Applied Surface Science 419 (2017) 540–545

Contents lists available at ScienceDirect

Applied Surface Science

journal homepage: www.elsevier.com/locate/apsusc

Graphene for amino acid biosensing: Theoretical study of the electronic transport

S.J. Rodríguez [a,*], L. Makinistian [c], E.A. Albanesi [a,b]

[a] Instituto de Física del Litoral (CONICET-UNL), Güemes 3450, 3000 Santa Fe, Argentina
[b] Facultad de Ingeniería, Universidad Nacional de Entre Ríos, 3101 Oro Verde (ER), Argentina
[c] Departamento de Física, e Instituto de Física Aplicada (INFAP), Universidad Nacional de San Luis-CONICET, Ejército de los Andes 950, D5700BWS San Luis, Argentina

ARTICLE INFO

Article history:
Received 7 March 2017
Received in revised form 29 April 2017
Accepted 3 May 2017
Available online 8 May 2017

Keywords:
Graphene
Biosensor
Amino acid
Adsorption

ABSTRACT

The study of biosensors based on graphene has increased in the last years, the combination of excellent electrical properties and low noise makes graphene a material for next generation electronic devices. This work discusses the application of a graphene-based biosensor for the detection of amino acids histidine (His), alanine (Ala), aspartic acid (Asp), and tyrosine (Tyr). First, we present the results of modeling from first principles the adsorption of the four amino acids on a graphene sheet, we calculate adsorption energy, substrate-adsorbate distance, equilibrium geometrical configurations (upon relaxation) and densities of states (DOS) for each biomolecule adsorbed. Furthermore, in order to evaluate the effects of amino acid adsorption on the electronic transport of graphene, we modeled a device using first-principles calculations with a combination of Density Functional Theory (DFT) and Nonequilibrium Greens Functions (NEGF). We provide with a detailed discussion in terms of transmission, current–voltage curves, and charge transfer. We found evidence of differences in the electronic transport through the graphene sheet due to amino acid adsorption, reinforcing the possibility of graphene-based sensors for amino acid sequencing of proteins.

1. Introduction

The analysis and quantification of biomolecules is crucial in clinical diagnosis and treatment, for this reason in the last years, the construction of biosensors with biomedical application has gained great importance [1–3]. For building biosensors, it is needed to explore materials with high biocompatibility, sensitivity, selectivity with fast response time, and feasible nanoscale fabrication procedures. Graphene, a single layer of carbon atoms, has exhibited superior physical and chemical properties than other 3D materials, positionning it as a strong candidate for the construction of biosensors [4,5]. This material is characterized as a semi-metal or zero gap semiconductor. As for its electrical properties, it has shown (i) a remarkably high electron mobility at room temperature—with experimentally reported values in excess of 15,000 $cm^2 V^{-1} s^{-1}$ [6]—, (ii) low resistivity (10^{-6} Ω cm), (iii) low Johnson noise, which along with its high electron mobility allow it to be utilized as the channel in a field effect transistor (FET), (iv) high surface area 2620 m^2/g for both sides of graphene [7], and 1310 m^2/g for one-side (e.g., supported on a substrate).

Theoretical and experimental advances in structures of graphene-based nanomaterials reported changes in electronic transport properties of a graphene sheet, due to interactions by covalent or non-covalent forces between graphene and severals organic molecules [8–12]. Viswanathan et al. [13] described an approach for the development of a graphene-based biosensor platform using glucose as an example of target molecule. The presence of external molecules can vary its conductivity and this variation can either be monitored using a simple chemiresistor or by a transistor based sensor. Ohno et al. [14] investigated graphene field-effect transistors (GFETs) for electrical detection of pH and protein adsorptions, the GFETs thus acted as highly sensitive electrical sensors for detecting biomolecule concentrations. Furthermore, smaller molecules have been sensed: dopamine [15], and nucleotides in a DNA chain, among others. Zou et al. [16] reported a DNA sensor based on graphene, the current signals of the four bases guanine (G), adenine (A), thymine (T) and cytosine (C), were separated efficiently. Zhen et al. [17] developed a novel FET nanobiosensor based on a chemical vapor deposition

* Corresponding author.
E-mail address: sindy.rodriguez@ifis.santafe-conicet.gov.ar (S.J. Rodríguez).

http://dx.doi.org/10.1016/j.apsusc.2017.05.031
0169-4332/

(CVD)-grown monolayer of graphene, their sensor turned out ultrasensitive, label-free, and highly specific for detection of DNA.

In order to evaluate the possibility of using graphene as an amino acid sequencer in a protein [18,19], in this work we studied the effects produced by the adsorption of amino acids on the electronic transport properties of a graphene sheet. The study is divided into two parts: (1) equilibrium configuration and charge transfer upon adsorption of four amino acids—histidine (His), Alanine (Ala), aspartic acid (Asp) and tyrosine (Tyr)—on a graphene sheet (throughout the article the optimized (i.e., relaxed) structures are notated as His/grap, Ala/grap, Asp/grap and Tyr/grap). (2) Evaluation of the non-equilibrium transport properties of graphene—probability of transmission and the current–voltage (*I*–*V*) curve—, before and after adsorption.

2. Computational details

All the calculations were performed within a pseudopotentials approach to the Density Functional Theory (DFT), utilizing the code OpenMX3.8 [20,21] and adopting a DFT-D3 approximation for the exchange-correlation potential (DFT-D3 corrections included van der Waals interactions [22,23]). First we studied the adsorption of the four amino acids on graphene: His, Ala, Asp and Tyr, basic, neutral, acid, and aromatic neutral amino acids, respectively. Amino acids are composed of a carboxyl group (—COOH), an amino group ($-NH_2$), and a side-chain (R group), which distinguishes the nature of each amino acid. Subsequently, we modeled a device to study the effects of the molecules on the electronic transport of graphene.

