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Rates and Equilibrium of Cu_A to Heme *a* Electron Transfer in *Paracoccus denitrificans* Cytochrome *c* Oxidase

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ABSTRACT Intramolecular electron transfer between Cu_A and heme *a* in solubilized bacterial *(Paracoccus denitrificans)* cytochrome *c* oxidase was investigated by pulse radiolysis. Cu_A, the initial electron acceptor, was reduced by 1-methylnicotinamide radicals in a diffusion-controlled reaction, as monitored by absorption changes at 825 nm, followed by partial restoration of the absorption and paralleled by an increase in the heme *a* absorption at 605 nm. The latter observations indicate partial reoxidation of the Cu_A center and the concomitant reduction of heme *a*. The rate constants for heme *a* reduction and Cu_A reoxidation were identical within experimental error and independent of the enzyme concentration and its degree of reduction, demonstrating that a fast intramolecular electron equilibration is taking place between Cu_A and heme *a*. The rate constants for Cu_A → heme *a* ET and the reverse heme *a* → Cu_A process were found to be 20,400 s^{-1} and 10,030 s^{-1}, respectively, at 25°C and pH 7.5, which corresponds to an equilibrium constant of 2.0. Thermodynamic and activation parameters of these intramolecular ET reactions were determined. The significance of the results, particularly the low activation barriers, is discussed within the framework of the enzyme's known three-dimensional structure, potential ET pathways, and the calculated reorganization energies.

INTRODUCTION

Cytochrome *c* oxidase (CcO) is the terminal enzyme in the respiratory chain of most aerobic organisms where it catalyzes the sequential four-electron transfer from cytochrome *c*, or c_{552} in the case of *Paracoccus denitrificans*, to dioxygen; for recent reviews, see Richter and Ludwig (1) and Wikström (2).

CcO has four redox active metal centers, a mixed-valence copper pair forming the so-called Cu_A center, the low-spin heme *a*, and heme a_3 with Cu_B, which together form the binuclear center. Cu_A serves as the electron acceptor from cytochrome *c*. Electrons are transferred from Cu_A to heme *a* and subsequently to the binuclear center where O_2 is reduced to water. The intramolecular electron transfer reactions are coupled to the translocation of protons across the membrane (3–9) by a mechanism that is still under discussion (5,10–12). The involvement of hydrogen-bonded water networks in proton transport in relation to ET, mainly the heme *a*/heme a_3–Cu_B transition, has been discussed recently (13). The electrochemical proton gradient resulting from the redox reactions is finally used by ATP synthase to generate ATP.

The electron transfer reactions between cytochrome *c* and CcO and within CcO have been investigated by several methods (14–22). Alternative approaches include flow-flash experiments of the reaction of the electrostatic CcO/cytochrome *c* complex with O_2 (23,24), time-resolved measurements of the reverse electron transfer from the binuclear center to the oxidized heme *a* and Cu_A upon photolysis of the three-electron reduced CO-inhibited enzyme (25) and light-induced electron injection into the oxidase (8,26–29) or the electrostatic cytochrome *c*/cytochrome oxidase complex (30–32). All these results support Cu_A being the electron acceptor from cytochrome *c*, which is then followed by ET to heme *a*.

Pulse radiolysis has been widely used to monitor intramolecular ET in several redox enzymes ranging from multicopper enzymes such as laccase, ascorbate oxidase, ceruloplasmin (33–35), and copper-containing nitrite reductase (36–40) to the heme containing cd_1-nitrite reductase (41–44) as well as the multicentered xanthine oxidase (45–47). The method has also been applied to studying intramolecular ET in bovine CcO where it was demonstrated that 1-methylnicotinamide radicals reduce oxidized Cu_A in a diffusion-controlled process, followed by intramolecular equilibration between Cu_A and heme *a* (48,49).

The available high-resolution three-dimensional (3D) structures of both mammalian and bacterial cytochrome *c* oxidases (50–57) make a correlation of the ET reactivity more meaningful. Hence, we investigated the intramolecular ET thermodynamics and kinetics of the Cu_A-heme *a* equilibration using pulse radiolysis to correlate the internal ET reactivities with their known 3D structures.

MATERIALS AND METHODS

All chemicals were of analytical grade and used without further purification. Milli-Q water (Millipore, Eschborn, Germany) was used throughout the studies.

