Mechanism of Charge Migration through DNA: Molecular Wire Behavior, Single-Step Tunneling or Hopping?

Ferdinand C. Grozema, Yuri A. Berlin,† and Laurens D. A. Siebbeles*

Contribution from the Radiation Chemistry Department, IRI, Delft University of Technology, Mekelweg 15, 2629 JB Delft, The Netherlands

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Abstract: In this work the mechanism of migration of positive charges through donor−DNA−acceptor systems is studied using a quantum mechanical model based on the tight-binding approximation. For DNA bridges containing only adenine-thymine (AT) base pairs the difference in ionization potential between the donor moiety and the AT base pairs (i.e., the injection barrier) is shown to determine the mechanism by which the charge migrates from the donor to the acceptor. For an injection barrier of 0.55 eV, corresponding to a guanine radical cation as the hole-donor, a β-value of 0.85 Å^{-1} is found. This agrees reasonably with the value of $\beta = 0.7$ Å^{-1} deduced from experimental studies on these sequences. For this injection barrier (0.55 eV) the charge density on the AT bridge was found to be very small, which is characteristic for charge transfer by single-step tunneling. For lower injection barriers the charge density on the AT bridge becomes substantial and the charge moves through the bridge according to a bandlike mechanism. The actual DNA base pair sequence is shown to have a large effect on the charge transport mechanism. For a series of DNA bridges with an increasing number of guanine-cytosine (GC) base pairs, mutually separated by 2 AT base pairs a weak distance dependence is found in agreement with experimental data for these sequences. It is shown that the charge migration mechanism is effectively hopping between GC base pairs.

I. Introduction

The nature of charge migration through DNA has received an enormous amount of attention over the last 40 years.[1−4] It is well-known that excess positive or negative charges created in DNA, either by excitation with (UV) radiation or chemical reactions, can migrate along the stacked base pairs in the double helical DNA strand. A detailed understanding of the mechanism of charge migration in DNA is of obvious importance since oxidation and reduction of nucleic bases are key steps in DNA damage.[1,5,6] The possibility of electrical conductivity in DNA was first proposed by Eley[7] in 1962, shortly after the helical structure of DNA was discovered by Watson and Crick.[8] Eley noted that the base pair stack in the interior of the double helix shows a striking resemblance to the stacking in one-dimensional aromatic crystals. High charge carrier mobilities have been reported in these aromatic crystals[9,10] and also in one-dimensional discotic materials.[11]

However, there are also important differences between DNA and these systems. For instance, natural DNA is a nonperiodic stack of two different aromatic moieties (adenine-thymine (AT) and guanine-cytosine (GC) base pairs), whereas in aromatic crystals and discotic materials the aromatic disks are all exactly the same. Furthermore, base pairs in DNA are held together by a sugar−phosphate chain and the conformation and flexibility of DNA depend very much on the actual base pair sequence and on the water content of the sample.[12−15] These differences may have a considerable effect on the efficiency of charge transport through the base pair stack.

An enormous amount of experimental work has been performed in order to unravel the mechanism of charge migration through DNA; however, there is still no generally accepted mechanism for this charge migration process.[2,3] In most of the more recent experimental studies a "hole" (or electron) donor and acceptor are covalently attached to a DNA oligonucleotide with a well-defined base pair sequence. The efficiency of hole transport from the donor to the acceptor is then determined, either by measuring the quenching of the fluorescence of the donor[14−21] or an analysis of the relative yield of

† Department of Chemistry and Materials Research Center, Northwestern University, 2145 N Sheridan Rd., Evanston, IL 60208-3113.

* Corresponding author. E-mail: siebbel@iri.tudelft.nl.

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strand breakages at different positions along the DNA strand.[22−26] The results of these studies are usually interpreted in terms of classical electron transfer theory, which implies that the rate of charge transfer, k_{CT}, exhibits an exponential dependence on the distance R, between the donor and the acceptor:

