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HOMO Energy Gap Dependence of Hole-Transfer Kinetics in DNA

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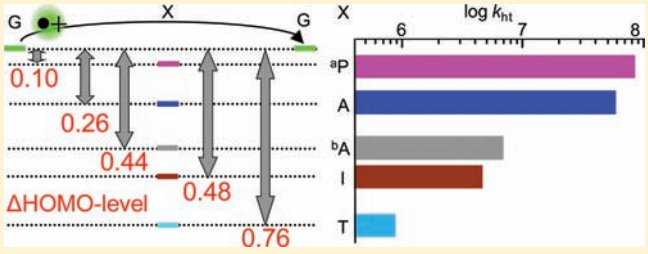
Supporting Information

ABSTRACT: DNA consists of two type of base-pairs, G-C and A-T, in which the highest occupied molecular orbital (HOMO) localizes on the purine bases G and A. While the hole transfer through consecutive Gs or As occurs faster than 10^9 s^{-1}, a significant drop in the hole transfer rate was observed for G-C and A-T mixed random sequences. In this study, by using various natural and artificial nucleobases having different HOMO levels, the effect of the HOMO-energy gap between bases (Δ_{HOMO}) on the hole-transfer kinetics in DNA was investigated. The results demonstrated that the hole transfer rate can be increased by decreasing the Δ_{HOMO} and can be finely tuned over 3 orders of magnitude by varying the Δ_{HOMO}.



INTRODUCTION

A hole (a positive charge) generated in DNA migrates along DNA over 20 nm,[1−10] which renders DNA an interesting bottom-up material for the design of nanoelectronic sensors and devices, and the hole transfer process in DNA has attracted wide attention.[11−19] Experimental and theoretical efforts of the last two decades have established that hole transfer in DNA is mediated primarily by π-stacked nucleobases. Among the four nucleobases, G exhibits the highest HOMO-level,[20,21] and the model of a series of the short-range hole transfer processes between G-C base pairs (i.e., a mixture of superexchange and hopping mechanisms) is the most widely adopted means of describing the long-range hole transfer process through DNA.[22−24] Lewis and co-workers reported that a hole transfer through consecutive A-T base-pairs proceeds with a rate constant of 1.2×10^9 s^{-1}.[25] Once a hole is trapped at G, the hole transfers through DNA via a series of short-range hole transfer processes between Gs, and among the natural sequences, hole transfer occurs fastest in consecutive Gs with a rate constant of 4.3×10^9 s^{-1}.[25] The hole transfer rate (k_{ht}) between Gs is strongly dependent on the distance between Gs, and superexchange is considered to be the main mechanism of hole transfer when no more than three A-T base-pair(s) lie in between Gs. While a hole does transfer between G-C base-pairs separated by more than three A-T base-pairs via a thermally induced hopping mechanism,[26−28] the hole transfer proceeds quite slow in such sequences ($<10^5$ s^{-1}),[8,29−31] which limits the potential applications of DNA as a conducting molecule in molecular-scale devices.

It was experimentally and theoretically demonstrated that hole transfer efficiency is sensitive to the HOMO level of nucleobases. By replacing one A in the middle of five A-T base-pairs with 7-deazaadenine, which has a higher HOMO level than A, i.e., closer to that of G, Nakatani et al. demonstrated that 7-deazaadenine serves as a stepping stone for increasing the hole transfer efficiency between Gs separated by the A-T tract.[32] Those results were theoretically supported by findings reported by Voityuk and Rösch,[33] and Bixon and Jortner,[27] i.e., the former investigated the superexchange regime, while the latter reported the contribution of a 7-deazaadenine in the sequential hole transfer process. Recently we reported that the hole transfer efficiency in DNA can be drastically increased in a manner that is less dependent on the G-C content by replacing As with 7-deazaadenines[34] or diaminopurines (D),[35,36] which has higher HOMO level than A close to that of G. In this study, to further understand how the HOMO energy gap between bases (Δ_{HOMO}) affects the hole transfer rate through DNA, we synthesized the following DNAs containing a region of six alternating bases of various combinations of natural and artificial bases with different HOMO levels in the strand of interest: G, A, T, inosine (I), D, 2-aminopurine (^{a}P), 8-bromoadenine (^{b}A), and 8-bromoguanine (^{b}G). The hole transfer efficiency through the DNA was evaluated by measuring the k_{ht} through the DNA using time-resolved transient absorption measurements. The k_{ht} through the DNA was found to be strongly dependent on the Δ_{HOMO} between the base components in the same strand of the alternating sequence region. It was clearly demonstrated that the hole transfer efficiency can be tunable by changing the Δ_{HOMO}, and can be increased by decreasing the Δ_{HOMO}.

