Eur. Phys. J. D **38**, 117–120 (2006)
DOI: 10.1140/epjd/e2006-00043-1

THE EUROPEAN PHYSICAL JOURNAL D

Amino acid adsorption on single-walled carbon nanotubes

T. Roman[1], W.A. Diño[1,2,3], H. Nakanishi[1], and H. Kasai[1,a]

[1] Department of Applied Physics, Osaka University, Suita, Osaka 565-0871, Japan
[2] Department of Physics, Osaka University, Toyonaka, Osaka 560-0043, Japan
[3] Physics Department, De La Salle University, Manila 1004, Philippines

Received 12 September 2005 / Received in final form 1st December 2005
Published online 21 February 2006 – © EDP Sciences, Società Italiana di Fisica, Springer-Verlag 2006

Abstract. We investigate and discuss the adsorption of a few amino acids on (3,3) carbon nanotubes and on graphite sheets through calculations within density functional theory. Results show weak binding of the biomolecules on both substrates, but through generally favourable adsorption pathways. Zwitterion adsorption through the charged amine and carboxylate groups are bound stronger to the nanotube surface in comparison to their nonionic counterparts, as well as on histidine, phenylalanine, and cysteine side chain groups fixed in specific orientations. Binding strengths on graphite suggest dissimilar trends for amino acid interactions with increasing nanotube diameter.

PACS. 85.35.Kt Nanotube devices – 81.05.Uw Carbon, diamond, graphite – 31.15.Ar Ab initio calculations – 87.14.Ee Proteins

1 Introduction

It wasn't very long after the debut of carbon nanotubes (CNTs) over a decade ago for much interest to grow in their potential applications in the life sciences. Initially generating a strong following due to their remarkable electronic properties and believed potential for nanoscale storage, a few years ago the role of CNTs as part of highly responsive sensing systems has been considered, motivated by experimental results suggesting considerable conductivity changes upon exposure of the tubes to some gases [1,2]. Prior to this, several studies have already been published on the immobilization of proteins and nucleic acids on nanotubes (see for instance Refs. [3–5]), though only more recent work [6–8] discussed appreciable changes in nanotube conductivity as biomolecules are immobilized, directly or indirectly, on the CNT sidewalls. Direct peptide binding on CNTs [9] suggests roles of specific amino acids in direct protein interaction with nanotubes, though it is acknowledged that we are still in need of a full understanding on the interfaces of these systems.

Whether for sensing or for any other intended application, a more detailed picture on bridging carbon nanotubes with biological systems should be essential in designing life sciences-related tools employing these nanomaterials. As a starting point in understanding interactions with much more complex biological systems, we carried out calculations within density functional theory on the interaction of armchair (3,3) carbon nanotubes and the amino acids glycine, histidine, phenylalanine, and cysteine. Our computational models for glycine involve the molecule in both its zwitterionic and non-ionic forms — the two forms amino acids take, differing essentially by the position of a proton. In aqueous environments amine protonation is favoured, which gives the amino acid zwitterion a much larger polar character. Data for the four amino acids are subsequently compared with corresponding results on graphite sheets, representative of the limit as carbon nanotube diameter is increased. Details on the model as well as on the computational methods employed are explained more thoroughly in the proceeding section, followed by a discussion of our results in Section 3 and a summary in the last section.

2 Computational details

The fact that amino acids have ten or more component atoms implies that a full simulation of the adsorption process should involve a number of degrees of freedom. We have however limited our calculations to the models described in Figures 1 (glycine) and 2 (histidine, phenylalanine, cysteine), varying the amino acid-substrate separation while holding all other parameters (i.e. adsorbate internal coordinates, rotational orientation) fixed. It should be further noted that separately optimized geometries for the carbon substrates and amino acids were used in the combined system. The orientation schemes employed in modelling nonionic glycine adsorption are shown in Figures 1a and 1b, and for the zwitterionic form in Figures 1c and 1d. Orientations and positions have been

