

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



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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.

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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, positioning 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 $15,000 \text{ cm}^2 \text{ V}^{-1} \text{ s}^{-1}$ [6]—, (ii) low resistivity ($10^{-6} \Omega \text{ cm}$), (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

$2620 \text{ m}^2/\text{g}$ for both sides of graphene [7], and $1310 \text{ m}^2/\text{g}$ 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 several 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

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(CVD)-grown monolayer of graphene, their sensor turned out ultra-sensitive, 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 ($-\text{COOH}$), an amino group ($-\text{NH}_2$), 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 different—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:

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

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

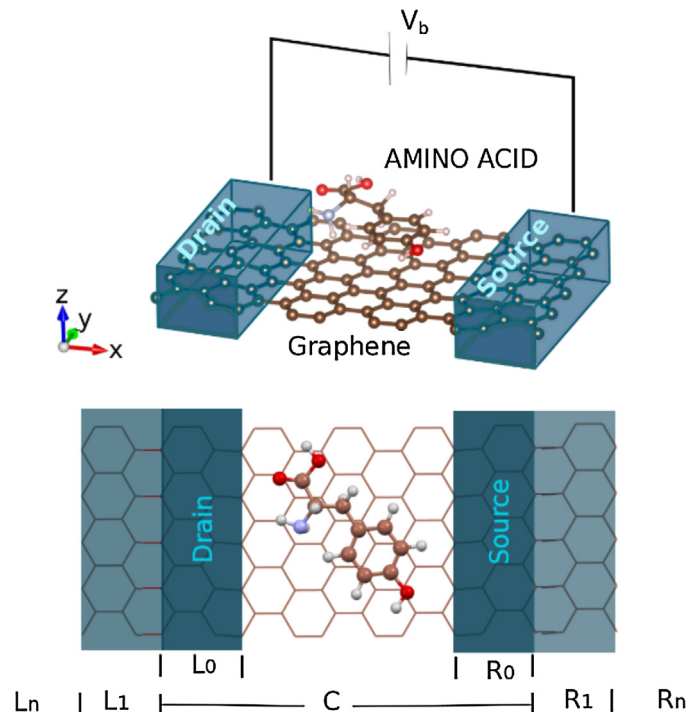


Fig. 1. Configuration of the system treated by the NEGF method, with infinite left and right graphene leads along the x -axis under a two-dimensional periodic boundary condition on the yz plane. The central region is determined as the equilibrium geometry of amino acids on graphene.

supercell had dimensions $21.30 \times 12.29 \times 25.00$ Å³ 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

