Base and Phosphate Electron Detachment Energies of Deoxyribonucleotide Anions

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Ionization and electron transfer in nucleic acids underlie a variety of normal and pathological processes in living tissue.[1−3] Molecular origins of these effects have been sought through measurements and calculations of electron binding energies of DNA and RNA fragments. Whereas free nucleobases have been studied thoroughly with ultraviolet photoelectron spectroscopy[4,5] and state-of-the-art calculations,[5−7] less is known of nucleotides and their oligomers. The instability of nucleotides under the conditions that prevail in a typical photoelectron experiment inspired attempts to infer their electron binding energies from more feasible measurements on base, sugar, and phosphate molecules and ab initio, self-consistent field calculations.[8,9] On this basis, the lowest ionization energies of 2′-deoxyribo guanosine 5′-monophosphate (dGMP) and its anion were assigned, respectively, to molecular orbitals localized on the guanine and phosphate regions. In these and similar works on nucleotides coordinated to a small number of water molecules[10] or in aqueous solution,[11] only Watson−Crick structures were considered. Photolysis experiments and density functional (DF) calculations have been performed on hydrated oligonucleotides.[12] A correlated ab initio study of dTMP⁻ in a Watson−Crick conformation also has appeared.[13]

Useful standards for theoretical study of electronic structure were provided by recent anion photoelectron spectra on gas-phase deprotonated nucleotides.[14] Broad, poorly resolved peaks occurred in all four cases, but only the spectrum of dGMP⁻ contained a well-separated, low-energy feature. The lowest vertical electron detachment energy (VEDE) of each anion was assigned by the authors to the highest occupied Kohn−Sham orbital obtained with the B3LYP[15] DF. (Numerical estimates of these VEDEs were based on total energy differences at the most stable, optimized, anionic geometries, which were held to be compatible with classical, force-field calculations on hundreds of isomers.[16]) The authors assigned the first VEDEs of 2′-adenosine-5′-monophosphate (dAMP⁻), 2′-cytidine-5′-monophosphate (dCMP⁻), and 2′-thymidine-5′-monophosphate (dTMP⁻) to phosphate-localized orbitals, but a π-orbital centered on the base was ascribed to the lowest VEDE of dGMP⁻.[14] This evidence and the presence of low-energy features in the spectra of guanine-containing di- and trinucleotides appear to confirm the supposition that guanine is the site of electron detachment in photoionization of nucleic acids.

In this communication, we interpret the photoelectron spectra of dAMP⁻, dGMP⁻, dTMP⁻, and dCMP⁻ with ab initio, electron propagator calculations,[17] which produce electron binding energies that include the effects of final-state, orbital relaxation, and electron correlation. The partial third order (P3) self-energy approximation[18] of the electron propagator has been applied successfully to nucleobases[7,8] and phosphate anions.[19] P3 calculations on dUMP⁻ have produced encouraging results and have established the

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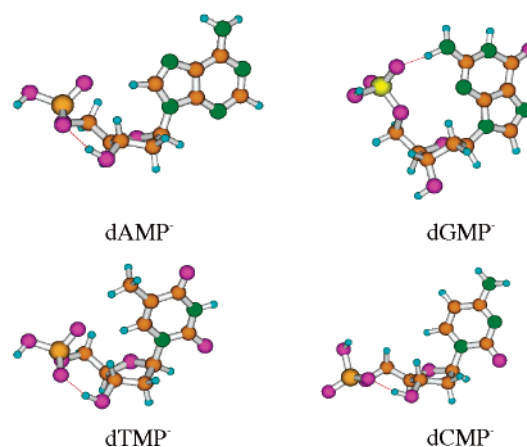
Figure 1. Ground-state conformations of anionic mononucleotides.

importance of electron correlation in determining the correct assignment of final states.[19]

An essential preliminary step is determination of the most stable conformations. Our B3LYP/6-311++G** optimizations agree with similar calculations[14] and with classical, force-field surveys of numerous conformations[16] in identifying the ground-state structures of Figure 1. The next most stable conformations were found to be 2.9 (dCMP⁻), 3.4 (dAMP⁻ and dGMP⁻), and 4.4 kcal/mol (dTMP⁻) higher. Under the room-temperature conditions of the experiment,[14] Boltzmann factors for these less stable conformations are negligible. Hydrogen bonds between phosphate oxygen atoms and sugar or base hydrogen atoms play an important role in determining the ground-state structures. Minima which resemble fragments of the Watson−Crick structures of DNA are unlikely to be relevant to gas-phase photoelectron spectra of these anions.

