

Current perceptions of Photosystem II

Örjan Hansson & Tom Wydrzynski*

*Department of Biochemistry and Biophysics, Chalmers University of Technology and University of Göteborg, S-412 96 Göteborg, Sweden; *Correspondence address: Max-Volmer-Institut der Technischen Universität Berlin, Sekr. PC 14, Strasse des 17. Juni 135, D-1000 Berlin 12, Germany*

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Abstract

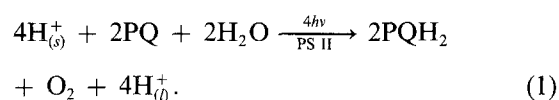
In the last few years our knowledge of the structure and function of Photosystem II in oxygen-evolving organisms has increased significantly. The biochemical isolation and characterization of essential protein components and the comparative analysis from purple photosynthetic bacteria (Deisenhofer, Epp, Miki, Huber and Michel (1984) *J Mol Biol* 180: 385–398) have led to a more concise picture of Photosystem II organization. Thus, it is now generally accepted that the so-called D1 and D2 intrinsic proteins bind the primary reactants and the reducing-side components. Simultaneously, the nature and reaction kinetics of the major electron transfer components have been further clarified. For example, the radicals giving rise to the different forms of EPR Signal II have recently been assigned to oxidized tyrosine residues on the D1 and D2 proteins, while the so-called Q₄₀₀ component has been assigned to the ferric form of the acceptor-side iron. The primary charge-separation has been measured to take place in about 3 ps. However, despite all recent major efforts, the location of the manganese ions and the water-oxidation mechanism still remain largely unknown. Other topics which lately have received much attention include the organization of Photosystem II in the thylakoid membrane and the role of lipids and ionic cofactors like bicarbonate, calcium and chloride. This article attempts to give an overall update in this rapidly expanding field.

1. Introduction

This article provides an update on current perceptions of Photosystem II (PS II) structure and function since the overall topic was last reviewed in this journal (van Gorkom 1985). During the interim time, many review articles have appeared in the literature on various aspects of PS II. Some of the more recent of these articles include the following: the light-harvesting components (Zuber et al. 1987, Peter and Thornber 1988), the primary photochemistry and reducing-side reactions (Diner 1987, Velthuys 1987, Mathis and Rutherford 1987, Rich and Moss 1987, Diner and Petrouleas 1988), the oxidizing-side reactions (Renger 1987a, b, Babcock 1987), the cofactor requirements (Homann 1987, Brudvig 1988), the protein components (Andersson

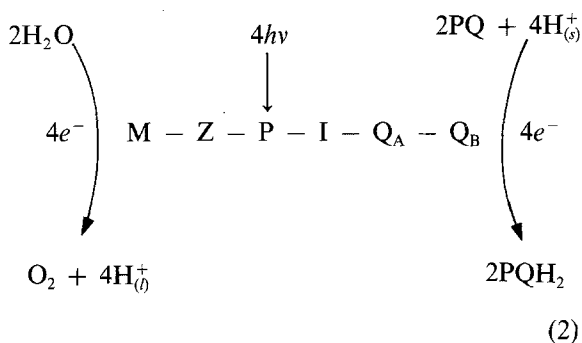
and Åkerlund 1987, Green 1988), the molecular biology (Gray 1987, Chitnis and Thornber 1988, Shinozaki et al. 1989), organization in the membrane (Staehlin 1987) and general reviews (Anderson 1987, Witt 1987, Andréasson and Vänngård 1988). The reader is referred to these articles for additional details.

Photosystem II can be defined as that part of oxygenic photosynthesis which catalyzes the photoinduced transfer of electrons from water to plastoquinone (PQ), i.e.



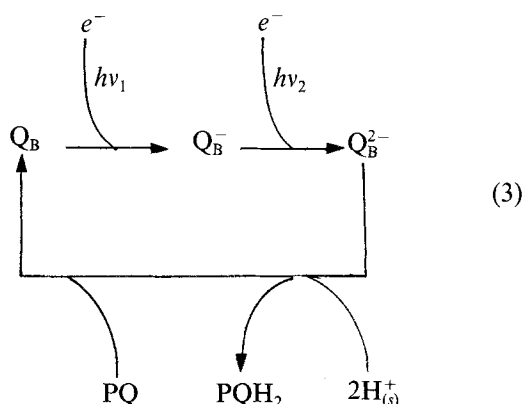
In this formulation, in order to denote the vectorial organization of the reaction sequence across the

thylakoid membrane, the proton release and uptake are designated by subscripts (*l*) and (*s*), respectively, from the luminal (*l*) to the stromal (*s*) side. The minimal scheme to describe the PS II reaction sequence is typically given as follows:



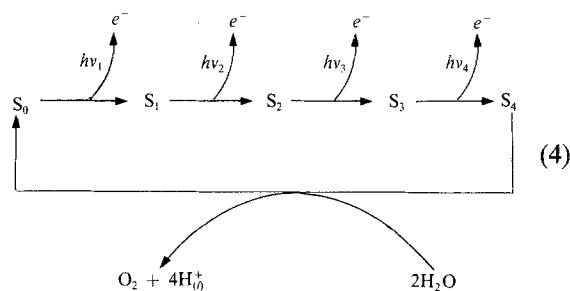
where P is the primary electron donor chlorophyll (Chl) *a* molecule (i.e. P680) that is activated by a light quantum, I, the primary electron acceptor molecule, which is considered to be a pheophytin (Pheo) *a*, Q_A, the first bound plastoquinone acceptor, Q_B, the second bound plastoquinone acceptor, Z, the first electron donor to P⁺ and M, the manganese-containing component that is involved in water oxidation and the release of O₂.

In order to couple the one-electron process of the primary reactants (P and I) with the two-electron process needed for PQ reduction and the four-electron process involved in H₂O oxidation (O₂ evolution), PS II has evolved unique binary and quaternary gating functions on the reducing and oxidizing sides, respectively. Thus, on the reducing side, Q_B is defined as a specially bound PQ molecule which undergoes a two-step reduction process (Velthuis 1981), i.e.



Upon one photochemical event of the primary reactants, the bound PQ becomes reduced to a semiquinone anion which is stabilized by the surrounding protein matrix. Upon a second photochemical event, the bound semiquinone becomes fully reduced, protonated and released from the Q_B binding site as plastoquinol (PQH₂). The binary cycle repeats itself as another PQ molecule binds at the Q_B site.

The quaternary gating function on the oxidizing side of PS II was at first elegantly demonstrated in the O₂-flash yield measurements of Joliot and coworkers (Joliot et al. 1969). As it is now well-established, the O₂ produced by a sequence of brief light flashes displays a damped oscillatory pattern with a periodicity of four beginning after the third flash in dark-adapted samples. Kok and coworkers (Kok et al. 1970) described the O₂-flash yield pattern in terms of a S-state cycle which is driven by successive photoactivations of PS II, i.e.



In Kok's original formulation, each S_{*n*} state (for *n* = 0–3) represented a charge distribution state of PS II, the advancement of which was governed by the ability of the primary reactants to undergo a charge separation upon photoactivation. The S₄ state was defined as that state of PS II which reacted to release O₂ and to regenerate the S₀ state. In more modern usage, the S_{*n*} states are often used in reference to the number of electrons extracted from the manganese-containing component on the oxidizing side of PS II (that is, M, as defined in Reaction Sequence 2 above).

Other reaction components of PS II which may interact with the flow of electrons from water to PQ, but are not designated in Reaction Sequence 2 above, include: cytochrome *b*559 (cyt *b*559), a dark-stable free radical component which gives rise to EPR Signal II_{slow} and usually has been denoted as

D^+ , a non-heme iron (Fe) which is associated with the reducing-side quinone acceptors, carotenoids, monomeric forms of Chl *a* and a second Pheo *a* molecule. Details on these components will be expanded in the following sections.

2. Structural aspects of Photosystem II

The most significant advancements in PS II research since 1980 have been in the biochemical characterization. More than 22 polypeptides have been suggested to be associated with PS II (Masojidek et al. 1987). One possible scheme to describe the organization of PS II is shown in Fig. 1. In this hypothetical picture, PS II is subdivided into four functional parts: (1) the Reaction Core, which contains the primary reactants, the O_2 -evolving components and the PQ-reducing components, (2) a Regulatory Cap, which is made up of a set of hydrophilic proteins that are extrinsically bound to

the luminal surface of the membrane, (3) a Proximal Antenna and (4) a Distal Antenna. In the following sections each of these functional parts is discussed along with the overall organization of PS II in the thylakoid membrane.

2.1. Reaction core

Within the last two years, the primary reactants and the reducing-side components of PS II have been assigned to the so-called D1 and D2 intrinsic proteins of PS II (D1 \approx 32 kDa and D2 \approx 34 kDa, where 'D' refers to 'diffuse bands' on Coomassie-stained urea SDS-PAGE gels). Originally, this assignment was based on homology arguments for the gene sequences between the D1 and D2 proteins and the L and M subunits of the reaction center complex of purple bacteria (see Hearst 1987). The recent isolation of a D1/D2/cyt

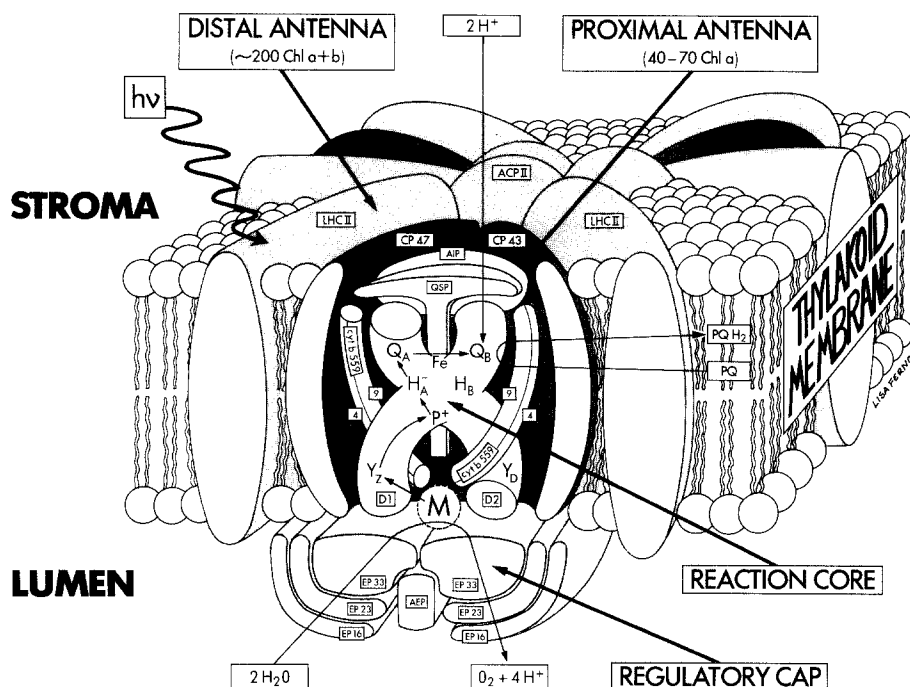


Fig. 1. A schematic representation of the functional organization of Photosystem II. The definition of symbols are as follows: P, the primary electron donor chlorophyll (Chl) (P680); H_A , the primary electron acceptor pheophytin (Pheo); H_B , a second Pheo; Q_A and Q_B , the first and second quinone electron acceptors, respectively; Fe, a non-heme iron atom; Y_Z , the tyrosine first electron donor to P; Y_D , a second tyrosine; M, the manganese-containing component involved in oxygen evolution; cyt *b*559, cytochrome *b*559 heterodimer; D1 and D2, Reaction Core subunits, QSP, quinone-shielding protein; AIP, accessory intrinsic proteins; EP 33, EP 23 and EP 16, extrinsic proteins of the Regulatory Cap; AEP, accessory extrinsic proteins; CP 47 and CP 43, Chl proteins of the Proximal Antenna; ACP II, accessory Chl proteins of the Distal Antenna; and LHC II, the Chl *a/b* light-harvesting complex. See the text for details.