$$k_{CT}(R) = k_0 \exp(-\beta R) \quad (1)$$

where k_0 is a preexponential factor and β is the so-called falloff parameter. The value of β is often used to distinguish between the different charge migration mechanisms that have been proposed for DNA. A large β ($\approx$1 Å^{-1}) represents a strong dependence of the charge-transfer rate on the donor−acceptor distance. This is characteristic for a single-step tunneling process,[27] as has been found for electron-transfer in proteins.[28] A small value for β ($\approx$0.1 Å^{-1}) indicates that the electron transfer rate depends only weakly on the distance between the donor and the acceptor. Two different charge migration mechanisms give rise to a weak distance dependence. The first is the "molecular wire" mechanism,[29,30] which implies that the donor and the acceptor are strongly coupled to each other through the intervening bridge. Therefore the charge can travel almost coherently through this "π-way", according to a bandlike charge transport mechanism in which the charge-transfer rate is almost independent of distance. The main difference between this type of transport and the single-step tunneling mechanism is that a substantial charge density on the bridge is present here, while in the single-step tunneling mechanism the charge density on the bridge is always negligible. A second mechanism that yields a small distance dependence is the incoherent hopping mechanism.[27,31] In this case the charge travels through the DNA bridge in a multistep process in which the charge "hops" between localization sites (base pairs) until it reaches the acceptor. It should be noted that in the case of multistep hopping the charge-transfer rate does not decay exponentially with the distance and hence β is not a suitable parameter. In a multistep hopping mechanism the logarithm of the charge migration rate is proportional to the logarithm of the number of hopping steps N:

$$\ln k_{CT} \propto -\eta \ln N \quad (2)$$

The power parameter η is equal to 2 for unbiased diffusive hopping from the donor to the acceptor, while it is between 1 and 2 for an acceptor-direction-biased random walk process.[27]

A wide range of experimental values has been obtained for β. A number of groups have reported relatively high values using a wide variety of different donor−DNA−acceptor systems.[17−21] These high values are in agreement with the values obtained from semiempirical quantum mechanical calculations performed by Beratan and co-workers.[32]

By contrast, low values for β have been observed, e.g., by the group of Barton[14−16] in fluorescence quenching studies and by the group of Schuster[22,23] who studied photoinduced strand breakages. The group of Barton has demonstrated that values as low as 0.2 Å^{-1} can be obtained depending on the way in which the donor and the acceptor are positioned in the DNA molecule.[16] Such weak distance dependencies have also been observed for sequences containing many intervening AT base pairs.[22,33]

Recently it was demonstrated by Porath et al. that a current can flow through a single 10.4-nm-long poly(G)-poly(C) DNA molecule trapped between two metal nanoelectrodes.[34] The current−voltage curves reported by these authors show features that are typical for wide band gap semiconductors. Earlier measurements of electrical conductivity in micrometer long DNA ropes[35] and in films containing many DNA molecules[36] have shown that DNA behaves as a good linear conductor is these cases.

The conductivity in pulse-irradiated calf-thymus DNA has been investigated using the time-resolved microwave conductivity technique. The signals observed at low temperatures in these studies were attributed to conduction through the ice-mantle of the DNA rather than to one-dimensional conduction through the base pair stack.[37] Other radiation chemistry studies by Melvin et al.[38,39] have shown that excess positive charges can migrate through DNA. Positive charges created on all nucleic acid bases by irradiation with 193-nm UV light were found to become trapped predominantly at guanine sites. Furthermore, recently Messer et al. have determined β-values for *electron* transfer in different forms of natural DNA at low temperatures and found rather large distance dependencies ($\beta \approx 1.0$ Å^{-1}).[40]

The aim of the present work is to provide theoretical insight into the actual mechanism of charge migration through DNA and to establish the conditions under which high or low values for β can be expected. A relatively simple tight-binding model is used to achieve this goal. It has been shown earlier in a preliminary account[41] that this model provides an appropriate description of the sequence dependence of charge transport through DNA in some of the sequences studied by Meggers et al.[24]

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The influence of the use different donor moieties will be discussed and the effect of the base pair sequence on the efficiency of charge migration through a DNA bridge is evaluated. The theoretical results are compared to the experimental results in refs 30 and 31, where a strong influence of the base pair sequence on the distance dependence of the charge-transfer rate has been reported. This large effect of the DNA base pair sequence was explained by assuming that a hole moves through the stack by hopping between GC base pairs. The same mechanism was employed by Nakatani et al. to explain their experimental results.[26] Furthermore, theoretical analysis by Berlin et al.[42] and also by Bixon et al.[31] have shown that the rates found by Meggers et al. can be reproduced by assuming hopping between GC base pairs. The present study differs from these accounts in the sense that no assumptions are made a priori about the charge migration mechanism. It is shown that a single model can describe different charge migration mechanisms depending on the donor−DNA−acceptor system under consideration.

In section II the theoretical model that was used is discussed and the details of the simulations are given. The results will be presented and discussed in section III.