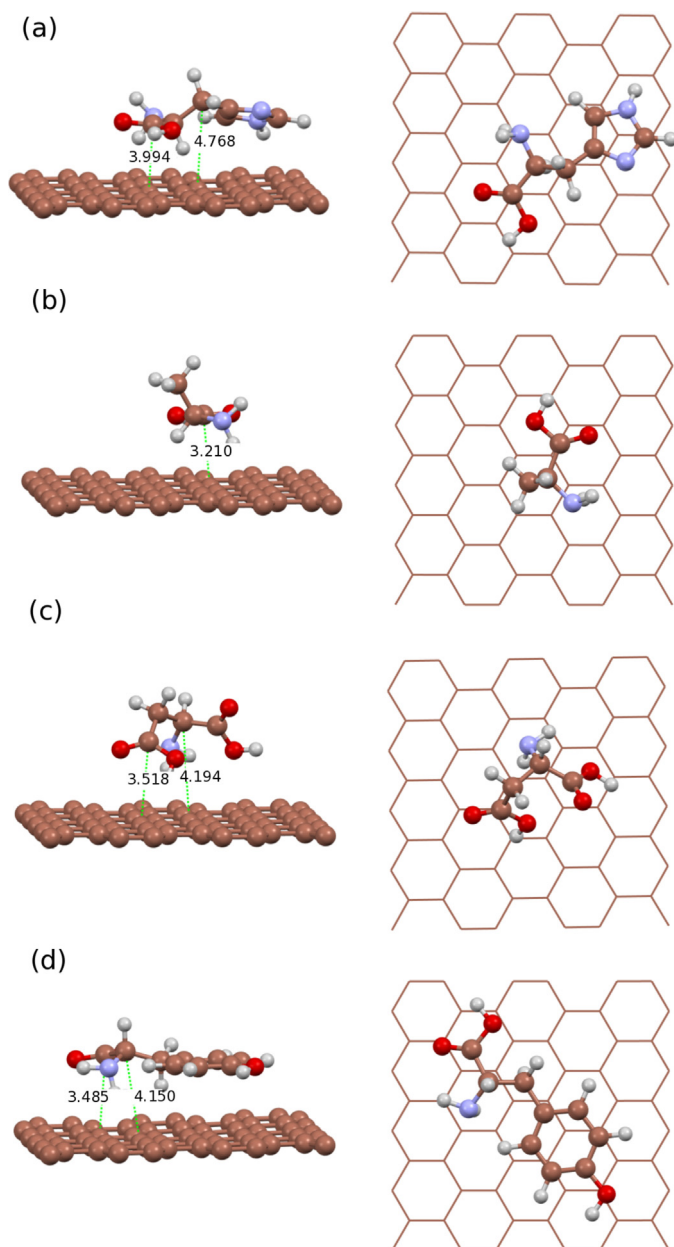


Fig. 2. Equilibrium geometry for amino acids on graphene (a) His/grap, (b) Ala/grap, (c) Asp/grap and (d) Tyr/grap. All distances are in Å.

a side-chain composed of an imidazole ring and a phenol group, respectively). In Tyr/grap the phenol ring is composed of an –OH group, the stronger interaction between the oxygen atom and the graphene sheet generates a completely parallel arrangement between the ring and the graphene sheet. The nature of tyrosine molecules to adopt a flat orientation is consistent with experimental studies on graphene oxide (GO) [7]. A parallel arrangement between the –COOH and –NH₂ groups and the graphene sheet is observed for all systems with minimal energy.

In Table 1 we present E^{ads} and d^{ads} (adsorption distance is measured from the geometric center of the biomolecule to the graphene sheet) for each system. We report that $E^{ads}_{Tyr/grap} > E^{ads}_{His/grap} > E^{ads}_{Asp/grap} > E^{ads}_{Ala/grap}$, whereas $d^{ads}_{Asp/grap} > d^{ads}_{Ala/grap} > d^{ads}_{His/grap} > d^{ads}_{Tyr/grap}$. The systems with the highest E^{ads} present lesser substrate-adsorbate distances (His and Tyr). The amino acids adsorbed on graphene present a strong physisorption with substrate-adsorbate distances

Table 1

Adsorption energy (E^{ads}), adsorption distance (d^{ads}), and transferred charge (Q) for substrate-adsorbate systems: His/grap, Ala/grap, Asp/grap and Tyr/grap.

Gap	Graphene acceptor or donor	Q (e)	d^{ads} (Å)	E^{ads} (eV)	Adsorbate
No	Donor	0.18	2.97	1.49	His
No	Donor	0.10	3.15	0.91	Ala
No	Donor	0.17	4.00	1.17	Asp
No	Donor	0.12	2.89	1.63	Tyr

greater than 2.8 Å –the values calculated for d^{ads} eliminate any chance of covalent bond formation, i.e. chemisorption is not viable.

We report a charge transfer from the graphene sheet to the biomolecules of 0.18 e, 0.10 e, 0.17 e and 0.12 e for, His, Ala, Asp and Tyr, respectively. Graphene is a weak electron donor in all cases. The order of magnitude of transferred charge is in accordance with other works [24]. For instance, graphene donates 0.99 electrons to molecules of 7'70'8'80'-tetracyano-p-quinonedimethane (TNCQ), in this systems, the adsorption opens a gap in the graphene [25]. For smaller adsorbates NO₂ and H₂O 0.09 e and 0.025 e are transferred from the graphene, respectively [26]. The results are shown in Fig. 3. The green regions correspond to $\Delta D > 0$, i.e., higher electron density due to adsorption. The blue regions correspond to $\Delta D < 0$, the lower charge density due to adsorption. The green surfaces are located between the molecule and the graphene sheet; the electrons that participate in π - π interactions cause the charge excess (interaction of the π -orbitals residing on the amino acids and the delocalized p-electrons of graphene). In His/grap, Ala/grap, and Tyr/grap, the transfer charge generates a vertical dipole, with the graphene sheet losing charge and the molecule gaining it, as shown in Fig. 3. The most important effect is a horizontal charge polarization over the graphene sheet forming a local longitudinal dipole. A significant charge density over the graphene sheet coming from the –COOH and –NH₂ groups is displayed by Asp/grap—in this system the local transversal dipole is mainly due to carboxyl and amine groups, breaking with the vertical dipoles symmetry of the other amino acids adsorbed. This result is consistent with studies of the adsorption of benzene rings with carboxyl groups [3,27], whose the interaction with carboxyl groups and graphene is predicted to induce adsorbate dipoles through charge transfer between the molecules and graphene substrates.