EXPERIMENTAL SECTION

DNA Synthesis. Cyanoethyl phosphoramidite of *N*-(3-hydroxypropyl)-1,8-naphthalimide and 10-(2-hydroxyethyl)phenothiazine, ^{b}A, and I were synthesized as previously reported.[37−40] All other reagents for DNA synthesis, including phosphoramidite of D, ^{b}G, and ^{a}P, were purchased from Glen Research. DNA were synthesized on an Applied Biosystems DNA synthesizer and purified by reverse phase HPLC and lyophilized. All of the DNA studied here was characterized

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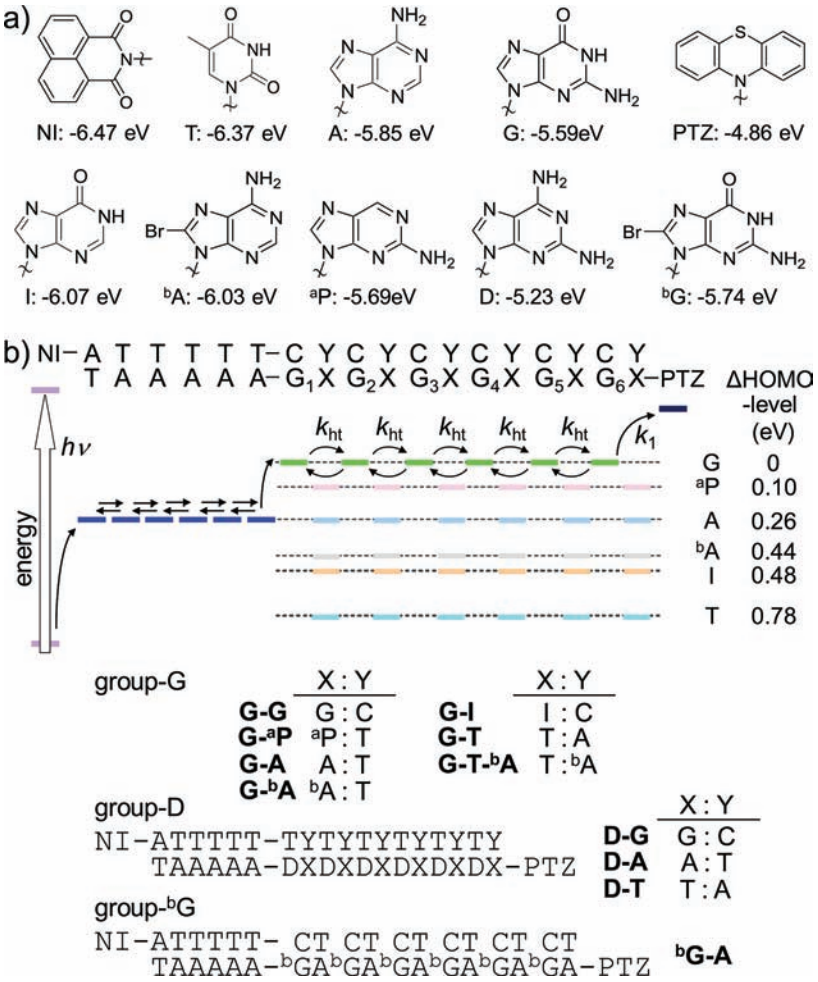

