

Temperature Dependence of the Reduction of P_{700}^{+} by Tightly Bound Plastocyanin in Vivo[†]

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ABSTRACT: The kinetics of reduction of P_{700}^{+} , the stably oxidized electron donor of Photosystem I, by plastocyanin (PC) has been investigated by pump–probe optical spectroscopy in living cells of the green alga *Chlamydomonas reinhardtii*, between 277 and 318 K. The reduction of P_{700}^{+} in vivo is described by two kinetic components with lifetimes of 6 ± 0.5 and 56 ± 1 μ s at room temperature. The rapid reduction phase, which is attributed to reduction of P_{700}^{+} by prebound PC, is thermally activated with an apparent activation barrier of 105–115 meV. The analysis of the in vivo reaction is consistent with (i) reduced PC and PS I forming a relatively tight binary complex that does not undergo kinetically limiting conformational reconfiguration and (ii) the activation barrier being determined principally by enthalpic contributions to the free energy change. Under the approximation that entropic contributions to the free energy change associated with this electron transfer reaction are negligible, a lower boundary value of the reorganization energy is estimated to be 0.54–0.63 eV, which is on the lower range of the distribution for intraprotein electron transfer reactions. This low activation barrier is discussed in terms of the optimization of primary donor reduction.

Electron transfer (ET)¹ reactions are of fundamental importance in bioenergetics. In biological systems, ET involves the movement of an electron from donor to acceptor molecules which are bound to proteins in a relatively rigid structure, so that the cofactors are often separated by distances which exceed the molecular radii. Hence, the diffusion of the electron acceptor and donor molecules, as well as the direct overlap of the molecular orbitals of the electron transfer partners, is hindered. Therefore, for the reaction to take place, the electrons need to tunnel through a potential energy barrier (reviewed in refs (1–3)). The oxidation and reduction of diffusible electron carriers can also proceed through the tunneling processes (reviewed in refs (1–5)), even though it involves the movement of electrons between different cofactor–protein complexes.

The simpler description of the rate of electron tunneling, in the nonadiabatic limit, is given by the modification of the semiclassical formulation, introduced by Marcus (6), which includes the quantum-mechanical coupling with solvent phonons (7–9):

$$k_{\text{et}} = \frac{2\pi|V_{\text{AD}}|^2}{\hbar\sqrt{2\pi}\vartheta(T)} e^{-(\Delta G^\circ + \lambda_t)^2/(2\vartheta^2(T))} \quad (1)$$

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Abbreviations: cyt, cytochrome; ET, electron transfer; PS I, Photosystem I; PhQ_A and PhQ_B, plastoquinones A and B, respectively; F_X, F_A, and F_B, iron–sulfur clusters X, A, and B, respectively; P_{700}^{+} , Photosystem I primary donor (cation); PC^{II}, oxidized plastocyanin; PC^I, reduced plastocyanin; RC, reaction center; λ_t , (total) reorganization energy; k_{et} , electron transfer rate.

where V_{AD} is the electronic coupling matrix element between the electron donor (D) and the electron acceptor (A) molecule, λ_t is the (total) reorganization energy, and $\vartheta(T)$ is the width of the Gaussian curve describing the Franck–Condon factors.

The ET rate would show an extremely weak temperature dependence when $\Delta G^\circ = -\lambda$. Still, k_{et} may depend on T , because of the $\vartheta(T)$ term which in its most simple formulation is described by

$$\vartheta^2(T) = \hbar\bar{\omega}\lambda_t \coth \frac{\hbar\bar{\omega}}{2k_bT} \quad (2)$$

where k_b is the Boltzmann constant, $\bar{\omega}$ is the mean phonon mode expressed in angular frequency units, and T is the absolute temperature. When k_bT is larger than $\hbar\bar{\omega}$, $\vartheta^2(T)$ tends to $2\lambda_t k_bT$. As a result, eq 1 becomes equivalent to the classical derivation of Marcus (6):

$$k_{\text{et}} = \frac{2\pi|V_{\text{AD}}|^2}{\hbar\sqrt{4\pi\lambda_t k_bT}} e^{-(\Delta G^\circ + \lambda_t)^2/(4\lambda_t k_bT)} \quad (3)$$

However, when $\hbar\bar{\omega} \gg k_bT$ (i.e., tunneling is coupled to high-frequency phonon modes), $\vartheta^2(T)$ tends to a constant value ($\hbar\bar{\omega}\lambda_t$), so that the ET rate becomes effectively temperature-independent (1, 2, 7). More accurate expressions, which consider full quantum-mechanical coupling with one (9) or more frequency modes (1, 2, 5), as well as specific tunneling pathways within the inhomogeneous protein medium (e.g., refs 10 and 11), have also been discussed.

Even though the rate of ET depends, in principle, on a limited number of parameters, accurate determination of the electronic coupling factor (V_{AD}) and total reorganization energy (λ_t) has

often proved to be difficult, yet to a first approximation, the value of $|V_{AD}|^2$ depends exponentially on the distance between the acceptor and donor molecules (3, 5, 12), scaled by a factor known as the tunneling barrier. Moreover, for systems in which the spatial arrangement of cofactors and the intervening medium is known with sufficient resolution, computational approaches based on ab initio quantum-chemical and molecular dynamics calculations (reviewed in refs 14 and 15) can also be employed.

Information relating to other parameters determining the Franck–Condon factors (i.e., the reorganization energy and the mean phonon mode coupled to electron donor and acceptor) can be, in principle, retrieved from the analysis of the temperature dependence of the ET reaction, particularly when the free energy change can be assessed from independent investigation. A survey of intraprotein ET reactions involving redox-active centers of numerous enzymes, including photosynthetic complexes, has led to average values of λ_t in the range of 0.6–0.7 eV (3, 5, 14, 15). Nevertheless, considerably lower values (~ 0.2 eV) were determined for ultrafast photochemical charge separation reactions, particularly in the reaction centers of purple bacteria (see ref 16 and references cited therein). Values of λ_t lower than 200 meV were also reported for the reduction of the cyt a_3 –Cu_B binuclear center in cytochrome *c* oxidase (17). On the other hand, the reorganization energy appears to increase for interprotein ET, which typically occurs on the microsecond time scale, with average values close to 1 eV (3–5). A complication associated with the analysis of interprotein ET reactions is that they often display polyphasic kinetics, reflecting diffusion-limited complex formation and heterogeneity of prebound acceptor–donor complexes (reviewed, e.g., in refs (18–20)). Still, the rates of the more rapid interprotein ET reactions taking place from preformed complexes have often been successfully described by tunneling theory (e.g., refs (1–5) and 21). This observation suggests that, within the time of the ET reaction, the binary donor–acceptor complex is stable enough for the Franck–Condon approximation employed in the derivation of the theoretical formulation to hold true. When this is the case, interprotein ET reactions can be treated analogously to intraprotein ET, for which the geometrical arrangement of the cofactor is defined by their binding to the protein matrix.

Probably the most extensively investigated interprotein ET reactions in photosynthetic systems are the donation of an electron from cytochrome c_2 (cyt c_2) to the primary donor of the purple bacterial reaction center (reviewed in ref 23) and the reduction of ferredoxin (reviewed in ref 24) by the acceptor side of Photosystem I (PS I). The reduction of the PS I primary donor P_{700}^+ by the diffusible carrier plastocyanin (PC) (reviewed in refs (18–20)) and cyt c_6 (19, 20) has also been extensively investigated in vitro. However, studies performed in vivo are far less abundant and have, in certain cases, produced results contradictory to investigations in purified systems (25, 26). Crystallographic structures of supercomplexes composed of PS I and its acceptor ferredoxin (27) and that of cyt c_2 and the reaction center (RC) of *Rhodospirillum rubrum* (28, 29) have been reported, supporting the formation of a tight binary complex. However, at present, the crystallization of a binary complex between PC and PS I has been unsuccessful.