Enzyme preparation

Cytochrome c oxidase from *P. denitrificans* was isolated in detergent micelles according to Hendler et al. (58). The pure CcO fractions eluted from

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Abbreviations used: CcO, cytochrome *c* oxidase; ET, electron transfer; MNA, 1-methyl nicotinamide; DM, *n*-dodecyl-β-D-maltoside.

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DEAE-Sepharose CL-6B (Amersham, Freiburg, Germany) with a NaCl-gradient in 20 mM KP_i, 1 mM EDTA, pH 8.0, containing 0.4 mM DM (Glycon, Luckenwalde, Germany) at 4°C were concentrated with buffer-washed VivaSpin concentrators (50 kD CO from VicaScience, Hannover, Germany). A concentrated sample of 68 mg CcO in 4 ml of the elution medium was added to a small column with 4 ml Q Sepharose FastFlow (Amersham, Freiburg, Germany), equilibrated with 10 mM KP_i and 0.5 mM DM pH 7.5 at 4°C, was washed with 100 ml of the same DM containing buffer. Elution with 600 mM KCl in 10 mM KP_i and 0.5 mM DM pH 7.5 provided concentrated fractions of CcO. To remove KCl, the chosen fractions were dialyzed at 4°C in Spectra/Por CE tubing (50 kD CO from Spectrum Laboratories (Rancho Dominguez, CA), for 3 days against 10 mM KP_i and 0.5 mM DM, pH 7.5 (three buffer changes). CcO concentration was determined at 425 nm on the basis of an extinction coefficient of 1.57×10^5 $M^{-1}cm^{-1}$. The activity, measured at 550 nm with 50 μM $Na_2S_2O_4$-reduced horse-heart cytochrome *c* (Biomol, Hamburg, Germany) under substrate saturation conditions in the presence of 0.5 nM CcO in 10 mM KP_i, 40 mM KCl, and 0.5 mM DM at 25°C and pH 7.5, provided a turnover number of 290 electrons s^{-1}.

Determination of extinction coefficient

For the determination of the Cu_A extinction coefficient in 10 mM KP_i and 0.5 mM DM pH 7.5 at 25°C, the visible spectrum of $Na_2S_2O_4$-reduced CcO was subtracted from that of the oxidized enzyme, which exhibits a maximal value at 830 nm. The Cu_A extinction coefficient was 2140 $M^{-1}cm^{-1}$. The apparent absorption of the reduced form above 700 nm is due to light scattering contributions of the mixed protein/detergent micelle.

Kinetic measurements

Time-resolved measurements were carried out using the pulse radiolysis system based on the Varian V-7715 linear accelerator at the Hebrew University in Jerusalem, Israel. Accelerated electrons (5 MeV) were employed using pulse lengths in the range from 0.1 to 1.5 μs in protein solutions containing 5 mM 1-methylnicotinamide (MNA^+), 10 mM KP_i, and 0.5 mM DM at pH 7.5. The yield of reducing MNA* radicals was ~1.5 μM/μs pulse width. All measurements were carried out anaerobically in solutions saturated with and kept under purified argon at a pressure slightly in excess of atmospheric pressure. The detergent also serves as a scavenger for OH radicals. A 1-cm spectrosil cuvette was employed, using one or three light passes that result in an overall optical pathlength of either 1 or 3 cm, respectively. A 150-W xenon lamp produced the analyzing light beam together with a Bausch & Lomb (Rochester, NY) double grating monochromator. Appropriate optical filters with cutoff at 385 or 590 nm were used to reduce photochemical and light scattering effects. The data acquisition system consisted of a Tektronix (Beaverton, OR) 390 A/D transient recorder attached to a PC. The temperature of the reaction solutions in the cuvette (15 different temperatures in the range from 4.1 to 36.4°C) was controlled by a thermostating system, and continuously monitored by a thermocouple attached to the cuvette. Reactions were generally performed under pseudofirst-order conditions, with typically a 20-fold excess of oxidized protein over reducing radicals. In each experiment 2000 data points are collected, divided equally between two different timescales. Usually the processes were recorded over at least three half-lives. Each kinetic run was repeated at least four times. The data were analyzed by fitting to a sum of exponentials using a nonlinear least squares program written in MATLAB (The MathWorks, Natick, MA).

