

## Review

# Correlation of electron transfer rate in photosynthetic reaction centers with intraprotein dielectric properties

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## Abstract

A number of the electrogenic reactions in photosystem I, photosystem II, and bacterial reaction centers (RC) were comparatively analyzed, and the variation of the dielectric permittivity ( $\epsilon$ ) in the vicinity of electron carriers along the membrane normal was calculated. The value of  $\epsilon$  was minimal at the core of the complexes and gradually increased towards the periphery. We found that the rate of electron transfer (ET) correlated with the value of the dielectric permittivity: the fastest primary ET reactions occur in the low-polarity core of the complexes within the picosecond time range, whereas slower secondary reactions take place at the high-polarity periphery of the complexes within micro- to millisecond time range. The observed correlation was quantitatively interpreted in the framework of the Marcus theory. We calculated the reorganization energy of ET carriers using their van der Waals volumes and experimentally determined  $\epsilon$  values. The electronic coupling was calculated by the empirical Moser–Dutton rule for the distance-dependent electron tunneling rate in nonadiabatic ET reactions. We concluded that the local dielectric permittivity inferred from the electrometric measurements could be quantitatively used to estimate the rate constant of ET reactions in membrane proteins with resolved atomic structure with the accuracy of less than one order of magnitude.

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## 1. Introduction

The processes of charge separation in photosynthetic reaction centers (RC) and further transfer of electron and proton along the photosynthetic chain are accompanied by generation of transmembrane electric potential difference ( $\Delta\psi$ ) that can be detected using instrumental methods. The direct electrometric method suggested in our laboratory at the Belozersky Institute of Physical–Chemical Biology provided an opportunity to detect the rise-time of  $\Delta\psi$  within the range from 200 ns to 100 ms [1–3]. This method was used to study bacteriorhodopsin [2], bacterial photosynthetic RC [3], as well as photosystem (PS) I [4,5] and PS II [6] of cyanobacteria.

Because the photoelectric signal amplitude measured by this method is proportional to dielectrically weighted distances, comparison of projections of the distance vectors between redox cofactors onto the membrane normal with the relative photovoltage amplitudes allows the local effective (i.e., determined within the reaction time interval) dielectric constant value ( $\epsilon$ ) to be estimated at the corresponding chain segment. Dielectric properties have a great influence on the mechanism of photoinduced electron transfer reactions in photosynthetic complexes, and their studies could provide a deeper advance in quantitative treatment of charge transfer reactions in membrane proteins. RCs seem to be an ideal object for such study because their 3D structure has been resolved with atomic resolution using X-ray diffraction analysis, and electron transport activity can be tested by various instrumental methods including laser spectroscopy, EPR, ENDOR, photoelectric techniques, etc. Photoelectric and

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dielectric properties of RCs were considered in our earlier works [7–10]. The results of the studies are briefly summarized in Fig. 1. It follows from Fig. 1 that the value of  $\epsilon$  is minimal at the core of the three complexes and gradually increases towards the periphery.

## 2. Dielectric and photoelectric properties of photosynthetic reaction centers

### 2.1. Photosystem I

Photoelectric and dielectric properties of PS I were studied using isolated PS I complexes and such complexes interacting with natural and artificial electron donors and acceptors. The results of X-ray diffraction analysis of crystals of the protein complex of photosynthetic RC were taken from the Brookhaven Protein Databank (<http://www.rcsb.org/pdb>). Distances between centers of molecules were measured using the HyperChem 7 Professional software.

The PS I electron transport chain includes P700 (special pair of chlorophyll (Chl) molecules),  $A_0$  (one or the two Chl monomer molecules),  $A_1$  (one or the two molecules of phyloquinone), and  $[FeS]_4$  iron–sulfur clusters  $F_X$ ,  $F_A$ , and  $F_B$ . Taking into account the distances between the PS I cofactors [11] and the structural model of the plastocyanin (Pc) docking site [12,13], as well as relative contributions of the electron transfer reactions  $P700 \rightarrow A_0$ ,  $A_0 \rightarrow A_1$  [14],  $A_1 \rightarrow F_X$  [15, 16],  $F_X \rightarrow F_B$  [17],  $Pc \rightarrow P700$  [18], and  $F_B \rightarrow Fld$  (flavodoxin) [19]

to the overall electrogenesis provided by PS I complex, the following assertions were made:

- (1) Let the minimal value of the dielectric constant for the  $P700 \rightarrow A_0$  protein region be  $\epsilon \sim 3$ . Then, the  $\epsilon$  value for the  $A_0 \rightarrow A_1$  and  $A_1 \rightarrow F_X$  domains was estimated to be  $\sim 5.4$ .
- (2) On the acceptor side, the  $\epsilon$  value further increases nonmonotonically along the PsaC subunit ( $F_X \rightarrow F_A$ ,  $\epsilon \sim 8.7$ ;  $F_A \rightarrow F_B$ ,  $\epsilon \sim 4.8$ ).
- (3) On the donor side between the Pc binding site and P700 Mg-porphyrin rings embedded into the PsaA/PsaB heterodimer ( $Pc \rightarrow P700$ ), the mean  $\epsilon$  value is 9.7.

The estimates of  $\epsilon$  are qualitatively consistent with the pattern of distribution of water molecules and ionizable amino acid residues (Asp, Glu, Lys, Arg, and His) in the loci of the electron transfer chain (Table 1). The numbers of ionizable amino acid residues in the vicinity of the iron–sulfur clusters  $F_X$ ,  $F_A$ , and  $F_B$  (at distances  $< 11$  Å from each cluster), determined from the X-ray diffraction analysis of the PS I protein crystals, are 13, 15, and 3, respectively. With regard to the effect of compensation of closely located opposite charges (distance,  $< 3.5$  Å) [20], these numbers are 5, 9, and 3, respectively. Although the general trend towards an increase in the value of  $\epsilon$  along the direction from the primary pair to the periphery of the complex is valid in this case too, there is a deviation from this trend at the site  $F_A \rightarrow F_B$ , where distribution of water molecules and polar amino acid residues is abnormal. The cause of the anomaly is presently obscure.

### 2.2. Photosystem II

Recently determined crystal structures of PS II core complex from the cyanobacteria *Synechococcus elongatus* and *Thermosynechococcus vulcanus* [21–24] were resolved at 3.8 Å, 3.7 Å, and 3.0 Å resolution. It follows from these data that the arrangement of the electron transfer cofactors in PS II is rather similar to that in RCs of purple bacteria. The cofactors form two branches organized symmetrically along the pseudo-C2 axis. This symmetry is broken at the luminal side of D1 protein by the redox-active Tyr 161 ( $Y_Z$ ) and the manganese cluster  $[Mn]_4$ , which is located  $\sim 15$  Å off the pseudo-C2 axis.

The kinetics and the quantum yield of the primary charge separation in pea chloroplasts were studied using the light-gradient technique [25,26]. The charge separation in PS II occurs with two electrogenic phases: the faster phase with the rise-time  $< 50$  ps being ascribed to the electron transfer from the primary donor Chl dimer P680 to the intermediary acceptor pheophytin (Pheo), whereas the slower phase ( $\sim 500$  ps) being attributed to the electron transfer from Pheo to the primary quinone acceptor  $Q_A$ . The relative photovoltage contributions of the faster and slower phases were approximately equal to each other.

Fast photovoltage measurements using PS II membranes electrically oriented in a microcoaxial cell [27] and using PS II-containing proteoliposomes attached to a planar phospholipid

