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Theoretical investigation of the interaction between glycine amino acid and fullerenes

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Abstract: In this paper, the possibility of the formation of glycine–C_{60} and glycine–C_{80} complexes were investigated by the Density Functional based Tight Binding (DFTB) treatment. It was found that the binding of glycine to C_{80} generated the most stable complexes via its amino nitrogen active site. We have also tested the stability of these complexes with density functional based tight binding molecular dynamics simulation which have been carried out at room temperature. These indicate that proteins might be able to form stable bindings to fullerenes, especially C_{80}, via their active sites.

Keywords: Fullerenes; Glycine; Adsorption; DFTB; Molecular simulation

Introduction

Fullerenes, the hollow carbon cages discovered in 1985 [1], are carbon clusters formed by the closing of a graphitic sheet among a given number of graphitic hexagons, of twelve pentagons. They are interesting class of compounds, because of many properties of them are unique.

Particular attention has been given to the most prominent representative of the fullerene class, C_{60}, which is the most abundant cluster in the solvent-extracted carbon soot. These last years, they have been widely considered for much interest to grow in their potential applications in the bio-area [2-10].

It's well known that proteins are instrumental in almost everything that the organism does. Hence, information about how the fullerene cage chemically interacts with proteins should be important for its applications to the bio-area. Glycine is often chosen as the simplest representative of a backbone unit of a protein therefore, glycine–fullerene complex can be chosen as a model for studying the interaction between a protein and a fullerene nano-cage. Furthermore, glycine (or other amino acid)–fullerene derivatives are of special interest as biologically active compounds [11–17]. These envisioned applications of fullerenes certainly demand a critical understanding of how such nanomaterials can impact biological systems. In one recent study [16], it was shown that glycine can directly react with C_{60} via its amino group in the presence of sodium hydroxide [16]. The possibility of the formation of glycine–C_{60} complex has been also discussed by using semi-empirical (AM1) quantum chemical calculations [18], and investigators have reported that the glycine may generate a stable complex with the C_{60} nano-cage via its amino nitrogen active site. More recently, by using B3LYP hybrid DFT method, Hu et al. [19] carried out interesting theoretical work regarding the glycine–C_{60} complex. They reported that the binding of glycine to C_{60} generated a slightly unstable complex via its amino nitrogen, a moderately unstable complex via its hydroxyl oxygen, and a very unstable complex via its carbonyl oxygen.

In the present work we intend to extend our understanding of the stability of glycine–C_{60} complex by means of Density Functional Theory (DFT) based calculations. The interactions between C_{60} and glycine were obtained for three active sites of glycine: the amino nitrogen (N), the hydroxyl oxygen (O), and the carbonyl oxygen (O) sites. To further investigate the formation of possible complexes between glycine and larger fullerenes we have also performed similar calculations for the glycine–C_{80} system.

Since the main factors which influence the stability of such systems are weak but numerous nonbonding van der Waals (vdW) interactions hence, for the first time, the dispersion corrects for the vdW interaction have also been considered. In view of the problems with designing life sciences-related tools employing these nanomaterials and the relatively easiness of performing computations using standard density functional theory based program packages the results presented in this paper deserve richly some comments.

Computational methods

The structural optimizations of C_{60} /C_{80} and glycine molecules are carried out using the recently developed DFTB+ code [20]. The DFTB+ uses the Density Functional based Tight Binding method based on a second-order expansion of the Kohn-Sham total energy in density functional theory with respect to charge

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density fluctuations. At second-order expansion a transparent, parameter-free, and readily calculable expression for generalized Hamiltonian matrix elements can be derived.

The DFTB approach, unlike the typical approximate Hartree-Fock/DFT methods, uses a tabulated set of integrals derived from *ab initio* DFT calculations [21], leading to a substantial speed-up of the method since explicit integration is not required in the method. Furthermore, unlike conventional tight-binding method it is possible to produce parameterizations capable of accuracy close to LDA/GGA with minimal adjustable parameters and also transferable between different systems. The basis functions of the DFTB method are also available, allowing the reconstruction of actual wavefunctions from the calculations. Further details of the method have been fully reviewed for instance in [20-23]. In this work the Slater-Koster (S-K) type parameter set [24] was implemented. Furthermore, the dispersion corrections for the nonbonding van der Waals interaction were implemented via the Slater-Kirkwood type model [25].

