# Unexpected Dissociation Energetics of Na<sup>+</sup> Counterion from GC Motifs in DNA Hole Migration

Jun Wang, Huifang Li, Liang Zhang, Yuxiang Bu\*

The Center for Modeling & Simulation Chemistry, Institute of Theoretical Chemistry, Shandong University, Jinan, 250100, P. R. China

### **Supporting information:**

#### 1. Molecular Dynamics Simulation Detail

To obtain the DNA configurations in which Na<sup>+</sup> ions, the counterions, directly interact with individual base pair, molecular dynamics (MD) simulations were carried out on a designed DNA decamer with the sequence d(AGGAGACCAA) with W-C pairing to make the corresponding duplex, with use of the AMBER 8.0 suite1<sup>S1</sup> of programs and the parm99 force field.<sup>S2</sup> Each structure was neutralized with 18 Na<sup>+</sup> ions and solvated with about 3000 TIP3P <sup>S3</sup> water molecules in a truncated octahedral box whose edges are approximately 10 Å in each direction from the closest decamer duplex. No salt was included. The SHAKE algorithm<sup>S4</sup> was employed to constrain all bonds involving hydrogens. After energy minimization to relax strains, the system was slowly heated from 0 to 300 K during 20 ps with harmonic restraints of 10.0 kcal/mol/Å<sup>2</sup> on the solute atoms, at constant volume. This was followed by another 300-ps MD run in which the restraints were gradually removed.<sup>S5</sup> After these equilibration procedures, 10 ns unrestrained molecular dynamics simulations were then carried out at constant pressure (1 atm) and temperature (300K) using the Particle Mesh Ewald algorithm<sup>S6</sup> and periodic boundary conditions.

The extended 10 ns long sampling was carried out to assess whether mobile Na<sup>+</sup> counterions can penetrate into the DNA groove and bind to a given base pair during the MD trajectory. The MD trajectory analysis revealed that the mobile Na<sup>+</sup> counterions are quite mobile. A Na<sup>+</sup> counterion was observed to penetrate into the major groove of the decamer to combine directly with purine residue during the first 6 ns of MD simulation and, subsequently, this Na<sup>+</sup> counterion slowly departed from the binding site. The DNA structures, including the presence or absence of Na<sup>+</sup> counterions at particular locations, were saved every 0.5 ps during the simulations for further

minimizations of the Na<sup>+</sup>-coupled configurations.

- S1. Case, D. A.; Darden, T. A.; Cheatham, T. E. III; Simmerling, C. L.; Wang, J.; uke, R. E.; Luo, R.; Merz, K. M.; Wang, B.; Pearlman, D. A.; Crowley, M.; Brozell, S.; Tsui, V.; Gohlke, H.; Mongan, J.; Hornak, V.; Cui, G.; Beroza, P.; Schafmeister, C.; Caldwell, J. W.; Ross, W. S.; Kollman, P. A. AMBER 8; University of California: San Francisco, 2004.
- S2. (a) Cornell, W. D.; Cieplak, P.; Bayly, C. I.; Gould, I. R.; Merz, K. M.; Ferguson, D. M.; Spellmeyer, D. C.; Fox, T.; Caldwell, J. W.; Kollman, P. A. J. Am. Chem. Soc. 1995, 117, 5179-5197. (b) Wang, J.; Cieplak, P.; Kollman, P. A. J. Comput. Chem. 2000, 21, 1049-1074.
- S3. Jorgensen, W. L.; Chandrasekhar, J.; Madura, J. D.; Impey, R. W.; Klein, M. L. J. Chem. Phys. 1983, 79, 926-936.
- S4. Ryckaert, J. P.; Ciccotti, G.; Berendsen, H. J. C. J. Comput. Phys. 1977, 23, 327-336.
- S5. Auffinger, P.; Westhof, E. J. Mol, Biol. 2000, 300, 1113-1131.
- S6. Darden, T.; York, D.; Pedersen, L. J. Chem. Phys. 1993, 98, 10089-10092.

#### 2. Relevant Figures



Figure S-1. Averaged DNA structure (*left*) obtained from MD trajectory averaged over a 10-ps MD run when a Na<sup>+</sup> binds with a base. MD-Na<sup>+</sup>GC was obtained from MD simulations on the d(AGGAGACCAA). The given Watson-Crick base pair bound with a Na<sup>+</sup> counterion is highlighted by ball and stick type in duplex, and also given in the top-view (*right*). The Na<sup>+</sup> counterion penetrating into the major groove with direct interaction with a Watson-Crick pair is represented as a big purple ball.