Figure 1. (a) Chemical structures of the photosensitizer naphthalimide (NI), hole acceptor phenothiazine (PTZ), thymine (T), guanine (G), inosine (I), 8-bromoadenine (^{b}A), adenine (A), 8-bromoguanine (^{b}G), 2-aminopurine (^{a}P), and diaminopurine (D). (b) A schematic representation of charge injection by the hole transfer between As, and sequential hole transfer through the alternating sequence region. The HOMO levels of bases are the values calculated at B3LYP/6-31G(d). (b) Sequence of DNA used in this study.

by MALDI-TOFF mass spectra and their concentrations were determined by complete digestion with nuclease P1 and AP to 2′-deoxyribonucleosides. Duplex solutions (DNA 80 μM, 100 mM NaCl, 10 mM $MgCl_2$, and 10 mM sodium phosphate buffer (pH 7.0)) were prepared by mixing equimolar amounts of the desired DNA complements and gradually annealing with cooling from 80 °C to room temperature.

Melting Temperature Measurements. The thermal denaturation profile was recorded on a JASCO V-530 spectrometer equipped with a Peltier temperature controller (ETC-505T). The absorbance of the DNA sample (at a strand concentration of 2 μM in 100 mM NaCl, 10 mM $MgCl_2$, 10 mM sodium phosphate (pH 7.0)) was monitored at 260 nm from 15 to 80 °C with a heating rate of 1 °C/min. The T_m value was determined as the maximum in a plot of $\Delta A_{260}/\Delta T$ versus temperature.

Laser Flash Photolysis. The nanosecond transient absorption measurements were performed using the laser flash photolysis technique.[6−8,34,41] Briefly, the third-harmonic oscillation (355 nm, fwhm of 4 ns, 8−12 mJ/pulse) from a Q-switched Nd:YAG laser (Continuum, Surelight) was used for the excitation light which was expanded to a 1-cm diameter. The light from a xenon flash lamp (Osram, XBO-450) was focused into the sample solution for the transient absorption measurement. Time profiles of the transient absorption in the UV−visible region were measured with a monochromator (Nikon, G250) equipped with a photomultiplier (Hamamatsu Photonics, R928) and digital oscilloscope (Tektronics, TDS-580D). The time profiles of the temperature dependence study were measured by using a JASCO Peltier temperature-controlled cell holder (EHC-716). The time profiles were obtained from the average of 32 laser shots.

Kinetic Modeling. The rate constants of the single-step hole transfer between Gs (k_{ht}) were determined from the kinetic modeling.[6,8] Analysis of time profiles based on the multistep hopping mechanism was performed with numerical analysis by using Matlab software. Kinetic model of multistep hole transfer process is shown in Figure 1a. Charge recombination process can be ignored because the charge separated state persists over several hundred microseconds when NI and the nearest G (or D or ^{b}G) are separated by six A-T base-pairs which works as an insulator.[41−43] According to Figure 1a, simultaneous differential equations are described as eq 1, where $[G_i]$ $(i = 1–6)$ corresponds to the hole population at each G-site (or D-site for group-D DNA or ^{b}G-site for group-^{b}G DNA), k_{ht} is hole transfer rate constants between Gs (or Ds or ^{b}Gs), and k_1 is hole transfer from $G_6^{\bullet+}$ (or $D_6^{\bullet+}$ or $^{b}G_6$) to PTZ.[8]