b559 complex (Nanba and Satoh 1987, Barber et al. 1987, Seibert et al. 1988b) which contains a minimal amount of Chl and Pheo and which can undergo photochemistry (Danielius et al. 1987, Takahashi et al. 1987, Chapman et al. 1988, Wasielewski et al. 1989) has greatly added support to this assignment. Furthermore, both reducing-side and oxidizing side properties of PS II are located on the same protein (i.e. on D1) (Metz et al. 1986, Bishop 1987, Ikeuchi and Inoue 1987). Finally, the chemical identity of the dark-stable free radical giving rise to EPR Signal II_{slow} (i.e. D⁺) has recently been assigned to a tyrosine residue (Barry and Babcock 1987) located on the D2 protein (Debus et al. 1988a, Vermaas et al. 1988a). The first electron donor to P⁺, which gives rise to EPR Signal II_{very fast} (i.e. Z), is most likely a tyrosine residues located on the D1 protein (Debus et al. 1988b, B. Diner, personal communication).

Due to these recent developments, we will depict the components Z and D as Y_Z and Y_D, respectively (Hoganson and Babcock 1988), where 'Y' is the biochemical symbol for tyrosine. Likewise, we will use the designation H_A for the primary electron acceptor molecule, where 'H' has been commonly used for the photosynthetic bacteria as the single letter notation for pheophytin. Consequently, a second Pheo *a* molecule (Nanba and Satoh 1987) will be designated as H_B. Thus, in Fig. 1, the primary reactants (P⁺ H_A⁻), the quinone electron acceptors (Q_A and Q_B), the associated non-heme iron (Fe), and the tyrosine electron donor to P⁺ (Y_Z) are shown to be located on a D1/D2 heterodimer within the Reaction Core. Although no experimental evidence exists at present, the second Pheo *a* (H_B) and the dark-stable tyrosine radical (Y_D⁺) may be located on a functionally separate part of the heterodimer. A separate 'non-functional arm' is known to exist in the purple bacteria (Michel et al. 1986). The D1/D2 heterodimer also contains β-carotene and some forms of Chl *a* other than P (Nanba and Satoh 1987) which are not depicted in Fig. 1. The additional Chl *a* may represent monomeric forms located between P and the pheophytins, as is known to be the case in purple bacteria.

The D1/D2 heterodimer is known to span the membrane. Initially, the D1 subunit (originally called the Q_B-protein) was inferred to have 7–8 transmembrane segments based on its primary structure

(see Kyle 1985). However, functional and sequence homologies with the L/M heterodimer of *Rhodospseudomonas viridis* (Deisenhofer et al. 1985), in combination with the analysis of amino-acid changes in herbicide-resistant plants (see Trebst and Depka 1985), led to the suggestion that both the D1 and D2 subunits have five transmembrane segments each. The latter folding pattern has received support in recent antibody studies (Sayre et al. 1986, Andersson et al. 1987). Apparently, the conformation of the D1 subunit is modulated depending on whether the Q_B site is occupied or not (Trebst et al. 1988). Both the D1 and D2 subunits can be phosphorylated (Millner et al. 1986, Ikeuchi et al. 1987, Marder et al. 1988).

A variety of spectroscopic methods have been used to investigate the nature and relative positions of the electron transfer components in the Reaction Core. In general, studies of the electric fields generated by the electron-transfer reactions show that the components are organized vectorially across the membrane, with the quinone acceptors towards the stromal side and P towards the luminal side (see Witt 1987).

The state of aggregation of P (whether it is Chl monomer or dimer) is controversial. Based on redox properties (Davis et al. 1979), optical (Mathis and Setif 1981, den Blanken et al. 1983) and EPR data (Rutherford et al. 1981) it is likely that the hole of the cationic form and the triplet state of P obtained on recombination reside on a monomeric species. It could be that P is a pair of Chl *a* molecules which interact strongly in the singlet excited state and weakly in the triplet state or when it is a cation. Studies on the triplet state of P indicate that the Chl is oriented with its macrocycle parallel to the membrane plane (Rutherford 1985a), markedly different to what is found in the purple bacteria (Tiede and Dutton 1981). Possibly, the triplet state of P in PS II migrates to an accessory monomeric Chl with a different orientation (Rutherford 1985b).

Studies of the electric fields generated by the electron transfers from P to the primary acceptor, H_A, and from H_A⁻ to the first quinone acceptor, Q_A, indicate that the distances between P and H_A and between H_A and Q_A are approximately equal (Trissl et al. 1987) [however, see (Meiburg et al. 1983)]. The orientation of H_A in PS II (Ganago et al. 1982)

is similar to what is observed in purple bacteria, where the Q_Y transition moment is parallel to the membrane normal. Resonance Raman spectroscopy shows that, as in purple bacteria, the 9-keto carbonyl of H_A is hydrogen-bonded to a glutamic residue (Glu130 of D1) (Moënne-Loccoz et al. 1989).

The electrochromic bandshifts in the blue and green parts of the Pheo optical spectrum when Q_A is reduced are stronger than when Q_B is reduced. This indicates that Q_A^- is closer to a Pheo molecule than Q_B^- (Schatz and Van Gorkom 1985). The EPR signals from the $Fe^{2+}Q_A^-$ complex (see Rutherford and Zimmerman 1984) are very similar to those observed in purple bacteria. This suggests that a 7 Å distance between the iron and the quinone ring of Q_A is conserved in PS II (see Mathis and Rutherford 1987).

The distance between P and Y_Z has been estimated to be 10–15 Å based on time-resolved EPR data (Hoganson and Babcock 1989). Since no change in the membrane potential was observed to accompany the Y_Z to P^+ electron transfer (Trissl et al. 1987), this electron transfer may occur laterally in the membrane. For the Y_D component, EPR studies indicate that the normal of its aromatic plane makes an angle of 60° with the membrane normal (Brok et al. 1986). A weak magnetic interaction between Y_D^+ and the manganese in the M component is detectable (de Groot et al. 1986, Styring and Rutherford 1988, Isogai et al. 1988) (however, see Innes and Brudvig 1989), suggesting that the distance between these two components is large (30–40 Å) (Evelo et al. 1989). The distances from the stromal and luminal membrane surfaces to Y_D^+ have been estimated to be 26 and 27 Å, respectively (Innes and Brudvig 1989).

In addition to the L and M subunits, the reaction center complex of purple bacteria contains a third polypeptide called the H-subunit. The H-subunit does not bind any of the electron transfer components, but is probably important in optimizing the conformation of the L/M heterodimer (Deisenhofer et al. 1985). A similar situation may exist in PS II (Renger 1986). In Fig. 1, a cap-like structure is depicted above the acceptor side of the D1/D2 heterodimer. It is simply designated as QSP for 'quinone shielding protein'. Based on gene sequence homologies, a phosphorylatable protein

with an apparent molecular mass of 9–10 kDa (Farchaus and Dilley 1986) has been suggested to be the PS II analog to the H-subunit (Packham 1988). The plastid-encoded gene for this protein yields a primary translation product of 73 amino acid residues with a calculated molecular mass of 7.8 kDa in spinach (Hird et al. 1986, Westhoff et al. 1986). The predicted primary structure reveals a single transmembrane segment and a large hydrophilic extension at the N-terminus which would presumably be located towards the stromal side of the membrane. There is about a 20% homology between this protein and the H-subunit. However, this protein has only been isolated from intact appressed thylakoid membranes and has not been associated with the Reaction Core. Nevertheless, its phosphorylation at threonine 2 on the N-terminal hydrophilic extension (Michael and Bennett 1987) is followed by a slight inhibition of O_2 evolution (Packham 1987) which is possibly mediated via an altered equilibrium between Q_A and Q_B (Hodges et al. 1987, Packham et al. 1988). Alternatively, another protein having an apparent molecular mass of 22 kDa has been implicated in the regulation of PS II reactions (Ljungberg et al. 1986a). This protein exhibits both hydrophilic and hydrophobic characteristics.

Although the similarities between PS II and purple bacteria are remarkable, there must also be very large differences since the purple bacteria do not evolve O_2 . Thus, PS II contains manganese which is required for O_2 evolution (see Ames 1983). The exact location of the manganese is unknown, since a functionally active manganese-containing protein has not yet been identified. However, there is indirect evidence based on mutant studies that the amount of bound manganese in PS II correlates inversely with a modified 34–36 kDa (Bishop 1987) [which is probably the precursor protein of D1 (see Gray 1987)]. It has been suggested that the functionally active manganese binds to the D1/D2 heterodimer (Coleman and Govindjee 1987, Sauer et al. 1988, Dismukes 1988). It is clear that the functionally active manganese is situated towards the luminal side of the membrane, probably within a restricted compartment (Miller and Cox 1984) which is formed between the Reaction Core and the extrinsic 33 kDa protein of the Regulatory Cap (see below)

(Seibert et al. 1988a, Yamamoto 1988). Until more information becomes available, the manganese-containing component, M, is simply depicted in Fig. 1 in such a way that it can be ligated to any number of the protein components.