RESULTS

In the presence of an ~100-fold excess of 1-methyl nicotinamide (MNA^+) over protein and under anaerobic conditions, the hydrated electrons produced by the radiation pulse react with the former species to produce MNA* radicals almost quantitatively. Formation and decay of this radical can be monitored at 420 nm ($\varepsilon_{420} = 3200$ $M^{-1}cm^{-1}$) (44); the formation takes place in the microsecond timescale whereas its decay, by dismutation, takes place in the time range of milliseconds. The oxidized Cu_A center, which exhibits a weak and comparatively broad absorbance around 830 nm, was found to be reduced according to its absorption change monitored at 825 nm concomitantly with the disappearance of the MNA* radical. The rate constant for this intermolecular ET process depends, as expected under pseudofirst-order conditions, on the enzyme concentration being in excess and the bimolecular rate constant was calculated to be 3×10^9 $M^{-1}s^{-1}$ at 25°C, i.e., an essentially diffusion-controlled process. Successive pulses were introduced into the same protein solution causing the stepwise reduction of the oxidized enzyme. The reduction yield of the enzyme per pulse could be determined from the absorption changes of the fast Cu_A reduction phase. After adding two reduction equivalents to the enzyme solution, the Cu absorption at 825 nm becomes negligible, indicating that the initial reduction phase appears to be complete. Introducing additional pulses into the solution only led to MNA* formation followed by dismutation of these radicals, but no further absorption changes of the enzyme were observed.

Under the conditions of incomplete reduction of the protein, subsequent to the fast bimolecular reduction of the binuclear copper center, the reduced Cu_A site was found to undergo partial reoxidation as revealed by an increase in absorption at 825 nm (Fig. 1 *A*). The observed rate constant k_{obs} of this step is $(3.05 \pm 0.25) \times 10^4$ s^{-1} at 25°C (pH 7.5) and was found to be independent of enzyme concentration or its degree of reduction. Because this reaction step occurs simultaneously with an absorption increase at 605 nm (Fig. 1 *B*), where the reduced heme *a* absorbs predominantly ($\Delta\varepsilon_{605} = 18{,}600$ $M^{-1}cm^{-1}$), we assign this reaction step to an intramolecular ET between reduced Cu_A [Cu_A(I)] and oxidized heme *a* [Fe_a(III)]. This is further substantiated by the observation that the amplitude ratio of the absorbance increases at 825 nm (Cu_A reoxidation) relative to that at 605 nm (heme *a* reduction) is as expected from their respective extinction coefficients. The process does not go to completion, however, and by determining the amplitudes of Cu_A reduction and reoxidation at 825 nm (cf. Fig. 1 *A*) an equilibrium constant was calculated for the reaction:

$$Cu_A(I)Fe_a(III) \rightleftarrows Cu_A(II)Fe_a(II), \qquad (1)$$

at 25°C, leading to $K = 2.0 \pm 0.1$. The experimentally observed rate constant of the equilibration process (Eq. 1) is the sum of the forward and the reverse ET steps: $k_{obs} = k_f + k_b$. Because the equilibrium constant K is equal to k_f/k_b, the individual rate constants could be calculated. Equilibrium and rate constants of this reaction were determined as a function of temperature in the range from 4.1 to 36.4°C (Fig. 1 *C*), and the results are summarized in Table 1.