II. Model and Computational Details

The model we used for studying charge migration through DNA combines a tight-binding description for an excess charge (hole) on the DNA chain with a simple description of dynamic disorder.[43,44] The donor−DNA−acceptor systems that were considered are represented by a one-dimensional chain of N sites. The first site ($n = 1$) corresponds to the donor site, the sites with $2 \le n \le N - 1$ represent the bridge sites (i.e., the DNA base pairs), the site with index N is the acceptor site. The charge is described by a tight-binding Hamiltonian:

$$H_q = \sum_n [\epsilon_n a_n^+ a_n - b(a_{n+1}^+ a_n + a_n^+ a_{n+1})] \tag{3}$$

where a_n^+ and a_n are the creation and annihilation operators for a charge at the nth site, respectively, b is the transfer integral (electronic coupling between neighboring sites), and ϵ_n is the energy of the charge when it is localized at the nth site. For the description of a hole on a DNA bridge this energy corresponds to the ionization potential of a base pair. At the acceptor site ($n = N$) a complex part is added to the energy ($\epsilon_N - i\Gamma$) in order to account for the irreversible trapping at the last site. The introduction of a complex part in the energy is a standard method to describe the irreversible decay of a charge due to coupling with a continuum of other states.[45−47]

In a perfectly ordered system without dynamic fluctuations causing dephasing the Hamiltonian of eq 3 leads to a coherent motion of the charge.[43,44] In general, dephasing effects cannot be neglected since at finite temperatures there are always dynamic fluctuations, either in the chain or its surroundings. This causes the site energies to become time-dependent. In the present model this is taken into account by considering the chain to be a series of coupled harmonic oscillators with mass M and a vibration frequency ω. The coupling between the charge and the oscillators is taken to be linear in the displacement with a proportionality constant g. The effect of dynamic disorder can thus be brought into account by the Hamiltonian:

$$H_v = \sum_n \left(\frac{p_n^2(t)}{2M} + \frac{1}{2} M\omega^{2+} [x_{n+1}(t) - x_{n(t)} - x_{eq}]^2 \right) + \sum_n g[x_{n+1}(t) - x_{n-1}(t) - 2x_{eq}] a_n^+ a_n \tag{4}$$

In this equation $p_n(t)$ and $x_n(t)$ are the momentum and the position of the nth oscillator at time t, respectively, and x_{eq} is the equilibrium distance between adjacent oscillators. The first term in eq 4 describes the harmonic oscillators, while the second term accounts for the coupling between the charge, which is described as a quantum particle, and the oscillators that are treated classically. The contribution of the dynamic disorder to the site energy of the charge is thus

$$\epsilon_n^d = g[x_{n+1}(t) - x_{n-1}(t) - 2x_{eq}] \tag{5}$$

The Hamiltonian described above is used to study the migration of a charge along a DNA chain numerically. The first step in these simulations consists of the assignment of initial velocities to the harmonic oscillators in the chain without a charge. These velocities are sampled from a Boltzmann distribution. This implies that the average vibrational energy per oscillator is $0.5k_BT$, where k_B the Boltzmann constant and $T = 293$ K. The initial positions of the oscillators are their equilibrium positions. The velocities and positions are first propagated in time until the system of coupled oscillators has reached equilibrium. After this the charge is introduced on the donor site. The wave function of the charge is expressed as a superposition of states $|n\rangle$ located on different sites:

$$|\Psi(t)\rangle = \sum_n c_n(t)\, |n\rangle \tag{6}$$

At $t = 0$ the charge is localized on the donor site, therefore $c_1(t = 0) = 1$ and $c_{n\neq1}(t = 0) = 0$. The wave function and the oscillators are then propagated in time by applying the time-dependent self-consistent-field formalism[48] with the total Hamiltonian, H_{tot} equal to the sum of eqs 3 and 4, $H_{tot} = H_q + H_v$. The wave function is propagated during a time step dt that is taken small enough that the positions of the nuclei (the harmonic oscillators) can to a good approximation be considered fixed. The coefficients $c_n(t)$ are obtained numerically by integration of the first-order differential equations that follow from substituting the wave function in eq 6 into the time-dependent Schrödinger equation $i\hbar(\partial|\Psi(t)\rangle/\partial t) = H|\Psi(t)\rangle$. To propagate the positions and velocities of the oscillators the total Hamiltonian is averaged over the wave function of the charge given in eq 6. This yields the classical vibrational Hamiltonian from which the first-order differential equations for the velocities and positions of the oscillators, can be obtained. These equations are integrated numerically to obtain the velocities and positions after a time step dt, during which the wave function of eq 6 is considered constant. This procedure is repeated until a preset time limit is reached.

The rate of charge migration through a DNA bridge can be calculated by this procedure by examining the probability $P(t)$ that the charge is still present on the chain (rather than absorbed at the acceptor site). This probability, hereafter referred to as the survival probability, is given by

$$P(t) = \sum_n^N |c_n(t)|^2 \tag{7}$$

Note that $P(t)$ decays in time due to absorption of the charge at the acceptor site, which is brought into account by the complex part of the acceptor site energy.