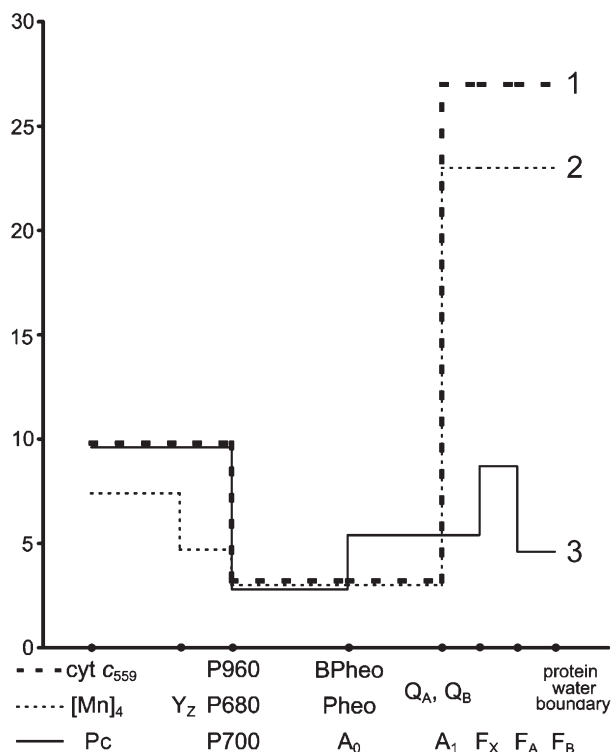


Fig. 1. Profile of changes of the effective dielectric constant  $\epsilon$  along the photosynthetic RC complex: (1) RC of *Blastochloris viridis*; (2) photosystem II; (3) photosystem I.

Table 1  
Distances  $d$  from iron–sulfur centers to closest polar amino acid residues and water molecules in PS I complexes

Iron– sulfur centers	Amino acid residues										Water				
	ASP (–)		GLU (–)		LYS (+)		ARG (+)		HIS (+ at pH=6.0)		Total <i>d</i> < 11 Å	Total <i>d</i> < 11 Å with regard to compensation	No.	<i>d</i> (Å)	Total
	No.	<i>d</i> (Å)	No.	<i>d</i> (Å)	No.	<i>d</i> (Å)	No.	<i>d</i> (Å)	No.	<i>d</i> (Å)					
F <sub>X</sub>	575	6.6	54 <sup>b</sup>	10.8	51 <sup>b</sup>	9.0	728 <sup>d</sup>	5.1			13	5	162	4.2	20
	579 <sup>a</sup>	8.3	62 <sup>a</sup>	14.2			712 <sup>c</sup>	5.6					43	5.3	
	566 <sup>b</sup>	8.6					694	9.4					12	5.3	
	593 <sup>d</sup>	8.6					674	9.6					190	6.0	
	580 <sup>c</sup>	9.2					583 <sup>a</sup>	9.7					73	6.3	
	568 <sup>a</sup>	14.2					570 <sup>b</sup>	10.5					37	6.4	
							65 <sup>b</sup>	11.2					67	6.4	
							52 <sup>a</sup>	12.0					6	6.6	
													26	6.9	
													145	7.0	
													36	7.0	
													56	7.4	
													132	8.1	
													64	8.3	
													76	8.4	
													160	8.4	
	F <sub>A</sub>	579 <sup>a</sup>	7.3	4 <sup>b</sup>	7.3	51 <sup>b</sup>	8.4	583 <sup>a</sup>	6.9	2			7.0	15	
23		8.3	62 <sup>a</sup>	8.1	5	8.9	52 <sup>a</sup>	7.7			188	8.7			
46 <sup>c</sup>		9.6	45	10.7			60	9.6			158	8.9			
568 <sup>a</sup>		11.3	71	10.7			43	9.9			157	9.2			
566 <sup>b</sup>		11.4					65 <sup>b</sup>	10.2			167	6.5			
							570 <sup>b</sup>	12.0			25	6.6			
							74 <sup>c</sup>	12.6			6.6	6.8			
											145	6.8			
											76	8.0			
											89	8.4			
											165	8.4			
F <sub>B</sub>	8	10.4	54 <sup>b</sup>	10.1	51 <sup>b</sup>	13.2	18	9.4			3	3	166	8.6	8
	566 <sup>b</sup>	13.4					65 <sup>b</sup>	11.4					34	8.8	
							570 <sup>b</sup>	11.7					119	9.4	
													120	10.4	
													182	6.9	
													126	7.1	
													183	7.6	
													82	7.8	
										184	9.0				
										81	9.5				
										167	10.0				
										148	10.6				

The structure file was taken from RCSB Protein Data Bank, PDB ID: 1JB0 [11]. Distance measurements were performed using VMD 1.7.1 software (Theoretical Biophysics Group, Beckman Institute for Advanced Science and Technology, University of Illinois).