The PS II Reaction Core also contains at least one heme, *cyt b559* (see Cramer et al. 1986). It has long been known that *cyt b559* can be photooxidized at 77 K, but its physiological role in PS II remains elusive. Although *cyt b559* can exist in high- and low-potential forms, the conversion between these does not correlate with activity changes (Briantais et al. 1985, Ghanotakis et al. 1986, Bergström and Franzén 1987). Likewise, the kinetics of *cyt b559* oxidation do not correlate with the overall kinetics of the main reaction sequence in PS II. Recently, it has been suggested that *cyt b559* may have a photoprotective role (Thompson and Brudvig 1988) or that it could be involved in a proton pump (Arnon and Tang 1988) in connection with a cyclic electron flow around PS II (Falkowski et al. 1986).

The apoprotein of *cyt b559* consists of two subunits with apparent molecular masses of 9 and 4 kDa. Each subunit contains a single histidine residue. Spectroscopic evidence shows that heme coordination in *cyt b559* is *bis*-histidine (Babcock et al. 1985). Consequently, it is usually suggested that the heme binds across the two subunits. The most recent information indicates that there are two copies of the *cyt b559* apoprotein per PS II unit and that the apoprotein spans the membrane with at least one heme located towards the stromal side (Tae et al. 1988). In Fig. 1, two *cyt b559* heterodimers are shown to be tightly coupled to the D1/D2 heterodimer.

The core of PS II may contain other intrinsic proteins with apparent molecular masses of 24 kDa (Ljungberg et al. 1984), 22 and 10 (10.8) kDa (Ljungberg et al. 1986a, Lautner et al. 1988), 7–6.5 and 3.7 kDa (Schröder et al. 1988), 4.8 (4.15) kDa (Ikeuchi and Inoue 1988) and 2 (4.28) kDa (Murata et al. 1988) (values within parenthesis have been calculated from gene sequences). The function of these proteins is not certain at present, but some may serve as structural components needed to optimize the Reaction Core conformation and others may merely represent protein remnants that are not needed for PS II function. These additional proteins are simply represented in Fig. 1 as a blob

labelled AIP, for 'accessory intrinsic proteins'.

2.2. *Regulatory cap*

In another contrast to the purple bacteria, PS II contains what is defined in Fig. 1 as a Regulatory Cap. It is comprised of a set of hydrophilic proteins that have apparent molecular masses of about 33, 23 and 16 kDa. These components are designated as EP 33, EP 23 and EP 16, where EP stands for 'extrinsic protein'. The Regulatory Cap proteins are extrinsically bound to the luminal surface of the membrane (see Andersson and Åkerlund 1987) and are usually assigned functions in regulating the ionic requirements for O₂ evolution (i.e. the chloride and calcium requirements) or in controlling the exchange of reactants with the manganese center (see Section 3.4). The genes for these proteins give predicted processed translation products of 247 (Tyagi et al. 1987), 186 and 149 (Jansen et al. 1987) amino acid residues and calculated molecular masses of 26.5, 20.2 and 16.5 kDa for the EP 33, EP 23 and EP 16, respectively. The EP 33, EP 23 and EP 16 are present in equimolar amounts (Murata et al. 1984, Andersson et al. 1984b). However, it is still controversial whether they exist as one or two copies per PS II unit, although crosslinking studies favor the latter possibility (Milner et al. 1987). In Fig. 1 two copies of each are depicted. The Regulatory Cap may contain another extrinsic protein as well, which has an apparent molecular mass of 5 kDa (Ljungberg et al. 1986b). In Fig. 1, possible additional extrinsic proteins in the Regulatory Cap are designated as AEP, for 'accessory extrinsic proteins'.

Based largely on cross-linking (Bowlby and Frasch 1986, Machold 1986, Milner et al. 1987, Enami et al. 1989), protease (Isoagai et al. 1985) and immunological studies (Ljungberg et al. 1984, Ivy and Berg 1985, Aoki et al. 1986, Camm et al. 1987), the EP 33 can link directly with the Reaction Core and Proximal Antenna components, whereas the two smaller proteins EP 23 and EP 16 appear to shield the EP 33 from the luminal space and can link to the LHC II complex of the Distal Antenna. Antibodies to CP 47 of the Proximal Antenna (see below) and D1 will not bind to the PS II complex unless EP 33 is removed (Bricker et al. 1988, Sayer

et al. 1986). Thus, the hydrophilic extensions of CP 47 and D1 (Alt et al. 1984) may constitute a border region with the EP 33 (Andersson et al. 1987).

It has been suggested that the binding site of the EP 33 on the luminal surface of the membrane is positively charged, while the binding site of the EP 23 is negatively charged (Isogai et al. 1987). This is related to the removal of these proteins by various types of salt washes (see Andersson and Åkerlund, 1987). Recent electron-microscopy studies show that the extrinsic proteins protrude from the membrane surface. The removal and reconstitution of them leads to a loss and recovery of multimeric (tetrameric) structures on the ESs surface (i.e. the luminal side of appressed membranes) of freeze-etched PS II membrane preparations (Simpson and Andersson 1986, Seibert et al. 1987, Bassi et al. 1988a). After removal of the extrinsic proteins, dimeric structures are observed which may indicate two-fold symmetry in the remaining parts of PS II or that PS II exists as dimeric units in the membrane. In another electron-microscopy study, a top view of isolated PS II core complexes lacking the extrinsic proteins was found to be triangular shaped and could represent half of a dimeric unit (Irrgang et al. 1988).

2.3. Proximal antenna

The light-harvesting array for PS II as indicated in Fig. 1 is divided into two major parts, the Proximal Antenna and the Distal Antenna. The Proximal Antenna has a long-wavelength absorption band essentially matching that of the primary donor, and therefore functions to couple energy transfer from the bulk of the light-harvesting pigments in the Distal Antenna to the Reaction Core. The possible modes of energy transfer among the light-harvesting pigments have recently been reviewed (van Grondelle 1985, Pearlstein 1987).

The Proximal Antenna consists of two pigment-protein complexes, often called CP 47 and CP 43 (or CPa-1 and CPa-2, where CP stands for 'Chl-Protein complexes') (see Green 1988). These two proteins have apparent molecular masses of 45–51 and 40–45 kDa, respectively. They both consist of single subunits with possibly seven transmembrane segments containing 11–12 His residues, presumably involved in Chl binding, and a large hydro-

philic segment towards the luminal side (Alt et al. 1984, Morris and Herrmann 1984). Only the CP 43 can be phosphorylated (Ikeuchi et al. 1987). Each protein binds 20–25 Chl *a* and about 5 β -carotene, but no Chl *b* or Pheo. Most of the Chl is oriented with the Q_x transition moment parallel to the membrane normal (Breton and Katoh 1987).

Recent low-temperature fluorescence and absorption spectroscopy have revealed several dissimilarities between CP 43 and CP 47 (Breton and Katoh 1987, van Dorssen et al. 1987). The fluorescence at 77 K peaks at 685 and 695 nm for CP 43 and CP 47, respectively, as was shown earlier (Nakatani et al. 1984). In addition to its main absorption at 669 nm, CP 43 also exhibits a band at 682 nm polarized perpendicular to the membrane normal. The absorption and linear dichroism in the red region of CP 47 is even more complex with bands at 660, 668, 677 and 690 nm. The latter band is probably associated with a single Chl *a* molecule with an unusual orientation of its Q_y transition moment parallel to the membrane normal. It was tentatively assigned to the species responsible for the low-temperature fluorescence band F695. In earlier work the F695 band was suggested to arise from the photoactive Pheo (Breton 1982) and therefore the CP 47 was believed to harbor the primary reactants (see Green 1988). However, with the recent developments now assigning the primary reactants to the D1/D2 heterodimer, this is evidently not the case. The presence of the Chl species responsible for the F695 band would mean that CP 47 contains an energy trap deeper than the primary reactants themselves.

The orientations of the β -carotenes are different between CP 43 and CP 47, which those of CP 43 being largely parallel, and those of CP 47 perpendicular, to the membrane normal. The absorption maxima of the β -carotenes of CP 43 were found to be blue-shifted by 10–15 nm as compared to those of CP 47 (Breton and Katoh 1987).

The Proximal Antenna is apparently tightly coupled to the Reaction Core. The CP 47 and CP 43 proteins are always present in O_2 -evolving preparations of PS II from higher plants. Recently, it has been shown that electron transfer from exogenous donors to Q_A can take place in the absence of CP 43 (Yamaguchi et al. 1988) but that the ability to reduce Q_A is lost when both CP 43 and CP 47 are removed (Akabori et al. 1988). Inactivation

of the genes for CP 47 or CP 43 by site-directed mutagenesis prevents or reduces, respectively, the assembly of the Reaction Core (Vermaas et al. 1988b). At present, the Proximal Antenna cannot be totally excluded from having functions in either direct binding or regulation of the electron transport components.

2.4. Distal antenna

The Distal Antenna contains accessory pigments at variable amounts with which the organism can extend its light absorption to other wavelengths and respond to varying conditions of light intensity and spectral distribution. The Distal Antenna as diagrammed in Fig. 1 is shown to consist of at least two parts, the LHC II and the ACP II. The LHC II is the classical light-harvesting Chl *a/b* complex, which is involved in the stacking of membranes (see Staehlin 1986, Anderson 1987) and the partitioning of energy between PS II and PS I (see Briantais et al. 1986). The LHC II contains several separable, oligomeric components (as many as six in spinach) consisting of proteins with apparent molecular masses of 25 and 27 kDa (see Peter and Thornber 1988). It has a Chl *a/b* ratio of 1.2 ± 0.2 and contains xanthophyll as the major carotenoid. About 30% of the total LHC II can be phosphorylated by membrane-bound kinase which is activated by high levels of reduced PQ. Part of the phosphorylated LHC II then constitutes a 'mobile' fraction which dissociates from PS II and migrates from the appressed to the non-appressed regions of the thylakoid membrane, where it is proposed to increase the light-harvesting capability of PS I (Larsson et al. 1987, Bassi et al. 1988b). The energy coupling between the LHC II, both the 'mobile' and 'non-mobile' parts, and the Reaction Core is also dependent upon the membrane surface charge (Zucchelli et al. 1988).

There are a number of other Chl proteins associated with the PS II Distal Antenna that are not part of the LHC II. We loosely denote these as 'ACP II' in Fig. 1, for 'accessory Chl proteins'. Among these components are CP 29 (see Green 1988) and the recently discovered CP 26 and CP 24 (Dunahay and Staehlin 1986, Bassi et al. 1987) (the numbers after 'CP' denote the apparent molecular masses in kDa). These Chl proteins are separable from LHC

II and generally have a slightly higher Chl *a/b* ratio of 2–3. None of these proteins are phosphorylated. The components of the ACP II may be more closely coupled to the Proximal Antenna and the Reaction Core and may serve as a 'linker' or 'anchor' for the LHC II proteins. One suggestion has been that these Chl proteins may participate in the dissipation of excess excitation energy arriving at the Reaction Core as a means to counteract photoinhibition (Bassi et al. 1987). In higher plants, the total Distal Antenna contains about 200 Chl (*a* + *b*) molecules per PS II unit.