The data that are presented in the next section were obtained by averaging over 100 different realizations of the initial velocities. The distance between the equilibrium positions of the oscillators was set equal to 3.4 Å, which corresponds to the distance between the base pairs in the DNA stack. The mass of the oscillators M, the oscillation period, and the coupling constant g were set to be 60 times the proton

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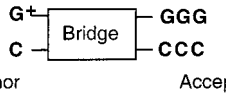
Table 1.



no.	bridge
1	T
	A
2	AT
	TA
3	ATT
	TAA
4	ATAT
	TATA
5	A**C**AT
	T**G**TA
6	TT
	AA
7	TT**G**TT
	AA**C**AA
8	TT**G**TT**G**TT
	AA**C**AA**C**AA
9	TT**G**TT**G**TT**G**TT
	AA**C**AA**C**AA**C**AA

mass, 0.45 ps and 0.51 eV/Å, respectively. These parameters were varied by a factor of 2 but it was found that this does not affect the results significantly. Furthermore the exact nature of the coupling between the charge and the classical vibrations is of minor importance for the present analysis, since the main focus is on the qualitative features of the charge transport mechanism. The coupling is only introduced to get some amount of dynamic disorder resulting in dephasing.

An estimate for the transfer integral b can be obtained by examining the HOMO − HOMO-1 energy difference that can be obtained from ab initio calculation[49] or from the bandwidths obtained from band structure calculations.[50] In this way the electronic coupling between neighboring base pairs can be estimated to range from 0.1 to 0.25 eV depending on the actual bases. The calculations mentioned above refer to perfectly regular B-DNA stacks while in real DNA the coupling will be hindered by static and dynamic fluctuations of the structure and different combinations of bases will give different values for b. The value used for b in these studies is $b = 0.11$ eV (0.004 atomic units), which can be considered as a reasonable estimate for the average electronic coupling between neighboring base pairs. The sequence of the base pairs is introduced in the model by taking the static components of the site energies ϵ_n in eq 3 equal to the different ionization potentials of the individual base pairs. The ionization potentials of the base pairs were taken from an ab initio study performed by Hutter and Clark.[51] For an AT base pair, this value was found to be 8.06 eV, while the ionization potential of a GC base pair was 7.51 eV, hence the energy difference between the two types of base pairs is 0.55 eV. It is well-known that the actual ionization potential of a DNA sequence, i.e., more than one base pair, depends considerably on the sequence. It should be noted that this sequence dependence of the ionization potential is caused by the electronic coupling between different base pairs and should therefore be accounted for through the parameter b which will in general be dependent on the actual sequence, see below.

The value of the parameter Γ, which determines the rate by which the charge decays on the acceptor site, was taken to be 0.04 eV, which was found to be sufficiently large to ensure that the results do not depend on Γ. Increasing or decreasing the value of Γ by a factor of 2 did not significantly influence the numerical results.

The model presented above is rather simple, for instance the value for b was assumed to be the same between all combinations of base pairs. It can be expected that the coupling between two AT base pairs is quite different from that between two GC pairs. Future investigations will include a detailed study of the transfer integrals between all possible combinations of base pairs which can then be used in the same model to provide a more detailed quantitative description. Another issue that should be taken into account in future work is the possible decay (trapping) of the charge carrier on GC sites on the bridge due to deprotonation or other irreversible reactions.

The main purpose of the present work is to provide a qualitative picture of the mechanism of charge migration and to explain the strong effects of the base pair sequence and the barrier for charge injection on this mechanism.

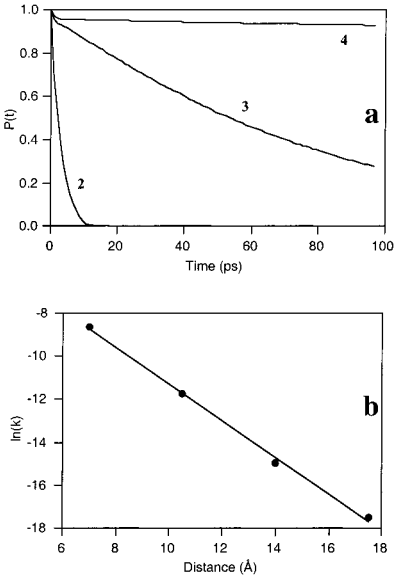


Figure 1. (a) Survival probability for sequences **2**, **3**, and **4** as a function of time. (b) ln(k) plotted against the donor−acceptor distance for sequences **1**−**4**. The value for β obtained from the slope of the linear fit is 0.85 Å^{-1}.