Distance  $d$  from amino acid residue to iron–sulfur center was measured as the shortest distance between the charged residue and the closest iron atom of the center. Groups of residues compensating each other are denoted as: a: ASP 579, ASP 568, GLU 62, ARG 583, ARG 52; net charge – 1; b: ASP 566, GLU 54, LYS 51, ARG 570, ARG 65; net charge + 1; c: ASP 580, ARG 712; net charge 0; d: ASP 593, ARG 728; net charge 0; e: ASP 46, ARG 74; net charge 0.

membrane [6,28] showed that electron transfer from  $Y_Z$  to  $P680^+$  spanned a dielectrically weighted distance of 13–18% of the distance between P680 and  $Q_A$ . The dielectrically weighted distance of the electron transfer from  $[Mn]_4$  to  $Y_Z^{ox}$  ( $S_1 \rightarrow S_2$  state transition of the oxygen-evolving complex) was estimated to be less than 3.5% [28, 29]. Larger electrogenic components (about 7%) were attributed to proton transfer from the oxidized cofactor X to the lumen phase during the transition  $S_2 \rightarrow S_3$  [28].

As it was shown earlier, the charge transfer reaction associated with protonation of double-reduced secondary plastoquinone  $Q_B^{2-}$  at the acceptor side contributes about 5% to the overall electrogenesis in PS II [30,31]. However, this estimate represented the lower limit of the relative contribution of this reaction, because: (i) the reconstruction of the  $Q_B$  function in the PS II particles used in these experiments was incomplete and (ii) slow component of  $\Delta\psi$  decay (characteristic of the oxygen-evolving complex activity [32]) contributed only ~50% to the overall laser flash-induced  $\Delta\psi$  decay [30]. It was shown recently in our laboratory using PS II preparations, in which the contribution of the slow component of the  $\Delta\psi$  decay reached ~90%, that the amplitude of the electrogenic phase attributed to  $Q_B^{2-}$  protonation was ~11% of the total amplitude of  $\Delta\psi$  [33]. The distance between the  $Q_B$ -binding site and protein globule boundary in PS II complexes is smaller than in bacterial RC [24]. Therefore, it is safe to suggest that the dielectric properties in the  $Q_B$ -protein boundary domain of PS II are similar to that of bacterial RC.

Like in the case of the bacterial RC, the  $\epsilon$  value in the protein domain between the Chl dimer P680 and  $Q_A$  is the lowest, whereas it gradually increases at the donor side. A similar (but less significant) increase in the effective dielectric constant is observed at the donor side of PS II.

### 2.3. Bacterial reaction centers

Although the PS I complex differs significantly from the RC of purple photosynthetic bacteria, there are features of remarkable similarity between PS I and bacterial RC, especially in the RC core and the donor sites. It was shown in our earlier studies that electrogenic reduction of the photo-oxidized bacteriochlorophyll dimer P960 in *Blastochloris* (formerly *Rhodospseudomonas*) *viridis* RC by the immediate electron donor, high-potential cytochrome  $cyt\ c_{559}$ , and further electron transfer from the second high-potential  $cyt\ c_{556}$  to oxidized  $cyt\ c_{559}$  account for 15% and 5% of the overall photoresponse amplitude  $\Delta\psi$ , respectively [34]. The same relative photovoltages and effective dielectric constant values were obtained for the donor sites of the *Rhodospirillum rubrum* and *Rhodobacter sphaeroides* RC [35].

Comparison of the distance vector projections onto the membrane normal with the relative photovoltage amplitudes in PS I and bacterial RC demonstrated that the  $\epsilon$  values corresponding to the electron transfer from the native donor proteins to P700 and P960 (or P870 in case of the other bacterial RC species) were close to one another. Note that the electron transport reactions at the donor side of PS I and bacterial RC

share the following features of similarity: (i) Gibbs energy difference ( $\Delta G$ ) between Pc/cyt  $c_6$  and P700 is close to  $\Delta G$  between cyt  $c_2$  and P870; (ii) electron transfer kinetics and proposed reaction mechanisms are very similar.

The main electrogenic step on the acceptor side of bacterial RC is due to the protonation of the double-reduced secondary quinone  $Q_B$  [36]. The  $\epsilon$  value in this region is ~20 [37], which is about 3 times higher than that in the acceptor region of PS I. The profiles of dielectric constant distribution over electron transfer cofactors in bacterial RC, PS I, and PS II are shown in Fig. 1.

Because similar patterns of distribution of dielectric constant are observed at least in three photosynthetic systems with different structures, it is safe to suggest that such a character of dielectric constant distribution is a general property inherent in photosynthetic charge transfer processes rather than a unique characteristic of specific pigment–protein complexes.

