

COMPUTATIONAL STUDY ON STRUCTURAL, ELECTRON STATES, AND MUON TRAPPING SITES IN GUANINE

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Abstract

Knowledge of muon trapping sites in matters is needed in the interpretation of Avoided Level Crossing-Muon Spin Resonance (ALC- μ SR) experiment. Additionally, accurate computation on the trapped muon hyperfine interaction is instrumental in the planning of applied magnetic field strength for the experimental measurement. Density Functional Theory quantum mechanical method was employed to predict the most probable sites of muon addition in isolated guanine nucleobase. Utilizing B3LYP functional coupled with 6-311G++(d,p) basis set, the HOMO-LUMO gap was calculated to be 5.147 eV. The frontier molecular orbitals show significant delocalization characteristics. Molecular electronic potential map indicates that N2, O5, and N7 areas are favoured for alkylation. Out of eight possible muon addition sites, C8 was found to have the lowest total energy and therefore is the most probable location for the trapping of implanted muon. Natural Population Analysis reveals that the trapped muon is covalently bonded to the C8 atom with a bond order of 0.903. The calculated muon hyperfine coupling constant at the C8 site is 337.4 MHz. The applied magnetic field strength for ALC- μ SR resonance to occur for C8 site is predicted to be around 14,000 Gauss. These findings provide valuable insights into muon behavior in nucleobases, contributing to a more precise interpretation of ALC- μ SR experimental data and enhancing the design of future studies on muon interactions in biomolecular systems.

Keywords: Density Functional Theory; DNA; Guanine; Hyperfine Interaction; Muon

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Introduction

DNA, the blueprint of life is a vital biopolymer because it determines how an organism function. The properties of DNA have attracted considerable interest from physicists, chemists, and material scientists due to its capability to act as a medium for electron transport and its great potential for eco-friendly applications in nanotechnology. Developing DNA-based devices requires a thorough understanding of their electronic structure and properties. Muon can be used as a sensitive probe to investigate the nature of electron state of various materials. It is employed in a collection of experimental method called μ SR (Muon Spin Rotation/ Relaxation/ Resonance). μ SR has been successfully applied to study microscopic properties of different materials including molecules of biological importance such as DNA (Hubbard *et al.*, 2006; Nagamine *et al.*, 2009). When a muon enters into an organic material, it may capture an electron and form a muonium (Mu). Knowledge on the Mu stopping sites would enable the computation of muon hyperfine coupling constant (HFCC).

Mu HFCC can be measured using Avoided Level Crossing μ SR (ALC- μ SR) technique. At a specific value of applied magnetic field, muon spin resonance can occur. There are three types of resonances, $\Delta 0$, $\Delta 1$, and $\Delta 2$, which depend on ΔM , where M is the sum of the m_z quantum numbers of the muon, electron, and proton spins (McKenzie, 2019). A review and details of the ALC- μ SR technique can be found in McKenzie's previous study (McKenzie, 2019). Muon hyperfine interaction involves the coupling between the magnetic dipole moment of muon and the surrounding unpaired electron spin. Its strength is represented by the so-called muon HFCC. These interactions are considerably smaller compared to the energy levels of the nucleus itself. The isotropic Fermi contact hyperfine coupling constant A is defined as follows (Sulaiman, 1992).

$$A = \frac{4}{3} \gamma_e \gamma_\mu \hbar (10^{-6} a_0^{-3}) [|\Psi_u^\uparrow(\mathbf{R})|^2 + \sum_v \{ |\Psi_v^\uparrow(\mathbf{R})|^2 - |\Psi_v^\downarrow(\mathbf{R})|^2 \}]$$

In the above equation, the gyromagnetic ratio of electron and muon are represented by γ_e and γ_μ , respectively. $\hbar$ is the plank constant, a_0 is the Bohr radius, and Ψ is the electronic wavefunction. The subscripts u and v denote the unpaired spin orbital and paired spin orbital. The up arrow $\uparrow$ and the down arrow $\downarrow$ denote the orbitals of α and β electrons respectively.

There are three main objectives in the work presented in this paper. First, is to computationally determine the electron state of the studied molecule.