[a] e-mail: kasai@dyn.ap.eng.osaka-u.ac.jp

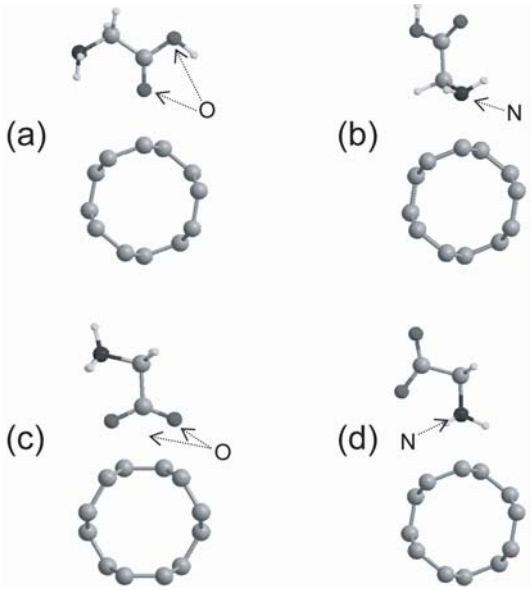

Fig. 1. Glycine on carbon nanotubes: (a) nonionic, through the carboxyl end; (b) nonionic, through the amine end; (c) zwitterionic, through the carboxylate end; (d) zwitterionic, through the amine end. The nanotube axis is directed out of the page.

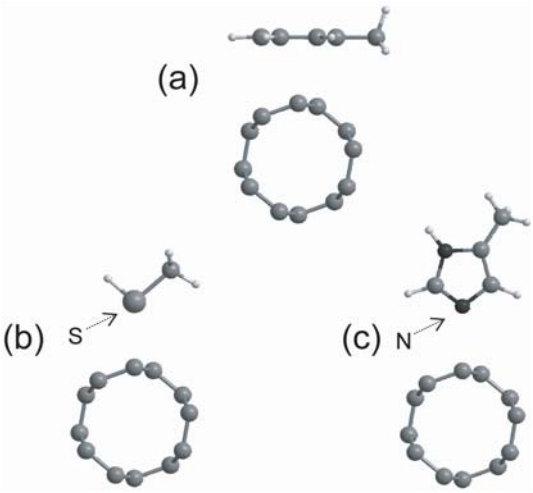

Fig. 2. Amino acid side chain clusters on carbon nanotubes: (a) phenylalanine, (b) cysteine, and (c) histidine models. The nanotube axis is directed out of the page.

specifically chosen so that the carboxyl (Figs. 1a and 1c) and amine (Figs. 1b and 1d) groups approach directly on top (*top* site) of substrate atoms. Top site positions have similarly been adopted for the side chains of histidine and cysteine, while the aromatic ring of phenylalanine is *AB* stacked with respect to the substrate geometry.

As illustrated in Figure 2, the sections that would form part of the polypeptide backbone ($NH_2CHCOOH$) for histidine, phenylalanine, and cysteine have all been replaced by terminating hydrogens. As the twenty most common amino acids primarily differ through their respective side chains, we decided to give focus on those sections alone, partly in light of minimizing the computational cost of the simulations. Histidine is hence hereby represented by an imidazole ring with an attached methyl group, phenylalanine with toluene, and the sulfur-containing cysteine with a methanethiol molecule. We however in this paper refer to these with their respective amino acid analogues.

All structural optimization and total energy calculations for the nanotube/graphite-amino acid systems were performed using Dacapo [10], an implementation of the supercell approach to density functional theory, using ultrasoft pseudopotentials in describing the ion cores. Plane waves with kinetic energies up to 916 eV were employed in the expansion of the Kohn-Sham single-electron wavefunctions, while the generalized gradient approximation (GGA) was adopted for the exchange and correlation energy [11]. The effectively one-dimensional Brillouin zone for the interactions with carbon nanotubes is sampled using the scheme of Monkhorst and Pack [12] through 6 k-points along the tube axis, while a $4 \times 4 \times 1$ sampling mesh was employed for calculations on graphite. On the nanotube we have used an adsorbate coverage of one amino acid for every 24 substrate atoms for all calculations save for that involving phenylalanine, in which 36 substrate atoms were included. The vacuum between periodic images was set to at least 10 Å to minimize interactions with neighbouring supercells. Calculated dispersion relations show non-negligible but small interactions between the adsorbate and its neighbouring images at these coverages. The corresponding computations on graphite were implemented with one amino acid molecule for every 18 substrate atoms, with the periodically stacked carbon sheets separated by about 20 Å.