The lower boundary value of the reorganization energy associated with the reduction of P_{700}^+ by reduced plastocyanin (PC^I) was estimated to be 545 meV, based on the effect of

site-directed mutants with altered P_{700} redox potential in whole cells of *Chlamydomonas reinhardtii* (30). Even considering the relatively small range of ΔG° values (–77 to –217 meV) explored in the study of Ramesh and co-workers (30), the lower bound value of λ_t appears to fall on the low edge of the spread reported for interprotein ET and is particularly low, considering that the reaction involves ET between different proteins, and that the redox-active center of PC is a Cu atom. Similar lower boundary values of $\lambda_t \approx 500$ meV were reported for another intercomplex reaction, the reduction of the oxidized primary donor in the RC of *R. sphaeroides* (P_{870}^+) by cyt c_2 , analyzing the effect of altering the driving force of the reaction (31). However, a successive investigation that took into account the temperature dependence of the ET rates measured in the same mutants, where ΔG° was varied between –65 and –420 meV, yielded a larger λ_t value of 920 ± 110 meV (21). This latter value close to ~ 1 eV is consistent with the temperature dependence of the P_{870}^+ reduction previously measured in *R. sphaeroides* wild-type reaction centers (32).

We have reinvestigated in whole cells of *C. reinhardtii* the temperature dependence of P_{700}^+ reduction by prebound PC^I. We estimate the activation enthalpy of the reaction ($\Delta H^\ddagger = 100$ –110 meV). Making the assumptions that (i) the high-temperature limit is an adequate description of the ET rate for the conditions employed in this study and (ii) the entropic contribution to the free energy difference is negligible, so that $\Delta H^\ddagger \approx \Delta G^\ddagger$, we estimate the lower bounds for the total reorganization energy to be 525–620 meV. The relatively small value of λ_t leads to an acceleration of P_{700}^+ reduction by 2 orders of magnitudes compared to what it would be if the average value for interprotein electron transfer (~ 1 eV) held true.

EXPERIMENTAL PROCEDURES

The *C. reinhardtii* strain containing the *FuD7* (*psbAΔ*) mutation in the *P71* low-antenna background, which accumulates wild-type levels of PS I and cyt b_6f , was used in these experiments. Cells were grown heterotrophically in TAP medium, which contains acetate as a carbon source. They were harvested by centrifugation at 1500g for 5 min and immediately resuspended to a concentration equivalent to 1.5 OD units at 678 nm (the peak in the Q_y absorption band of chlorophyll *a*) in 50 mM Hepes–NaOH (pH 8) buffer containing Ficoll (20%, w/v) to prevent sedimentation of the cells during the measurements. The uncoupler FCCP was added at a final concentration of 10 μ M to collapse the transmembrane ionic gradients. The temperature of the samples was controlled with a circulating water bath. The sample was left to incubate for 15 min once the temperature was reached before the kinetics were recorded.

Time-Resolved Difference Absorption Spectroscopy. The kinetics of electron transfer in whole cells of *C. reinhardtii* were recorded using a pump–probe spectrometer, which has been previously described in detail (34). In brief, the excitation pulse is provided by a Nd:YAG pumped dye (LDS 698) laser. The excitation wavelength was set to 700 nm and the intensity regulated by a neutral metal grid so as to excite approximately 70% of the complexes during the ~ 6 ns actinic pulse. The kinetics were probed at discrete wavelengths, using the output of an OPO (Panther, Continuum) pumped by a frequency-tripled Nd:YAG laser (Surelite I, Continuum). The temporal resolution of the instrument is better than 7 ns, without deconvolution of the actinic pulse profile.

Analysis of ET Kinetics at Room Temperature. The kinetics (monitored every 5 nm in the 350–540 nm range) at 298 K were globally fitted by a sum of exponentials:

$$\Delta A(t, \lambda) = \sum_{i=1}^n a_i(\lambda) e^{-t k_i} + b(\lambda) \quad (4)$$

where $a_i(\lambda)$ is the amplitude (at wavelength λ) of the decay-associated spectrum (DAS) with (apparent) rate constant k_i and $b(\lambda)$ is the amplitude (at wavelength λ) of the DAS of the nondecaying component. All DAS are reported in Figure S1 of the Supporting Information.

Analysis of the Temperature Dependence of ET Kinetics. (i) *Global Analysis.* At each temperature investigated, in the 277–318 K interval, the kinetics recorded at 430, 445, 460, and 480 nm were fitted simultaneously (globally) by a fit function of the form of eq 4, but which explicitly describes the temperature dependence:

$\Delta A(t, \lambda, T) = \sum_{i=1}^n a_i(\lambda, T) e^{-t k_i(T)} + b(\lambda, T)$. In this type of analysis, the rate constants $k_i(T)$ are only global fit parameters (i.e., they assume the same value for each wavelength investigated, at a given temperature), while the amplitudes of the DAS are unconstrained. The thermodynamic parameters associated with the temperature dependence of the reaction were extracted by the Arrhenius plot of $\ln[k_i(T)]$ as a function of T^{-1} . (The Arrhenius relation is often expressed as $k_i(T) = k_{\max} e^{-E_a/k_b T}$ where E_a is the activation barrier and $k_{\max}$ is the maximal rate constant. It is easily shown that, in this form, $E_a \approx \Delta H^\ddagger$, the activation free enthalpy difference, rather than $E_a \approx \Delta G^\ddagger$, the activation free energy difference, and that the pre-exponential term is $k_{\max} = k_{\max}^{\text{eff}} e^{\Delta S^\ddagger/k_b}$).

(ii) *Global-Target Analysis.* In the global-target analysis, which is analogous to the case of global analysis, the data are fitted to the function $\Delta A(t, \lambda, T) = \sum_{i=1}^n a_i(\lambda, T) e^{-t k_i(T)} + b(\lambda, T)$. However, while in the global analysis no particular assumption is made about the temperature dependence of the rate constants, in global-target analysis, a theory-based assumption is introduced: $k_i(T)$, which is described by eq 1, in the high-temperature approximation ($k_b T > \hbar \omega$), reduces to

$$k_i(T) = C T^{-1/2} e^{-\Delta H^\ddagger/k_b T} \quad (5)$$

where C is a temperature-independent constant, equivalent to $C = C' e^{\Delta S^\ddagger/k_b}$, where $C' = \pi^{1/2} |V_{AD}|^2 / [\hbar (k_b \lambda_i)]$ and $\Delta S^\ddagger$ is the activation entropy difference. Equation 5 is equivalent to eq 1 (in the high-temperature limit) but does not require any assumption about the specific value of λ_i , which is implicitly contained in the terms C' and $\Delta G^\ddagger = \Delta H^\ddagger - T \Delta S^\ddagger$. With this definition of $k_i(T)$, all kinetic data sets, monitored between 430 and 480 nm, and in the 277–318 K temperature range, are fitted simultaneously. Thus, the rate constant $k_i(T)$ is not a fit parameter in the global-target analysis; it is described by the values of C and $\Delta H^\ddagger$, which are common to all data sets. The amplitudes $a_i(\lambda, T)$ and $b(\lambda, T)$ are, as for the non-model-based global analysis, unconstrained. The principal advantage of the global-target analysis is that, as all data are fitted simultaneously, the number of possible numerical solutions, and hence the errors in the parameter estimates, are largely reduced (35). Second, the activation enthalpy ($\Delta H^\ddagger$) is extracted directly from the fitting rather than from subsequent analysis, which also increases the precision of the estimation.