Secondly, this study aims at identifying the most probable sites in the molecule where a muon would stop after its implantation. The third objective is to compute the value of muon HFCC at the trapping sites. By understanding how guanine interacts with an implanted muon, this study provides insights into its electronic behavior and structural stability. Guanine has been chosen as the molecule to be studied because it is one of the four nitrogenous bases found in DNA that is known to allow electron transport to occur (Kratochvílová *et al.*, 2008).

Materials and Methods

The DFT calculation involved the use of structural data from the non-muonated molecule (host system). The non-optimized coordinates of the atoms in the host system were generated using the data provided in the PubChem substance and compound database (Kim *et al.*, 2015). The atomic coordinates of the host atoms were then optimized such that the resulting geometry corresponds to the lowest in total energy. Subsequently, this optimized host structure was added with a Mu at various possible sites in DNA nitrogenous base. As a result, Mu will be bonded covalently to one of the host atoms, either a carbon, nitrogen, or oxygen (Hubbard *et al.*, 2004). There are five carbon atoms labeled as atom number 2, 4, 5, 6, and 8 in Figure. 1 that are suitable as Mu sites. Additionally, nitrogen atoms number 3 and 7, as well as oxygen number 6 can be possible sites too.

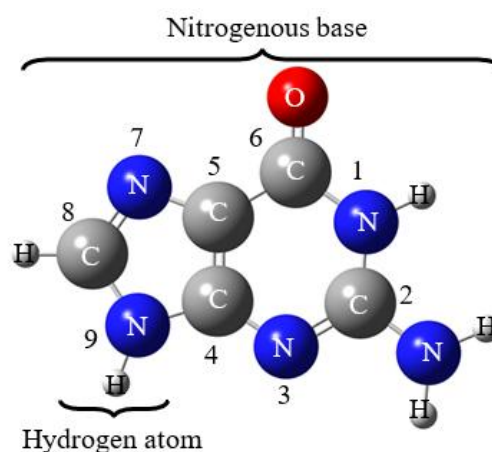


Figure 1. Geometrical structure of isolated guanine. The number follows the IUPAC nomenclature. The atomic symbols are labeled in the sphere

The orbital shape, size, and energy of Mu and hydrogen are virtually the same, making hydrogen a reliable substitute for Mu in theoretical calculations. Since the reduced mass of Mu is 0.995 that of hydrogen, their quantum mechanical behavior is nearly identical. This allows the Born-Oppenheimer approximation to be applied. Thus, in this study, Mu is represented by a hydrogen atom (Zaharim *et al.*, 2021). Once a Mu was added, all atoms were allowed to relax to a new position by executing further geometry optimization procedure. The electronic properties such as the highest occupied molecular orbital (HOMO), and the lowest unoccupied molecular orbital (LUMO), as well as muon HFCC were analyzed and evaluated using the converged electronic structure. Possible Mu trapping sites were predicted by examining the total energy of the muoniated systems (Sulaiman, 1992; Zaharim *et al.*, 2024).

DFT method at B3LYP/6-311++G(d,p) level was employed for all calculations in this study. Gaussian 16 Revision B0.1 made available at the RIKEN Hokusai GreatWave Supercomputing facility was used for the geometry optimization and electronic structure calculation (Frisch *et al.*, 2016). The input files for Gaussian 16 calculations were created using GaussView 6 package (Dennington *et al.*, 2016). This software was also used to generate visual images such as molecular orbital surface plot. The quality of all open shell calculations is excellent as the value of $\langle S^2 \rangle$ is between 0.75 to 0.76. In the Gaussian 16 output, the Fermi contact value A is given in the atomic unit. The muon HFCC was then calculated using the isotropic Fermi contact hyperfine coupling constant equation.