3 Results

In Figures 3 and 4 we show energy curves describing the interaction of nonionic and zwitterionic glycine, respectively, with the carbon substrates through the two adsorption configurations described in the preceding section. Energy origins are obtained from the sum of the energies of the substrate and adsorbate calculated separately, i.e. setting $E = 0$ at infinite amino acid-CNT/graphite separation. Figures are drawn to the same scale for easier comparison. Quantitative results suggest that glycine is weakly bound to the nanotube sidewall, having adsorption energies comparable to that for gas molecules (see for instance Refs. [13,14], which reported adsorption energies in the range of about 0.1 to 0.8 eV). The relatively far equilibrium glycine-carbon substrate separation, small adsorption energy, and absence of significant charge localization associated in strong chemical bonds all suggest the involvement of only non-covalent interactions in the adsorption.

While the adsorption strength for nonionic glycine regarding the two orientations does not show much difference whether on the nanotube sidewall or on graphite, the carboxyl-first orientation is significantly favoured in the case of the zwitterion. Glycine approaching the substrate through its deprotonated carboxyl (i.e., carboxylate) group adsorbs the strongest among all adsorption

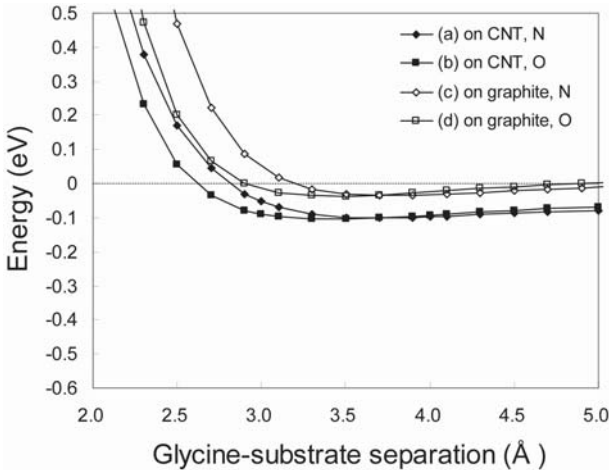

Fig. 3. Energy curves for nonionic glycine adsorption on the carbon nanotube and graphite (solid marks for the nanotube, hollow marks for graphite): (a) on the nanotube, through the amine end; (b) on the nanotube, through the carboxyl end; (c) on graphite, through the amine end; (d) on graphite, through the carboxyl end.

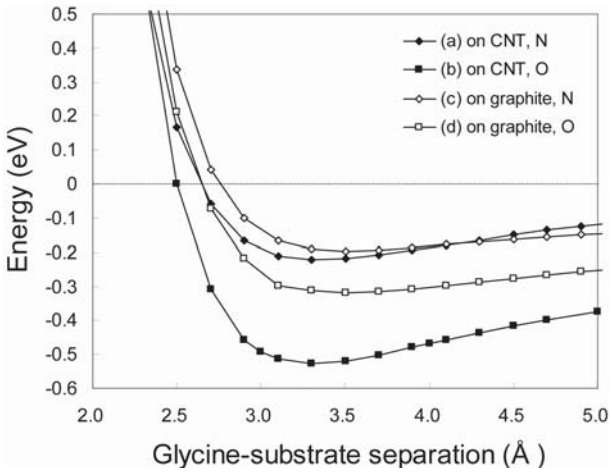

Fig. 4. Energy curves for zwitterionic glycine adsorption on the carbon nanotube and graphite (solid marks for the nanotube, hollow marks for graphite): (a) on the nanotube, through the amine end; (b) on the nanotube, through the carboxyl end; (c) on graphite, through the amine end; (d) on graphite, through the carboxyl end.

models (E_a = 0.53 eV), this particular configuration involving direct interaction with both carboxylate oxygen atoms simultaneously. A quick comparison of the two figures furthermore shows that glycine zwitterions bind more strongly onto the substrates compared to their nonionic counterparts, through both orientations. Though neutral as a whole, the zwitterion is oppositely charged in its amine and carboxylate ends, and we surmise this dipolar nature should promote adsorption of the molecule in introducing an ionic character to the amino acid-carbon substrate interaction, which is accompanied by small charge transfers ($<0.1e$) observed to and from the carbon substrate.