The data were fitted by laboratory-written software operating in MatLab, which minimizes the reduced sum of the squared residuals, using a combination of the Simplex (initial search) and Levenberg–Marquardt (refine minimization) algorithms. Errors are estimated by the Covariance matrix, and the stability of the solution was tested by an iterative search as described by Beechem (35) and Venturoli et al. (21).

RESULTS

The temperature dependence of the light-induced ET kinetics in the PS I reaction center was investigated in living cells of *C. reinhardtii* by pump–probe transient optical spectroscopy. The kinetics were monitored at four discrete wavelengths in the 430–480 nm range and from 5 ns to 20 μ s after the pump flash, after incubation of the cells at a set temperature. These wavelengths were selected as they allowed preferential monitoring of the kinetics of either P_{700}^+ reduction (430 and 445 nm) or the electro-chromic band shift (ECS, 460 and 480 nm) associated with vectorial electron transfer in the PS I RC (e.g., ref 36). The latter process (ECS) dominates the kinetics at wavelengths longer than 460 nm, and although it does not directly monitor PhQ^- oxidation, it has been shown to relax with exactly the same kinetic lifetimes as the actual ET reaction, as expected from its electro-chromic origin (see DAS in Figure S1 of the Supporting Information as well as refs (36–39)). Furthermore, it has been shown that, in vitro, the activation barriers of the PhQ^- oxidation reaction estimated from the temperature dependence of the kinetics recorded at 480 nm (ECS) and 390 nm (PhQ^-) are virtually indistinguishable (40).

Figure 1 shows the transient flash-induced absorption changes as well as the global-target fits at selected temperatures. A satisfactory description of the experimental data at all wavelengths requires at least three exponential decay components, which are characterized by lifetimes of 20 ± 1 ns, 228 ± 6 ns, and 6.3 ± 0.2 μ s at 298 K, in agreement with previous investigations of the same organism at room temperature (Figure S1 of the Supporting Information and refs 35 and 36). On the basis of the differential absorption in the near UV, the 20 and 228 ns components have been assigned to the oxidation of phylosemi-quinone (PhQ^-) molecules bound by the PsaB and PsaA subunits, respectively (36–39), and the 6.3 μ s phase has been assigned to the reduction of P_{700}^+ by prebound PC^I on the basis of the bleaching at 432 nm (e.g., refs 36 and 37).

Figure 2A also shows the Arrhenius plot of the rate derived from the global-target fitting of the experimental results as a function of temperature. The temperature dependence of the amplitudes associated with each of the kinetics components at the four wavelengths investigated is reported in Figure S2 of the Supporting Information. As the data are subjected to a model-based analysis (see Experimental Procedures for further details), the activation enthalpies ($\Delta H^\ddagger$) are extracted directly from the fitting of the kinetics acquired at different set temperatures, and they are determined to be 47.1 ± 0.5 , 107 ± 2 , and 104.5 ± 0.1 meV for the 20 ns, 228 ns, and 6.3 μ s components, respectively.

Also shown in Figure 2A (Δ) is the Arrhenius plot of the 6.3 μ s phase for an unconstrained three-exponential fit, which shows that even dropping the assumption of particular temperature dependencies of the rate constants does not much influence the result of the fits. The value of $\Delta H^\ddagger$ is 106.2 ± 0.8 meV in this case. However, the value of the lifetimes of the fast (~ 20 ns) and slow (~ 230 ns) phases of PhQ^- reoxidation retrieved from the free-running, three-exponential fit displayed a significant statistical

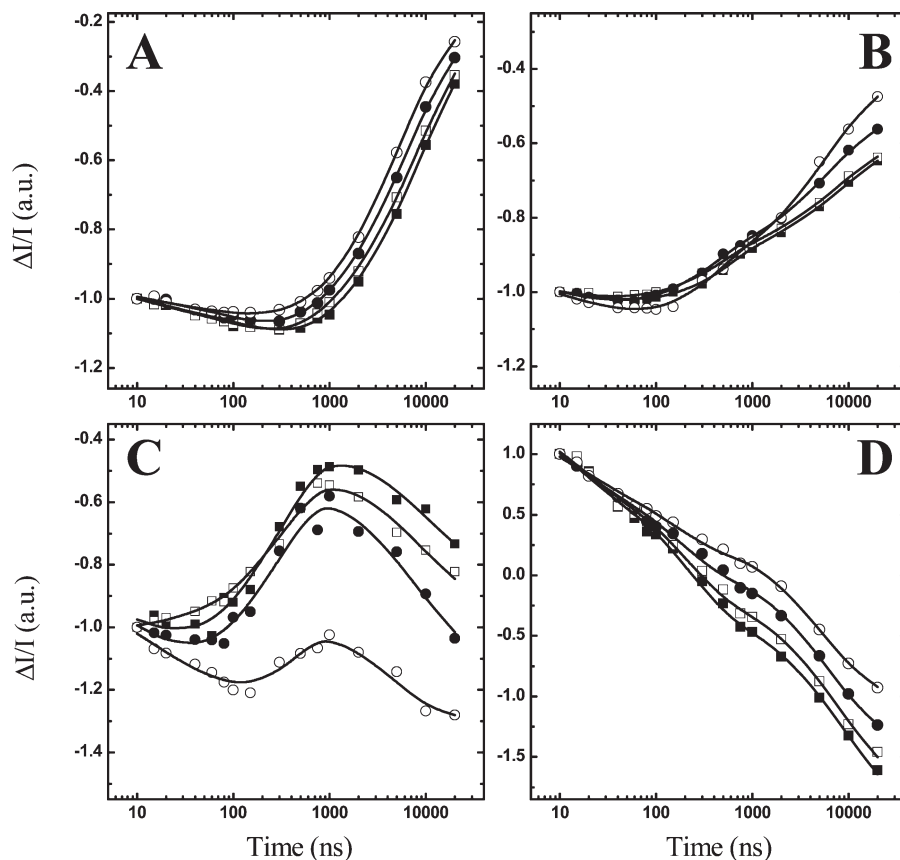


FIGURE 1: Temperature dependence of the kinetics of light-induced ET in PS I monitored at 430 (A), 445 (B), 460 (C), and 480 nm (D), in living *C. reinhardtii* cells maintained at 277 (■), 288 (□), 298 (●), or 305 K (○). Solid lines are the global fit to the experimental results considering a four-exponential decay model.