$$\frac{d[G_1]}{dt} = -k_{ht}[G_1] + k_{ht}[G_2]$$

$$\frac{d[G_2]}{dt} = k_{ht}[G_1] - 2k_{ht}[G_2] + k_{ht}[G_3]$$

$$\vdots$$

$$\frac{d[G_6]}{dt} = k_{ht}[G_5] - (k_{ht} + k_1)[G_6]$$

$$\frac{d[PTZ]}{dt} = k_1[G_6] \quad (1)$$

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RESULTS AND DISCUSSION

The HOMO level of the nucleobases used in the present study was calculated at B3LYP/6-31G(d) by replacing a sugar moiety with a methyl group. The HOMO level of the bases increased along the order of T < I < ^{b}A < A < ^{b}G < ^{a}P < G < D (Figure 1). DNA sequences were designed such that they contained six consecutive A-T base-pairs at one end of the duplex, followed by six alternating bases of interest, to form an octadecamer. The synthesized DNAs were categorized as follows into three groups according to the nucleobase with the higher HOMO level in the alternating-sequence region: (1) group-G: **G-G**, **G-^{a}P**, **G-A**, **G-^{b}A**, **G-I**, **G-T**, **G-T-^{b}A**; (2) group-D: **D-G**, **D-A**, **D-T**; and (3) group-^{b}G: **^{b}G-A**. The Δ_{HOMO} of the bases in the same strand of alternating sequence varied from 1.14 eV (**D-T**) to 0 eV (**G-G**). The k_{ht} through the DNA was determined by nanosecond time-resolved transient absorption measurements. A photosensitizer naphthalimide (NI), was attached at one end of the DNA containing consecutive A-T base-pairs, and a hole was injected into the DNA upon laser-flash excitation of NI. Such an injected hole will rapidly migrate through DNA by hopping between As to become trapped at G, D, or ^{b}G in the alternating-sequence region, which is accomplished within 10 ns. Once a hole reaches the alternating region, the six A-T base-pairs serve as an insulator to slow down the charge recombination (<1 × 10^{4} s^{-1}).[41−43] Then, a hole is transferred through the DNA by hopping through nucleobases with the higher HOMO level in the alternating sequences. Phenothiazine (PTZ), which has a much higher HOMO level than the nucleobases used in this study,[38] was attached to the other end of the duplex as a hole trap, and hole transfer through the DNA was monitored by the formation of the PTZ radical cation (PTZ$^{\bullet+}$), with a peak at around 520 nm.[6−8,34] The rate constant of each hole-transfer step was determined based on kinetic modeling, as described in the Experimental Section.

First the k_{ht} of the DNA of group-G, in which G served as a hole carrier, was investigated. Excitation of the NI-site with a 355-nm laser resulted in the immediate formation of an NI radical anion (NI$^{\bullet-}$) with a peak at 400 nm (Figure 2a). Then, a transient absorption spectrum with a peak at 520 nm, assigned to PTZ$^{\bullet+}$, emerged in a time-dependent manner, which corresponded to the hole transfer through DNA to the PTZ site.[6−8,34] Time profiles of the transient absorption of PTZ$^{\bullet+}$, monitored at 520 nm for group-G sequences, are shown in Figure 2b,c. The k_{ht} obtained in the present study was summarized in Table 1. In the case of **G-G**, the hole transfer was accomplished faster than the time resolution of our setup, showing that k_{ht} was larger than 1 × 10^{9} s^{-1} (Figure 2b). The k_{ht} between Gs across a single G (**G-G**) was also added in Table 1 by applying the k_{ht} value reported by Lewis and co-workers for adjacent Gs (k_{GG} = 4.3 × 10^{9} s^{-1})[25] and eq 2,[44]

$$k_{ht} = k_{GG}N^{-2} \quad (2)$$

where N is a hopping number, and N = 2 was applied to obtain the k_{ht} between Gs across a single G. Interestingly, the formation rate of PTZ$^{\bullet+}$ correlated well with Δ_{HOMO} between G and the other base in the same strand of alternating sequence, and the k_{ht} increased with decreasing Δ_{HOMO} (Table 1).

According to the semiclassical Marcus theory, the k_{ht} is described as

$$k_{ht} = \sqrt{\frac{\pi}{\hbar^2 \lambda k_B T}}\,|H_{DA}{}^2|\,\exp\left[-\frac{(\Delta G + \lambda)^2}{4\lambda k_B T}\right] \quad (3)$$