Note also that the thermodynamic and kinetic properties of the terminal acceptors in bacterial RC complexes significantly differ from those in PS I. The redox midpoint potential ( $E_m$ ) values of the  $Q_A/Q_A^-$  and  $Q_B/Q_B^-$  redox couples in bacterial RC fall within the range from –50 to +100 mV, whereas the  $E_m$  values of  $F_X$ ,  $F_A$ , and  $F_B$  in PS I are much more negative (range from –500 to –700 mV). The lifetimes of the electron and proton transfer reactions on the acceptor side of bacterial RC (submillisecond time range) are at least three orders of magnitude lower than those values in the domain of the iron–sulfur clusters in PS I (range of tens to hundreds of nanoseconds). Perhaps, the three-order-of-magnitude difference between the rate constants of charge transfer on the acceptor side of bacterial RC and PS I, and threefold increase in the estimated value of  $\epsilon$  reflects hypothetical correlation between the reaction rates and the dielectric properties of the corresponding protein domains between redox cofactors suggested in our earlier works [7–10]. Indeed, the primary processes of electron transfer in photosynthesis are characterized by high rates (reaction time, from pico- to nanoseconds), low value of  $\epsilon$ , and large value of the free energy gap  $\Delta G$ . As the electron goes farther from the primary pair of Chl (or bacteriochlorophyll) molecules, the value of  $\epsilon$  gradually increases and reaction rate decreases.

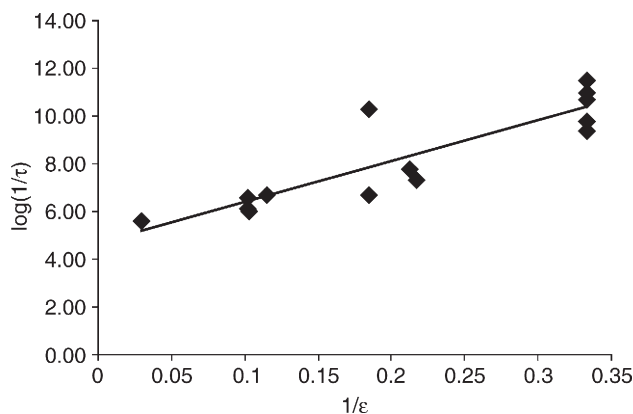


Fig. 2. Dependence of electron transfer rate constant on dielectric permittivity in photosynthetic RC complexes. The experimental points correspond to the donor–acceptor pairs listed in Table 2.

Quantitatively, correlation between dielectric permittivity and electron transfer rate constant is illustrated by empirical data summarized in Fig. 2. Let us consider possible mechanism of the correlation between kinetic and dielectric properties of reaction centers in more detail.

### 3. Possible mechanism of correlation between kinetic and dielectric properties of reaction centers

Electron transfer reactions in protein complexes occur from a donor ( $D$ ) to an acceptor ( $A$ ), which are often held at fixed distance and orientation apart from each other. Two alternative mechanisms of ET could be considered depending on whether the rate of polar environment relaxation is faster or slower than the rate constant of electron tunneling  $k_0$ . If the distance between reactants is small enough and  $k_0$  is higher than the rate of medium relaxation (the adiabatic mode), the ET is controlled by the solvent dynamics [38]. In the alternative case, when the rate of solvent relaxation is fast (the nonadiabatic limit), the rate constant of ET could be calculated by the first order time-dependent perturbation theory and, in the high-temperature limit, this approach gives the semiclassical nonadiabatic theory [39]. In ordinary solvents, the medium relaxation is complete in several picoseconds, so the ET reactions which are slower than several picoseconds are usually treated as nonadiabatic ones. In proteins, however, the nonadiabatic ET mechanism might be complicated by relaxation processes in the microsecond time scale, such as slow conformational motion of protein subdomains or proton redistribution at pH-buffering groups. If the driving force of the ET reaction is less or about 0.1 eV, relaxation processes might partially control the ET dynamics [40]. Such relaxation control apparently takes place for slow components of  $Q_A \rightarrow Q_B$  ET reaction in bacterial RC from *R. sphaeroides* [41],  $P960^+$  reduction by four-heme cytochrome  $c$  in RC from *B. viridis* [40], and the reduction of photo-oxidized

primary donor  $P680^+$  by a redox-active tyrosine  $Y_Z$  in photosystem II [42,43]. Further we would consider only those ET reactions that occur by the nonadiabatic mechanism.