III. Results and Discussion

Distance Dependence. The method described above was used to study the mechanism of charge migration through the DNA bridges listed in Table 1, which were studied experimentally by the Meggers et al.[24,25] In these experiments a radical cation, G^+, was generated site-selectively in a DNA double-strand with a well-known base pair sequence. The hole was found to migrate to a GC triad. The ionization potential of such a GC-triad was calculated to be 0.7 eV lower than that of a single GC base pair[52] and therefore it acts as an acceptor for holes. Relative reaction rates were derived from these experiments by determining the yield of DNA strand breakages at different positions. These strand breakages, induced by treatment with an enzyme, occur at places where the G^+ radical has reacted with the surrounding water. This reaction can occur at the donor GC base pair but also at other GC bases on the bridge or at the acceptor site since the charge can migrate through the DNA. From the relative amounts of strand breakages at the different GC positions relative charge-transfer rates are obtained.

The first series of DNA bridges that were considered in the work of Meggers et al.[24] consists of sequences containing an increasing number of AT base pairs between the donor (a GC site of which the guanine is oxidized initially) and the acceptor (GC-triad), these sequences are listed in Table 1 (**1**−**4**). The time evolution of the survival probability, $P(t)$, calculated for bridges **2**−**4** is shown in Figure 1. The decay curve for sequence **1** is not included because it nearly coincides with the vertical

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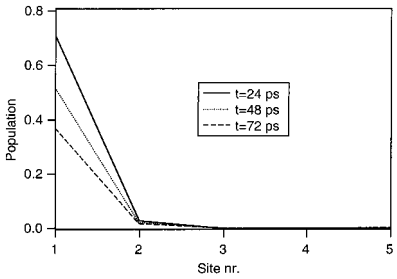

Figure 2. Analysis of the charge distribution on a DNA bridge consisting of three AT base pairs (sequence **3**) at three different times for an injection barrier of 0.55 eV. Sites 1 and 5 are the donor and the acceptor, respectively.

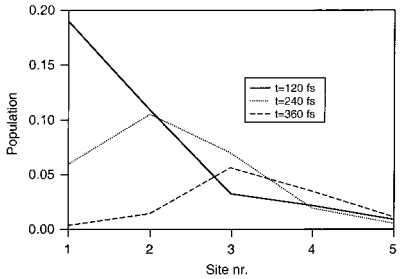

Figure 3. Analysis of the charge distribution on a DNA bridge consisting of three AT base pairs (sequence **3**) at three different times for an injection barrier of 0.14 eV. Sites 1 and 5 are the donor and the acceptor, respectively.

Table 2. Effect of the Injection Barrier on the Falloff Parameter for Charge Transfer through Bridges Consisting of AT Base Pairs Only

$\Delta E_{\text{inj, eV}}$	β in Å^{-1}
0	0.09
0.14	0.13
0.27	0.34
0.41	0.53
0.55	0.85
0.70	~1

axis. The decrease of the survival probability with time is due to the migration of the charge from the initial site (the donor) to the acceptor site where it is trapped irreversibly. The time evolution of the survival probability can be approximated by an exponential function:

$$P(t) = \exp(-k_{CT}(R)t) \tag{8}$$

in which k_{CT} is the effective decay rate. The natural logarithm of the decay rates, obtained by fitting the numerical data in Figure 1a to eq 8, are plotted against the donor−acceptor distance in Figure 1b. It is clear that the rate constant exhibits a rather strong exponential dependence on the distance. The falloff parameter β obtained from Figure 1b is 0.85 Å^{-1}, which is in reasonable agreement with the experimental value of 0.7 Å^{-1} obtained by Meggers et al.[24,25] This relatively large value for the falloff parameter is characteristic for single-step hole tunneling from the donor to the acceptor.

More information on the mechanism of charge migration in these bridges can be obtained by examining the population on the bridge and the donor sites (the population on the acceptor will be negligible at all times since the charge decays irreversibly after arriving at this site). Such a charge distribution is shown in Figure 2 for a bridge containing through AT base pairs (bridge **3**) at three different times. The only site that has an appreciable population is the donor (GC) site, the population on the AT sites remains very small at all times. Examining the population at different times shows that the charge "leaks" through the bridge without localization on the bridge. Thus the charge migration mechanism is effectively a single-step tunneling process, which is reflected in the large value found for β. This may not be very surprising since the ionization potential of the donor (and the acceptor) GC sites is 0.55 eV[51] lower than that of the AT bridge sites. This energy gap determines the value of the injection barrier E_{inj}, which controls the injection of holes into the bridge. Since the total vibrational energy present in the model system is less than this injection barrier, the hole can never become localized on the bridge.

