca cluster, by HO[•] appears to initiate a cascade of amino acid oxidation events at the C termini of the D1 and D2 proteins. Later, formation of HO[•] at the nonheme iron may be associated with hydrogen abstraction from D2:²⁴⁴Y, with subsequent oxidation events occurring in amino acids of the D-de loop of the D2 protein. Finally, O₂^{•-} formed by the reduction of O₂ by Pheo_{D1}^{•-} and/or Q_A^{•-} may oxidatively modify the residues D1:¹³⁰E and D2:²⁴⁶M.

Materials and Methods

PSII Membrane Isolation. PSII membranes were isolated from fresh spinach leaves (*Spinacia oleracea*) purchased from a local market, by using the method of Berthold et al. (41–43). Before PSII isolation, spinach leaves were kept in darkness to allow for dark adaptation. The PSII membranes were suspended in a buffer solution containing 400 mM sucrose, 10 mM NaCl, 5 mM CaCl₂, 5 mM MgCl₂, and 50 mM Mes-NaOH (pH 6.5) and stored at –80 °C until use.

Timecourse for Photoinhibition. For these experiments (and the oxidative modification mapping studies described below), the PSII membranes were isolated from spinach leaves incubated overnight at room temperature at a low light intensity (<5 μmol photons·m⁻²·s⁻¹) to facilitate the partial repair of PSII. After isolation, as described above, the PSII membranes were suspended at 100 μg Chl·mL⁻¹ in 400 mM sucrose, 50 mM Mes-NaOH (pH 6.0), 15 mM NaCl, and either incubated in darkness or exposed to red light (663 nm) at 1,400 μmol photons m⁻²·s⁻¹ at room temperature for 0–30 min, either in the presence or absence of 0.4 mM 2,6-dichlorobenzoquinone (DCBQ) + 1 mM potassium ferricyanide. After exposure, the samples were immediately removed from the chamber and assayed for O₂ evolution activity by polarography at room temperature (Hansatech Instruments) using 400 μM DCBQ as an electron acceptor. The control O₂ evolution rate was >400 μmol O₂·mg Chl⁻¹·h⁻¹. For mass spectrometry, samples were removed after 0, 15, and 30 min illumination and stored at –80 °C before electrophoresis. At these time points, the samples exhibited 100, 55, and 40% of control O₂ evolution capability, respectively.

EPR Spin-Trapping Spectroscopy. Free O₂ radicals were detected by EPR spin-trapping spectroscopy. The spin trapping of O₂^{•-} and HO[•] was accomplished by using the spin traps EMPO (Alexis Biochemicals) or POBN (Enzo), respectively. PSII membranes (150 μg Chl·mL⁻¹) were illuminated in a glass capillary tube (Blaubrand intraMARK) with 25 mM EMPO or 50 mM POBN, 170 mM ethanol, and 40 mM Mes buffer (pH 6.5). The spectra were recorded by using an EPR spectrometer Mini Scope MS400 (Magnetech). The EPR conditions used were as follows: microwave power, 10 mW; modulation amplitude, 1 G; modulation frequency, 100 kHz; sweep width, 100 G; and scan rate, 1.62 G·s⁻¹. For quantification, intensity of the EPR signal was evaluated by the relative height of the peak of the first derivative of the EPR absorption spectrum. In these studies, PSII membranes were illuminated with continuous red light (>600 nm, 1,000 μmol photons m⁻²·s⁻¹) at room temperature. In some experiments, the following compounds were added individually to the PSII membranes before the onset of illumination: 400 U·mL⁻¹ superoxide dismutase, 400 U·mL⁻¹ catalase, 5 mM desferal, 100 mM sodium chloride, 100 mM sodium acetate, 10 mM DIDS, 50 mM mannitol, 10 mM sodium formate, 20 μM potassium ferricyanide, and 30 μM DCPIP.

Immunoblot Analysis. For the identification of D1 fragments and aggregates induced by illumination, proteins were resolved by using a Tricine-SDS-polyacrylamide gel electrophoresis (Tricine-SDS/PAGE) (44). Concentrations of acrylamide were 4% (wt/vol) in the stacking and 10/16% (wt/vol) in the resolving gels. PSII membranes (10 μg Chl) were loaded into each well. For Western blot analysis, separated proteins were transferred by using a semidry electroblotter to a nitrocellulose membrane (Bio-Rad Laboratories) and blocked by incubating with 5% (wt/vol) BSA in 25 mM Tris pH 7.6, 150 mM NaCl, 0.05% Tween-20 overnight, and detected by using an antibody against the D-de loop of the D1 protein (anti-D-de loop antibody) (Agrisera). Goat anti-rabbit IgG (H+L) horseradish peroxidase conjugate (Bio-Rad Laboratories) was used as the secondary antibody. Blots were developed by using the Immobilon Western Chemiluminescent HRP substrate (Merck Spol. s.r.o.) and documented by using a high-resolution digital chemiluminescence imager (Amersham Imager 600, GE Health Care Europe).

Immunoblot Detection of Protein Radicals. Before illumination of the PSII membranes, 50 mM DMPO (Dojindo) was added as a spin trap. After illumination of PSII membranes, electrophoresis, immunoblotting, and blocking the nitrocellulose membrane was probed with a primary rabbit polyclonal antibody against the DMPO nitron adduct (anti-DMPO antibody) (Abcam) and detected as described above.

Immunoblot Detection of Protein Carbonyl Groups. After illumination of PSII membranes, electrophoresis, and immunoblotting, carbonyl groups in the protein side chains were derivatized to DNP by reaction with 50 mM DNPH for 30 min. After derivatization, the nitrocellulose membrane was blocked as described above and probed with a primary polyclonal rabbit antibody specific to the DNP moiety of the proteins (anti-DNP antibody) (Molecular Probes Europe BV) and detected as described above.

Protein Digestion and Mass Spectrometry. For the identification of oxidatively modified residues, the D1 and D2 proteins were resolved on 12.5–20% acrylamide lithium dodecyl sulfate-PAGE gradient gels by using a nonoxidizing system as was described (17, 45, 46). This nonoxidizing gel system exhibited significantly lower levels of artifactual protein oxidation (see fig. S1 of ref. 17). After electrophoresis, the gels were stained with Coomassie Blue, destained, and the D1 and D2 protein bands were excised. The protein bands were processed for trypsin digestion by using standard protocols. After digestion, the tryptic peptides were processed by using a C18 ZipTip before mass analysis and were resolved by using reversed-phase chromatography. Mass spectrometry was performed on a Thermo Scientific LTQ-FT. For details of the mass spectrometry experimental conditions, see ref. 17.

MassMatrix version 1.3.2 (47, 48) was used for the identification and analysis of peptides containing oxidative mass modifications and was programmed to

search for the presence of oxidative modifications on 18 amino acids, excluding glycine and alanine (49, 50). For the identification of oxidative modifications, a P value $\leq 1 \times 10^{-5}$ was required, as was a precursor ion mass precision of ≤ 5.0 ppm. A FASTA library containing the D1, D2, CP47, CP43, PsbO, PsbP, and PsbQ protein sequences and a decoy library containing the same proteins, but with reversed amino acid sequences, were searched. For these experiments, peptides were required to exhibit 0% hits to the decoy library for further consideration.

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