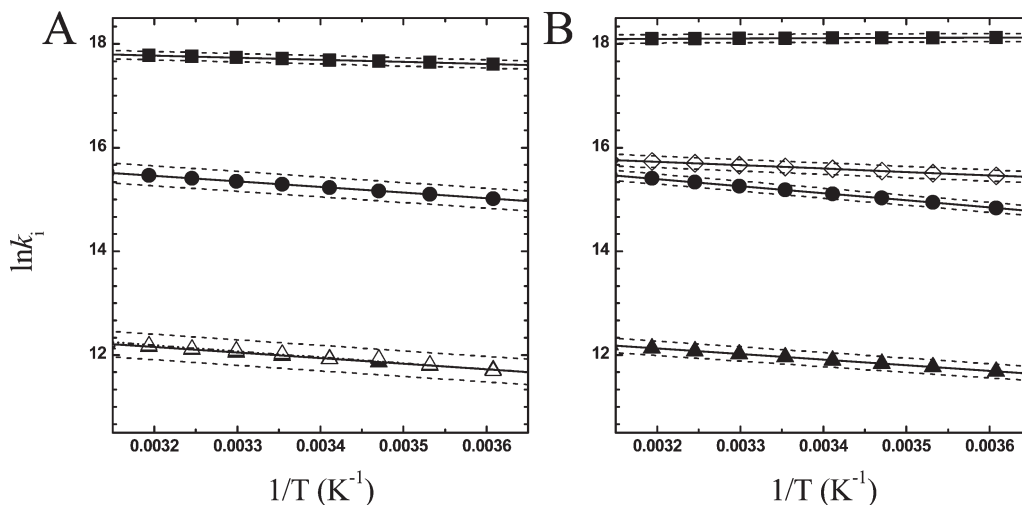


FIGURE 2: Dependence of the apparent rate constants upon temperature, shown as conventional Arrhenius plots. (A) Rate constants obtained from a three-exponential global-target fit: (■) $\tau_{1,298K} = 20.3$ ns ($C = 5.32 \times 10^9$ s⁻¹ K^{1/2}), (●) $\tau_{2,298K} = 228$ ns ($C = 4.61 \times 10^9$ s⁻¹ K^{1/2}), and (▲) $\tau_{3,298K} = 6.2$ μ s ($C = 1.67 \times 10^8$ s⁻¹ K^{1/2}). Empty triangles represent an unconstrained global fit ($\tau_{3,298K} = 6.3$ μ s). (B) Rate constants obtained from a four-exponential global-target fit: (■) $\tau_{1,298K} = 13.6$ ns ($C = 1.79 \times 10^9$ s⁻¹ K^{1/2}), (●) $\tau_{2,298K} = 255$ ns ($C = 1.56 \times 10^9$ s⁻¹ K^{1/2}), (◇) $\tau_{3,298K} = 164$ ns ($C = 1.08 \times 10^{10}$ s⁻¹ K^{1/2}), and (▲) $\tau_{4,298K} = 6.4$ μ s ($C = 1.68 \times 10^8$ s⁻¹ K^{1/2}). For both panels, the solid lines are extrapolations from the fitting parameters for the temperature dependence of the rates while the dashed lines mark the confidence interval (within 2 σ). For the unconstrained analysis of the ~ 6 μ s component in panel A, the dashed-dotted line is the linear regression through the data points, the slope of which ($E_a k_b^{-1}$) is obtained from the derivation of $\ln K_{et}$, which is $E_a = \Delta H^\ddagger - k_b T/2$.

scatter, albeit distributed around the same average value obtained from the model-based fitting approach (Figure S3 of the Supporting Information).

Figure 2B shows the Arrhenius plot obtained from fitting the experimental data with a four-exponential function (the amplitudes are shown in Figure S2). An additional decay component

was considered, based on prior results from the investigation of both the temperature dependence of PhQ⁻ oxidation in purified cyanobacterial PS I (40) and the effects of PhQ_A site mutations in living *C. reinhardtii* cells (38, 39), which revealed the presence of an intermediate component with a τ of ≈ 170 –180 ns. At 298 K, the best fit to the kinetics is obtained with lifetimes of 13.7 ± 0.4 ns,

164 ± 6 ns, 255 ± 3 ns, and 6.4 ± 0.2 μ s. The activation enthalpies for these four kinetic components are then 8.0 ± 0.5 , 69 ± 1 , 129.8 ± 0.6 , and 105.9 ± 0.3 meV, respectively. After taking into account the contribution of this additional component decaying on the nanosecond time scale, we determined a higher rate for the fast component of PhQ^- oxidation, which is associated with a lower activation barrier, while the slow component is shifted to a slightly slower rate with a larger activation barrier. However, it is important to note that the kinetics of P_{700}^+ reduction, and the associated $\Delta H^\ddagger$ value, are, substantially, independent of the specific kinetic model adopted to fit the transient optical data.

DISCUSSION

Temperature Dependence of PhQ^- Oxidation. Investigation of the temperature dependence of the ET reactions occurring in vivo in the nanosecond-to-microsecond time range in the PS I reaction center allows the determination of the activation enthalpy difference ($\Delta H^\ddagger$) associated with the oxidation of PhQ^- by F_X and with the reduction of P_{700}^+ by PC^I prebound to the RC. The values of $\Delta H^\ddagger$ associated with the fast phase of PhQ^- oxidation (8–47 meV), which is attributed to oxidation of PhQ_B^- , are in agreement with the conclusions (7–15 meV) drawn from a previous study of PS I RCs isolated from *Synechocystis* sp. PCC 6803 (40). A relatively good agreement is also obtained for the slow phase of PhQ^- oxidation, which is attributed to the oxidation of PhQ_A^- (36–41) and was estimated to be 65–110 meV in isolated particles (40). It is noteworthy that the values of $\Delta H^\ddagger$ are relatively insensitive to the specific kinetic model used to describe the experimental data, as shown from the relatively narrow spread of values (107–130 meV) obtained from the analysis using either a three- or four-exponential decay (Figure 2). When the kinetics are fitted with a sum of four exponential functions, larger values of $\Delta H^\ddagger$ (130 meV) for the oxidation of PhQ_A^- are obtained compared to the value extracted from the three-component fitting (106 meV). A comparable difference is observed for the fast phase (20 ns) attributed to oxidation of PhQ_B^- . Thus, after taking into account the intermediate component (~ 160 ns), we found the apparent activation of the fast (~ 20 ns) and slow (~ 200 ns) components, attributed to PhQ_A^- and PhQ_B^- , respectively, is in very close agreement with the estimates obtained in cyanobacterial PS I RCs (40).

The additional kinetic phase is characterized by a lifetime of ~ 164 ns at 298 K, in agreement with the previous investigation of mutations of the PhQ_A binding site in *C. reinhardtii* (38, 39) and the investigation of the temperature dependence of PhQ^- oxidation in isolated cyanobacterial PS I (40). This kinetic component was tentatively attributed to the oxidation of reduced F_X by the terminal acceptors (F_A and F_B (38, 39)). The presence of two closely spaced lifetime components in the midnanosecond range in the wild-type reaction center has also been predicted by kinetic simulations of the PhQ^- oxidation kinetics, based on electron tunneling theory (42). However, in the previous investigation performed in isolated cyanobacterial PS I RCs (40), it was not possible to evaluate the activation energy associated with this intermediate component, because of excessive statistical scatter in the fitted lifetimes. From our fitting of the in vivo kinetics in *C. reinhardtii*, we estimate that $\Delta H^\ddagger = 69$ meV for this component, which is hardly negligible. This also explains the difference in $\Delta H^\ddagger$ calculated for the slow component (~ 200 ns) of PhQ^- oxidation using different kinetic models, since the estimated value would tend toward the weighted average

of the unresolved lifetimes when the ~ 160 ns component is neglected.

To apply electron tunneling theory reliably to experimentally determined activation barriers (and maximal rates), the free energy difference (ΔG°) and the rate constant of the individual reaction should be accurately known. Neither of these two requirements is met in the case of the PhQ^- oxidation reactions (see the reviews in refs (42–44) for more extensive discussion of this issue), precluding any further application of electron transfer theory to the experimental results at this stage.