We calculated the density of states (DOS) of graphene alone, His/grap, Ala/grap, Asp/grap and Tyr/grap. The solid black line of Fig. 4a displays the well-known DOS for graphene, with its zero gap and zero states at Fermi energy (Diracs points). His, Asp and Tyr amino acids introduce states near the Fermi energy level of graphene at –1.2 eV, –1.8 eV, and –1.3 eV, respectively. These states do not produce an open-gap in graphene. Ala/grap introduces states in E_F : –2.3 eV (states close to typical DOS of graphene alone).

On the other hand, Fig. 4b shows the states-contribution of the –COOH and –NH₂ groups to the total DOS, for each system. In all systems studied, the states at energies –3.8 eV and –2.1 eV are typical contributions of the –COOH (red line with symbols) and –NH₂ (dotted turquoise line) groups, respectively (see arrows in Fig. 4b). The states nearer the Fermi Energy are introduced by the R groups in His/grap and Tyr/grap (systems with greater adsorption energy), while for Ala/graphene the states are introduced by carboxyl and amine groups. Only in the Asp/grap, there are states at energy –3.1 eV due to carboxyl and amino groups, this explains the difference in charge distribution for this system Fig. 3c.

3.2. Electronic transport

In Fig. 5, the transmission for the five systems studied, for $V_b = -1, -1.5$ and -2 V, is presented, and significant differences in transmission are given for these bias voltage values. The transmis-

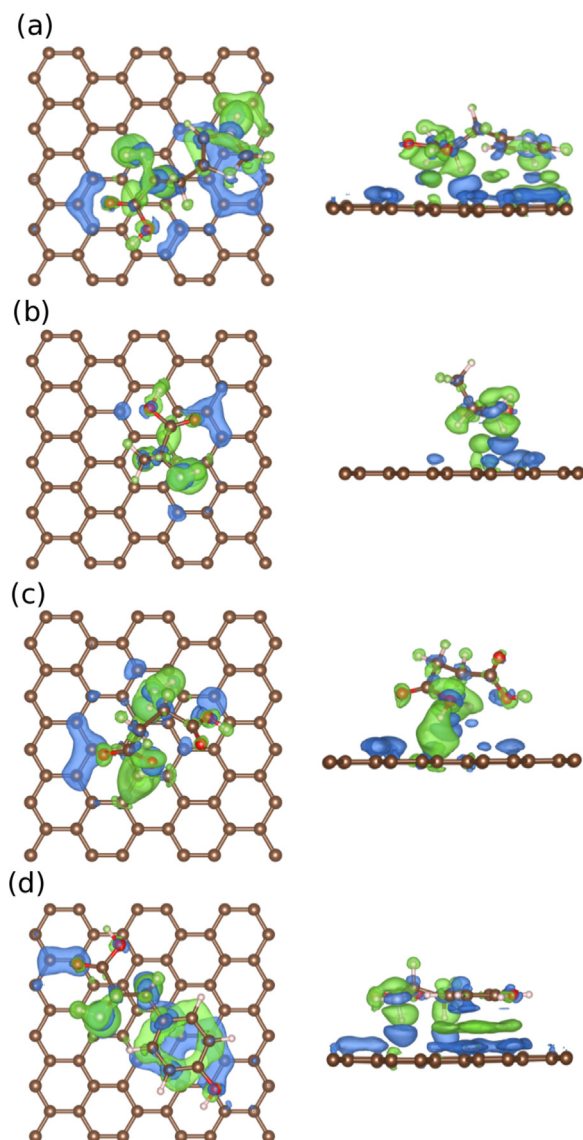


Fig. 3. Charge density. Light grey regions (green color online) accepted electrons ($\Delta D > 0$), while the dark grey regions (blue color online) lost electrons ($\Delta D < 0$). (a) His/grap. (b) Ala/gra. (c) Asp/graph. (d) Tyr/graph. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

sion for adsorbed His, Ala and Asp amino acids (1) increases for $V_b = -1, -1.5$ and -2 V, (2) is different in comparison to the graphene sheet alone, and (3) is different for each adsorbed amino acid. Tyr amino acid shows an increased transmission for $V_b = -1, -1.5$ V, but Tyr causes a decrease for $V_b = -2$ V. Differences in the transmissions of the amino acids are important if a highly selective device is required. The calculated transmissions are in accordance with the current–voltage curves.