Effect of Injection Barrier. In experimental studies on charge migration in DNA a wide variety of hole donors have been used. These different donor moieties will, in general, have an ionization potential that differs from that of a GC base pair as used in the study of Meggers et al. Therefore it is interesting to investigate the effect of the difference between the ionization potentials of the donor and that of the AT base pairs on the bridge (which determines the injection barrier) on the charge-transfer rate and its distance dependence. The calculations described above have been repeated for bridges of AT base pairs only using a number of different injection barriers. The β values obtained from the dependence of the charge-transfer rate on the number of AT base pairs in the bridge are listed in Table 2 for different injection barriers. The falloff parameter decreases as the injection barrier becomes lower and attains a limiting value of 0.09 Å^{-1} for $\Delta E_{inj} = 0$ eV. A similar tendency has also been observed experimentally for a series of synthetic tetracene−bridge−pyromellitimide compounds.[53] The bridges used in these studies were *p*-phenylene−vinylene chains of increasing length. The present calculations show that the actual type of donor that is used in experimental studies has a pronounced influence on the results that are obtained. This may offer an explanation for the very low values for β that were reported by the group of Barton for donor−DNA−acceptor systems with ethidium as the hole donor.[14−16] The data presented in Table 2 suggest that a β value of 0.2 Å^{-1} found by this group is obtained by using an injection barrier of about 0.2 eV. Table 2 also shows that a β value of 0.7 Å^{-1}, as reported in refs 17 and 18, would be obtained for $E_{inj} \sim 0.5$ eV, while $\beta = 1.4$ Å^{-1}, as found in the work of ref. 20, suggests the injection barrier to be higher than 0.7 eV.

When the charge distribution on a bridge of three AT base pairs is considered (see Figure 3) in a case with a small injection barrier ($E_{inj} = 0.14$ eV), it becomes clear that the charge rapidly spreads out over the entire bridge and the population of the bridge becomes quite substantial. The maximum of the charge density shifts from the donor site to the bridge and moves toward the acceptor. It can be concluded from Figures 2 and 3 and the data in Table 2 that the actual mechanism of charge migration changes as the injection barrier is lowered. At high injection barriers the population on the bridge is negligible. When the injection barrier is lowered a substantial charge density is present on the bridge during the migration of the charge. The charge migration mechanism changes from a single-step tunneling process at high injection barrier to a type of transport that can be designated as a "molecular wire" or bandlike conduction at low injection barriers. The latter type of transport corresponds to an almost coherent motion of the charge from the donor to the acceptor. This coherent transport is hindered by dynamic fluctuations in the DNA bridge.[12−15] Thus the absolute value

(53) Davis, W. B.; Svec, W. A.; Ratner, M. A.; Wasielewski, M. R. *Nature* **1998**, *396*, 60−63.

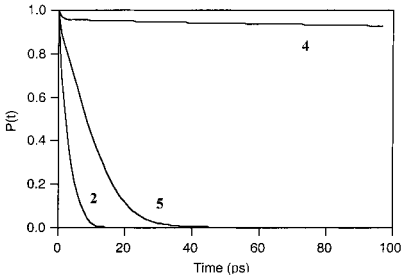

Figure 4. Survival probability for sequences **2**, **4**, and **5** as a function of time.

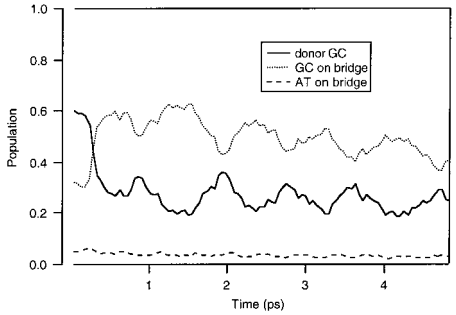

Figure 5. Population on different sites in sequence **5** as a function of time.

of the rate of charge migration (which is not the main concern in this study) will depend on the details of the coupling between the charge and the (vibrational) degrees of freedom in the DNA and its surrounding. It should therefore be noted that the time scales in the figures cannot be compared directly to experimental data on the absolute magnitude of the charge migration rates in DNA that have been reported recently by two different groups.[54,55]