Temperature Dependence of P_{700}^+ Reduction by Prebound PC^I . The reduction of P_{700}^+ in vivo, which is characterized by a lifetime of ~ 6 μ s at 298 K, exhibits a clear temperature dependence that is satisfactorily described by an activation enthalpy difference ($\Delta H^\ddagger$) of 105–110 meV (Figure 2). Since the reduction of P_{700}^+ requires the formation of a binary complex between PS I and PC^I , several factors could lead to a thermally activated reaction. These include the equilibrium of PC binding at the PS I luminal side, possible rearrangements of the complex to a metastable “active” intermediate from which ET takes place, and the dependence of the ET rate upon parameters already discussed for interprotein ET reactions.

Most of the previous investigations of P_{700}^+ reduction have been performed in isolated systems. The kinetics in vitro are markedly biphasic, showing components of ~ 6 –20 and 50–150 μ s (18–20). The rate of the fast phase of P_{700}^+ reduction is independent of PC^I concentration, as expected for a monomolecular rate constant, while the rate of the slower component increases with an increase in PC^I concentration, indicating the bimolecular character of this reaction (18–20). Conflicting conclusions have been reached relating to the rate-limiting step of the P_{700}^+ reduction reaction. Sigfridsson and co-workers (45–47) proposed that rearrangement of the PS I– PC^I binary complex imposes the main kinetic constraint in vitro. Structural microrearrangements would require some flexibility of the PS I– PC^I binary complex conformation, such that the active configuration would represent only one of many possible microconformational states. Hence, this process is expected to be associated with a non-negligible entropic contribution to the Gibbs free energy difference, and potentially heterogeneous kinetics due to distributed lifetimes. Díaz and co-workers (48) estimated a large value (~ 2 meV K^{-1}) for the entropy change associated with the bimolecular reduction of P_{700}^+ by either PC^I or $\text{cyt } c_6$ and attributed it to ET rather than the binding process. However, Drepper et al. (33) argued against the occurrence of significant structural reconfiguration of bound PC at the PS I docking complex, principally because of the absence of kinetic intermediates associated with the reorganization of the binary complex which, for instance, was observed in the case of P_{870}^+ reduction by $\text{cyt } c_2$ (e.g., refs 23, 31, and 32). The lifetime of the fast P_{700}^+ reduction phase was shown to be virtually independent of PC^I concentration (33). Only the amplitude of the fast phase increased as a function of PC^I concentration, as expected if it were determined by the binding equilibrium. These results argue against a significant distribution of substrates, as the number of statistically populated microconformational states should scale with the overall P_{700}^+ – PC^I binary complex concentration but are consistent with the fast phase representing the reaction within a tight preformed complex, limited by the actual ET rate (33).

Occurrence of Kinetic Intermediates Associated with Reconfiguration of the PS I(P_{700}^+)– PC^I Complex. To investigate the presence of the aforementioned intermediate

components of P_{700}^{+} reduction kinetics, we have analyzed the light-induced absorption changes on an extended time scale (up to 250 μ s) and throughout the near-UV and up to 500 nm in the visible absorption spectrum, at room temperature (298 K). The kinetics on the microsecond time scale are described satisfactorily by a biphasic decay characterized by lifetimes of 6 and ~ 56 μ s. The optical transients and global fits at a few selected wavelengths are shown in Figure 3A, while the DAS of the 6.4 and 56 μ s components are shown in Figure 3B. (The DAS of the nanosecond components were the same as those obtained in the 5 ns to 20 μ s time interval, and hence, they were omitted from Figure 3B.) It is clear that, apart from a difference in amplitude between the DAS of the ~ 6.4 and ~ 56 μ s phases, they have similar spectral profiles and are both dominated by the bleaching due to the P_{700}^{+} – P_{700} absorption difference (e.g., refs 36, 49, and 50). On the basis of the amplitude of the DAS, we estimate that the fast phase of P_{700}^{+} reduction (in preformed PS I– PC^I complexes) occurs in $>85\%$ of the PS I RCs (Figure 3B). The remainder display a slower P_{700}^{+} reduction phase with a lifetime of ~ 56 μ s at 298 K, which we attribute to the bimolecular reaction. This could be limited by PC diffusion, docking of PC^I , and release of PC^{II} at the PS I donor side. Thus, the binary complexes of PS I with PC^I represent the vast majority of PS I RCs in dark-adapted cells of *C. reinhardtii*, in agreement with previous investigations (e.g., refs (36–39)). While we cannot completely exclude the presence of a potential intermediate phase between the ~ 6 and ~ 56 μ s phase, it would have to have a small fractional amplitude ($<10\%$) to escape detection.

Occurrence of the Lifetime Distribution of P_{700}^{+} Reduction Kinetics. Structural heterogeneity in the P_{700}^{+} – PC^I binary complex would give rise to a distribution of rate constants and hence observable lifetimes (reviewed in ref 51). This should lead to a deviation from strictly exponential kinetics, which can be accommodated by stretched exponential functions (51, 52). Moreover, as the heterogeneity of the binary population is expected to depend on the temperature, so too will the lifetime distribution. To explore the presence of lifetime (rate) distributions associated with P_{700}^{+} reduction, we have globally fitted the kinetics acquired at different temperatures using stretched exponentials. This analysis was restricted to the 5 ns to 20 μ s time window, and stretching of the microsecond component only was considered. In the temperature range investigated, the stretching parameter ranged from 0.88 (277 K) to 0.97 (313 K), which indicates a relatively narrow distribution of rate constants (Figure 3C,D). This result is in agreement with experiments performed in PS I isolated from higher plants (33). The value of activation enthalpy $\Delta H^{\ddagger}$ obtained from the Arrhenius plot of the mean value of the rate constant, $\langle k(T) \rangle$, is 103 ± 1 meV, which agrees closely with the estimate obtained from global and global-target fits employing simple exponential functions. Thus, although the apparent lifetime of the fast phase of P_{700}^{+} reduction might still be determined by the kinetics of binary complex reconfiguration, our data provide little support for this hypothesis.

Estimation of the Reorganization Energy of P_{700}^{+} Reduction. If the rate of the fast phase of P_{700}^{+} reduction were determined exclusively by the ET process, then the temperature dependence of the reaction should be described consistently by electron transfer theory. In Figures 1 and 2, it is shown that the experimental results can be fitted satisfactorily using a simple model based on this theory. The only assumption, justified by the relatively high temperatures employed in these studies, is that

the coupling of the ET process with (protein) phonon modes does not deviate from that of a classical nonquantized oscillator. Then, according to Marcus (6), the free energy of activation will be defined by the equation

$$\Delta G^{\ddagger} = \frac{(\lambda_t + \Delta G^{\circ})^2}{4\lambda_t} = \frac{(\lambda_t + \Delta H^{\circ})^2}{4\lambda_t} + \frac{(T\Delta S^{\circ})^2}{4\lambda} - \frac{T(\lambda_t + \Delta H^{\circ})\Delta S^{\circ}}{2\lambda_t} \quad (6)$$

The value of $\Delta H^{\ddagger}$, which is determined experimentally, closely approximates that of $\Delta G^{\ddagger}$, which is required to obtain a lower-boundary estimate of λ_t , when $|\Delta S^{\circ}| \ll |\Delta H^{\circ}|$. A vanishing value of ΔS° might be seen as the absence, or small contribution, of reconfiguration of the solvent (protein scaffold in this case) outside the inner coordination sphere of the redox cofactors (3). It is also worth noting that the derivation of eqs 1–3 assumes that the potential surfaces of the donor–acceptor molecules in their ground and ionic states are harmonic and have the same width (1–3). As explicitly discussed by Hopfield (8), this is equivalent to the absence of large entropic (i.e., $\Delta S^{\ddagger} \cong 0$) contributions to the ET reaction, yet even in the presence of low values of ΔS° , the condition $\Delta G^{\ddagger} \cong \Delta H^{\ddagger}$ is expected to be valid, so that lower-boundary values of λ_t can be determined on the basis of independent estimates of ΔG° (53–56).