Fig. 6 displays the current–voltage (I – V) curve for His/grap, Ala/gra, Asp/graph, Tyr/graph and graphene alone. The I – V curve of the graphene sheet alone exhibits a clear nonlinear behavior, consistent with it being a zero-gap semiconductor. In all systems the value of the current is very low for an applied V_b between -0.5 V and 0.5 V, subsequently, there are significant variations of the current, which depend on each amino acid adsorbed. Between 0.5 V and 2 V the proposed device has the same sensitivity for His and Ala amino acids, this is due to the current corresponding to the His remains close to the current of the Ala. The device has high specificity and sensitivity for V_b between -1 V and -2 V, e.g., for

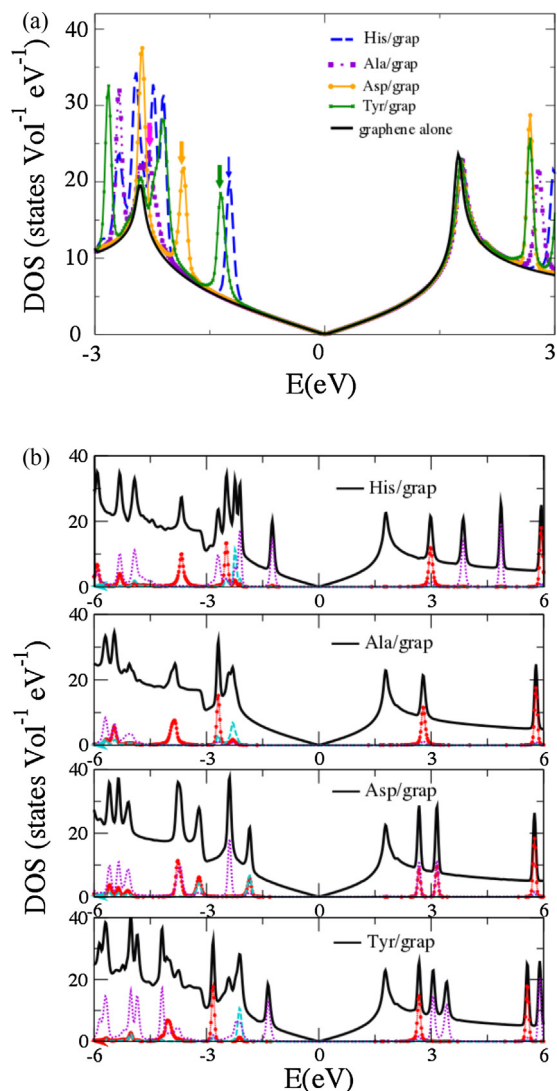


Fig. 4. (a) Total DOS His/grap, Ala/gra, Asp/graph, Tyr/graph and graphene alone. (b) Total DOS His/grap, Ala/gra, Asp/graph and Tyr/graph. Including for each amino acid, the individual contribution to the DOS of the lateral chain (violet dotted lines), the $-\text{COOH}$ group (red lines with symbols), and the $-\text{NH}_2$ group (turquoise dashed lines). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

$V_b = -1.5$ V, the current difference ΔI between each amino acid adsorbed and the graphene sheet is $0.84 \mu\text{A}$, $1.05 \mu\text{A}$, $1.52 \mu\text{A}$, and $0.27 \mu\text{A}$ for His, Ala, Asp and Tyr, respectively (in Table 2, ΔI for different V_b is reported). The values of ΔI , are in the order of magnitude of the μA . Given that this difference is compared with electrical sensitivity for graphene-based devices, we propose that through measurements of the differential drain-source current, the sensor could detect amino acids in the range of -1 V to -2 V, which could be useful for protein sequence determination (see Table 2).

It is worth mentioning that the electronic response of some materials, particularly the 2D systems, can be improved not only by manipulation of the charge and spin, but also of the valley degrees of freedom [32–34], which result from the anisotropies in a local minimum of the conduction bands, or in a maximum of the valence bands. While this is a plus [35] in carrying and storing information, it requires more complicated sample geometries, magnetic fields, or the use of circularly polarized light to read the additional information. In our case, however, we consider convenient to keep our device as simple as possible, as a sensor driven by just an electric field. Our calculations demonstrate that our standard device