1.3. Organization of PS II in the thylakoid membrane

Crucial to the overall organization of PS II within the thylakoid membrane are the inherent lipids (see Murphy 1986, Gounaris et al. 1986, Anderson 1987). The lipids constitute about 25–30% of the total thylakoid mass. The neutral galactolipids monogalactosyldiglyceride (MGDG) and digalactosyldiglyceride (DGDG) make up the major fraction (75%), while the remaining fraction consists of the negatively charged lipids phosphatidylglycerol (PG) (10%) and sulphoquinovosyldiacylglyceride (SQDG) (10%), and a small amount of other phospholipids (5%). The lipid distribution in thylakoid membranes is most likely asymmetric, both transversely across the membrane as well as laterally. The asymmetric transverse distribution is difficult to determine, but studies with rightside- and inside-out thylakoids indicate that about 60% of the total neutral galactolipids occurs towards the stromal side of the membrane (Sundby and Larsson 1985). Thus, the luminal side of the membrane may contain more of the other lipid components and hence would be more negatively charged. The lateral asymmetric distribution of lipids is more easily determined, since appressed and non-appressed regions can be separated. The appressed regions have a higher MGDG/DGDG ratio and an enrichment of anionic lipids relative to the non-appressed region. In the appressed regions the lipids make up only 14% of the membrane mass, while in non-appressed regions they make up 40%.

It has been found that the addition of DGDG or the phospholipid phosphatidylcholine (PC) stimulates O_2 -evolution activity of PS II-enriched

samples, while the anionic lipids SQDG and PG inhibit activity (Gounaris et al. 1983). Also, it was shown that the degree of saturation of the membrane lipids influences PS II activity (Horváth et al. 1987). Although it has been shown that the processed D1 subunit is post-translationally palmitoylated (Mattoo and Edelman 1987), there has been no direct evidence for specific association of membrane lipids within PS II. It has been observed, however, that the D1 subunit is more resistant to glutaraldehyde crosslinking than the D2 subunit and cyt *b559*, unless the sample is perturbed with specific detergents (i.e. glucosides having 7–9 carbon atom alkyl chains) (Adir and Ohad 1987). This suggests that the D1 confirmation might be stabilized by interactions with adjacent saturated lipids containing 7–9 carbon atom chains and would imply that the lipids may serve an important role at the heart of the Reaction Core. In support of this conclusion are the observations that lipids are essential for a stable charge separation between P^+ and Q_A^- (Jordan et al. 1983, Eckert et al. 1987b, Akabori et al. 1988) and that addition of linolenic acid blocks electron transport at Q_A (Warden and Csatorday 1987). Likewise, lipids are probably essential for the O_2 -evolving step itself since, of the S-state transitions only the S_3 to S_4 to S_0 step shows a break in an Arrhenius plot (Koike et al. 1987), characteristic of a phase transition. Finally, the O_2 -evolving step can be specifically inhibited by lauroyl choline, a lipid analog (Wydrzynski et al. 1985).

The division of thylakoid membranes into appressed and non-appressed regions is associated with an asymmetric distribution of PS II (see Murphy 1986, Gounaris et al. 1986, Staehlin 1986, Anderson, 1987). Thus, it is believed that PS II is primarily located in the appressed (or granal) regions and PS I in the non-appressed (or stromal) regions, although some PS II exists in the non-appressed regions as well. Functional heterogeneity of PS II described as α and β units (see Black et al. 1986) and arguments concerning PS II to PS I stoichiometry (McCauley and Melis 1986, Chylla et al. 1987) may be related to the asymmetric distribution of PS II. For example, in non-appressed regions, it may be that PS II units are being newly synthesized or reprocessed such that the acceptor side is altered. It is known that the D1 subunit turns over rapidly (see Kyle and Ohad 1986), perhaps in

response to photoinhibition at the Q_B site (Kirilovsky et al. 1988, Ohad et al. 1988) and/or at the primary reactants (Arntz and Trebst 1986, Cleland et al. 1986), and that the 34.5 kDa precursor protein to the D1 subunit is processed for incorporation into the thylakoid membrane in the non-appressed regions (see Gray 1987).

There may be additional protein components associated with PS II other than those defined in the previous section. For example, a 62 kDa protein has recently been identified in intact thylakoid samples and was suggested to be involved in a chloride channel through the membrane (Vambutas and Beattie 1987). Since the chloride requirement for photosynthesis is believed to be restricted to PS II (see Section 3.4), it would be interesting to determine whether this protein is associated with PS II. Often 60 kDa proteins are observed in PS II preparations, but these are usually considered to be aggregates of D1/D2 and/or smaller proteins (Steinmetz et al. 1986, Satoh et al. 1987).

The functional organization of PS II as depicted in Fig. 1 can be used to illustrate the properties of various PS II preparations. Thus, the entire PS II complex as shown would represent the PS II-enriched inside-out thylakoid vesicles (i.e. the appressed regions of the membranes) (Åkerlund and Andersson 1983) and the oxygen-evolving detergent-treated PS II preparations (Berthold et al. 1981, Kuwabara and Murata 1982). The PS II complex as shown but excluding the Distal Antenna, with or without ACP II components, would represent the first non-oxygen-evolving core preparations (see Yamada et al. 1985) and the later oxygen-evolving core preparations (Ikeuchi and Inoue 1985, Tang and Satoh 1985, Satoh et al. 1985, Franzén et al. 1986, Ghanotakis et al. 1987), which have various degrees of damage on the reducing side. Finally, the Reaction Core itself would correspond to the newly developed D1/D2/cyt *b559* preparations, which currently show damages on both the oxidizing and reducing sides and are relatively unstable (Nanba and Satoh 1987, Barber et al. 1987, Seibert et al. 1988b, Ghanotakis et al. 1989).

Although spinach represents the most commonly used higher plant source for PS II preparations, there is also a wealth of literature on the use of preparations from the prokaryotic cyanobacteria.

The function of PS II in these organisms is basically the same as in higher plants, but there are some major structural differences (see Glazer 1984, Staehlin 1986, Zuber et al. 1987). The cyanobacteria do not form appressed regions of thylakoid membranes and thus do not have the same type of separation of PS II and PS I as in higher plants. In addition, the thylakoid membranes are also believed to be the site of the respiratory chain. The organization and composition of the Distal Antenna in cyanobacteria are very different as well. The cyanobacteria do not contain Chl *b* but use phycobilins instead as the accessory light-harvesting pigments. These pigments are organized into well-defined structures called phycobilisomes which protrude from the membrane surface and are connected to the Reaction Core complexes within the membrane via special anchor proteins.

The proteins of the Proximal Antenna and Reaction Core in cyanobacteria are similar to those found in higher plants (see Bricker et al. 1986). However, in the Regulatory Cap, the EP 16 and EP 23 are not present (Stewart et al. 1985a). Instead, another extrinsic protein with an apparent molecular mass of 9–10 kDa may be important in function (Stewart et al. 1985b, Rolfe and Bendall 1989). Highly O₂-evolving PS II preparations can be made from cyanobacteria using zwitterionic detergents with 12 carbon atom long chains (e.g. LDAO and SB 12) but these preparations usually require the presence of a high osmoticum (e.g. glycerol) and high concentrations of Ca²⁺ ions in order to exhibit maximum activity. As in higher plants, electron microscopy of PS II particles from cyanobacteria indicate dimeric structures (Rögner et al. 1987). Certainly, the optical properties of cyanobacterial PS II preparations have greatly assisted in the spectroscopic characterization of the PS II primary photochemistry (Schlodder et al. 1984) and the ability to perform site-directed mutagenesis in cyanobacteria (e.g. with *Synechocystis* sp. PCC 6803) was essential for the identification of Y_D as a tyrosine residue in the D2 protein (Debus et al. 1988a, Vermaas et al. 1988a).

3. Functional aspects of photosystem II

A division of PS II into structural and functional aspects may seem artificial since these concepts are

so strongly interrelated. However, in the following sections, emphasis will be put on the more mechanistic details such as the nature of the reactants involved, their relative ordering in the sequence of electron transfer reactions and the kinetics and regulation of these reactions. Topics covered will include (1) electron transfer via the primary acceptor, H_A, to the first quinone acceptor, Q_A, (2) the two-electron quinone gate, Q_B, (3) electron transfer via the tyrosine components, Y_Z and Y_D, and (4) the manganese-containing four-electron oxygen gate, M.

3.1. Electron transfer via the primary acceptor, H_A, to the first quinone acceptor, Q_A

As indicated in Section 2.1 above, there are many structural similarities between the Reaction Cores of PS II and purple bacteria and it is natural to expect also a functional resemblance. At present, our understanding of the early electron transfer events in purple bacteria is particularly detailed (see Kirmaier and Holten 1987). To a large extent this has been achieved through the application of time-resolved optical spectroscopy to reaction center preparations. In contrast, similar studies of PS II have been hampered by the fact that the absorption bands of the chromophores in the Reaction Core are not as well separated spectrally as they are in purple bacteria and also by the lack of pure preparations. However, the recent development of the D1/D2/cyt *b559* preparation (Nanba and Satoh 1987), which is free of antenna Chl, has opened up a new perspective in PS II research in this respect.

In PS II preparations where an antenna is present, the rate of the primary charge separation will be determined by the migration and trapping of the excitation energy, a process which takes place on the 100 ps timescale (Trissl et al. 1987, Schatz et al. 1987, Hodges and Moya 1988, Kischkoweit et al. 1988). However, for the recently developed D1/D2/cyt *b559* preparation the time constant for the primary charge separation (P* → P⁺H_A⁻) has now been measured and found to be 3.0 ± 0.6 ps based on the risetime of the P⁺H_A⁻ absorption band around 820 nm (Wasielewski et al. 1989). A photochemical hole-burning study of the D1/D2/cyt *b559* preparation at 4.2 K gave a value of 1.9 ± 0.2 ps (Jankowiak et al. 1989), while a model

calculation of excitation energy trapping in PS II resulted in a similar value of 3 ps (Schatz et al. 1988). These rates for the primary charge separation are close to those reported for purple bacteria (see Kirmaier and Holten 1987).