The standard midpoint potentials of the electron acceptor (P_{700}^{+}) and electron donor (PC^I) are 475 ± 10 mV (e.g., refs 33, 53, and 54) and 360 ± 10 mV (18, 55, 56), respectively, so that the average value of ΔG° is -115 meV. Following the studies of Drepper et al. (33) with isolated PS I, the free energy of P_{700}^{+} reduction in the binary complex is reduced by ~ 45 meV, to account for differences in the binding constant for oxidized and reduced PC, so that the effective free energy $\Delta G^{\circ}_c = -70$ meV (where the subscript c will be used hereafter to refer to the ΔG° of the ET reaction in the binary complex).

Assuming that (to a first approximation) the coupling with high-energy phonons is negligible in the temperature range investigated² and considering the values of ΔG° (-115 meV) and ΔG°_c (-70 meV), applying eq 6 leads to λ_t estimates of 0.62 ± 0.01 and 0.55 ± 0.01 eV, respectively.³ These values are in good agreement with the λ_t of ≥ 545 meV determined by altering the driving force for the reaction (30), confirming the validity of the assumption that $\Delta G^{\ddagger} \cong \Delta H^{\ddagger}$. $\Delta G^{\ddagger}$ would lie in the range of 85–105 meV, using the value of λ_t determined in ref 30 and the ΔG° described above, indicating that the entropic contribution to the activation free energy is quite small.

The lower bounds of λ_t can be considered accurate (within the high-temperature limit, which was also employed in ref 30) if the measured lifetimes correspond to the actual reaction rate. In the most general case, the kinetics of reduction of P_{700}^{+} in the binary complex are determined by the rates of both P_{700}^{+} reduction (k_1)

²This approximation is substantially valid provided that mean phonon frequencies $\bar{\nu} \leq 150$ cm^{-1} . Neglecting coupling with phonons might lead to underestimation of the value of λ_t .

³Deriving λ_t from $\Delta G^{\ddagger}$ involves solving a second-order equation (eq 5), so two possible values of the reorganization energy are found. Independent of the choice of ΔG° , the low boundary value of λ_t that numerically describes the activation barrier is ~ 10 meV. This would place P_{700}^{+} reduction in the so-called inverted Marcus regime, a condition in which coupling with phonon modes cannot be neglected. However, 10 meV is too small to be considered reliable. Thus, we have excluded this value.

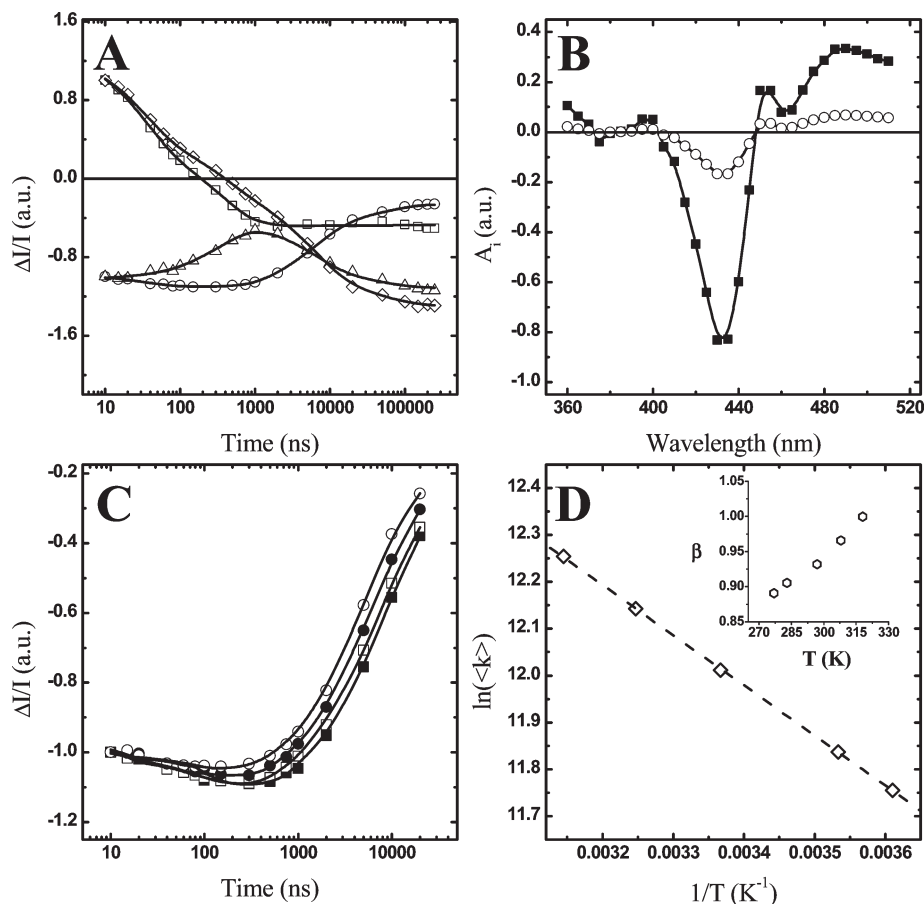


FIGURE 3: (A and B) Kinetics of flash-induced changes recorded on an extended time scale (5 ns to 300 μ s) at 298 K. (A) Kinetics recorded at selected wavelengths at 298 K: 390 ($\square$), 430 ($\circ$), 460 ($\triangle$), and 480 nm ($\diamond$). Solid lines are the best fits. (B) DAS of the components with time constants of $6.3 \pm 0.1 \mu$ s ($\blacksquare$) and $55.6 \pm 0.4 \mu$ s ($\circ$). The amplitudes are normalized to the sum of the two DAS. (C and D) Temperature dependence of P_{700}^+ reduction, fitted using the stretched exponential model function (in the 5 ns to 20 μ s temporal interval): $f(t) = e^{-(t/\tau)^\beta}$. (C) Kinetics monitored at 430 nm at 277 ($\blacksquare$), 288 ($\square$), 298 ($\bullet$), or 305 K ($\circ$). Solid lines are best fits to the experimental results. (D) Arrhenius plot of average rate constant $\langle k \rangle$, which is obtained as $\langle k(T) \rangle^{-1} = [\tau(T)/\beta(T)]\Gamma[1/\beta(T)]$ (49), where Γ is the gamma function. The slope was calculated as described in the legend of Figure 2 and yields a $\Delta H^\ddagger$ of 103 ± 1 meV. The inset in panel D shows the temperature dependence of stretching parameter β .