If the edge-to-edge distance  $d$  between donor  $D$  and acceptor  $A$  exceeds 5–7 Å, the electronic interaction between them is relatively weak and the rate constant for the ET could be estimated by the semiclassical nonadiabatic theory [39]. This theory separates the classical movement of nuclear subsystem from the quantum electron tunneling between  $D$  and  $A$  and considers the three following stages of the ET reaction: (i) the classical subsystem oscillates stochastically around an equilibrium reactant conformation and reaches randomly the transition state where the energy of reactants matches the energy of products, that requires an activation energy  $E_a$ . (ii) In the transition state, the electron tunneling becomes possible with rate constant  $k_0$ . (iii) After the electron tunneling, the heavy-atom subsystem relaxes towards an equilibrium product conformation. The criterion of the nonadiabatic mechanism is that the frequency of classical heavy-atom motion around equilibrium and the relaxation towards product state is faster than the rate of electron tunneling  $k_0$ . Under this condition, the rate constant of ET  $k_{ET}$  is broken up into nuclear and electronic terms:

$$k_{ET} = k_0 \exp(-E_a/k_B T). \quad (1)$$

Here the electronic term  $k_0$  is the rate of electron tunneling (it is proportional to the electronic coupling between redox sites  $|H_{AD}|^2$  determined by the protein atomic structure) and the exponential nuclear term relates the activation energy of the transition state to the nuclear reorganization energy  $\lambda$  and the reaction driving force  $-\Delta G$ :

$$E_a = (\lambda + \Delta G)^2 / 4\lambda. \quad (2)$$

The values  $\Delta G$  and geometrical parameters of the electron carriers of bacterial RC, PS I, PS II, and soluble ferredoxin

Table 2

Experimental characteristics of some electron transfer reactions in bacterial photosynthetic reaction center, PS I, PS II, and soluble ferredoxins (Fd)

ET reaction	$\epsilon_D$	$\epsilon_A$	$\Delta G$ (meV)	$d$ (Å)	$a_D$ (Å)	$a_A$ (Å)	$R$ (Å)	$E_a$ (meV)	$\tau$ (s)	Reference for $\Delta G$	Reference for $\tau$
BRC: $c_{556}^+ \rightarrow c_{551}^+$	34	34	300	7.9	5	5	16.5	366	$2.2 \times 10^{-6}$	[50]	[50]
BRC: $c_{559}^+ \rightarrow P960^+$	34	9.8	−130	12.3	5	7	21	40	$3 \times 10^{-7}$	[34,51]	[34,51]
BRC: $P960^+ \rightarrow B_A$	3	3	−87	5.2	7	5	11.6	0	$3.5 \times 10^{-12}$	[52]	[52]
BRC: $B_A \rightarrow H_A$	3	3	−161	4.9	5	5	10.9	8	$1.2 \times 10^{-12}$	[52]	[52]
BRC: $H_A \rightarrow Q_A$	3	4	−500	9.3	5	4	15	54	$2 \times 10^{-10}$	[53]	[54]
BRC: $Q_A \rightarrow Q_B^a$	4	20	−100	13	4	3.5	18	151	$2 \times 10^{-5}$	[53]	[55]
BRC: $Q_A \rightarrow P960^+$	4	3	−580	22.3	4	7	28	78	$10^{-1}$	[53]	[55]
PS I: $A_0^- \rightarrow A_1$	3	5.4	−300	6.7	5	4	9	2	$3 \times 10^{-11}$	[56,57]	[58]
PS I: $A_1^- \rightarrow F_X$	5.4	8.7	−100	9	4	3.9	13	211	$2-15 \times 10^{-8}$	[57,59]	[60]
PS I: $F_X^- \rightarrow F_A$	8.7	6.6	−150	11.5	3.9	3.9	14.1	208	$3-5 \times 10^{-7}$	[59,61]	[62]
PS I: $F_A^- \rightarrow F_B$	6.6	4.8	50	9.5	3.9	3.9	12	263	$3-5 \times 10^{-7}$	[61]	[62]
PS II: $Y_Z \rightarrow P680^+$	6.4	3	−90	9	3	7	17	107	$3.5-5 \times 10^{-8b}$	[63]	[63]
PS II: $^1P680^+ \rightarrow B_A$	3	3	0	4.4	7	5	11.3	20	$6 \times 10^{-12}$	[64]	[65]
PS II: $B_A \rightarrow H_A$	3	3	−150	5	5	5	10.7	5	$7 \times 10^{-13}$	[67]	[66]
PS II: $H_A \rightarrow Q_A$	3	4	−340	8.6	5	3.5	13	3	$3-4 \times 10^{-10}$	[68]	[69]
Fd: $(FeS)_4 \rightarrow (FeS)_4$	6.6	6.6	0	8.5	3.9	3.9	11.7	253	$3 \times 10^{-7}$	[70]	[70]