The charge separation is further stabilized by the rapid transfer of the electron away from H_A^- . When Q_A is oxidized, this electron transfer occurs with a time constant of 250–300 ps in a spinach PS II core preparation (Nuijs et al. 1986) (based on the decay of an absorption band around 655 nm ascribed to the electrochromic effect of H_A^- on a nearby Chl). Slower kinetics with a time constant of 510 ± 50 ps were observed in the thermophilic cyanobacterium *Synechococcus* sp. (Schatz et al. 1987).

There are several reports to indicate the possible presence of other intermediates between H_A and Q_A (see Diner 1986, Mathis and Rutherford 1987). However, it was concluded from double-flash optical studies that no high-yield acceptor exists which could stabilize an electron for more than a few ns when Q_A is prereduced (Brettel et al. 1985). Recently, the time constant for Q_A reduction was inferred to be 350 ± 100 ps in a time-resolved UV study (Eckert et al. 1988a). Thus, these results seem to exclude the possibility of an intermediate between H_A and Q_A in the major electron pathway.

When the forward electron transfer is blocked by reduction of Q_A , either chemically or by preillumination, there is an increase in the fluorescence yield from the PS II antenna. The origin of this so-called variable fluorescence as well as the related question of the yield and lifetime of the radical pair ($P^+H_A^-$) formed under these conditions is at present controversial. The theories discussed can be summarized with a simple kinetic model (van Gorkom 1985, Schatz and Holzwarth 1986, Mathis 1987), in which it is assumed that $P^+H_A^-$ is in equilibrium with the antenna Chl singlet excited state (A^*): $A^* \leftrightarrow P^+H_A^-$. Originally, it was suggested that the variable fluorescence is a luminescence resulting from the $P^+H_A^-$ charge recombination with the energy reexciting the Chl (see Klimov and Krasnovskii 1981). Alternatively, the above equilibrium might be much displaced to the left, either because of a large antenna or because of a lower possibility for the $P^*H_A \rightarrow P^+H_A^-$ charge separation when Q_A is reduced. In this model, the variable fluorescence is a direct fluorescence from excited antenna Chl with little involvement of the

radical pair (Trissl et al. 1987, Schatz et al. 1988).

In a number of recent reports, the radical pair formation was studied directly using time-resolved flash-absorption spectroscopy. Large variations in the yield and lifetime of $P^+H_A^-$ were found between different PS II preparations. For the D1/D2/cyt *b559* complex the observed absorption changes suggested a significant yield of flash-induced pair that subsequently decayed with an $1/e$ -lifetime of *ca.* 40 ns (Danielius et al. 1987, Takahashi et al. 1987). Time-resolved fluorescence studies revealed a component with a similar lifetime (Seibert et al. 1988b, Mimuro et al. 1988, Hansson, Janot and Moya, unpublished observations). Thus, for these particles the original Klimov model seems applicable, although it should be emphasized that the D1/D2/cyt *b559* preparations used in these studies lack Q_A and, thus, the acceptor side properties may be altered.

In more intact PS II preparations (in the presence of Q_A^- and an antenna) the radical pair decays faster. Very rapid decay kinetics with half-lifetimes less than 500 ps were reported for O_2 -evolving PS II-enriched membranes and these were found to slow down to half-lifetimes of 2.7 (70%) and 15 ns (30%) after repeated light/dark cycles in the presence of $Na_2S_2O_4$ (Eckert et al. 1987a). In a study of a series of PS II preparations differing in antenna size, the half-lifetimes of $P^+H_A^-$ ranged from 3 to 32 ns. The shorter values were obtained from the preparations with a larger antenna (Hansson et al. 1988). A radical-pair $1/e$ -lifetime of *ca.* 11 ns was found in an O_2 -evolving PS II particle from *Synechococcus* sp. (Schlodder and Brettel 1988). In the two latter studies, the yield of radical pair was estimated to be 40–75%. Significantly lower yields were inferred from a combined fluorescence and absorbance study of the above-mentioned particle from *Synechococcus* sp. (Schatz et al. 1987) and from a photovoltage study of pea chloroplasts (Trissl et al. 1987).

The observed yields and lifetimes of the radical pair show a trend towards smaller values with increasing antenna size. This is in accordance with a displacement of the above-mentioned equilibrium to the left, but generally, the radical-pair lifetimes are longer than the lifetime of the variable component in the fluorescence decay ($1/e$ -lifetimes, 1–2.5 ns). To account for the discrepancy between absorbance and fluorescence studies, an extension

of the simple equilibrium model above was recently proposed (Schlodder and Brettel 1988). In this model, which is similar to an earlier model for purple bacteria (Woodbury and Parson 1984), the radical pair is assumed to relax irreversibly to an energetically more favourable conformation. It was concluded that the radical pair recombination does not give rise to the variable fluorescence (Schlodder and Brettel 1988).

The recombination of the radical pair in PS II units with Q_A reduced or absent can also occur via an intermediate triplet state of P (3P) with a lifetime of about 100 μ s. The triplet formed in such a radical-pair mechanism gives rise to an EPR signal with a characteristic spin polarization pattern (see Rutherford 1985b). Indeed, the observation of such an EPR signal in the D1/D2/cyt *b559* preparation conclusively showed that a primary charge separation can occur in this particle (Okamura et al. 1987). With flash-absorption spectroscopy it was found that the quantum yield of 3P increased from 23% at 276 K to 80% at 10 K (Takahashi et al. 1987), similarly to what has been found for purple bacteria (Schenck et al. 1982). Formation of the triplet state of a carotenoid can also be observed, but with a very low, essentially temperature independent quantum yield (Takahashi et al. 1987, Schlodder and Brettel 1988). Thus, although it is known that at least one [possibly two (van Dorssen et al. 1987)] β -carotene molecule is bound to the Reaction Core (Nanba and Satoh 1987), the triplet energy is not transferred to it.

3.2. The two-electron quinone gate, Q_B

As discussed in the previous section, H_A^- most likely reduces Q_A directly. Under normal conditions Q_A is a one-electron acceptor (see Crofts and Wraight 1983, Mathis and Rutherford 1987). The formation of Q_A^- is not accompanied by a protonation of the semiquinone. Instead, the electron is transferred to Q_B , which occurs in the 100–200 μ s timerange. Although a proton uptake may be associated with the formation of Q_B^- , the protonation event most likely occurs at a protein group close to the Q_B site and not on the semiquinone. Upon the second reduction to Q_B^{2-} , which occurs in the 400–500 μ s timerange, a true protonation occurs, forming bound plastoquinone (Q_BH_2). Since the

binding affinity for Q_BH_2 is low, another PQ molecule from the pool can readily displace it.

A certain proportion of Q_B^- (ca. 30%) is stable in the dark. The loss of Q_B^- , when not driven forward by the light reactions, occurs via charge recombination with the M component. For M in the S_2 and S_3 states, this recombination reaction occurs with half-life times of about 30 s (Rutherford et al. 1984), while for M in the S_1 state the loss of Q_B^- takes hours (Hide and Demeter 1985).

The unique electron transfer events that take place at the Q_A and Q_B sites depend upon the special binding of the PQ molecules to the protein. The PQ molecules at both the Q_B (Wydrzynski and Inoue 1987) and the Q_A (Diner et al. 1988) sites can be extracted and replaced with other quinone molecules, leading to altered acceptor-side properties. There is a wealth of literature to show that many herbicides interact with PS II at the Q_A/Q_B level (see Renger 1986). Indeed, radioactively labelled herbicides were originally used to tag the D1 protein and identify it as the location of the Q_B site (see Böhman et al. 1987). Upon addition of a herbicide inhibitor, such as DCMU, electron transfer from Q_A to Q_B is blocked. It is thought that the inhibitor molecule binds at or close to the Q_B site in competition with PQ binding, although recent evidence suggests that there may be two herbicide binding sites in the Reaction Core (Hsu et al. 1986, Giardi et al. 1988, Vasil'ev et al. 1988). Nevertheless, in the presence of an inhibitor, with Q_B in the semiquinone state, a reverse electron transfer back to Q_A takes place, i.e. $Q_A Q_B^- + \text{inhibitor} \leftrightarrow Q_A^- (\text{inhibitor}) + \text{PQ}$. The lifetime of Q_A^- under this condition depends upon the availability of the oxidizing charges on the M component (Koike et al. 1986).

Closely associated with Q_A and Q_B is a non-heme Fe^{2+} ion which interacts magnetically with the semiquinones, rendering them EPR invisible at room temperature. However, the non-heme iron is detectable by Mössbauer spectroscopy (see Diner and Petrouleas 1988). At low temperatures, EPR signals similar to the FeQ signals from purple bacteria can be seen at $g = 1.8$ and 1.9 (see Rutherford and Zimmermann 1984). In a thermophilic cyanobacterium, an unusual signal at $g = 1.6$ was observed in addition to the $g = 1.8$ signal (McDermott et al. 1988). In contrast to the purple bacteria, the Fe^{2+} in PS II can be oxidized (e.g. by

ferricyanide), giving rise to an Fe^{3+} EPR spectrum with g -values at about 8 and 5.5 (Petrouleas and Diner 1986, Zimmermann and Rutherford 1986, Aasa et al. 1988). The Fe^{3+} EPR signal disappears when the sample is illuminated. Redox titrations give a midpoint potential of 400 mV for the $\text{Fe}^{2+}/\text{Fe}^{3+}$ redox couple. This value correlates well with the midpoint potential of a component, termed Q_{400} , that has been proposed to accept electrons directly from Q_A^- in a DCMU-insensitive path (see Diner and Petrouleas 1988). It has been demonstrated that flash-induced semiquinones of some exogenous quinone acceptors (such as phenyl-*p*-benzoquinone) bound at the Q_B site can also oxidize the iron to Fe^{3+} . This reductant-induced oxidation of the Fe^{2+} follows a periodicity of two in a sequence of flashes (Zimmerman and Rutherford 1986).

Bicarbonate has a major effect on the acceptor side of PS II (see van Rensen and Snel 1985, Govindjee and Eaton-Rye 1986, Blubaugh and Govindjee 1988a). In the absence of HCO_3^- , electron transfer from Q_A to Q_B is slowed down, although this effect may be induced by formate which is used in the HCO_3^- depletion procedure (Jursinic and Stemler 1986). In any event, under HCO_3^- -depleting conditions (using formate) the reduction of Q_{400} or its ability to form is slowed down, the oxidation of the Fe^{2+} ion is blocked and changes occur in the environment surrounding the Fe^{2+} ion, as determined by Mössbauer spectroscopy (see Diner and Petrouleas 1988). Although there appears to be several sites at which HCO_3^- can bind in PS II (see Blubaugh and Govindjee 1988b), one of these sites has recently been suggested to be the Fe^{2+} ion, involved in the protonation of Q_B^{2-} (van Rensen et al. 1988, Eaton-Rye and Govindjee 1988, Blubaugh and Govindjee 1988a, B. Diner, personal communication).