*Figure S-2.* The maps of two molecular orbitals (HOMO-6 and HOMO-8) for the Na<sup>+</sup>G<sup>+</sup>C complex. HOMO denotes the highest occupied molecular orbital.



*Figure S-3.* The optimized structures of the [Na(H<sub>2</sub>O)<sub>n</sub>]<sup>+</sup>G<sup>+</sup>C (n=1, 2, 3, 4) complexes, obtained at the B3LYP/6-311++G\*\* level.



*Figure S-4.* Effects of  $R_{Na^{+}\cdots O6}$  (the distance between Na<sup>+</sup> and O<sub>6</sub>) on  $\Delta E_1$ , the dissociation energies of the Na<sup>+</sup>-N<sub>7</sub>/O<sub>6</sub> bonds in all considered complexes: Na<sup>+</sup>G<sup>+</sup>C and its corresponding hydrates  $[Na(H_2O)_n]^+G^+C$  (n=1, 2, 3, 4), and  $\Delta E_2$ , the vertical dissociation energies of the Na<sup>+</sup>-N<sub>7</sub>/O<sub>6</sub> bonds in Na<sup>+</sup>G<sup>+</sup>C, viz.  $[Na(H_2O)_n]^+G^+C$  for n=0 (no water molecules attached). All data for this figure is given in Table S-5.



Na<sup>+</sup>(G-NH-H<sub>2</sub>O)<sup>+</sup>(C-NH<sub>2</sub>-H<sub>2</sub>O) Na<sup>+</sup>(G-NH-H<sub>2</sub>O)<sup>+</sup>(C-NH-H<sub>2</sub>O) Na<sup>+</sup>(G-NH<sub>2</sub>-H<sub>2</sub>O)<sup>+</sup>(C-NH-H<sub>2</sub>O)

*Figure S-5.* The optimized structures of the Na<sup>+</sup>[G-R(H<sub>2</sub>O)<sub>n</sub>]<sup>+</sup>[C-R(H<sub>2</sub>O)<sub>n</sub>] (R=NH<sub>2</sub>, NH; n=0, 1, 2) complexes, the hydrates of Na<sup>+</sup>G<sup>+</sup>C, obtained at the B3LYP/6-311++G\*\* level.



*Figure S-6.* The optimized structures: (a) Na<sup>+</sup>G<sup>+</sup>C-min, (b) Li<sup>+</sup>G<sup>+</sup>C, and (c) K<sup>+</sup>G<sup>+</sup>C, obtained at the B3LYP/6-311++G\*\* level. The complex Na<sup>+</sup>G<sup>+</sup>C-min denotes the hole-trapped one when Na<sup>+</sup> resides in the minor groove of the DNA duplex, while Li<sup>+</sup>G<sup>+</sup>C and K<sup>+</sup>G<sup>+</sup>C are the corresponding hole-trapped those when Li<sup>+</sup>, or K<sup>+</sup> resides in the major groove of the DNA duplex.

I

## 3. Relevant Tables

Table S-1: The dissociation energies (ΔEs) of Na<sup>+</sup>-N<sub>7</sub>/O<sub>6</sub> bond and Watson-Crick H-bond (WC HB) in these complexes Na<sup>+</sup>GC, Na<sup>+</sup>G<sup>+</sup>C, and Na<sup>+</sup>G(-H<sup>+</sup>)C<sub>p</sub> at the B3LYP/6-311++G\*\* level (Method 1), and those dissociation energies of Na<sup>+</sup>G<sup>+</sup>C were also calculated at the MP2/6-311++G\*\*//MP2/6-31+G\* level (Method 2) and M05-2X/6-311++G\*\* level (Method 3) for comparison.