Results and Discussion

Host System

Guanine is a derivative of purine. It is made up of a pyrimidine and an imidazole ring that are fused together at C4-C5. The initial geometry of the pyrimidine-imidazole ring is planar. The ring's planarity was not affected by optimizing all atoms' coordinates to achieve minimum total energy configuration. The computed total energy of the optimized structure is -14,761.3 eV. The HOMO and LUMO energies for the optimized isolated guanine system are -6.002 eV and -0.866 eV, respectively. The HOMO-LUMO energy gap was then calculated to be 5.147 eV. Figure. 2 shows the electrostatic potential map and the atomic charges of isolated guanine. The electron concentration at the molecular electrostatic potential surface is

indicated by different colours as in Figure. 2(a). The red area is the most negative electrostatic potential where most electrons are located, while the most positive electrostatic potential appears in blue. The potential value in this molecule ranges from -0.03 a.u. (red) to +0.03 a.u. (blue).

The most negative values of electrostatic potential are found at the molecular plane that is associated with the guanine base ring and carbonyl oxygen. Based on the results obtained, isolated guanine has three minimum electrostatic potentials that are near to the N3, O6, and N7 atoms, which is in agreement with previous study (Pullman and Pullman, 1981). These three areas are the most negative parts that are electron abundant, and an electrophile would preferentially be attracted to these three positions. In the remaining region (other than N3, O6, and N7 areas) of guanine base, the electrostatic potential is positive. As can be seen in Figure 2(b) all nitrogen atoms have negative charge values. For carbon atom, only C5 atom has a slight negative effective charge.

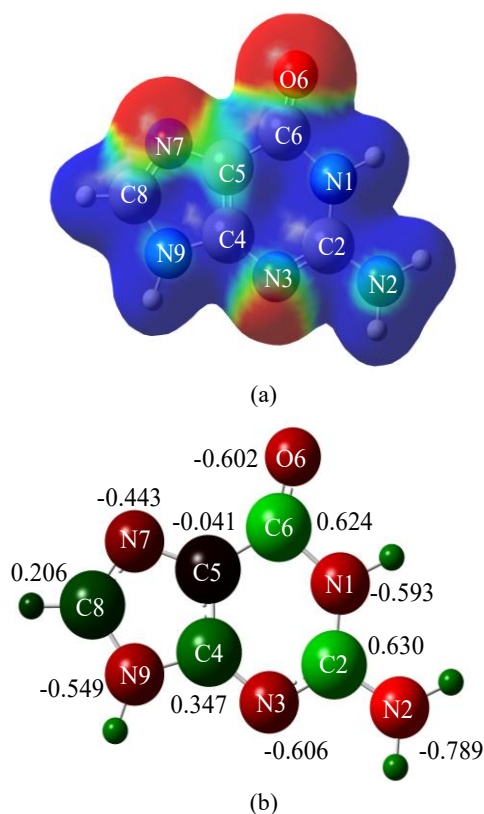


Figure 1. (a) Map of molecular electrostatic potential and (b) atomic charge distribution in the isolated guanine optimized geometry