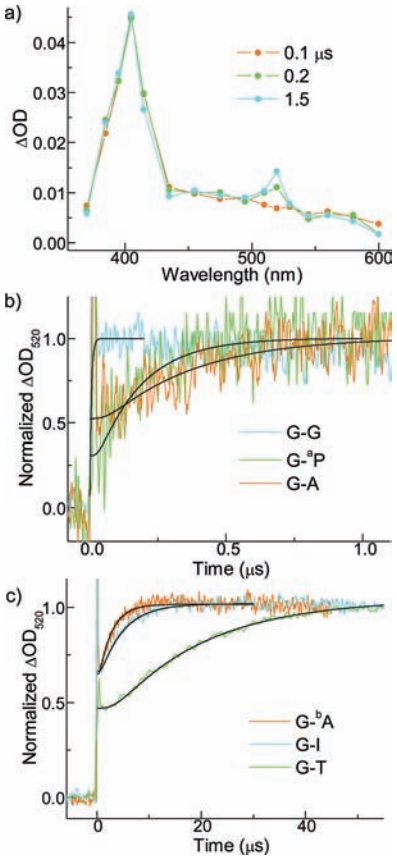

Figure 2. (a) The transient absorption spectrum of **G-^{a}P** obtained at 0.1, 0.2, and 1.5 μs. (b,c) Time profiles of the transient absorption of PTZ$^{\bullet+}$ monitored at 520 nm during the 355-nm laser flash photolysis of group-G DNA (b) **G-G**, **G-^{a}P**, **G-A**, and (c) **G-^{b}A**, **G-I**, **G-T**. The smooth black curves are the fit derived from the kinetic model using k_{ht} values depicted in Table 1.

Table 1. HOMO Energy Gap of Bases (Δ_{HOMO}) and Base-Pairs (Δ_{bp}), Hole Transfer Rate (k_{ht}), Activation Energy (E_a), and the UV Melting Temperature (T_m)

DNA	Δ_{HOMO} (eV)[a]	k_{ht} (s^{-1})[b]	Δ_{bp} (eV)[a]	E_a (eV)[c]	T_m (°C)
G-G	0	1.1 × 10^{9}[d]	0	0.12[d]	67.5
G-^{a}P	0.10	7.6 × 10^{7}	0.54	0.18	53.0
G-A	0.26	3.8 × 10^{7}	0.71	0.18	59.4
G-^{b}A	0.44	5.0 × 10^{6}	0.88	0.45	45.5
G-I	0.48	2.8 × 10^{6}	0.72	0.32	45.0
G-T	0.78	7.0 × 10^{5}	0.71	0.39	65.1
G-T-^{b}A	0.78	7.2 × 10^{5}	0.88	0.12	54.9
D-G	0.36	>1 × 10^{9}	0.05	–	65.7
D-A	0.62	3.5 × 10^{7}	0.76	0.21	54.2
D-T	1.14	1.7 × 10^{6}	0.76	0.35	48.3
^{b}G-A	0.11	7.3 × 10^{7}	0.53	0.06	39.7

[a]HOMO-levels of bases and base-pairs are calculated at B3LYP/6-31G(d). [b]Rate constants were obtained from the kinetic modeling at 22 °C. Estimated fitting error for the average of 32 laser shots was ±10%. [c]Calculated according to eq 5 using the k_{ht} values measured at various temperatures. Estimated fitting error was ±20%. [d]Derived from the report of Lewis and co-workers and using eq 2.[25]

where λ is the reorganization energy, ΔG is the reaction free energy, k_B is Boltzmann's constant, $\hbar$ is the reduced Planck constant, T is the temperature, and H_{DA} is the electronic coupling between the donor (D) and the acceptor (A), which

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subsumes the description of the bridging medium (B) for hole transfer.[45] McConnell developed a mathematical model (eq 4) describing the overall electronic coupling (H_{DA}) in a system in which the donor and acceptor are separated by a bridge.[46]