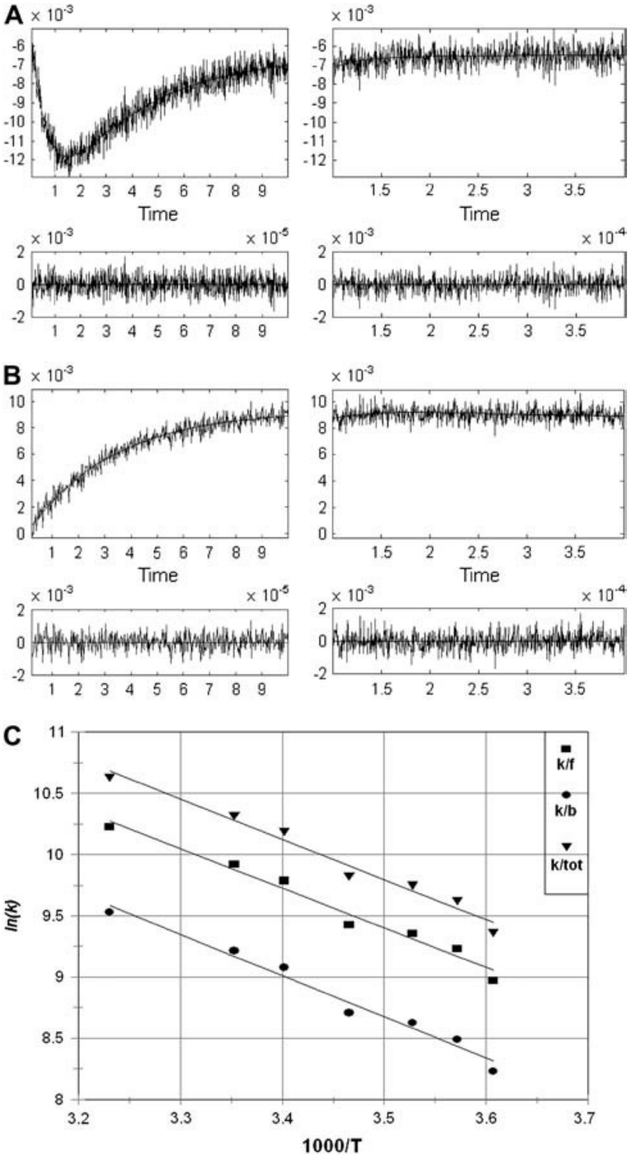

FIGURE 1 Time-resolved absorption changes. In the left-hand panel the initial reaction phase is shown. The reaction is followed further at a slower timescale in the right panel. (*A*) Cu_A reduction and reoxidation monitored at 825 nm. Enzyme concentration, 52 μM; MNA concentration, 5 mM; argon saturated buffer, 10 mM phosphate, 0.5 mM DM, pH 7.5. Temperature, 298 K. Optical pathlength, 3 cm. Pulse width, 1.0 μs. (*B*) Heme *a* reduction monitored at 605 nm. Enzyme concentration, 15.4 μM; MNA concentration, 5 mM; argon saturated buffer, 10 mM phosphate, 0.5 mM DM, pH 7.5. Temperature, 298 K. Optical pathlength, 3 cm. Pulse width, 0.3 μs. (*C*) Temperature dependence of rate constants for the forward (k_f), reverse (k_b), and total (k_{tot}) reaction as depicted in Eq. 1.

TABLE 1 Kinetics and thermodynamics of Cu_A-heme *a* ET equilibration at 25° C and pH 7.5

Kinetic parameters	k / s^{-1}	$\Delta H^{\neq}$/kJ mol^{-1}	$\Delta S^{\neq}$/J K^{-1} mol^{-1}
Forward (bacterial)*	20,400 ± 1500	22.2 ± 1.2	−88 ± 2
(bovine)†	13,000 ± 1200	11.4 ± 0.9	−128 ± 11
Reverse (bacterial)*	10,030 ± 800	24.6 ± 1.3	−86 ± 2
(bovine)†	3700 ± 300	13.4 ± 1.0	−131 ± 11
Equilibrium data	K	ΔH^0/kJ mol^{-1}	ΔS^0/J K^{-1} mol^{-1}
(bacterial)*	2.0 ± 0.1	−2.4 ± 0.7	−2.6 ± 2.4
(bovine)†	3.4 ± 0.5	−2.0 ± 0.3	3 ± 5

*This work.

†Farver et al. (49).

DISCUSSION

The reaction scheme for the ET processes monitored in this study can be depicted as follows:

$$e^-_{aq} + MNA^+ \rightarrow MNA^* \quad (2)$$

$$MNA^* + Cu_A(II)Fe_a(III) \rightarrow Cu_A(I)Fe_a(III) + MNA^+ \quad (3)$$

$$Cu_A(I)Fe_a(III) \rightleftarrows Cu_A(II)Fe_a(II). \quad (4)$$

The MNA* radicals formed, as indicated in Eq. 2, reduce the Cu_A site in a diffusion-controlled bimolecular reaction (Eq. 3). The reduction of Cu_A was found to be followed by a rapid partial reduction of heme *a* (Eq. 4). The bimolecular rate constant of the reaction between the enzyme and MNA* of 3×10^9 $M^{-1}s^{-1}$ at 25°C is identical with that obtained earlier for bovine CcO (49). The reduction of heme *a* takes place by an intramolecular ET from reduced Cu_A, as evidenced by the simultaneous absorption changes taking place at 825 nm (Cu_A) and 605 nm, where heme *a* contributes ~65% to the total absorption (cf. Fig. 4 in Hellwig et al. (59)). These time-resolved absorbance changes are illustrated in Fig. 1. The rate constant of the intramolecular electron transfer from Cu_A to heme *a* of $(3.05 \pm 0.25) \times 10^4$ s^{-1} observed here at 298 K is almost twice as large as that has been determined earlier for intramolecular ET in the bovine CcO $(1.67 \pm 0.23) \times 10^4$ s^{-1} (49). The latter value is similar to the reciprocal τ-value determined by Kobayashi et al. (48), also by employing pulse radiolysis. The equilibrium constant for the internal electron equilibration is $K = 2.0 \pm 0.1$, i.e., half of the value determined earlier for the bovine protein (cf. Table 1). It is noteworthy that the activation enthalpies of the intramolecular ET in both proteins are quite small, and that the higher rate observed for the bacterial enzyme is therefore due to a more advantageous activation entropy. Studies of intramolecular ET reactivity in *P. denitrificans* CcO were performed in the presence of a detergent (18) and with a reconstituted system (8). The reported reciprocal τ-value of 4.6×10^4 s^{-1} obtained with the reconstituted enzyme is close to our results. Some studies of the *Rhodobacter spheroides* enzyme or its complex with cytochrome *c* (28,29,31) were characterized by higher rate constants than those observed for the *P. denitrificans* protein. All other investigations were done on the bovine enzyme in the pH range of 7.0–8.1, mostly close to room temperature and under low ionic strength conditions, with the free enzyme or its complex with CO or cytochrome *c* or in its chemically modified state. The majority of these studies provide only τ-values of the ET process (23,26,29,30,60) rather than specific rate constants of individual steps as reported here. Similar rate constants were reported or can be deduced for the bovine enzyme by Morgan et al. (25) and Szundi et al. (32). Although the hitherto published dynamic and thermodynamic parameters vary, they agree within one order of magnitude.

No direct reduction by free radicals of the heme *a* site, which is mainly shielded by the hydrophobic residues of the protein, was observed. Also, there is no indication in these experiments, under conditions where the enzyme is present in considerable stoichiometric excess, for reduction of the heme a_3 site directly or by electron transfer from the reduced heme *a* or Cu_A, even on a 10-s timescale. Intramolecular ET between heme *a* and heme a_3 would result in an absorbance decrease at 605 nm where heme *a* contributes considerably more to the absorption than heme a_3. Heme a_3 exhibits, in the case of the bacterial enzyme, a maximum value at 609 and a shoulder at 588 nm, as determined in the absence of inhibitors (59). Our observation that no changes could be resolved in absorption properties of the oxidized heme a_3-Cu_B binuclear center is in full agreement with results of earlier studies where no reoxidation of heme *a* by the heme a_3-Cu_B binuclear center was not observed (26,30,48,60). Still, it is noteworthy that in the presence of a large excess of reducing agent and absence of O_2, Richter et al. (61) observed a comparatively slow process in the time range of seconds, which was assigned to the electron transfer between heme *a* and a_3.

Heme a_3 and Cu_B are strongly coupled, implying that separate reactivities of the individual components in electron transfer is not probable. As discussed by Wikström et al. (62,63) reduction of heme a_3 by heme *a* should, in principle, be a very fast process provided that several conditions are fulfilled concerning protolytic reactions within the oxygen reduction site and possibly also the involvement of structural features. Thus, electron transfer from heme *a* to a_3 cannot be excluded but, under the conditions of our study (excess oxidase over reductant) has not been observed within a time range of 10 s. Using published reduction potentials of the redox centers in CcO, and assuming no cooperativity between sites we find that a given number of added electrons at full equilibrium should be distributed in the following way: reduced Cu_A, 26%; reduced heme *a*, 53%; reduced heme a_3, 21%. It has, however, been suggested earlier that the redox state of heme *a* does influence the potential of the heme a_3/Cu_B couple, implying that coupling exists between these two centers (63). Therefore, assuming that the sites do interact, the potentials might change with electron uptake, making ET to heme-a_3 less likely. Further, the path leading from Cu_A to heme a_3 is much longer (12 covalent bonds and two H-bonds) than the Cu_A to heme *a* path (seven covalent bonds and two H-bonds). By careful examination of the stoichiometry of the reactions monitored, our results clearly demonstrate that under these experimental conditions, only two reduction equivalents are taken up by the enzymes. One rationale for this observation could thus be kinetic (weaker electronic coupling between Cu_A and heme a_3-Cu_B) whereas the other rationale could be thermodynamic (reduction potentials).