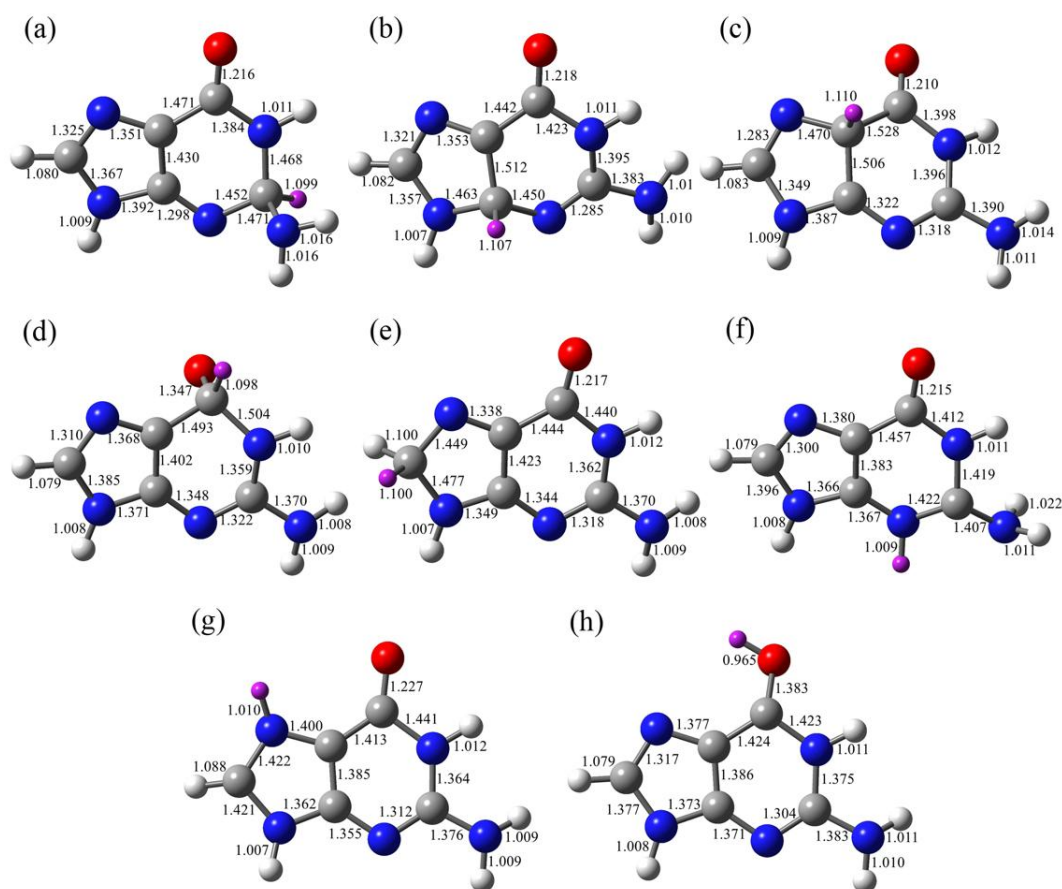


Figure 3. Optimized geometries of the muoniated isolated guanine systems. Mu (purple color) is trapped at (a) C2, (b) C4, (c) C5, (d) C6, (e) C8, (f) N3, (g) N7, and (h) O6

Muoniated System

Figure 3 shows the optimized geometries of muoniated isolated guanine with Mu at different trapping sites. The bond distances in the optimized geometries are also shown in the figure. Isolated guanine has an NH_2 (amine) group attached to the purine ring at position 2. In the host system, the nitrogen atom of the NH_2 group and the purine ring lie in a plane. The NH_2 group bends out by 58° from the initial position when Mu is trapped at C2 while maintaining the purine ring's planar geometry. Extensive geometrical alterations were observed when a Mu is added to C4 or C5 atoms. For these two trapping sites, the purine ring adopts a “butterfly” conformation, which agrees with the observations made in previous studies for the case of hydrogen or Mu addition (Goli, 2018).

For C6 trapping site, the oxygen atom located at position 6 moves out of the plane but does not distort the purine ring. The isolated guanine base's planarity was not affected after the addition of a Mu at C8. To achieve a minimum total energy conformation, the hydrogen atom at C8 atom

moved to a new position such that it makes an angle of 60° with the molecular plane. For N3 trapping site, the muoniated radical formed exhibits a slight puckering in the pyrimidine ring. The NH_2 group is twisted such that one hydrogen atom is located below the molecular plane while the second hydrogen atom lies above the molecular plane. The formation of muoniated radical when Mu is trapped at N7 atom causes a slight distortion to the imidazole ring. In the unmuoniated system, O6 atom is located in-plane with purine ring. The addition of Mu at O6 dislodged the O6 atom from the plane where the dihedral angle formed by O6-C6-C5-C4 is 146° .

Table 1 summarizes the main findings of our computational investigations on Mu trapping sites and Mu hyperfine interaction in isolated guanine, arranged in increasing order of relative energy. The bond order of Mu trapped at different possible Mu trapping sites varies from 0.750 to 0.910, an indication that the stability of Mu is site dependent. For Mu attached to the carbon atoms (C2, C4, C5, C6, and C8), the bond order values are greater than

0.840. In contrast, when Mu is attached to nitrogen (N3 and N7) or oxygen (O6) the bond order values are smaller than 0.830. These results show that a Mu trapped at the carbon atoms has greater stability than a Mu trapped at the nitrogen or oxygen atoms. Mu attached to the C8 atom (Mu-C8) in the guanine base ring has the largest value of bond order. Consequently, Mu-C8 covalent bond is also the strongest, an indication that C8 could be the most stable site.