Although the Fe^{2+} ion may assume an important function on the acceptor side, it is too premature at this time to assign an exact function. It may only contribute in optimizing the conformation of the acceptor side. For example, replacement of the Fe^{2+} ion in purple bacteria with any number of divalent transition metal does not significantly alter the rate of electron transfer from Q_A to Q_B (Debus et al. 1986).

Numerous types of acceptor-side heterogeneity have been reported in the literature (see Black et al.

1986). This heterogeneity has been variously described in terms of non-B-type acceptors, Q_1 , Q_2 , X_a and, more recently, A_q (Jursinic and Dennenberg 1988). The non-B-type acceptors may be associated with PS II β units which are believed to be located in the non-appressed regions of the membranes (see Section 2.5). The very high midpoint potential measured for these acceptors (higher than that for the PQ pool) would correlate with the lack of characteristic period-two oscillation. Recently, analyses of O_2 and delayed-fluorescence flash-yield patterns reveal two different types of period-four behavior which may be related to the different acceptor-side properties of PS II α and β units (Delrieu and Rosengard 1988). The other cases of acceptor heterogeneity represent proposed additional acceptor components in PS II prior to Q_B . This acceptor heterogeneity, however, may be a consequence of experimental conditions and/or inhomogeneous PS II samples. Certainly, it is known that various extents of damage occurs on the acceptor side among different PS II preparations (see Section 2.5). Clarification of acceptor-side heterogeneity will most likely require further biochemical advances to produce well-defined and homogeneous PS II preparations.

3.3. Electron transfer via the tyrosine components, Y_Z and Y_D

The oxidized form of Y_Z (the physiological electron donor to P^+ as depicted in Fig. 1) was originally identified as a light-induced kinetic component of the well-known EPR Signal II (see Babcock 1987). In intact, O_2 -evolving PS II preparations it is designated as the organic radical giving rise to the flash-induced Signal II_{very fast}. A chemically identical, though separate, organic radical giving rise to the dark-stable Signal II_{slow} is designated as Y_D in Fig. 1. At first, these organic radicals were thought to be specially bound plastoquinone cations (O'Malley and Babcock 1984) and considerable amount of spectroscopic evidence was used to support this assignment (Dekker et al. 1984b, O'Malley et al. 1984, Rutherford 1985, Brok et al. 1985, Brok et al. 1986). However, quantitation of the plastoquinone content of PS II preparations revealed too few plastoquinone molecules present to account for all the proposed quinone com-

ponents on both the oxidizing and reducing sides (Takahashi and Katoh 1986, de Vitry et al. 1986). This conflict led to a re-evaluation and to the current assignment of Signal II as oxidized forms of tyrosine (Barry and Babcock 1987, 1988). Subsequent studies using site-directed mutagenesis (Debus et al. 1988a, Vermaas et al. 1988a) appear to establish firmly that Signal II_{slow} arises from the oxidized form of Tyr160 in the D2 subunit. Optical (Gerken et al. 1988) and EPR (Hoganson and Babcock 1988, 1989) evidence have since strongly indicated that Signal II_{very fast} also arises from an oxidized form of tyrosine. More recent site-directed mutagenesis studies indicate that it is Tyr161 in the D1 subunit (Debus et al. 1988b, B. Diner, personal communication).

The reduction of P⁺ during normal electron transport in PS II must necessarily be fast since charge recombination of P⁺Q_A⁻ occurs in about 100 μs (see Conjeaud and Mathis 1986). The reduction kinetics of P⁺ are quite complex, being multiphasic and dependent upon the S states. Based on optical kinetic measurements, for the S₀ and S₁ states, P⁺ is reduced with a major phase at about 20 ns and a minor phase of 35 μs and for the S₂ and S₃ states, with major phases at about 50 and 250 ns and again a minor phase at 35 μs (Brettel et al. 1984). The S-state dependence of the submicrosecond kinetics can be understood in terms of coulombic effects of the charge stored on M, but the origin of the slow 35 μs kinetics (whose amplitude is also S-state dependent) is still controversial (see van Gorkom 1985).

Due to kinetic limitations ($\geq 2 \mu\text{s}$) in early studies using time-resolved EPR and UV spectroscopy to monitor Y_Z⁺ directly (Boska and Sauer 1984, Dekker et al. 1984b, Weiss and Renger 1986), it was difficult to show that the oxidation kinetics of Y_Z followed directly the reduction kinetics of P⁺. The uncertainty in the oxidation kinetics of Y_Z left open the possibility that another component could exist between Y_Z and P. Indeed, the biphasic nanosecond reduction kinetics for P⁺ in the S₂ and S₃ states were interpreted to indicate that another component did exist (Brettel et al. 1984). With recent improvements in time resolution to the nanosecond time range for UV measurements, the oxidation kinetics of Y_Z was shown to follow exactly the reduction kinetics of P⁺ (Gerken et al. 1988). The biphasicity in the reduction kinetics of

P⁺ was reinterpreted to indicate different protonation states of M. Recent results using improved time-resolved EPR also support the above UV results (Hoganson and Babcock 1988). Thus, it is generally agreed that Y_Z is the immediate electron donor to P⁺.

Upon elimination of O₂ evolution, the kinetics of P⁺ reduction is altered from the ns to the μs time range, with half-lifetimes dependent upon the experimental conditions. In Tris-treated samples, for instance, after the first excitation following dark-adaptation, the P⁺ reduction kinetics exhibit pH-dependent half-lifetimes of 2–40 μs due to electron donation from the oxidizing side. In subsequent flashes, P⁺ becomes reduced through a recombination with Q_A⁻ having a half-lifetime of 120 μs (Conjeaud and Mathis 1986). Similar treatments to inhibit O₂ evolution convert EPR Signal II_{very fast} to the so-called Signal II_{fast}, which has identical spectral characteristics but a slower rise kinetics (Boska et al. 1983, Bock et al. 1988, Hoganson and Babcock 1989). The rise kinetics correlate with the P⁺ reduction kinetics (Conjeaud and Mathis 1986, Weiss and Renger 1986, Bock et al. 1988). Thus, it seems likely that Y_Z donates electrons directly to P⁺ under these conditions as well.

Although Y_D is now chemically identified, its role in PS II is obscure (see Mathis and Rutherford 1987). The kinetics of formation and disappearance of Y_D⁺ are far too slow to have a direct role in the main electron transport sequence. However, evidence has been provided that Y_D can donate electrons to M in the S₂ and S₃ states after 1 or 2 light flashes (see Vermaas et al. 1984) while Y_D⁺ can accept electrons from M in the S₀ state in the dark (Styring and Rutherford 1987, Nugent et al. 1987). The specific modification of the Tyr160 in the D2 subunit by site-directed mutagenesis reduces the photoautotrophic growth of the cyanobacterium, although the number of intact PS II units in the mutants remained normal with respect to the wild type (Vermaas et al. 1988a). This suggests that an intact Y_D may be needed for PS II O₂ evolution.

3.4. The four-electron oxygen gate, M

3.4.1. Manganese requirement

In Section 1 we defined M as that component which governs the S states, i.e. as electrons are sequen-

tially extracted from M, PS II advances to the next higher S state. In the main path of electrons through PS II the reduction kinetics of Y_2^+ (as well as of P^+ — see above) are modulated by the S-state turnover. The half-lifetimes for the S-state transitions of M as determined by UV measurements (Dekker et al. 1984c, Renger and Weiss, 1986, Saygin and Witt 1987) are: S_0 to S_1 , 30–50 μ s; S_1 to S_2 , 40–110 μ s; S_2 to S_3 , 100–350 μ s; S_3 to S_4 to S_0 , 1.0–1.5 ms. The kinetic parameters for Y_2^+ reduction are: S_0 to S_1 , \approx 50 μ s; S_1 to S_2 , \approx 50 μ s; S_2 to S_3 , 400–600 μ s; S_3 to S_4 to S_0 , 1–1.3 ms (Boska and Sauer 1984, Cole and Sauer 1987). Thus, it seems clear that Y_2^+ is reduced directly by the M component. There is some recent evidence to indicate a transitory state (that is not photo-induced) between S_2 and S_3 (Koike and Inoue 1987). Such a state was originally described by Bouges-Bocquet (see Wydrzynski 1982). The final S_3 to S_4 to S_0 transition is taken to be rate-limited by electron transfer (see Babcock 1987); however, it has recently been suggested that O_2 release (and not water oxidation) may be the overall rate-limiting step (Plijter et al. 1988) [see also (Meunier and Popovic 1988)].

Upon perturbation or removal of the manganese from PS II, the S-state dependence in Y_2^+ reduction, as well as all other period-four phenomena, is lost. Since manganese is a transition metal that can take on a number of oxidation states, functionally bound manganese in PS II has long been associated with the redox reactions involved in the M component (see Ames 1983, Babcock 1987). Despite extensive studies, the exact location and functional operation of the manganese is still under considerable debate. It is generally agreed, however, that (1) stoichiometrically, four Mn ions are associated with each PS II unit, (2) at least some of the Mn ions are arranged in a multinuclear cluster, (3) valence state changes of the Mn ions are associated with the S-state transitions, and (4) the Mn ions are located within a restricted compartment towards the luminal side of the membrane.

The manganese stoichiometry has been determined by various extraction procedures (Yocum et al. 1981). For example, upon removal of the Regulatory Cap by treatment with $CaCl_2$, urea or $LaCl_3$, there is a variable release of the functional manganese (10–50%) depending upon the ionic conditions used during the extraction (Ono and Inoue 1984a, Miyao and Murata 1984a, b,

Kuwabara et al. 1985, Ghanotakis et al. 1985, Imaoko et al. 1986). However, when a reductant is included during the extraction procedure, up to 90% of the manganese is solubilized (Ghanotakis et al. 1984b, Tamura and Cheniae, 1985) and this amount corresponds to about four Mn ions per PS II unit. The release of either half or all of the manganese under different extraction conditions implies that there are at least two manganese binding domains. Such heterogeneity in manganese binding has been implied in other studies (Allakhverdiev et al. 1986, Takahashi and Asada 1986, Tamura and Cheniae 1987, Isogai et al. 1988).