In order to calculate the adsorption energy E^{ads}(eV) and adsorption distance d^{ads}(Å) a set of relaxations were carried. First, for each amino acid (His, Ala, Asp and Tyr), an initial geometry was obtained by optimizing the amino acid structure. Later, with the aim to eventually find the most stable system geometry, the relaxed molecule was located on a graphene sheet at heights and orientations diferents—with and within carboxyl and amine groups parallels to graphene sheet—, and for each atomic arrangement, a total relaxation of the system was carried out (amino acids and graphene atoms). The interaction energy (E_{int}) was calculated according to:

$$E_{\text{int}}(h) = E_{sub-ads}(h) - E_{ref} \quad (1)$$

where the $E_{sub-ads}$ (h), is the energy of the substrate-adsorbate system for each distance (h) and E_{ref} is the total energy when the interaction between substrate-adsorbate system is negligible (there is no interaction between amino acids and graphene when $h = 12.5$ Å). Finally, the E^{ads} is the minimum interaction energy.

A cut-off energy of 180 Ry was used in the numerical integrations and the solution of Poisson equation, and a k-mesh of $5 \times 5 \times 1$ was used for the self-consistency. For the relaxation, the convergence criterion was of 0.02 eV/Å. The charge transfer was calculated from Mulliken population analysis. The electronic density redistribution over the graphene sheet induced by the adsorbed amino acids was defined as:

$$\Delta D = D_{amino.acid+graphene} - D_{amino.acid} - D_{graphene} \quad (2)$$

where D is the charge density.

The effects of the adsorption on the electronic transport properties of graphene were investigated by first-principles calculations within a combination of DFT and Nonequilibrium Green's Functions (NEGF). We defined three regions L, R and C. A central scattering region (C) sandwiched between a semi-infinite source (left, L) and a drain (right, R) electrode regions. We considered infinite left L and right R graphene leads along the *x*-axis under a two-dimensional periodic boundary condition on the *yz* plane (see Fig. 1). The central region C contained the molecules adsorbed on graphene. The

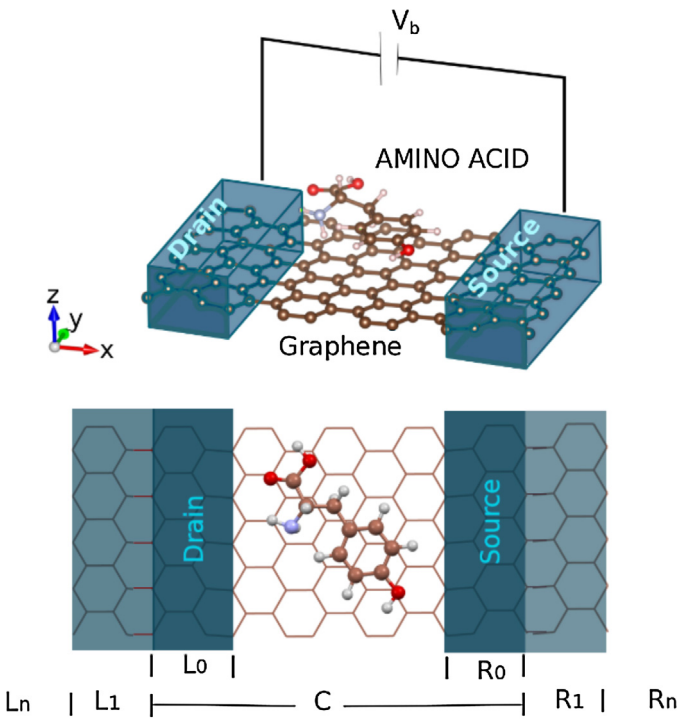

Fig. 1. Configuration of the system treated by the NEGF method, with infinite left and right graphene leads along the *x*-axis under a two-dimensional periodic boundary condition on the *yz* plane. The central region is determined as the equilibrium geometry of amino acids on graphene.

supercell had dimensions $21.30 \times 12.29 \times 25.00$ Å^3 with the two electrode regions containing 20 carbon atoms each, whereas the central (scattering) region contained 60 carbon atoms belonging to graphene, plus the amino acid. The voltage was applied along the *x*-axis, and a temperature of 600 K was used in the Fermi-Dirac distribution, which yields a good compromise between accuracy and efficiency in the implementation of the non-equilibrium Green function method [21].

We modeled five devices: His/grap, Ala/grap, Asp/grap, Tyr/grap and graphene alone. We applied bias voltages (V_b) between the two electrodes of the device in the interval of −2 V to 2 V, with the aim of obtaining the probability of transmission and the current–voltage (*I*–*V*) curve. The transmission probability of electrons incident at an energy E through the device under the potential bias V_b was calculated using Landauer's formula:

$$T(E) = \frac{1}{V_c} \int_{BZ} dk^3 T^k(E) \quad (3)$$

where $T^k(E)$ is the k-resolved transmission, expression within a Green's functions formalism.

The current is evaluated by

$$I = \frac{e}{h} \int dE T(E) \Delta f(E) \quad (4)$$

where $f(E)$ is the difference of Fermi-Dirac distribution functions centered at the electrodes' electrochemical potentials.

3. Discussion of results

3.1. Amino acid adsorption

In Fig. 2 the equilibrium configurations are presented. A tendency to a parallel configuration between rings and graphene is observed for His/grap and Tyr/grap (amino acids His and Tyr have