The LUMO energy values are in the range of -0.591 eV to -0.932 eV. There are no significant differences in the LUMO values for all possible Mu trapping sites. However, there is a significant difference in the HOMO energies. The HOMO energy for all possible Mu trapping sites is in the ranges of -3.557 eV to -6.050 eV. The corresponding HOMO-LUMO energy gap values are in the range of 2.771 eV to 5.281 eV. The atomic charge on Mu of different muoniated radicals varies from 0.121 to 0.133. These atomic charge values are small and show that it is a paramagnetic Mu state and not a diamagnetic state.

The trapping positions of Mu were computationally determined by analyzing the possible sites and their corresponding total energy (Sulaiman *et al.*, 1994; Cammarere, 2000). The difference between the lowest energy and the highest energy states is 1.372 eV. The lowest energy Mu site was found to be the C8 atom in the guanine base. The next sites in the increasing order of energy are N7, C2, C4, C5, O6, N3, and C6, where the energy increases by 0.425 eV, 0.554 eV, 0.555 eV, 0.703 eV, 0.761 eV, 0.871 eV, and 1.372 eV, respectively. The calculated Mu HFCC values are all positive except for Mu trapped at the O6 atom, which is -24.8 MHz. A negative value of HFCC is caused by the polarization effect of Mu *1s* electron. The calculated values HFCC for Mu at the C4, C5 and C8 are high where the values are 366.3 MHz, 446.9 MHz and 337.4 MHz, respectively.

McKenzie conducted ALC- μ SR experiment to measure the Mu hyperfine interaction in the nitrogenous bases (3). For guanine base, a resonance signal was reported at 1.5 T. Based on his analysis using computational and experimental data, the 1.5 T signal is due to the formation of a muoniated radical corresponding to an addition of Mu to C8 atom. The associated muon HFCC was calculated to be 400.8 MHz. It can be seen in the last column of Table 1, C4, C5 and C8 Mu trapping sites have the closest predicted resonance positions to McKenzie's ALC- μ SR experimental results. However, C4 and C5 sites are unlikely due to the much higher total energy as compared to the C8 trapping site. Thus, based on this DFT study, C8 is the only Mu radical that could form in the isolated guanine system which is in agreement with McKenzie's experimental findings (McKenzie, 2019).

Conclusion

In this paper, the results of DFT computation to determine muon's trapping position in isolated guanine are presented. It is found that the introduction of a single Mu into guanine molecule causes significant atomic relaxation. It is crucial for the muoniated molecule to undergo full geometry relaxation procedure so that the system can achieve minimum energy configuration. Mu can have profound effects on the purine ring geometry. For some sites, however, the distorting effect due to the presence of a Mu is compensated by the reorientation and relaxation of the surrounding atoms. Based on the DFT computational investigation, Mu prefers to be trapped at the C8 atom of the isolated guanine.

Table 1. Main findings on Mu trapping sites and Mu hyperfine interaction of isolated guanine. The Mu sites are listed in ascending order of their relative energy as given in column two. The relative energy is calculated by subtracting the particular site's energy with the energy of C8 sites which is the lowest. Theoretically predicted ALC resonances field was evaluated by assuming the condition that $|\Delta M|=1$

Mu site	Relative energy (eV)	Bond order	HOMO (eV)	LUMO (eV)	Mu charge (a.u)	HFCC (MHz)	Estimated ALC resonance (T)
C8	0.000	0.903	-4.429	-0.932	0.191	337.4	1.2
N7	0.425	0.806	-3.557	-0.808	0.405	81.6	0.3
C2	0.554	0.897	-6.050	-0.769	0.171	122.4	0.5
C4	0.555	0.869	-5.183	-0.747	0.195	366.3	1.4
C5	0.703	0.846	-3.994	0.713	0.219	446.9	1.6
O6	0.761	0.751	-3.557	-0.591	0.482	-24.8	0.1
N3	0.871	0.805	-4.355	-0.892	0.405	0.7	0.0
C6	1.372	0.890	-5.719	-0.733	0.172	64.5	0.2

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