Calculation of the equilibrium electron distribution from the difference in midpoint reduction potentials of hemes *a* and a_3 of the *P. denitrificans* enzyme (at pH 7 and 5°C in the presence of 100 mM KCl) of 230 and 205 mV versus SHE (59), respectively, indicates that heme *a* reduction would be favored relative to that of heme a_3. The ET process between heme *a* and heme a_3 is likely to be influenced by conformational properties of the enzyme, and obviously in the presence of O_2 additional driving force would promote this process. As already stressed, we have not been able to introduce more than two reduction equivalents into the enzyme, indicating that ET to the heme a_3-Cu_B system does not take place under these experimental (i.e., anaerobic) conditions, which is in accordance with the above-mentioned reduction potentials.

The observed equilibrium constant of the rapid Cu_A/heme *a* electron exchange step (cf. Eq. 4) is 2.0 ± 0.1 at 25°C, pH 7.0, which corresponds to a difference in reduction potentials between the heme *a* [Fe(III)/Fe(II)] and Cu_A [Cu(II)/(I)] couples of +18 ± 1 mV. For Cu_A in the *P. denitrificans* CcO, a midpoint potential of 213 mV versus SHE was determined under the conditions mentioned above (P. Hellwig, Institute of Biophysics, J. W. Goethe-University, Frankfurt, Germany; personal communication, 2005). The equilibrium constant determined here is thus in excellent agreement with the differences between the reduction potentials of heme *a* and Cu_A (+17 mV = 230 − 213 mV).

The electron distribution at equilibrium between heme *a* and Cu_A exhibits an exceptionally small temperature dependence; thus we find $\Delta H^0 = -2.4 \pm 0.7$ kJ mol^{-1} and $\Delta S^0 = -2.6 \pm 2.4$ J K^{-1} mol^{-1}. These very small values are also in good agreement with earlier results (49) obtained for the bovine CcO. The equilibrium and kinetic data enable us to calculate the activation parameters for both forward and reverse ET reactions between Cu_A and heme *a* (cf. Fig. 1 *C* and Table 1). For comparison, earlier results obtained for intramolecular ET in the bovine enzyme are also presented here.

Electron transfer between electron donor (D) and acceptor (A) in a weakly coupled system can be described by the semi-classical Marcus equation for nonadiabatic processes (64):

$$k = \frac{2\pi}{\hbar} H_{DA}^2 (FC), \tag{5}$$

where H_{DA} is the electronic tunneling matrix element coupling D and A:

$$H_{DA} = H_{DA}^0 \exp\left\{ -\frac{\beta}{2}(r - r_0) \right\}. \tag{6}$$

H_{DA}^0 is the maximal electronic coupling at van der Waals contact distance (r_0). FC is the Franck-Condon factor, which in the classical limit ($k_B T > h\nu$) is

$$FC = \frac{1}{(4\pi\lambda_{TOT}RT)^{1/2}} \exp\{-(\Delta G^0 + \lambda_{TOT})^2 / 4\lambda_{TOT}RT\}. \tag{7}$$

ΔG^0 is the standard free-energy difference between D and A, λ_{TOT} is the reorganization energy required for changes in the nuclear configuration of the redox centers accompanying ET.