<sup>a</sup> This reaction is coupled to a proton transfer, but it is not kinetically limited by the proton transfer.

<sup>b</sup> According to [43], reduction of  $P680^+$  by the redox active tyrosine  $Y_Z$  is multiphasic. Only the component with largest amplitude was taken into account. The components with lower amplitudes and slower kinetics could be explained by relaxation processes and different conformational states of the system that determine the overall time course. Obviously, the rates of these processes were not simply derived from the Marcus theory.



found in the literature are summarized in Table 2. The reorganization energy of the heavy-atom subsystem  $\lambda$  could be broken up into two terms: the reorganization of redox cofactors themselves and the reorganization of external medium (the inner-sphere and outer-sphere parts  $\lambda_{\text{in}}$  and  $\lambda_{\text{out}}$ , respectively). In many cases, the molecules of redox cofactors are fairly rigid and the redox transition occurs without considerable conformational changes of the cofactors that leads to negligibly small  $\lambda_{\text{in}}$  values, but in the case of  $[\text{FeS}]_4$  cluster, the  $\lambda_{\text{in}}$  value exceeds 0.2 eV [44], and the latter figure was used for  $[\text{FeS}]_4$  clusters in further calculations. In homogeneous medium  $\lambda_{\text{out}}$  could be approximated by the equation:

$$\lambda_{\text{out}} = e^2 \left( \frac{1}{\epsilon_0} - \frac{1}{\epsilon_s} \right) \left( \frac{1}{2a_D} + \frac{1}{2a_A} - \frac{1}{R} \right) \quad (3)$$

where  $e$  is the electron charge,  $\epsilon_0$  and  $\epsilon_s$  are optical and static dielectric constants of the external medium,  $a_D$  and  $a_A$  are the effective radii of the donor and acceptor, and  $R$  is the center-to-center distance between the cofactors. The optical dielectric permittivity of protein is about 2.5; the static dielectric constant might vary in a wide range from 3 to 30 [41,45]. The effective radii of cofactors could be either estimated by their van der Waals volume, or calculated more precisely by numeric integration of the Poisson–Boltzmann equation using special software [46].

The electronic term,  $k_0$ , is directly related to the strength of the electronic interaction between the donor and acceptor, which decays exponentially upon increasing the edge-to-edge distance  $d$ . Although the secondary and tertiary protein structures might affect the magnitude of the electronic coupling (see, e.g., the discussion in a special issue of *J. Biol. Inorg. Chem.* 2 (1997), and in particular, Ref. [47]), to a first approximation the electronic term could be estimated by the empirical Moser–Dutton expression that describes a simple exponential decay of tunneling rate with the distance  $d$  [48]:

$$k_0 = 10^{13-0.6(d-3.6)} (\text{s}^{-1}). \quad (4)$$

Quantitatively, Eqs. (1), (2), and (3) describe the dependence of the rate constant  $k_{\text{ET}}$  on the local dielectric permittivity of the protein  $\epsilon_s$  in the vicinity of cofactors completed by the geometry factor specified by Eq. (4). To compare the ET reactions occurring at different distances, it is worthwhile excluding the dependence of the ET rate on the distance and to use a corrected rate constant

$$k_{\text{ET}}^0 = k_{\text{ET}} \cdot 10^{0.6(d-3.6)}. \quad (5)$$

The corrected rate constant of a given ET reaction is an ideal rate at very strong electronic coupling of reactants (if the reactants are in direct contact). The usage of distance-excluded rate constant  $k_{\text{ET}}^0$  is complementary to the usage of free-energy-optimized ET rate by Moser and Dutton who excluded the nuclear term ( $-\Delta G_{\text{opt}} = \lambda$ ) and quantified the effect of distance on the ET rate [48].