Geometries of the fullerenes and glycine are optimized separately prior to the optimization of the whole system. Structural optimizations were performed using the conjugate gradient algorithm. The accuracy of our method is tested by comparison of optimized geometries of fullerene C_{60} and glycine molecule against the existing experimental data.

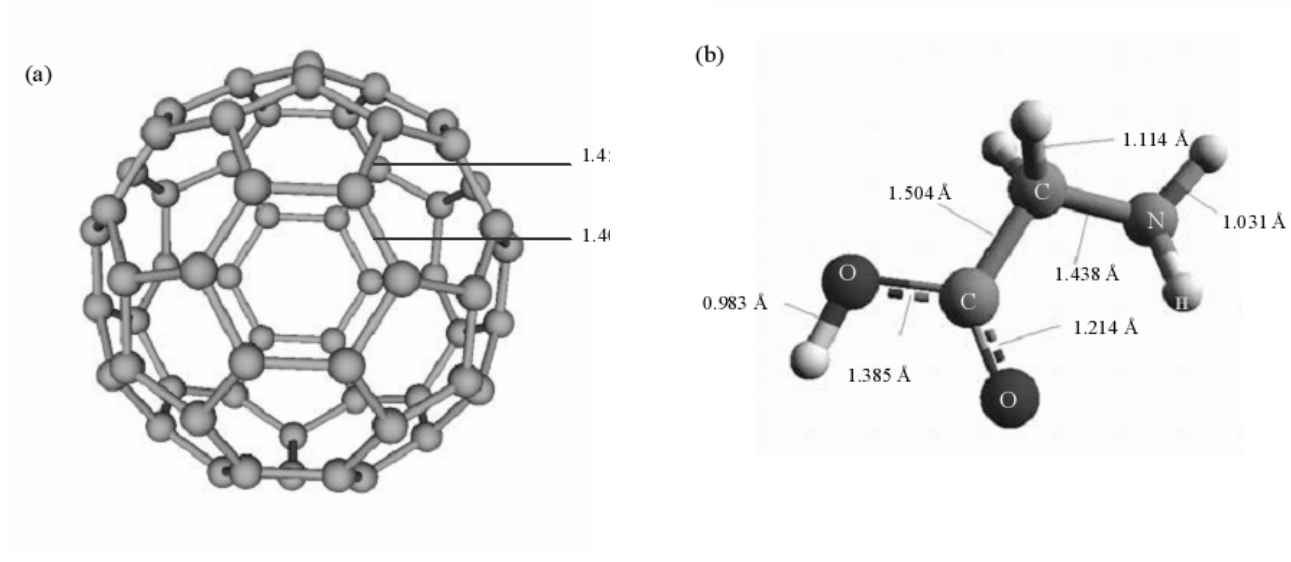
We have also tested the stability of the glycine–C_{60} and C_{80} complexes with density functional based tight binding molecular dynamics (DF-TBMD) simulation. The DF-TBMD simulations are done by DFTB+ in the canonical regime; i.e., the thermodynamical system under consideration is described by the number of particles *N*, volume *V*, and temperature *T* as variables. The structure under study is in contact with Andersen thermostat [26] having fixed temperature 300 K. The MD time step is 1.0 fs.

3. Results and discussion

To study the glycine binding to the C_{60} cage we start with atomic structures of C_{60}. The structure of C_{60} has widely been examined theoretically using quantum chemical calculations [27-34]. The structure of C_{60} obtained (Fig. 1a) is consistent with the literature [27-34], and the prediction of bond lengths (1.454 Å for single bond and 1.404 Å for double bond) is in excellent agreement with the experimental values (1.458 and 1.401 Å, respectively) [35-37].