3.4.2. Arrangement and valence changes of manganese

Several spectroscopic methods, including X-ray absorption spectroscopy (XAS), near-infrared optical absorption and EPR spectroscopy, have recently been employed for investigations of the structural organization of the manganese in PS II. The information provided so far strongly suggests that at least some of the four Mn ions are arranged in a cluster. The XAS results obtained by Klein, Sauer and coworkers have recently been summarized (Sauer et al. 1988) and the reader is referred to this review for further details and references. A μ -oxo-bridged binuclear structure with a Mn–Mn distance of 2.70 Å was found to be consistent with the data, although more recent data does not exclude other types of bridging structures (George et al. 1989). A feature identified in a preliminary report as possible evidence for a second Mn–Mn distance of > 3 Å (Guiles et al. 1987) has been shown to exhibit significant dichroism (George et al. 1989). Simulations indicate that tetranuclear cubic (Brudvig and Crabtree 1986) or ‘butterfly’ (Vincent and Christou 1987) structures are unlikely to be present, while binuclear, trinuclear or highly distorted tetranuclear structures are all still possible (McDermott et al. 1988, George et al. 1989). The rapid development of model manganese complexes (Sheats et al. 1987, Bhula et al. 1988, Kulawiec et al. 1988, Matsushita et al. 1988, Wiegardt et al. 1988) should in the future help to clarify the organization of the Mn in PS II.

The XAS data also indicates that the ligands in the first coordination shell surrounding the Mn in PS II are light elements, predominantly O and N. A

study of an O₂-evolving PS II preparation from the thermophilic cyanobacterium *Synechococcus* sp. revealed that the Mn environment in this organism is very similar to that seen in spinach PS II (McDermott et al. 1988). No changes in the fine structure of the XAS spectra were found to accompany the S₁ to S₂ to S₃ transitions, indicating that no significant rearrangement of ligands occurs on these steps. However, for a state analogous to S₀, obtained by illumination of a NH₂OH-treated sample, indications of structural changes were found (see Sauer et al. 1988).

S-state-associated absorbance changes in the near IR have been observed in O₂-evolving PS II-enriched membranes from spinach (Dismukes and Mathis 1984). The absorption spectrum associated with the S₂ and S₃ states (see Dismukes 1986) was strikingly similar to intervalence charge-transfer bands observed for the Mn₂(III, IV) mixed-valence state in synthetic binuclear Mn complexes. However, in a subsequent study, only a much weaker absorption band could be seen. Based on theoretical considerations it was suggested that the observed absorption change could result from scattering changes (Velthuys 1988).

Two different light-induced EPR signals can be detected from the M component, a multiline signal centered at $g \approx 2.0$ and a featureless signal at $g = 4.1$ (see Dismukes 1986, Brudvig 1988). Most probably, both can be ascribed to manganese, as suggested from spectral similarities with low-molecular weight complexes and from correlations between their appearance and changes in the manganese X-ray absorption region (Goodin et al. 1984, Cole et al. 1987a). They are both associated with the S₂ state of M, as demonstrated from their oscillating behavior as a response to light flashes (Dismukes and Siderer 1981, Zimmermann and Rutherford 1986). Also, the disappearance of the multiline signal was shown to correlate with the decay of the S₂ state (Brudvig et al. 1983, Styring and Rutherford 1988b).

The multiline signal was originally assigned to a mixed-valence cluster of Mn ions (Dismukes and Siderer 1981). A single Mn ion can be ruled out from the lack of large-scale anisotropies in the signal (Hansson et al. 1984, 1987). Although small signal anisotropies can be detected (Rutherford 1985a), especially at a lower microwave frequency (Haddy et al. 1989), this will not alter the conclu-

sion. Recent magnetic susceptibility data also rule out a single Mn ion (Sivaraja et al. 1989). Spinach grown on ¹⁵NO₃ showed a normal multiline signal, suggesting the absence of nitrogen in the first coordination sphere (Andréasson 1989). Temperature studies show that both the multiline (Hansson et al. 1984) and the $g = 4.1$ signals (de Paula et al. 1986) arise from ground state doublets. A recent proposal that the multiline signal may arise from an excited state doublet (de Paula et al. 1986) has not been confirmed (Hansson et al. 1987, Aasa et al. 1987, D. Stehlik, personal communication).

To account for the appearance of the EPR signals, two alternative models for the arrangement of the manganese in M have been proposed. The EPR signals may either arise from two different conformations of a tetranuclear Mn cluster (de Paula et al. 1986, Zimmermann and Rutherford, 1986b) or from a bi(tri)nuclear mixed-valence Mn complex (the multiline signal) in redox equilibrium with a monomeric Mn⁴⁺ ion (the $g = 4.1$ signal) (Hansson et al. 1987). A definitive conclusion does not seem possible based only on the presently available EPR data. Recently it was suggested that the $g = 4.1$ signal arises from an inactive conformation of M (Beck and Brudvig 1988). However, no correlation was found between the magnitude of this signal, abolished by small amounts of ethanol, and the steady-state or flash-induced O₂ evolution (L.-E. Andréasson, personal communication).

The appearance of the multiline EPR signal shows that the Mn ions have a mixed valence in the S₂ state but a definitive assignment of oxidation states is difficult. The lack of EPR signals from the other S states may be taken as evidence for oxidation-state changes of manganese, although other interpretations are possible. Whereas S₁ and S₃ might be difficult to detect since they are even-electron systems, it should be possible to observe S₀ and S₄. S₄ is too short-lived; for S₀, structural rearrangements may weaken the magnetic interactions, rendering the EPR signals highly anisotropic and difficult to detect. Such a rearrangement may also explain why, at low chloride concentrations, no multiline signal can be seen, although an apparent S₂ state may be attained (Ono et al. 1986).

Studies of the X-ray absorption-edge energies suggested an increase in the manganese oxidation state for an analogue S₀ state (see above) to S₁ and for the S₁ to S₂ but not for the S₂ to S₃ transitions

(see Sauer et al. 1988). Similar conclusions have also been drawn from studies of the relaxation properties of protons (Srinivasan and Sharp 1986a, b) and EPR Signal II_{slow} (Y_D^+) (Styring and Rutherford, 1988a). It is not clear where the additional oxidizing equivalent in S_3 resides, but it may be sufficiently close to the Mn ions to make the EPR signals disappear (Goodin et al. 1984).

A part of the flash-induced absorption changes in the UV region can be ascribed to the M component based on a characteristic period-four oscillation pattern. In one study, it was suggested that the absorption changes reflected Mn^{3+} to Mn^{4+} oxidations on all S-state transitions from S^0 to S_3 (Dekker et al. 1984a). The analysis of the data is complicated by interfering contributions from the acceptor side quinones (see Renger and Hanssum 1988) and several different interpretations exist. However, there now seems to be an agreement that the absorption change from the S_0 to S_1 transition is different from those due to the S_1 to S_2 and S_2 to S_3 transitions (Lavergne 1987, Saygin and Witt 1987, Kretschmann et al. 1988).

Taken together, the presently available spectroscopic data now seem to support that manganese is oxidized on the S_0 to S_1 and S_1 to S_2 transitions. However, it is still controversial whether the manganese is oxidized on the S_2 to S_3 transition. No information is available for the S_3 to S_4 transition. The XAS data suggest that manganese is predominantly in the +3 oxidation state in the S_1 state. This is consistent with the manganese extraction experiments (see previous subsection), which suggest that at least part of the manganese is stabilized in oxidation states higher than +2 in the dark, and with the general observations that manganese needs to be photoactivated (photooxidized) in order to be incorporated into its functional site (Callahan and Cheniae 1985, Callahan et al. 1986, Tamura and Cheniae 1987, Ono and Inoue 1987).

3.4.3. Protein interactions

The protein environment is essential for the overall water-oxidation reaction. Thus, the EP 33 of the Regulatory Cap is known to shield the manganese center and has also been called the 'manganese-stabilizing protein' (Kuwabara et al. 1987, Tyagi et al. 1987, Philbrick and Zilinskas 1988). However, perturbations to the Regulatory Cap can lead to various extents of inhibition of O_2 evolution (40–

95%) without necessarily changing the properties of manganese. For example, removal of the Regulatory Cap proteins under high ionic conditions has no effect on the manganese environment as determined by XAS measurements (Cole et al. 1987b), does not prevent the formation of the S_2 -state multiline EPR signal (Styring et al. 1987) and allows S-state turnover to occur up to S_3 (Ono and Inoue 1985, Vass et al. 1987), yet O_2 evolution is low or non-existent (depending upon the ion conditions) (Kuwabara et al. 1985, Tang and Satoh 1986, Ono and Inoue 1986) and the rate of O_2 release is markedly slowed down (Miyao et al. 1987). Recently, it has been shown that the two conserved cysteines in the EP 33 (Kuwabara et al. 1987, Philbrick and Zilinskas 1988) form a disulfide bridge which upon reduction alters the conformation such that the protein cannot bind and activate O_2 evolution (Tanaka and Wada 1988). Reoxidation of the reduced protein will subsequently lead to binding and restoration of O_2 activity. Mutational analysis of the cyanobacterial *Synechocystis* 6803 strain shows that the EP 33 is required for O_2 evolution activity and photoautotrophic growth (Philbrick and Zilinskas 1988).

Calcium and chloride are generally taken to be cofactors for PS II and are closely associated with the function of the Regulatory Cap proteins (see Critchley 1985, Homann 1987, Boussac and Rutherford 1988). Under certain conditions, removal of the EP 16 and EP 23 reduces the O_2 evolution activity by as much as 50%, but this loss in activity can be restored by the readdition of sufficient amounts of calcium and/or chloride. Such results indicate that the EP 23 regulates the binding affinities for these ionic cofactors (Andersson et al. 1984a, Ghanotakis et al. 1984a, Boussac et al. 1985). However, the nature of the calcium and chloride binding sites are still obscure and a matter of much controversy.

It is generally assumed that calcium has a specific structural role and it now seems that there are two Ca atoms tightly bound per PS II unit (Cheniae 1988, Ono and Inoue 1988a). At least one of these Ca atoms is essential for O_2 evolution activity (Ono and Inoue 1988a, Boussac and Rutherford 1988). A Ca^{2+} -binding, calmodulin-like protein with an apparent molecular mass of 13–15 kDa (but is not EP 16) has been isolated from PS II preparations (Sparrow and Evans 1984) while a Ca atom appears

to be associated with CP 29, a component of the ACP II (K. Irrgang, personal communication). However, there are many different opinions as to where the Ca^{2+} ions interact in the reaction sequence (i.e. on which S-state transition) (see Boussac and Rutherford 1988). Part of the controversy may be explained by the recent observation that the standard procedure for removing calcium from the sample (by extracting the EP 23 and subsequent EGTA treatment) does not actually remove the two tightly bound Ca^{2+} ions, despite the fact that addition of CaCl_2 to these samples increases O_2 evolution activity (Shen et al. 1988). Treatment of intact samples with chelators may influence the observed O_2 evolution (Wydrzynski and Renger 1986), which may occur through membrane surface charge effects on the oxidizing side (Dreschler and Neumann 1987).