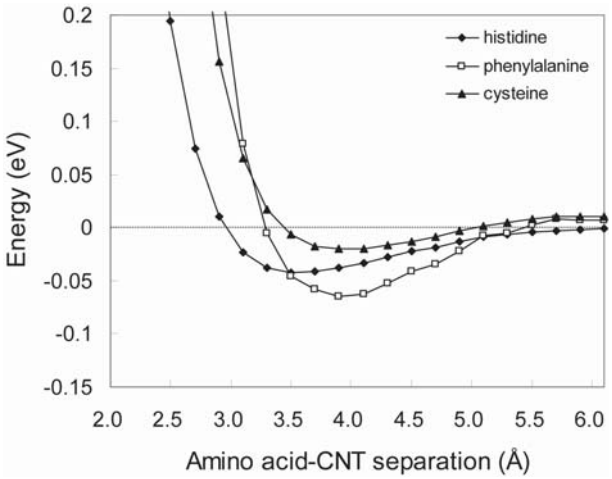

Fig. 5. Energy curves for the interaction of representative side chain models of histidine, phenylalanine, and cysteine with carbon nanotubes.

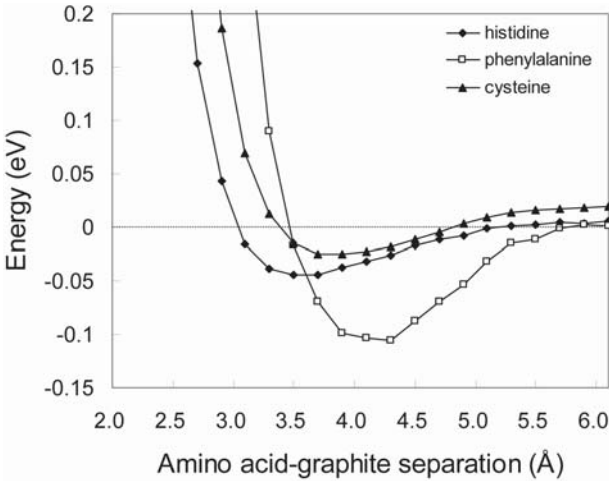

Fig. 6. Energy curves for the interaction of representative side chain models of histidine, phenylalanine, and cysteine with graphite.

The energy relations likewise show substrate dependence of glycine adsorption, binding stronger on the CNT sidewall than on the graphite sheets. Since analogous on-CNT and on-graphite orientations of amino acids were employed, the results may correspondingly imply weaker binding on carbon nanotubes of larger diameters. This result may be attributed to higher substrate chemical reactivity arising from the higher coordination brought about by orbital mixing induced by the high curvature of the (3,3) nanotube, viz. the sp^3-like character of the CNT atoms are more likely to form chemical bonds with adsorbates than those on graphite sheets. Such a trend however is not visible in our results for the side chain groups of histidine, phenylalanine, and cysteine, as shown in Figures 5 and 6. Phenylalanine in particular behaves the other way around, which should be attributed to π-stacking weakening from the nanotube curvature. On the other hand, histidine and cysteine side chain interaction

do not show much substrate-dependent profiles aside from slight increases in their activation energies on graphite. This result should be related to the fact that these molecules in their given spatial configurations showed very weak substrate binding (the weakest in fact in this study, $E_a < 0.05$ eV), something we are currently looking into in more detail. We however surmise from the results for the phenylalanine side chain that it should be possible for histidine to adsorb more strongly with the imidazole ring oriented parallel to the substrate, from its aromatic character. One trend that all the energy curves share is that amino acid adsorption should proceed favourably, i.e. activation barriers are either absent or very small (<0.02 eV). The adsorption processes modelled here suggest that if for specific applications peptides or even entire proteins are to be attached on the nanotubes through, but limited to, the groups discussed in this paper, then doing so through deprotonated carboxyl and fully protonated amine groups may give the most favourable results — here even better than aromatic groups, generalizing from the behaviour of glycine zwitterions. Though additional modelling may be necessary, the current results provide base information on possible contributions of polypeptide chain-terminating amine and carboxyl groups, if not to the same groups in side chains of amino acids not included in the current investigation (e.g., among others, lysine and aspartate).