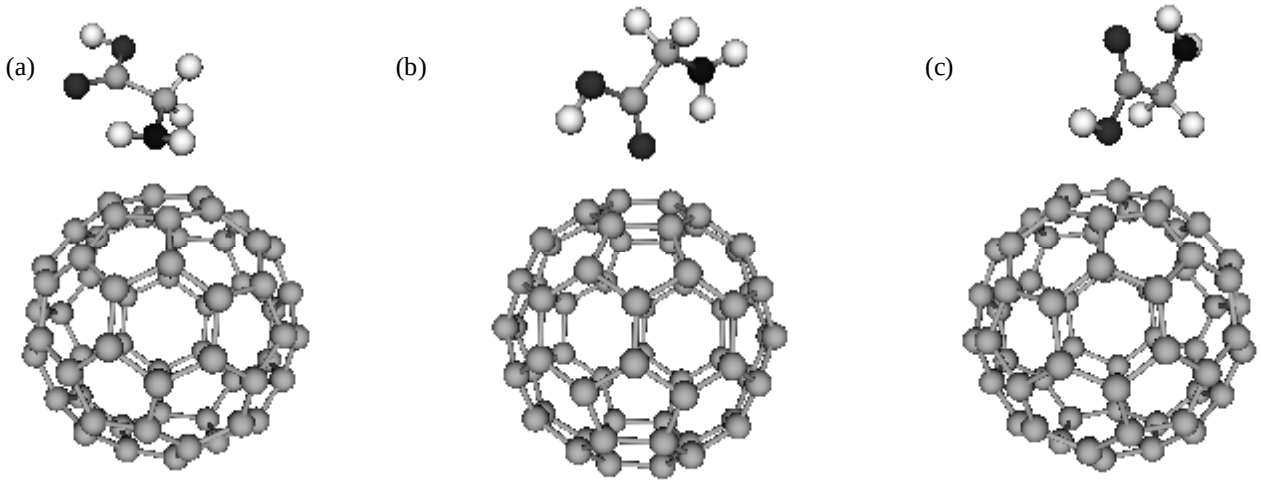
As the simplest representative of a backbone unit in a protein, glycine has been widely studied [38, 39]. Its most stable structure, which we obtained using DFTB, is presented in Fig. 1b.

Figure 1. The optimized geometric structures of (a) C_{60} fullerene cage and (b) glycine molecule.



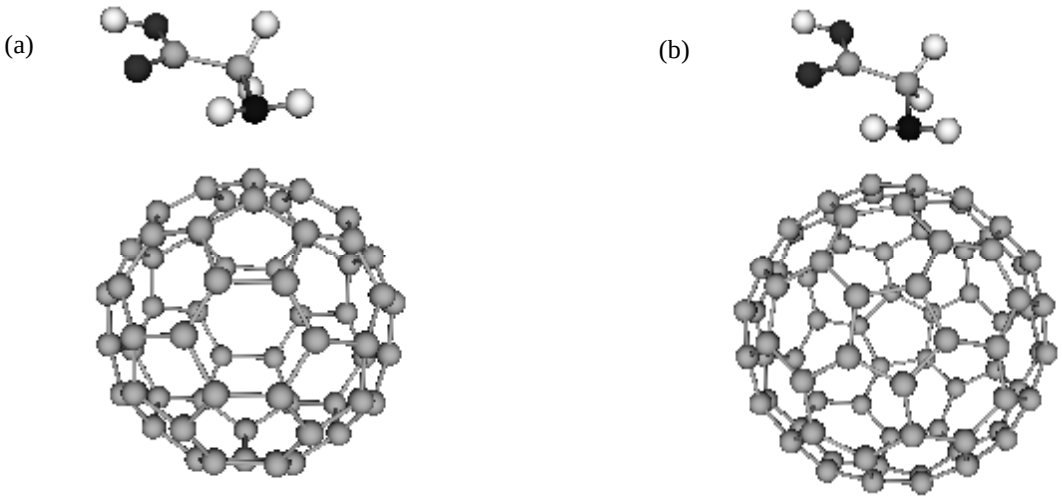
The geometric parameters of this structure are consistent with the literature [38-40]. Furthermore, it is well known that a glycine molecule has three active sites, the amino nitrogen (N), the hydroxyl oxygen (OH) and the carbonyl oxygen (O) sites. Therefore, it is expected for glycine to interact with the fullerenes cage via these three active sites. In order to examine the adsorption of a glycine on the fullerene cage, three possible configurations, called (A), (B) and (C), were selected for a molecule approaching the center of a hexagon/pentagon of carbon atoms: (A) denotes the amino nitrogen, (B) the hydroxyl oxygen and (C) the carbonyl oxygen active sites approach. The three configurations are shown in Fig. 2.

Figure 2. Model for three different adsorption states for a glycine molecule on the C_{60} cage above a hexagon via (a) the amino nitrogen (N), (b) the hydroxyl oxygen (OH) and (c) the carbonyl oxygen (O) active sites.



The optimized C_{60} structure was used for the molecule adsorption. After full structural optimization of the considered systems we find that the glycine prefers to interact with the C_{60} cage via its amino nitrogen (N) active sites, as represented in Fig. 3-a.

Figure 3. Stable structure for (a) glycine–C_{60}, (b) glycine–C_{80} complexes.