$$H_{DA} = \frac{h_{DB}h_{BA}}{\Delta\varepsilon^2} \quad (4)$$

In the group-G DNA, the donor and acceptor are both G, and the bridge is the other base in the alternating-sequence region. H_{DA} depends on the electronic coupling between the donor and the bridge (h_{DB}), the coupling between the bridge and the acceptor (h_{BA}), and the tunneling energy gap Δ_{tun}, which is the difference between the energy of the donor−acceptor system at the transition-state configuration and the energy of the bridge-localized states. While Δ_{tun} is not readily accessible from experiment, Δ_{tun} is reported to be closely related to the hole injection free energy into the bridge,[23,45,47−49] namely, Δ_{HOMO} in the present study. Thus, Δ_{tun} can be approximated using the Δ_{HOMO}. Beratan, Achim, Waldeck, and co-workers adopted the modified McConnell superexchange model to capture the general trend in the k_{ht} in single-stranded PNAs and PNA/PNA duplexes.[48,49] In the modified McConnell model, it was assumed that h_{DB} and h_{BA} do not vary significantly with the bridge base, and thus the differences in k_{ht} result from the Δ_{HOMO}. Since H_{DA} is proportional to $1/\Delta_{HOMO}$, the k_{ht} is proportional to $(1/\Delta_{HOMO})^2$, and the plot of k_{ht} versus $(1/\Delta_{HOMO})^2$ should be linear. In Figure 3, the k_{ht}

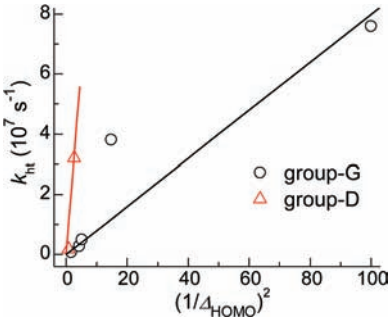

Figure 3. Plot of k_{ht} with respect to $(1/\Delta_{HOMO})^2$. Guidelines are shown to facilitate visualization.

values were plotted against $(1/\Delta_{HOMO})^2$ where the k_{ht} increase as the Δ_{HOMO} decrease, and the obtained plot was quite similar to that derived in the literature.[48,49] However, Beratan, Achim, and Waldeck concluded that in their short PNA duplexes system the primary premise of the modified McConnell model, namely h_{DB} and h_{BA} are relatively constant, does not hold and that hole transfer mechanism is neither strictly coherent superexchange nor hopping, but rather, a hybrid of the two mechanisms at the near-resonant limit. Several researchers have reported that thermal fluctuations in HOMO energies can range up to 0.4 eV.[31,50−52] The contribution of the hopping mechanism may be one of the reasons for some deviation from the linear plots especially when Δ_{HOMO} value is relatively low.[22]

Similar results were also obtained for group-D DNA, in which the k_{ht} increased with decreasing Δ_{HOMO} (Figures 3 and 4 and Table 1). In the case of **D-G**, the hole transfer was accomplished faster than the time resolution of our setup ($k_{ht} > 1 \times 10^9$ s^{-1}). The k_{ht} values obtained for group-D DNA were somewhat higher than those for group-G DNA with a

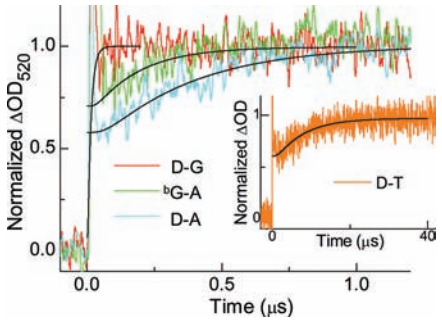

Figure 4. Time profiles of the transient absorption of $PTZ^{\bullet+}$ monitored at 520 nm during the 355-nm laser flash photolysis of group-D and group-^{b}G DNA: **D-T**, **D-A**, **D-G**, and **^{b}G-A**. The smooth black curves are the fit derived from the kinetic model using k_{ht} values depicted in Table 1. For **D-G**, curve was obtained using the k_{ht} value of 1×10^9 s^{-1}.

similar Δ_{HOMO} value. The H_{DA} depends on the overlap of HOMO between bases,[53,54] and thus the difference in the HOMO spatial distribution between G and D affects the k_{ht}. It is also well documented that H_{DA} is sensitive to the conformational changes and thermal fluctuations of DNA (discussed below). Lewis and co-workers suggested that the higher mobility of 7-deazaadenine may partially account for the observed faster k_{ht} between 7-deazaadenines compared to that between Gs.[55]