and the back-reaction (i.e., P_{700} oxidation by PC^{II} , $k_2 = k_1 K_{\text{eq}}^{-1}(T)$). According to the simple reaction scheme $P_{700}^+ - PC^{\text{I}} \xrightleftharpoons[k_2]{k_1} P_{700} - PC^{\text{II}}$ and neglecting the rate of dissociation of PC^{II} from the complex, the P_{700}^+ reduction kinetics is expected to be monotonic and characterized by the observable lifetime $\tau_{\text{obs}}^{-1} = k_1 + k_2 = k_1[1 + K_{\text{eq}}^{-1}(T)]$. It is thus clear that $\tau_{\text{obs}}^{-1} \cong k_1$ when $K_{\text{eq}}(T)$ is large. This is definitely the case [i.e., $K_{\text{eq}}(T) > 60$] over the temperature range investigated if ΔG° is calculated from the standard midpoint potentials of isolated complexes [i.e., assuming that the binding equilibrium of oxidized and reduced PC in vivo does not differ, as observed in vitro (33)]. However, even when the correction for the free energy of binding (i.e., using $\Delta G^\circ_{\text{c}} \sim -70$ meV) is taken into account, the value of $K_{\text{eq}}(T)$ lies in the range of 10–15, changing the rate by only $\sim 10\%$. Using this correction ($\Delta G^\circ_{\text{c}} = -70$ meV), $\Delta G^\ddagger$ is increased to 113 meV and λ_t becomes 580 meV. The effect of the back-reaction upon the apparent lifetime would be more relevant if the free energy difference associated with the oxidation of PC^{I} were to be decreased. However, in the case of previous studies in which the midpoint potential of P_{700}^+/P_{700} was altered by site-directed mutagenesis (30), the driving force was increased with respect to the wild type.

Thus, in a manner independent of the details of the kinetic model employed to describe the data, and within the range of free energy values reported in the literature, the results obtained in

this study confirm the previous conclusions based on altering the standard midpoint potential of P_{700}^+/P_{700} (30). This shows that the rate of ET occurring between two bound redox proteins can be described in a manner analogous to those of intraprotein ET reactions. This strongly indicates the formation of a tight complex between PS I and PC^{I} , which is stable within the lifetime of the ET reaction (i.e., tens of microseconds).

The value calculated for λ_t (≥ 0.54 – 0.6 eV) lies on the lower edge of the distribution for intracomplex ET reactions, which typically range from 0.7 to 1.3 eV (e.g., refs (3–5)). Such a low value is somewhat surprising, given that the redox center in PC is a copper ion, for which one would expect a larger value of λ_t associated with reduction and oxidation, compared to those of large conjugated systems like hemes and chlorins (1–5). However, these high values of λ_t are principally due to the large contribution of the rearrangement of water molecules within the metal's hydration sphere (which increases the reorganization energy of the reactant, λ_i) and the large dielectric constant of water (which increases the reorganization energy of the medium, λ_o). In cytochromes, the effect of solvent reorganization of the redox-active Fe atom is mitigated by coupling with the extended π -system of the porphyrin ring. The coordination sphere of Cu in PC includes donor bonds from the sulfur atoms in the thioether and thiolate groups of Met92 and Cys84, and from nitrogen atoms in the imidazole groups of His37 and His87 (e.g., ref 57, for

the structure of *C. reinhardtii* PC). Thus, the electron spin density of the copper ion can, in part, be shared with the ligands in the coordinating sphere; in particular, the imidazole group has some aromatic character, so that it could contribute, in a manner analogous to that of the extended tetrapyrrole rings of Chls and hemes, to a lower λ_t in the copper center of PC. In fact, mutations of the His ligands to the Cu center of PC are known to cause a remarkable slowing of the P_{700}^+ oxidation kinetics (e.g., refs 58 and 59).

Moreover, the donor side of PS I immediately above P_{700} is also very flat and hydrophobic, very much like the face of PC that binds there. It has been discussed before that this should lead to the exclusion of water molecules upon binding of PC to PS I (e.g., refs 25 and 60), minimizing their impact on the reorganization energy within the PS I– PC^I binary complex. The aromatic side chain of highly conserved Trp residues of PsaA (Trp651) and the PsaB (Trp627) also play a crucial role in modulating the affinity of the PC (and cyt c_6) binding to PS I (e.g., refs 25 and 60). Both residues are close to the primary donor, so that the large hydrophobic patch at the interface between PC and PS I might serve not only in the optimization of binding but also in providing a preferential route for ET, while excluding water at the interface of the binary complex. In fact, site-directed mutations targeting PsaB Trp627 and PsaA Trp651 had the effect of both reducing the affinity of binding for PC (and cyt c_6) and slowing the fast phase of P_{700}^+ reduction by the residual fraction of bound donor (25, 60).

Is the Optimization of P_{700}^+ Reduction Physiologically Significant? Ramesh and co-workers (30) calculated a maximal rate of $2.6 \times 10^6 \text{ s}^{-1}$ for reduction of P_{700}^+ in vivo at 298 K, using the relationship $\Delta G^\circ = -\lambda_t = -545 \text{ meV}$. We obtained a similar, albeit slightly larger, value of $\sim 9 \times 10^6 \text{ s}^{-1}$ from our independent estimation of λ_t (0.55–0.62 eV), which yields the electronic coupling element ($|V_{AD}|$) value of $\approx 0.16 \text{ cm}^{-1}$. These values, while realistic, are at least somewhat inaccurate, because of the limited intervals of ΔG° and T spanned in the two investigations. Nonetheless, these values can be used to calculate, to a first approximation, the rate constant of P_{700}^+ reduction for λ_t of $\approx 1 \text{ eV}$, the average value for interprotein electron transfer, all other conditions remaining unchanged (including coupling with phonons).

Depending on the precise value of $|V_{AD}|$ used, the calculated maximal rate constant for ET would lie in the range of $1.5\text{--}3.5 \times 10^3 \text{ s}^{-1}$. This value is ~ 2 orders of magnitude smaller than the experimentally observed rate ($\sim 2 \times 10^5 \text{ s}^{-1}$), indicating that the low value of λ_t plays a significant role in the optimization of this electron transfer reaction, by lowering the activation barrier. In the more general case (i.e., when dropping the high-temperature limit), lowering of the barrier can also be the result of coupling ET with phonons of midhigh frequencies ($\bar{\nu} \geq 350 \text{ cm}^{-1}$) when $\lambda_t \geq 0.8 \text{ eV}$. For instance, the calculated ET rates for a λ_t of 1 eV would yield observed lifetimes of P_{700}^+ reduction in the range of 250–750 μs . Alternatively, similar lengthening of the reaction kinetics is predictable by considering a communal “large” value of λ_t ($\sim 1 \text{ eV}$) when the frequency of the mean phonon is decreased from that of a “hard” environmental mode (i.e., $\geq 350 \text{ cm}^{-1}$) to that of a “soft” mode ($\leq 50 \text{ cm}^{-1}$). The calculated rates of P_{700}^+ reduction in the 250–750 μs interval are not only significantly slower than those of the diffusion-limited process (50–70 μs , in vivo) but also enter the same time scale of P_{700}^+ reduction by charge recombination from either PhQ^- (10–100 μs ; reviewed in refs 43 and 44) or F_X ($\sim 1 \text{ ms}$ (43, 44)).

It seems unlikely that charge recombination would impose a limitation on electron transport through the whole chain under typical growth conditions, as ET from PhQ to F_X and then to F_A and F_B takes place on the submicrosecond time scale (e.g., refs (42–44) and Figure 1). However, it is conceivable that the overall turnover rate of PS I, which is principally determined by donation of electrons from PC, might impose a kinetic bottleneck if it became comparable to that of cyt b_6f turnover.