To evaluate the stability of the glycine–C_{60} complexes, we calculated the energy of formation (binding energy) of the complex between the glycine and C_{60} molecules, by using the equation:

$$E_b = E_{C60\text{-}Glyc} - E_{C60} - E_{Glyc} \qquad (1)$$

Where $E_{C60\text{-}Glyc}$ is the total energy of the C_{60} with an adsorbed glycine molecule, $E_{C60}$is the total energy of the pure C_{60}, and E_{Glyc} is the total energy of the isolated glycine molecule.

For the energetically favorable configuration the calculated binding energy E_b and C–N equilibrium distance are about -0.2321 eV (-5.350 kcal/mol) and 2.317 Å, respectively, they are comparable with DFT results of Roman et al. for glycine adsorption on the CNTs and also comparable with those of gas adsorption on the CNTs [40-42]. The large distance of adsorbed molecule from the cage and the adsorption energy of -0.2321 eV indicate a weak interaction of glycine with the C_{60} fullerene. Furthermore, the results show that the bond lengths of glycine exhibit only small changes during its binding to the C_{60} cage [the lengths of the N-H and C-C bonds of glycine become longer (increasing from 0.970 to 1.030 Å and from 1.385 to 1.436 Å, respectively)].

One can see that the formation of the complex (via the amino nitrogen active site) decreases the energy of the system by -5.350 kcal/mol. This indicates that the binding of glycine to C_{60} is slightly stable via its amino nitrogen. This is consistent with both the experimental observation [16] and theoretical result of Messaouda et al. that showed that the addition of a glycine on C_{60} via amino group leads to a stable complex [18]. The calculated binding energies, E_b, of the hydroxyl oxygen (OH) and the carbonyl oxygen (O) active sites are about -0.1378 and -0.1921 eV, respectively.

To further investigate the adsorptive capability of glycine by fullerenes we have also performed similar calculations for the possibility of formation of glycine–C_{80} complex. After full structural optimization of the glycine–C_{80} systems (six configurations) we find that the glycine prefers to interact with the C_{80} cage via its amino nitrogen (N) active site. The calculated binding energy and C–N equilibrium distance are about -0.2809 eV (-6.475 kcal/mol) and 2.243 A, respectively. The large distance of adsorbed molecule from the cage and the adsorption energy of -6.475 kcal/mol indicate also a weak interaction of glycine with the C_{80} fullerene. The optimized geometric structure of the energetically favorable glycine–C_{80} complex is represented in Fig. 3-c. Mulliken analysis indicates that there is about 0.11 *e* and 0.20 *e* transfer from glycine toward the C_{60} and C_{80} cage, respectively. This indicates that there exist a stronger interaction between C_{80} and glycine amino acide in comparison with the C_{60} fullerene.

As a result, we find that glycine molecules prefer to interact with fullerenes via their amino group active site. Furthermore, the C_{80} fullerene can form the most stable complex with glycine in comparison with the C_{60} fullerene. As we know, as we reduce the number of atoms, these structures (fullerenes) would become more reactive [43-45] but however the present results indicate that these structures become more reactive with increasing of the number of atoms.

In order to investigate the stability of the glycine–C_{60} and C_{80} complexes, we have performed density functional based TBMD simulation for the most stable configurations. We put the systems in contact with a thermostat at room temperature and then a 2000 fs time MD simulation was performed. It does suggest that the glycine–C_{60} and C_{80} complexes are quite stable at room temperature. Therefore, from the calculation results involving glycine, one can predict that glycine amino acid might readily form stable bindings with fullerenes, especially C_{80}, via their amino nitrogen (N) active sites.

Conclusions

In summary, we have investigated the interaction of glycine molecule with C_{60} and C_{80} fullerenes by *first-principles* Density functional based Tight Binding (DFTB) method. The calculations results revealed that the binding of glycine to C_{60} and C_{80} fullerenes generated stable complexes with binding energies of -5.350 and -6.475 kcal/mol, respectively, via its amino nitrogen (N) active site. The DF-TBMD simulation, carried out at room temperature, shows that the glycine–C_{60} and glycine–C_{80} complexes are stable and that is possible to adsorb the glycine molecule by the fullerenes. Since all proteins contain amino nitrogen (N), hydroxyl oxygen (O) and carbonyl oxygen (O) active sites therefore, from the calculation results involving glycine, one can predict that fullerene cages, especially C_{80}, might be able to form stable bindings to proteins via their amino nitrogen (N) active sites.

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