We also calculated the HOMO of each base-pair and the HOMO energy gap between base-pairs (Δ_{bp}) in the alternating-sequence region (Table 1). The HOMO for D-T base-pair was calculated to be almost identical to that of G-C base-pair, which is consistent with the large k_{ht} value obtained for **D-G**. However, in overall, the correlation between Δ_{bp} and k_{ht} was less obvious compared to that between Δ_{HOMO} and k_{ht}, and a large deviation was observed especially when the HOMO mainly populates on the base of complementary non-G (**G-T**) or non-D strand (**D-T**). It is well documented that hole transfer also occurs in the interstrand fashion[7,34,49] and in such case the HOMO of the complementary strand also affects the k_{ht}. To investigate the possibility of the occurrence of hole transfer in a zigzag pathway, we synthesized an additional DNA strand (**G-T-^{b}A**) in which the HOMO-level of the non-G strand of **G-T** was decreased by bromine substitution at A C8. In sharp contrast with **G-^{b}A**, the change in the HOMO-level of the complementary strand only slightly affected the hole transfer kinetics (**G-T-^{b}A**), demonstrating that hole transfer proceeds in an intrastrand fashion and contribution of the HOMO of the complementary base is small in the present system.

An increase in the k_{ht} was also observed for **^{b}G-A** compared to **G-A** (Figure 4 and Table 1). In **^{b}G-A**, Δ_{HOMO} was reduced by decreasing the HOMO-level of G by introducing an electron-withdrawing bromine group rather than increasing the HOMO of the other base A in the alternating sequence. It is noteworthy that the decrease in the HOMO level of G (**^{b}G-A**: $\Delta_{HOMO} = 0.11$) gave a similar rate constant with **G-^{a}P** ($\Delta_{HOMO} = 0.1$), in which the HOMO-level of A is increased (Figure 5). These results clearly showed that Δ_{HOMO}, rather than an absolute value of the HOMO-level, plays a key role in the hole-transfer kinetics in DNA.

As DNA is such a flexible molecule, changes in the molecular conformation due to thermal fluctuations, which take place over a wide range of time scales (fs−μs), can significantly alter orbital overlap, and in turn the electronic coupling between

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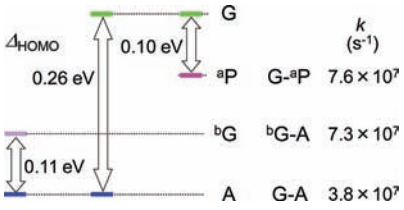

Figure 5. Schematic illustration of changes in the Δ_{HOMO} achieved by a decrease in the HOMO-level of G (**^{b}G-A**) and those achieved by an increase in the HOMO-level of A (**G-^{a}P**).

π-stacked bases.[23] Hole transfer through conformationally dynamic DNA is thought to be controlled by the frequency of occurrence of structures that are particularly amenable to hole transfer.[52,56−58] The use of multiple conformations from MD simulations to better simulate the dynamic environment of DNA has now gained popularity in the theoretical calculation of the hole-transfer dynamics in DNA.[31,50−52,59−63] In order to investigate the relationship among the temperature dependence of k_{ht}, DNA conformational mobility, and Δ_{HOMO}, the k_{ht} was measured at various temperatures (T). To analyze k_{ht} in the adiabatic regime, we analyzed the data using the conventional Arrhenius model eq 5[31]

$$k_{ht}\sqrt{T} = A \exp\left(-\frac{E_a}{k_B T}\right) \quad (5)$$

where A and E_a are a preexponential factor and activation energy, respectively. Time profiles of the transient absorption of PTZ$^{\bullet+}$, monitored at 520 nm between 15 and 55 °C for **G-^{a}P**, are shown in Figure 6a. The k_{ht} increased with increasing T,