To evaluate semiquantitatively the possible limitation imposed by a “slow” reduction of P_{700}^+ by PC^I , we have simulated the reduction kinetics of P_{700}^+ considering two different scenarios that occur in photosynthetic organisms. The first corresponds to the situation found in eukaryotes, such as *C. reinhardtii*, in which the binding equilibrium of PC is largely in favor of the PS I– PC^I binary complex, making the $\sim 6 \mu\text{s}$ phase the predominant P_{700}^+ reduction component. On the basis of the results obtained in this study, we estimated an equilibrium binding constant ($K_{\text{bin}}^{\text{eq}}$) of ~ 6 . The second scenario is that found in certain cyanobacterial strains, in which the lifetime of P_{700}^+ reduction is largely determined by the rate of formation of the PS I– PC^I binary complex. In this case, P_{700}^+ is reduced with an average lifetime of $\sim 100 \mu\text{s}$ (e.g., refs (18–20)). Fast components (6–10 μs) of P_{700}^+ reduction are also observed in cyanobacteria in vivo and generally account for 15–20% of the total amplitude (e.g., refs 20, 26, and 48), yielding $K_{\text{bin}}^{\text{eq}}$ values of ≈ 0.2 . We have considered a simplified kinetic scheme (Figure 4) in which only two reactions are considered: (1) formation of the PS I(P_{700}^+)– PC^I complex and (2) the subsequent ET reaction leading to reduction of P_{700}^+ and oxidation of PC^I . As the dissociation of the PS I(P_{700}^+)– PC^{II} binary complex is not taken into account, this represents an only first-order approximation. The simplified model describes relatively well the biphasic reduction of P_{700}^+ for the eukaryotic-like as well as the prokaryotic-like scenario, both in terms of lifetime and in terms of relative amplitudes (Figure 4). In the two cases considered, the mean lifetime $\bar{\tau}^4$ has values of 103 and 258 μs when the electron transfer rate is determined with a λ_t of 0.65. With an increase in the reorganization energy to 1 eV, the value of $\bar{\tau}$ increases to 147 μs (eukaryote-like scenario) or 455 μs (prokaryote-like scenario). This is determined by two factors, the lengthening of the lifetime associated with the electron transfer component (from ~ 6 to $\sim 50 \mu\text{s}$) and a small redistribution of the phases’ amplitudes in favor of the diffusion-controlled rate. Interestingly, the prokaryotic-like scenario shows a larger sensitivity to a change in λ_t , the slowing of P_{700}^+ reduction being more evident than in the case of the eukaryotic-like scenario. This stems from the fact that, in this case, the pure ET phase is barely present. It is clear from this relatively simple approach that a decrease in the pure ET rate would lead to overall P_{700}^+ reduction times that are comparable to that of cyt f turnover, which, under conditions in which photosynthetic ET is coupled to ATP synthesis, display average lifetime values of $\sim 200\text{--}300 \mu\text{s}$ for cyt f oxidation and $\sim 2 \text{ ms}$ for cyt f and cyt b reduction at the Q_o site (e.g., refs 19 and 61).

Hence, for the situations described above, one would expect to accumulate a fraction of P_{700}^+ under moderate steady-state illumination conditions. This might lead to an overall lowering of the rate of photosynthetic electron transport, as well as its

⁴The mean lifetime is defined as the first moment of the (normalized) function $f(t)$ describing the time dependence of the concentration of a given species. $\bar{\tau} = \int t f(t) dt$. The nondecaying component (Figure 4) has been omitted from the evaluation of $\bar{\tau}$.

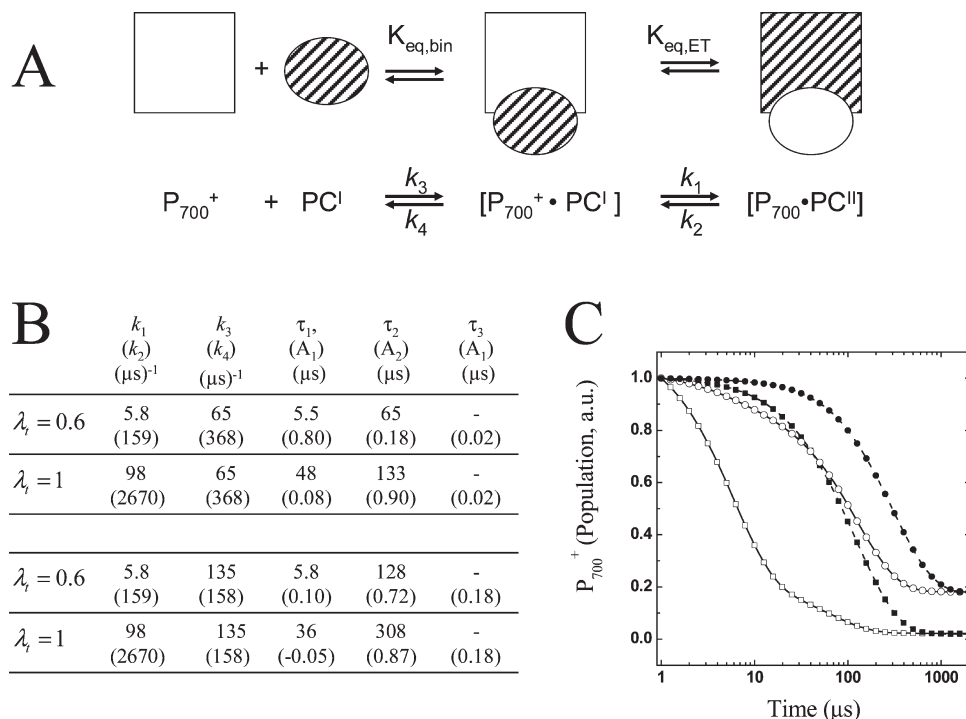


FIGURE 4: Simulations of the P_{700}^{+} reduction by prebound and diffusible PC^I . (A) Schematic representation of the kinetic model employed in the calculations, the principal parameters of which are given in panel B for four considered scenarios. Note that k_3 is a second-order rate constant, while the other three are first-order constants. The system is solved for an approximate value of $k_3' = k_3 \gamma_{PC^I}$, where γ_{PC^I} is the molar fraction of unbound PC^I , which is thought not to change significantly during the course of the kinetics (i.e., $[PC^I] \gg [PS II]$). (C) Temporal evolution of the total P_{700}^{+} molar fraction, calculated for four different scenarios: ($\square$) $\lambda_t = 0.65$ meV, $\Delta G^\circ = -85$ meV (this value of ΔG° is used in all of the simulations), and $K_{bin}^{eq} = 5.6$; ($\blacksquare$) $\lambda_t = 1$ eV ($K_{bin}^{eq} = 5.6$); ($\circ$) $\lambda_t = 0.65$ meV and $K_{bin}^{eq} = 0.25$, and ($\bullet$) $\lambda_t = 1$ eV ($K_{bin}^{eq} = 0.25$). Further details are given in the text.

efficiency, by the accumulation of photochemically incompetent PSI units. In this respect, the results of these simulations, although admittedly using a somewhat overly simplified reaction scheme, are qualitatively in agreement with the results obtained in mutants of *C. reinhardtii* either deficient or carrying substitutions in conserved residues of the N-terminal extension of the PsaF subunit, which is found only in eukaryotes and has been shown to be necessary for tight docking of PC and cyt c_6 . These mutants display slow kinetics of P_{700}^{+} reduction, and they are sensitive to light intensities exceeding $400 \mu\text{E m}^{-2} \text{s}^{-1}$ under aerobic conditions (25, 60).

SUPPORTING INFORMATION AVAILABLE

Decay-associated spectra from the fit of room-temperature kinetics, temperature dependence of the pre-exponential factors derived from the global-target fit of the experimental results, and temperature dependence of the lifetimes of nanosecond lifetimes derived from the global analysis of the experimental data. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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