As the local dielectric permittivity might be significantly different in the vicinity of donor and acceptor, it seems

reasonable to plot the dependence of the distance-excluded rate constant  $k_{\text{ET}}^0$  on the activation energy calculated from Eq. (2) using the following approximation for the reorganization energy [49]:

$$\lambda = \lambda_{\text{in}} + \frac{e^2}{2a_D} \left( \frac{1}{\epsilon_0} - \frac{1}{\epsilon_D} \right) + \frac{e^2}{2a_A} \left( \frac{1}{\epsilon_0} - \frac{1}{\epsilon_A} \right) - \frac{e^2}{R} \left( \frac{1}{\epsilon_0} - \frac{\epsilon_D + \epsilon_A}{2\epsilon_A \epsilon_D} \right). \quad (6)$$

This equation takes into account dielectric heterogeneity of protein by using different values of static dielectric permittivity  $\epsilon_D$  and  $\epsilon_A$  in the vicinity of donor and acceptor, respectively.

Fig. 3 shows the dependence of the distance-excluded rate constant on the activation energy calculated from Eqs. (2) and (6) using experimental results and data available from the literature and summarized in Table 2. The solid line shows the ideal dependence at direct contact between cofactors ( $d=3.6$  Å,  $k_0=10^{13} \text{ s}^{-1}$ ), whereas each experimental point corresponds to individual donor–acceptor pair with specific geometric parameters ( $a_D$ ,  $a_A$ ,  $R$ ,  $d$ ), dielectric properties ( $\epsilon_D$  and  $\epsilon_A$ ), and driving force value ( $-\Delta G$ ).

The correlation of experimental points obtained for various donor–acceptor pairs in different pigment–protein complexes of three photosynthetic systems (RC of purple bacteria and PS I and PS II of cyanobacteria) and soluble ferredoxin with the ideal theoretical dependence demonstrates that:

- (1) All ET reactions considered in this work follow the nonadiabatic mechanism and can be semiquantitatively described in terms of the Marcus theory using the Moser–Dutton empirical rule for electronic coupling term.
- (2) The local dielectric permittivity of membrane proteins inferred from the electrometric experiments could be used

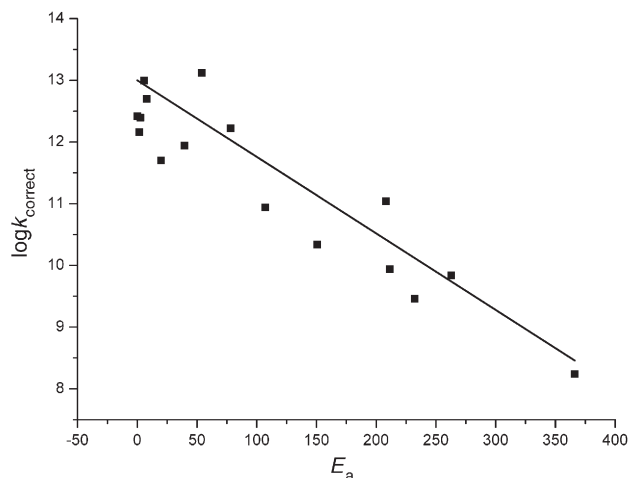


Fig. 3. Comparison of calculated (solid line) with experimental (squares) distance-excluded rate constants  $k_{\text{ET}}^0$  for various electron transfer reactions in bacterial photosynthetic reaction centers, photosystems I and II and soluble ferredoxin. Measured rates,  $\Delta G$ , geometric and dielectric parameters are taken from Table 2, reorganization energy  $\lambda$  and activation energy  $E_a$  are calculated from Eqs. (2) and (6), respectively.

for calculation of the ET reorganization energy by methods of continuum electrostatics.

- (3) Simple models of macroscopic electrostatics could be successfully applied to the ET reactions in membrane proteins with resolved atomic structure predicting the rate constant with the accuracy of less than one order of magnitude.

Further research into the possible mechanism of correlation between these parameters is a subject of our planned experimental and theoretical study.

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