All calculations were performed with the Gaussian 03 suite of programs.[20] All valence orbitals were retained in P3/6-311++G** determinations of VEDEs. For each VEDE, electron propagator calculations also yield the corresponding Dyson orbital (DO) and pole strength.[17] DOs for VEDEs are defined to be overlaps between N-electron, anionic states, and neutral final states with N-1 electrons whose normalization integrals equal their pole strengths. All of the VEDEs shown in Table 1 have pole strengths that exceed 0.85 and therefore validate the employment of the P3 method. Table 1 also displays the regions that contribute chiefly to each DO, uncorrelated predictions based on Hartree−Fock orbitals and the theorem of Koopmans (KT) and experimental values. In the latter case, error bounds accompany the data that were explicitly stated in the experimental report,[14] but our estimates for the higher VEDEs of each anion are based on inspection of the spectra.

dAMP⁻. KT results give the following order of VEDEs: π_1 adenine, π_2 adenine, four PO_4^- levels, and n_1 adenine. P3 results are completely different: $n_1\ PO_4^- \sim \pi_1$ adenine, three PO_4^- levels,

Table 1. Vertical Electron Detachment Energies (eV)

		KT	P3	expt.[14]
dAMP⁻	PO₄⁻	7.84	6.07	6.05 ± 0.50
	A π₁	6.16	6.15	6.05 ± 0.50
	PO₄⁻, S	8.21	6.39	∼6.4
dGMP⁻	G π₁	5.25	5.01	5.05 ± 0.10
	PO₄⁻	7.94	6.18	∼6.1
	PO₄⁻	8.31	6.54	∼6.4
dTMP⁻	T π₁	6.71	6.16	5.85 ± 0.50
	PO₄⁻	8.08	6.24	∼6.2
	PO₄⁻, S	8.41	6.60	∼6.6
dCMP⁻	PO₄⁻	7.72	6.00	5.80 ± 0.50
	PO₄⁻	8.10	6.41	
	C π₁	7.12	6.47	

π_2 adenine, and n_1 adenine. Large relaxation and correlation effects accompany electron detachment from phosphate-centered orbitals. Two VEDEs correspond to phosphate and base orbitals and are in close agreement with the experimental value. The near coincidence of these two final states is compatible with the spectral plateau that occurs near 6.1 eV. The remaining VEDE predictions in Table 1 and in the Supporting Information also display close agreement with experimental features. The most prominent spectral peak at ∼7.1 eV belongs to electron detachment from the n_1 orbital of adenine.

dGMP⁻. There are several important differences between the most stable structures of dGMP⁻ and dAMP⁻. The former has a compact, cyclic structure with a short (1.66 Å) H-bond formed by a phosphate oxygen and an amino hydrogen. The guanine fragment is almost perpendicular to the ring of deoxyribose with the pyrimidine ring directed inward. Both guanine and phosphate are above the sugar ring. The first VEDE predicted by the P3 calculations is very close to the experimentally observed peak position at 5.05 ± 0.10 eV and corresponds to a π_1 orbital localized on guanine. The second electron detachment energy is placed at ∼6.2 eV by P3 and corresponds to a clearly visible peak at ∼6.1 eV in the experimental spectrum. The corresponding orbital is localized on the phosphate group with no admixture of other molecular fragments. To the higher electron detachment energies the following orbitals are assigned: n_2 on PO₄⁻ at ∼6.5 eV, two mixed orbitals at ∼6.8 eV, and a π_2 orbital distributed over guanine and the sugar molecule (S) at ∼7.0 eV. All P3 energy values correspond rather well to the experimental features.

dTMP⁻. The most stable structure of dTMP⁻ resembles the one for dAMP⁻, with a H-bond in the phosphate−sugar fragment. The first and second VEDEs are assigned, respectively, to the π_1 orbital of thymidine and to the phosphate group. Qualitatively similar conclusions were reached on the basis of ab initio, variational calculations that were performed on a structure that corresponds to a Watson−Crick fragment.[13] Our geometry optimizations disclose that such a structure is less stable than the one shown in Figure 1 by approximately 4 kcal/mol. Given the small energy spacing between the two final states, it is likely that both are responsible for a plateau at ∼6.0−6.2 eV in the experimental spectrum of dTMP⁻. Another set of closely spaced VEDEs appears at 6.60, 6.83, and 6.84 eV, and all of these belong to electron detachment from orbitals that are delocalized over the phosphate group and the sugar molecule.

dCMP⁻. The lowest energy structure of dCMP⁻ also contains a H-bonded, phosphate−sugar fragment. The structure is less compact

than that of dTMP⁻. Unlike other mononucleotide anions, the first VEDE of dCMP⁻ belongs to an orbital on the phosphate group, and the energy separation between the first two final states is ∼0.4 eV. Two VEDEs that follow are almost degenerate and correspond to electron detachments from PO₄⁻ and cytosine π_1 orbitals. Another set of very close detachments is placed at 6.86, 6.98, and 7.18 eV. In each case, electron detachment occurs from orbitals that are delocalized over the whole nucleotide.

In conclusion, for dCMP⁻, the lowest VEDE may be assigned to a phosphate-centered DO. Phosphate- and base-centered DOs are very close in dAMP⁻ and dTMP⁻. Only dGMP⁻ presents a first VEDE that corresponds to a base π orbital and that is well-separated from other final states. This transition occurs at an energy that is markedly smaller than those which contribute to the broad experimental feature centered at 7 eV. In all cases, the presence of a negative ion reduces the ionization energies of the bases by several eV. VEDEs of the phosphate anion are increased by H-bonding to the nearby sugar or base molecules.[19] A detailed study of the dependence of VEDEs on conformations is in progress.

Supporting Information Available: Computational details, full Table 1, atomic coordinates, and complete ref 20. This material is available free of charge via the Internet at http://pubs.acs.org.

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