Sequence Dependence. An interesting recent observation on charge migration through DNA is the large influence of the actual base pair sequence in the DNA bridge on both the charge-transfer rate and its distance dependence. It was found experimentally by Meggers et al.[24] that the charge-transfer rate increases dramatically when one of the base pairs in a sequence of four AT base pairs is replaced by a GC base pair (sequence **5**). The computational results obtained for this sequence is shown in Figure 4a. It is evident that the motion of the charge through sequence **5** is almost as fast as the decay on a bridge containing only two AT base pairs (sequence **2**). This is in agreement with the experimental findings by Meggers et al.[24] The observed sequence dependence can be explained by assuming that a hole moves along the bridge by undergoing successive series of "hops" between G bases.[24,25,27,31,42] These "hops" are in fact super-exchange steps through regions containing only AT base pairs. The validity of this explanation can be verified by examining the population on the bridge sites. These populations are shown in Figure 5 as a function of time. Note that the horizontal axis does not start at time equal to zero, the first point in the graph corresponds to the first population that was obtained from the simulation after 0.05 ps, at this time the charge is already distributed over the donor and the GC site in the bridge. It can clearly be seen that the population on the GC site in the bridge is quite large, while the population on the AT sites is always negligible. The hole oscillates back and forth between the donor site and the GC site on the bridge, while it slowly leaks through the barrier that is formed by the last two AT base pairs of the bridge as evident from the overall decay of the full population. This last step is the rate-determining step in the process of charge migration through this particular bridge, hence it is easily understood that the rate of charge migration through this bridge is of the same order of magnitude as that found for a bridge containing only two AT base pairs.

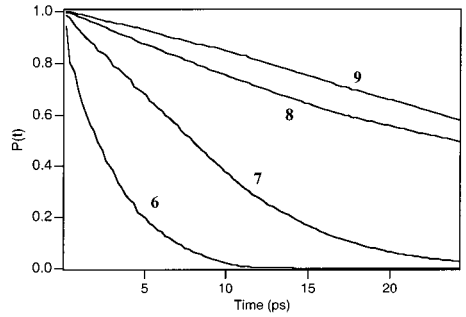

Figure 6. Survival probability for sequences **6**−**9** as a function of time.

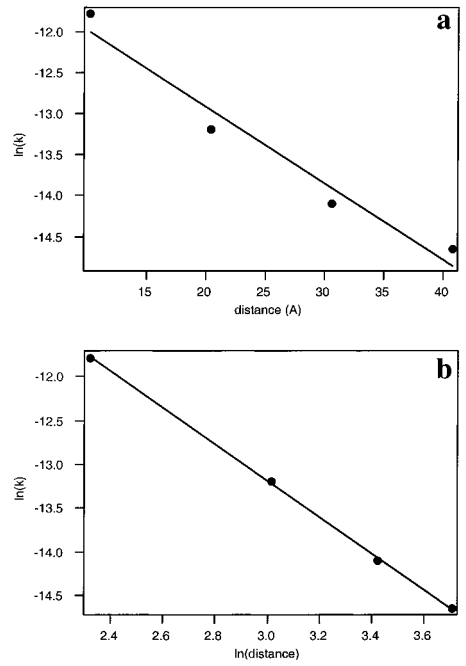

Figure 7. (a) ln(k) plotted against the donor−acceptor distance for sequences **6**−**9**. The value for β obtained from the slope of the linear fit is 0.09 Å^{-1}. (b) ln(k) plotted against the logarithm of the donor−acceptor distance for sequences **6**−**9**. The value for η (see eq 2) obtained from the slope of the linear fit is 2.09.

An interesting experimental test of the proposed mechanism of hopping between GC base pairs was published recently by Giese et al.[25] In this study a series of DNA bridges with an increasing number of GC base pairs mutually separated by two AT base pairs was considered. These sequences are denoted as **6**−**9** in Table 1. The time evolution of the survival probability obtained from simulations on these DNA sequences is shown in Figure 6. It is evident that the distance dependence is rather weak. A value for β can be derived again by plotting the logarithm of the effective decay rate (obtained by fitting to eq 9) against the distance as shown in Figure 7a. The β-value derived from Figure 7a for this series of sequences is 0.09 Å^{-1}. This value agrees nicely with the experimental values of 0.07 Å^{-1} reported by Giese et al. for this series.[25] The low β indicates that the mechanism of charge migration through this bridge is

(54) Lewis, F. D.; Wu, T.; Liu, X.; Letsinger, R. L.; Greenfield, S. R.; Miller, S. E.; Wasielewski, M. R. *J. Am. Chem. Soc.* **2000**, *122*, 2889−2902.