The optimal electron tunneling pathway (65) from Cu_A to heme *a* has been calculated using the HARLEM program (66) and proceeds via a hydrogen bond between the His-224 ligand and the carbonyl group of Arg-473. Another hydrogen bond connects the Arg-474 amide nitrogen to one of the heme *a* propionyl side chains (cf. Fig. 2). Altogether the path includes 14 covalent bonds and two hydrogen bonds (cf. Fig. 2). This corresponds to an effective tunneling length, $\sigma_\ell = 2.52$ nm and an electronic coupling decay factor, $\Pi = 1.0 \times 10^{-4}$. The metal-to-metal distance is 1.98 nm. The same pathway has been proposed for the bovine CcO for which we have calculated the electronic coupling energy, H_{DA}, to be 2.9×10^{-6} eV (49) in good agreement with Brzezinski (67) who had estimated the electronic coupling energy between Cu_A and heme *a* to be 3.8×10^{-6} eV. From Eqs. 5 and 7 we now find $\lambda_{TOT} = 0.32$ eV, in rather good agreement with the value of 0.3 eV, estimated by Brzezinski (66). To account for the maximum (activationless) rate constant of 8×10^5 s^{-1}, Ramirez et al. (68) calculated, from a driving force of 0.05 eV, that the value of the reorganization energy must be between 0.15 and 0.5 eV. Paula et al. (6) have estimated the lower limit of the electron transfer rate constant between Cu_A and heme *a* to be $\sim 2 \times 10^5$ s^{-1} during the reduction of O_2 to water by fully reduced oxidase using the flow-flash method. Electron transfer between Cu_A and heme *a* was found to be limited by proton uptake (6), and the rate constant would correspond to a reorganization energy close to 0.3 eV (68), which is in good agreement with the value reported here. Finally, comparing the reorganization energies for internal ET in bacterial and bovine CcO it is interesting that in the former enzyme λ_{TOT} is smaller (0.32 eV) than in the latter (0.40 eV). Thus, the reason for the higher rate of internal ET in bacterial CcO is a smaller energy requirement for reorganization of the redox centers in *P. denitrificans* CcO. This is in accordance with the observation that in bovine CcO, the subunits containing the heme regions are possibly surrounded by additional water molecules that are not seen in the bacterial enzyme; the medium surrounding an active site in a metalloprotein will affect the reorganization energy associated with the ET reaction. Thus, a hydrophobic active site will lead to smaller reorganization energies than a hydrophilic one, and consequently the kinetics of intraprotein ET will be highly sensitive to the active site environment.

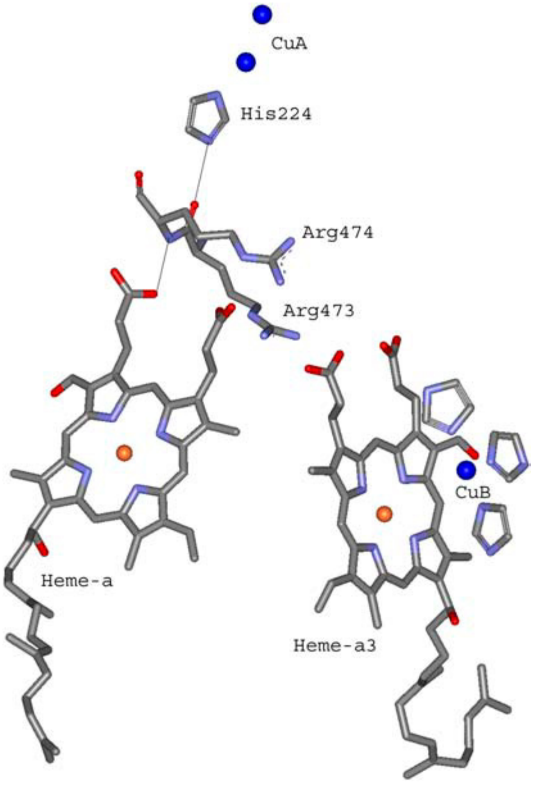

FIGURE 2 Electron transfer pathway between Cu_A and heme *a* in *P. denitrificans* CcO. The center-to-center pathway consists of 14 covalent bonds and two hydrogen bonds. The figure is based on the published 3D structure of *P. denitrificans* CcO (50). The two Cu_A atoms (*top*) are bound to the protein subunit II, whereas heme *a* (*left*) and heme a_3 (*right*) are bound to subunit I.

CONCLUSIONS

Analysis of both the time course and amplitudes of the intramolecular electron transport between Cu_A and heme *a* in bacterial cytochrome *c* oxidase has yielded the microscopic rate constants, activation parameters, and equilibrium constant as presented in Table 1. These results extend significantly the rigorous framework for understanding the electron transfer interactions between Cu_A and heme *a*.

The experimentally determined rate constants agree well with those theoretically calculated using results of previous work on intramolecular ET in both copper and heme containing proteins.

The ET process is characterized by an unusually small reorganization energy requirement.

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