Likewise, there are considerable controversies over where Cl^- ions interact in the reaction sequence (Itoh et al. 1984, Theg et al. 1984, Preston and Pace 1985, Imaoka et al. 1986, Damoder et al. 1986, Homann et al. 1986, Ono et al. 1986, Pistorius and Schmid 1987, Vass et al. 1987, Ono et al. 1987). The number of chloride binding sites is unknown, although there appears to be several (Sandusky and Yocum 1986, Coleman et al. 1987). However, the number of anion binding sites should not be based only on steady-state O_2 evolution or Hill-reaction measurements (Jursinic and Stemler 1988). Recently, a chloride binding site has been associated in close proximity to an iodination site on the D1 subunit (Ikeuchi et al. 1988).

Unlike the calcium requirement, the chloride requirement is not specific since other anions can replace chloride (in the order $\text{Cl}^- > \text{Br}^- \gg \text{NO}_3^- > \text{I}^-$). Generally, in order to observe a chloride dependence on O_2 evolution, samples must be pre-treated with high concentrations of sulfate and/or high pH, conditions which are likely to complicate the interpretations of the results. Alkaline pH treatment, for example, may have both reversible and irreversible effects (Cole et al. 1986, Vass et al. 1985, 1986, Schlodder and Meyer 1987) while sulfate effects may be variable depending upon the presence of EP 33 (Vass et al. 1987).

There are several suggestions that chloride ligates to the manganese ions directly and that this accounts for its effect on O_2 evolution activity (Critchley and Sargesson 1984, Damoder et al.

1986, Sandusky and Yocum 1986). However, there has been no direct evidence from XAS (see Sauer 1988) or the S_2 -state multiline EPR measurements (Yachandra et al. 1986, Haddy et al. 1989) to indicate that chloride ligates to the manganese ions. In another hypothesis, chloride that is located in the proteinaceous compartment surrounding the manganese center facilitates deprotonation of the substrate H_2O molecules (Coleman and Govindjee 1987). This was based on pH-dependence studies which indicated a competitive behaviour between OH^- and Cl^- ions. However, changes in pH were recently found to have additional effects on the EP 23 (Homann 1988a, b). In view of the complications, it may be that many chloride effects are expressed indirectly through electrostatic interactions (Itoh and Uwano 1986) that alter protein conformations which affect the water-oxidation chemistry (Homann 1988c).

In the organization of PS II as depicted in Fig. 1, the Regulatory Cap forms a barrier between the manganese and the aqueous phase. Oxygen-17 (Wydrzynski et al. 1978) and proton (Sharp and Yocum 1980) NMR water relaxation measurements indicate that water exchange across the thylakoid membrane is slow (1–2 ms). Likewise, it has been found that the accessibility of exogenous electron donors to the manganese center, such as H_2O_2 , NH_2OH and NH_2NH_2 , increases when the Regulatory Cap is perturbed by the removal of the EP 23, EP 16 and/or EP 33 proteins (Ghanotakis et al. 1984b, Schröder and Åkerlund 1986, Berg and Seibert 1987, Frasch and Mei 1987, Mano et al. 1987). The Regulatory Cap may, in part, serve to control the exchange of reactants with the manganese center. This could be an advantage for the intact system to allow water to react only at the appropriate step so as to produce oxygen rather than other, potentially destructive water-oxidation intermediates.

3.4.4. Site of water-oxidation

Of fundamental importance for understanding the mechanism of water oxidation is a detailed knowledge of the electronic distribution and nuclear geometry within the M component among the various S states. The above sections clearly show that manganese is a central constituent. However, the oxidizing equivalents need not be restricted to

the manganese ions themselves, but could be located on redox active ligands, including water-oxidation intermediates, or on more distant redox groups within the protein matrix.

It is generally assumed that the manganese ions form the matrix on which two water molecules meet to form the dioxygen bond. Two lines of evidence based on the use of water analogues and isotopically labelled water indicate that water binds directly to manganese. Ammonia, which is isoelectronic with water, inhibits O₂ evolution and dramatically alters the S₂-state multiline EPR signal (Beck et al. 1986). Subsequent electron spin echo studies do show that ammonia binds directly to manganese in the S₂ state (Britt et al. 1989). However, EPR measurements also indicate that, although ammonia binds at two sites in both the S₁ and S₂ states, in neither state does the binding account for the observed inhibition of O₂ evolution (Andréasson et al. 1988). Rather, there is a separate NH₃ interaction on the S₃ to S₄ to S₀ transition (Ono and Inoue 1988b). It has been reported that the ammonia-induced modification of the S₂-state multiline EPR signal can be mimicked by Sr²⁺ ions, an unlikely water analogue (Boussac and Rutherford 1988).

In the second line of evidence, the linewidth of the S₂-state multiline EPR signal is found to increase with H₂¹⁷O, indicating that oxygen ligates directly to the manganese center, interpreted either as peroxide, hydroxide or water itself, but not as superoxide or hydroxyl (Hansson et al. 1986, Andréasson et al. 1988). However, the isotope exchange conditions are not well-defined and it has been shown, for example, that μ -oxo bridges in iron complexes can undergo relatively fast isotopic exchange (Lippard 1988). In addition, the ¹⁷O isotopic effect on the S₂-state multiline EPR signal are still observed in the presence of ammonia, which would suggest that there is at least one site in which ammonia and water do not compete with each other (Andréasson and Hansson, 1987, Andréasson et al. 1988). Line broadenings induced by D₂O have also been reported (Nugent 1987), but the effects are not easily reproducible (Yachandra et al. 1986, Haddy et al. 1989).

In general there are two views on how the water oxidation chemistry occurs, either as a concerted reaction on the S₃ to S₄ to S₀ transition or in a stepwise reaction which involves a bound water-

oxidation intermediate formed prior to the S₃ to S₄ to S₀ transition. From a thermodynamic analysis, it has been argued that either two two-electron steps or one four-electron step are more likely than four single-electron step reactions (Krishtalik 1986). In the original Kok hypothesis, water could bind during any step in the S-state cycle, but water oxidation occurred as a concerted reaction on the final S₃ to S₄ to S₀ transition. Evidence has been obtained to support this view based on mass spectroscopic measurements using ⁸O-labelled water. It was concluded that no non-exchangeable, partially oxidized water species are formed in the lower S states (Radmer and Ollinger 1986, Bader et al. 1987). Likewise, UV flash absorption measurements indicate a sequential oxidation of the manganese center through the S₃ state and an extraction of four electrons from two bound water species on the final S₃ to S₄ to S₀ transition (Saygin and Witt 1987). In this model, as in other (e.g. see Brudvig 1988), the concerted mechanism involves a peroxide-type intermediate during the O–O bond formation step.

In contrast to the view of a concerted reaction, several models consider that water molecules bound to the manganese center become partially oxidized (usually, for energetic reasons, to peroxide-type intermediates) particularly in the S₃ state (see Renger and Govindjee 1985). The measured proton release from the oxidizing side of PS II is known to be modulated in a pattern of 1, 0, 1, 2 as the S-state cycle progresses from S₀ to S₄ (see Förster and Junge 1985). Similarly, an intrinsic proton release interpreted from flash-induced electrochromic measurements yields the same stoichiometry (Saygin and Witt, 1985). In the past, the proton release pattern has been used to support the partial oxidation of water during the S-state cycle. However, the measured proton release in the early S-state transitions may only arise from the dissociation of bound water molecules (Saygin and Witt 1987) or from membrane Bohr effects (Chandrasekar et al. 1986) or conformationally controlled proton transport processes (Renger et al. 1987) that are only indirectly coupled to the water-oxidation chemistry. On the other hand, the XAS and magnetic relaxation studies (see Section 3.4.2) which indicate that the manganese center is not sequentially oxidized through the entire S-state cycle, also has been used to support a stepwise

water-oxidation reaction. But in these measurements the ligand-centered redox chemistry that is implied need not necessarily involve bound water, but could be mediated through other ligands (Matsushita et al. 1988) often suggested to be redox active ligands of the protein matrix (Goodin et al. 1984, Renger 1988) such as histidines (Padhye et al. 1986). The water oxidation mechanism, therefore, still remains largely unknown.

Several reports have indicated that under certain inhibitory conditions (Wydrzynski et al. 1985, Eckert et al. 1988) and in certain sample preparations (Frei et al. 1988) [including salt-washed PS II samples where the EP 23 and EP 16 have been removed (Ono and Inoue 1984b)] electron flow through PS II after multiple turnover can be greater than what is accounted by the measured oxygen yield. A similar situation has recently been found in PS II samples suspended under low osmotic conditions (Wydrzynski et al. 1988). In this case [as well as possibly for salt-washed PS II samples (Schröder and Åkerlund 1986)] H_2O_2 appears to be formed, presumably via reactions on the oxidizing side of PS II. The possible production of H_2O_2 by PS II could imply that the M component is perturbed by these treatments in such a way that it leads to the release of partial water oxidation intermediates rather than oxygen.

4. Prospects for future research

Certainly, there have been many significant advances in PS II research in the last few years, which have led to our current perceptions of PS II structure and function. There remain, however, several important problems which will need to be addressed in the future. Some of the areas for future research are listed as follows:

- (1) There is a need for a Reaction Core preparation which maintains a functional O_A . This is important not only to establish the primary photochemistry, but also to unequivocally identify the location of all Reaction Core components.
- (2) The role of the CP 47 needs to be clarified. Why, for example, does it appear to be essential for Q_A function as well as O_2 evolution if it does not bind any of the reaction components?
- (3) The role of cyt *b*559 needs to be determined.

This component must be tightly coupled to the Reaction Core for some reason.

(4) The protein matrix has become recognized as extremely important for the PS II reaction sequence. It will be necessary to know in the future whether redox active sites other than Y_Z and Y_D are also located in the protein matrix and how protein dynamics ultimately regulate PS II function.

(5) The role of the calcium and chloride cofactors needs to be clarified. It remains to be demonstrated whether these cofactors have a specific interaction in the reaction sequence or whether their effects are mediated through protein conformation changes. In this area of research electrostatic effects as well as the lipid structure of the membrane must be taken into consideration.

(6) Finally, despite all recent major efforts, the location and redox chemistry of the manganese ions must be further clarified. In addition, where is the site of the water oxidation chemistry — does it actually take place on the manganese ions or does it occur at some other location in the complex?

The future promises to be both fruitful and exciting in PS II research.

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