(55) Wan, C.; Fiebig, T.; Kelley, S. O.; Treadway, C. R.; Barton, J. K.; Zewail, A. H. *Proc. Natl. Acad. Sci. U.S.A.* **1999**, *96*, 6014−6019.

effectively a process in which the charge hops from GC site to GC site over a sequence of AT base pairs. This was confirmed by examining the population on the AT base pairs, which was found to be negligible at all times, while a significant amount of charge appeared on the GC sites. As noted in the Introduction, in cases where the charge moves by a multistep hopping mechanism, there is no exponential relation between the length of the chain and the rate. This is also evident if the linear fit is compared to the numerical data points in Figure 7a; there are considerable deviations from linearity in the data points. These deviations are in fact very similar to the deviations from linearity in the experimental results by Giese et al. A more appropriate description is obtained when the logarithm of the rate is plotted against the logarithm of the distance according to the relation in eq 2 (see Figure 7b). A much better linear fit is obtained in this case; the value the proportionality factor η (eq 2) obtained from the fit is 2.09, which is reasonably close to the experimental value of 1.7.[25] The dependence of the results on the ionization potential of GC base pairs in the bridge has not been considered in this study. Possibly the ionization potential difference between AT and GC base pairs is somewhat lower than the 0.55 eV used in this study. A lower energy difference between the AT and GC sites on the bridge would decrease the values for β and for η, yielding a better correspondence with the experimental values.

It is important to note that each hop is in fact a tunneling step through an AT bridge and therefore this hopping-like transport is quite distinct from thermally activated hopping over barriers as has been proposed for charge transport in conjugated polymers. Thermally activated hopping over the AT base pairs is impossible in the present description, since the total energy present in the chain (vibrational and electronic) is smaller than the activation energy necessary for hopping onto an AT base pair.

Although tunneling rates are independent of temperature, there may still be an effect of temperature on the observed charge-transfer rate caused by static or dynamic disorder in the energies of the different GC base pairs. Static disorder in the ionization potentials of the GC base pairs will cause a temperature activated behavior, however, with an activation energy that is much lower than the energy necessary for a hole to become localized on an AT base pair. Dynamic disorder due to coupling of the charge with vibrations in the chain and the surrounding medium could cause the charge migration rate to vary with temperature. These effects of disorder are not expected to have a large influence on the distance dependence of the charge-transfer rate (i.e., on β) but are quite important in the determination of the absolute value of the rates. The precise nature of the dynamic disorder is especially important for modeling the exact time dependence of charge transfer, which was recently obtained experimentally by Wan et al.[55] and by Lewis et al.[54] A description of these dynamic fluctuations based on the sound velocity in DNA as recently described by Conwell et al.[56] may provide an improved description in this respect. More information on the effects of lattice vibrations on the site energies and in particular on the value of the transfer integral b is essential for predictions concerning the absolute charge-transfer rates without employing experimental information on these rates as used by Berlin et al.[42] and Bixon et al.[31] Other improvements in the present model should include a more detailed parametrization of the transfer integral b; at present this is taken the same for all combinations of base pairs, whereas there may be considerable differences in reality.

(56) Conwell, E. M.; Rakhmanova, S. V. *Proc. Natl. Acad. Sci. U.S.A.* **2000**, *97*, 4556−4560.

IV. Summary and Conclusions

In this work the mechanism of charge migration in donor−DNA−acceptor systems was studied using a tight-binding model combined with a classical description of vibrational degrees of freedom in the system. The model was found to provide a consistent description of the sequence and distance dependencies of the charge migration rate in DNA.

The rate of charge migration through a DNA bridge containing only AT base pairs was found to show a rather strong exponential dependence on the donor−acceptor distance with a falloff parameter β of 0.85 $Å^{-1}$ for an injection barrier of 0.55 eV. This injection barrier corresponds to the difference in energy between a GC base pair as the hole-donor and an AT base pair on the DNA bridge. This value for β is in reasonable agreement with the experimental value of 0.7 $Å^{-1}$. In this case charge migration occurs effectively by single-step tunneling, since the charge density on the AT bridge is negligible at all times.

When the injection barrier is lowered the calculated β-value rapidly decreases. Hence, the falloff parameter depends strongly on the type of donor that is used in experimental studies. This may provide an explanation for the wide variety of experimental values that have been obtained for β. When the injection barrier is decreased the charge rapidly spreads out over the entire bridge, indicating that the charge transport mechanism changes from a single-step tunneling process to a molecular wire type behavior.

The actual DNA base pair sequence was shown to have a strong effect on both the charge migration rate and its distance dependence. Interrupting a sequence of four AT base pairs with one GC base pair increases the charge migration rate by almost 2 orders of magnitude, in agreement with experimental results. Systems in which the DNA bridge consists of an increasing number of GC base pairs mutually separated by two AT pairs was shown to exhibit a weak distance dependence of the charge migration rate in agreement with experimental results. From the functional dependence of the charge migration rate on the distance it was concluded that the charge transfer effectively occurs by hopping between GC base pairs. This was confirmed by examining the charge distribution on the bridge during the transfer process. The population on the AT base pairs was found to be negligible at all times, while there is a considerable population on the GC base pairs. It should be noted that the hops are in fact tunneling steps and the tunneling rate depends exponentially on the number of AT base pairs between the GC sites.

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