Complexes		Na <sup>+</sup> GC	Na <sup>+</sup> G <sup>+</sup> C	$Na^+G(-H^+)C_p$	
Method 1	$\Delta E^{a}$	Na <sup>+</sup> -N <sub>7</sub> /O <sub>6</sub> bond	62.30	-15.49	-6.38
		WC HB	30.70	53.56	-16.32
	$\Delta E_{bsse}^{\ b}$	Na <sup>+</sup> -N <sub>7</sub> /O <sub>6</sub> bond	61.51	-16.18	-7.15
		WC HB	29.57	52.32	-18.14
Method 2	$\Delta E^{a}$	Na <sup>+</sup> -N <sub>7</sub> /O <sub>6</sub> bond		-18.03	
		WC HB	51.96		
	$\Delta E_{bsse}{}^{b}$	Na <sup>+</sup> -N <sub>7</sub> /O <sub>6</sub> bond	-19.35		
		WC HB	47.64		
Method 3	$\Delta E^{a}$	Na <sup>+</sup> -N <sub>7</sub> /O <sub>6</sub> bond	-15.20		

Notes:  $\Delta E^{a}$  are the dissociation energies,  $\Delta E_{bsse}^{b}$  are the BSSE-corrected ones. All of the dissociation energies are in kcal/mol.

**Table S-2:** AIM parameters  $\rho$  (the electron density) and Lap (the Laplacian of electron density) for the Na<sup>+</sup>GC and Na<sup>+</sup>G<sup>+</sup>C complexes.  $\rho$  and Lap are in atomic units.

Chemical bond	Na <sup>+</sup> GC		Ν	$Na^+G^+C$	
	ρ	Lap	ρ	Lap	
$Na^+N_7$	0.0225	0.1330	0.0161	0.0869	
$Na^+O_6$	0.0245	0.1500	0.0184	0.1050	
$O_6H-N$	0.0251	0.0790	0.0152	0.0508	
$N_1$ -HN	0.0366	0.0971	0.0479	0.1140	
N <sub>2</sub> -HO	0.0374	0.1230	0.0761	0.2058	

*Table S-3:* The dissociation energies ( $\Delta$ Es) of the Na<sup>+</sup>G<sup>+</sup>C-min, Li<sup>+</sup>G<sup>+</sup>C, and K<sup>+</sup>G<sup>+</sup>C complexes according to the dissociation mode, M<sup>+</sup>G<sup>+</sup>C $\rightarrow$  G<sup>+</sup>C + M<sup>+</sup> (M<sup>+</sup>= Li<sup>+</sup>, Na<sup>+</sup> or K<sup>+</sup>). The Na<sup>+</sup>G<sup>+</sup>C-min complex denotes the hole-trapped one when Na<sup>+</sup> resides in the minor groove of the DNA duplex, while Li<sup>+</sup>G<sup>+</sup>C and K<sup>+</sup>G<sup>+</sup>C are the hole-trapped those when Li<sup>+</sup>, or K<sup>+</sup> resides in the major groove of the DNA duplex, respectively.

complexes	B3LYP/6-311++G**	
	$\Delta \mathrm{E}$	$\Delta E_{\mathrm{BSSE}}{}^{\mathrm{a}}$
Na <sup>+</sup> G <sup>+</sup> C-min	-44.33	-44.89
$Li^+G^+C$	-3.12	-3.69
$K^+G^+C$	-24.39	-24.64

<sup>a</sup> the dissociation energies corrected with basis set superposition error (BSSE). All the dissociation energies are in kcal/mol.

**Table S-4:** R<sub>Na<sup>+</sup>...O6</sub> (the distance between Na<sup>+</sup> and O<sub>6</sub>), attraction (interaction between Na<sup>+</sup> and GC in Na<sup>+</sup>GC), added electrostatic repulsion (the increased electrostatic repulsion upon one-electron oxidation).

R <sub>Na+06</sub>	Attraction	Added electrostatic repulsion
(angstroms)		kcal/mol
2.38	-65.06	77.53
2.68	-61.64	75.51
2.98	-56.86	73.35
3.28	-51.57	70.96
3.58	-46.05	68.24
3.88	-40.63	65.32
4.18	-35.51	62.32
4.48	-30.86	59.33
4.78	-26.77	56.46
5.08	-23.25	53.77
5.38	-20.25	51.28
5.68	-17.73	48.98
5.98	-15.62	46.89
6.28	-13.84	44.97
6.58	-12.35	43.21

**Table S-5:**  $\Delta E_1$ , the dissociation energies ( $\Delta E_8$ ) of the Na<sup>+</sup>-N<sub>7</sub>/O<sub>6</sub> bond in these complexes: Na<sup>+</sup>G<sup>+</sup>C and its corresponding hydrates [Na(H<sub>2</sub>O)<sub>n</sub>]<sup>+</sup>G<sup>+</sup>C (n=1, 2, 3, 4);  $\Delta E_2$ , the vertical dissociation energies of the Na<sup>+</sup>-N<sub>7</sub>/O<sub>6</sub> bond in Na<sup>+</sup>G<sup>+</sup>C, viz. [Na(H<sub>2</sub>O)<sub>n</sub>]<sup>+</sup>G<sup>+</sup>C (n=0, no water molecules). Both  $\Delta E_1$  and  $\Delta E_2$  are obtained at the B3LYP/6-311++G\*\* level. R<sub>Na<sup>+</sup>...O6</sub> denotes the distance between Na<sup>+</sup> and O<sub>6</sub>.