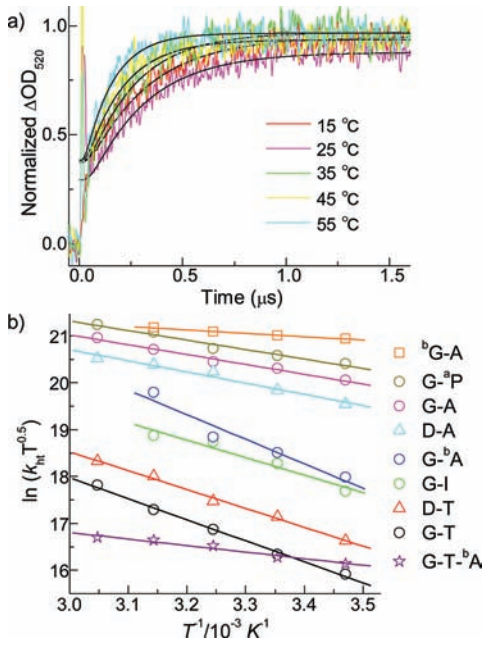

Figure 6. (a) Time profiles of the transient absorption of PTZ$^{\bullet+}$ monitored at 520 nm during the 355-nm laser flash photolysis of **G-^{a}P** at various temperatures. (b) Plots of ln ($k_{ht}T^{0.5}$) versus T^{-1}.

and similar trends were observed for all other sequences. A plot of ln ($k_{ht}T^{0.5}$) versus T^{-1} provides the E_a value for k_{ht} (Figure 6b and Table 1). As an overall trend, a higher E_a value was observed for DNAs with a slower k_{ht}, that is, for DNAs with a larger Δ_{HOMO}, suggesting that greater DNA conformational motion is required for DNAs with a high Δ_{HOMO} to adopt a conformation amenable to hole transfer. The E_a values for group-D DNA were lower than those of group-G DNA with a similar Δ_{HOMO} value. It is well-known that the donor−donor−acceptor type of hydrogen bond in G-C-type pairs is stronger than the donor−acceptor−donor type of hydrogen bond seen in D-T base pairs.[64] The higher flexibility of D-T base pairs compared to that of G-C base pairs may account for the observed faster k_{ht} for group-D DNA compared to that of group-G DNA with a similar Δ_{HOMO} value.[55] The highest E_a value was obtained for **G-^{b}A**, which may have been partly due to changes in the local fluctuation of DNA caused by an A C8 bromine group, which shifts the equilibrium to a *syn* glycosyl conformation.[65] On the contrary, substitution of A C8 bromine group in the complemental strand of **G-T** resulted in a lowering of the E_a value (**G-T-^{b}A**). We measured the melting temperature (T_m) of the duplex (Table 1), but no clear correlation between T_m and k_{ht} was observed. These results suggested that local fluctuation of DNA rather than global duplex stability plays a key role in the hole transfer kinetics. Although the computational calculation mainly targets fast DNA fluctuations within a few nanoseconds, long-range hole transfer is achieved as a consequence of the hole transfer process within a much slower time scale, which is directly related to the time scale of the reactions leading to DNA oxidative decomposition.[41,42,66−68] Further theoretical analysis in the extended time regions, as performed by Steinbrecher et al.,[31] will be necessary to understand the relationship among the temperature dependence of k_{ht}, DNA conformational mobility, and Δ_{HOMO}.

CONCLUSIONS

In conclusion, we demonstrated that k_{ht} is controlled by Δ_{HOMO} and is tunable by varying the Δ_{HOMO}. The present results can be potentially exploited for the future development of programmable DNA-based nanoelectronics, which would require a more rapid hole transfer than that of natural DNA duplexes. Recently we established a system for reading out the sequence information of nucleic acids that is based on single molecule-level k_{ht} measurements.[69] Epigenetic modification of RNA, such as A to I editing, methylation of A and G, and the conversion of G to wyosine[70−73] will cause significant changes in HOMO levels, as well as in k_{ht}. Attempts to read out information regarding the epigenetic RNA modification by measuring k_{ht} in DNA/RNA hybrids are currently underway.

ASSOCIATED CONTENT

Supporting Information

Supporting figures. This material is available free of charge via the Internet at http://pubs.acs.org.

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Notes

The authors declare no competing financial interest.

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