We have focused on direct adsorption of biomolecules on carbon nanotubes (i.e., without employing linking molecules covalently or noncovalently anchored to the nanotube sidewalls), which may or may not significantly disturb the ordered arrangement of substrate atoms, hence the physical properties of the tube. On this subject matter we are pursuing further calculations involving more computation-intensive structure relaxations during adsorption, though the weak noncovalent interactions implied by the results, even on small-diameter nanotubes, propose that only minor changes may take place.

4 Summary

In light of understanding interactions with more complex biomolecules, we have looked into the adsorption of the amino acids glycine, histidine, cysteine and phenylalanine on (3,3) carbon nanotubes and graphite sheets, taking into account dependence on: (1) amino acid form — zwitterions adsorb stronger than their nonionic counterparts; (2) spatial configurations — binding is strongest through the amino acid carboxyl-first orientation; and (3) substrate curvature — while glycine on graphene has been found to be weaker as compared to adsorption onto the (3,3) nanotube surface, the trend however was not observed for cysteine, histidine and phenylalanine side chains, the latter showing significantly much more affinity for the flat graphite arrangement of carbons. The amino acids adsorb through noncovalent interactions, having adsorption energies comparable to previous results involving gas molecules. The current study has been limited to energetics of the biomolecule interactions, and a discussion relating to substrate effects of the amino acid adsorption will be discussed in further related studies.

This work is partly supported by: a Grant-in-Aid for Scientific Research from the Ministry of Education, Culture, Sports, Science and Technology of Japan (MEXT); the 21st Century Center of Excellence (COE) Program "Core Research and Advance Education Center for Materials Science and Nano-Engineering" supported by the Japan Society for the Promotion of Science (JSPS); the New Energy and Industrial Technology Development Organization's (NEDO) Materials and Nanotechnology program; and the Japan Science and Technology Corporation (JST) Research and Development Applying Advanced Computational Science and Technology program. Some of the calculations were done using the facilities of the Information Technology Based Laboratories Project of the Japan Atomic Energy Research Institute (ITBL, JAERI), and the High Performance Computing Laboratory of De La Salle University, Manila.

References

1. J. Kong, N.R. Franklin, C. Zhou, M.G. Chapline, S. Peng, K. Cho, H. Dai, Science **287**, 622 (2000)
2. P.G. Collins, K. Bradley, M. Ishigami, A. Zettl, Science **287**, 1801 (2000)
3. F. Balavoine, P. Schultz, C. Richard, V. Mallouh, T. Ebbesen, C. Mioskowski, Angew. Chem. Int. Ed. **38**, 1912 (1999)
4. S.C. Tsang, J.J. Davis, L. Malcolm, H. Green, H. Allen, O. Hill, Y.C. Leung, P.J. Sadler, J. Chem. Soc. Chem. Commun. **17**, 1803 (1995)
5. S.C. Tsang, Z. Guo, Y.K. Chen, M.L.H. Green, H. Allen, O. Hill, T.W. Hambley, P.J. Sadler, Angew. Chem. Int. Ed. Engl. **36**, 2197 (1997)
6. R.J. Chen, S. Bangsaruntip, K.A. Drouvalakis, N.W.S. Kam, M. Shim, Y. Li, W. Kim, P. Utz, H. Dai, Proc. Natl. Acad. Sci. **100**, 4984 (2003)
7. K. Besteman, J. Lee, F.G.M. Wiertz, H. Heering, C. Dekker, Nano Lett. **3**, 727 (2003)
8. A. Star, J.C.P. Gabriel, K. Bradley, G. Gruner, Nano Lett. **3**, 459 (2003)
9. S. Wang, E.S. Humphreys, S.Y. Chung, D.F. Delduco, S.R. Lustig, H. Wang, K.N. Parker, N.W. Rizzo, S. Subramoney, Nature Mat. **2**, 196 (2003)
10. B. Hammer et al., DACAPO-2.4.6, `http://www.fysik.dtu.dk/campos` (2004)
11. J.P. Perdew, J.A. Chevary, S.H. Vosko, K.A. Jackson, M.R. Pederson, D.J. Singh, C. Fiolhais, Phys. Rev. B **46**, 6671 (1992)
12. H.J. Monkhorst, J.D. Pack, Phys. Rev. B **13**, 5188 (1976)
13. J. Zhao, A. Buldum, J. Han, J.P. Lu, Nanotechnology **13**, 195 (2002)
14. S. Peng, K. Cho, Nanotechnology **11**, 57 (2000)