Complexes	$\Delta E_1$	$\Delta E_{1(BSSE)}{}^{a}$	$\Delta E_2$	$R_{\text{Na}+\ldots O6}$
Na <sup>+</sup> G <sup>+</sup> C	-15.49	-16.19	-12.47	2.38
$[Na(H_2O)]^+G^+C$	-18.08	-18.89	-13.14	2.43
$[Na(H_2O)_2]^+G^+C$	-22.92	-23.78	-14.14	2.49
$\left[\mathrm{Na(H_2O)_3}\right]^+\mathrm{G}^+\mathrm{C}$	-28.59	-29.48	-15.64	2.56
$[Na(H_2O)_4]^+G^+C$	-30.04	-31.06	-16.25	2.65

<sup>a</sup> the dissociation energies corrected with the basis set superposition error (BSSE). All of the dissociation energies are in kcal/mol.

Table S-6: ΔE, the dissociation energies (ΔEs) of the Na<sup>+</sup>-N<sub>7</sub>/O<sub>6</sub> bonds in these complexes: Na<sup>+</sup>G<sup>+</sup>C and its corresponding hydrates Na<sup>+</sup>[G-R(H<sub>2</sub>O)<sub>n</sub>]<sup>+</sup>[C-R(H<sub>2</sub>O)<sub>n</sub>] (R=NH<sub>2</sub>, NH; n=1, 2) as shown in Fig. S-5; R denotes the groups with which water molecules interact. ΔE<sub>s</sub> are obtained at the B3LYP/6-311++G\*\* level. R<sub>Na<sup>+</sup>...O6</sub> denotes the distance between Na<sup>+</sup> and O<sub>6</sub>.

Complexes	ΔE	$\Delta E_{(BSSE)}{}^{a}$
$Na^+G^+C$	-15.49	-16.19
$Na^+(G-NH_2-H_2O)^+C$	-12.43	-13.15
$Na^{+}(G-NH-H_2O)^{+}C$	-11.74	-12.46
$Na^{+}G^{+}(C-NH_2-H_2O)$	-10.93	-11.64
$Na^+G^+(C-NH-H_2O)$	-10.10	-10.81
$Na^{+}(G-NH_2-NH-2H_2O)^{+}C$	-7.94	-8.65
$Na^{+}(G-NH_2-H_2O)^{+}(C-NH_2-H_2O)$	-7.12	-7.84
$Na^{+}(G-NH_2-H_2O)^{+}(C-NH-H_2O)$	-7.61	-8.36
$Na^{+}(G-NH-H_2O)^{+}(C-NH-H_2O)$	-6.79	-7.51
$Na^{+}(G-NH-H_2O)^{+}(C-NH_2-H_2O)$	-5.66	-6.40

<sup>a</sup> the dissociation energies corrected with the basis set superposition error (BSSE). All of the dissociation energies are in kcal/mol.

**Table S-7:** Various of dissociation energies ( $\Delta$ Es-PCM) using the polarizable continuum (PCM) self-consistent reaction field method when Na<sup>+</sup> is separated from the complex Na<sup>+</sup>G<sup>+</sup>C in the gas phase and ten solvents with different dielectric constants ranging from the gas phase ( $\epsilon$ =1) to water ( $\epsilon$ =78.39), RE denotes the released energies in dissociation of Na<sup>+</sup> from the Na<sup>+</sup>G<sup>+</sup>C complex, and  $\epsilon$  denotes dielectric constants.

solvent	3	$\Delta E$ -PCM	$RE(-\Delta E)$
gas phase	1.00	-15.49	15.49
ether	4.22	-6.57	6.57
chlorobenzene	5.62	-6.06	6.06
aniline	6.89	-5.40	5.40
quinoline	9.03	-5.35	5.35
acetone	20.7	-3.37	3.37
ethanol	24.55	-3.03	3.03
methanol	32.63	-2.56	2.56
DMSO	46.70	-2.85	2.85
water	78.39	-1.66	1.66

l