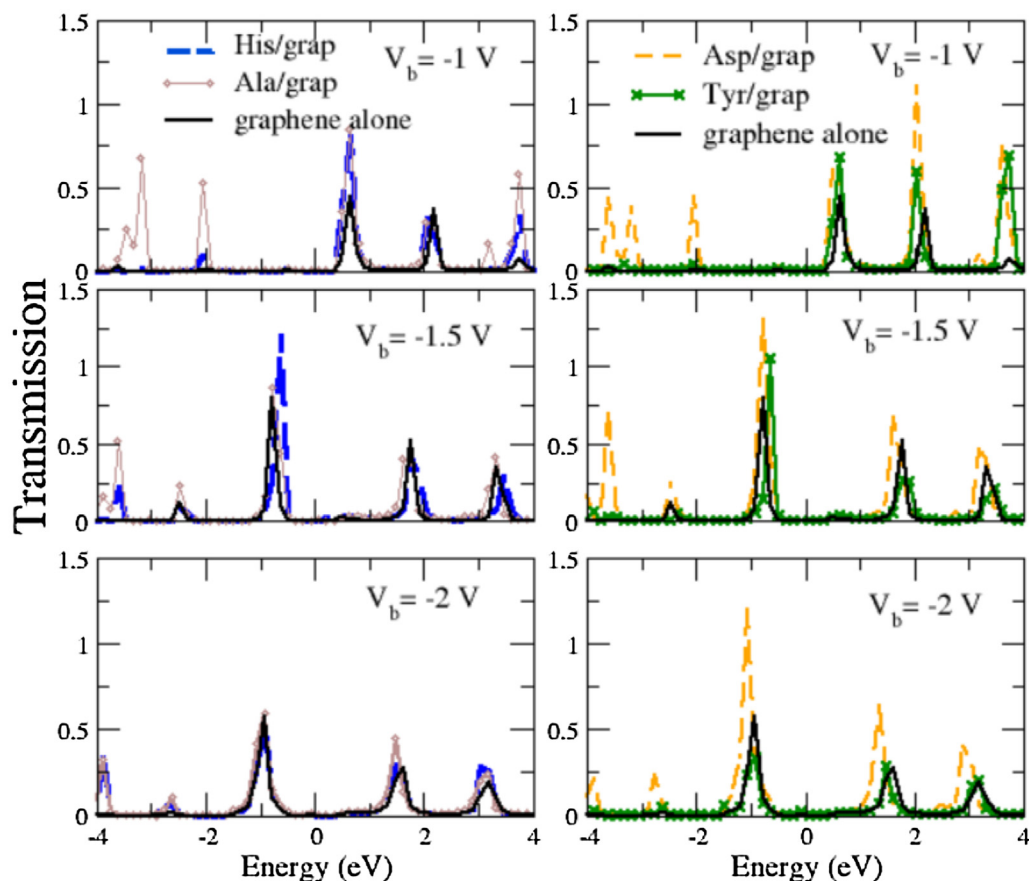


Fig. 5. Transmission for $V_b = -1, -1.5$ and 2 V for the graphene sheet alone, His/grap, Ala/grap, Asp/grap, and Tyr/grap. In general, the adsorbed amino acid increases transmission, only for Tyr/grap a decrease in transmission at $V_b = -2$ V is observed.

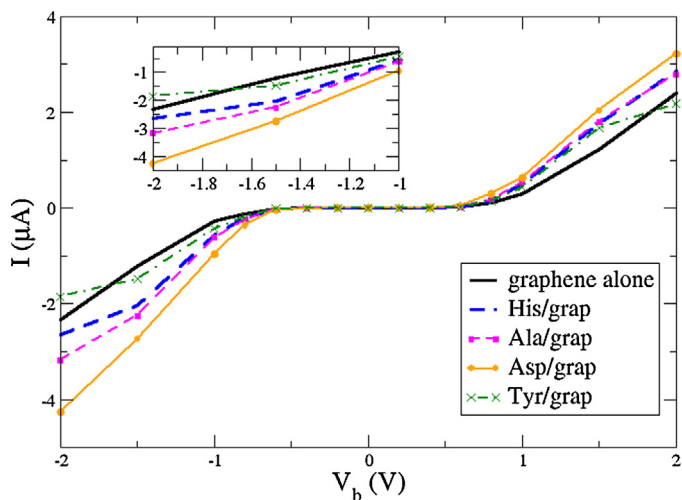


Fig. 6. Current–voltage curves.

model is highly sensitive to amino acids adsorption for a bias voltage, without the need of using the more sophisticated valleytronic mechanisms.

4. Conclusions

We modeled a graphene-based device for amino acid sensing. The modification of the electronic properties of the graphene sheet through noncovalent functionalization (simple molecular adsorp-

Table 2

Our theoretical calculations of current sensibility ($\Delta I = |I_{\text{graphene.alone}} - I_{\text{amino.acid.adsorbed}}|$) upon amino acid adsorption on graphene (upper part of table). For comparison, we also show (lower part of the table) orders of magnitude of experimentally measured currents on biosensing applications based on graphene FETs available in the literature.

Theoretical graphene-based amino acid biosensing (this work)			
$\Delta I, \mu\text{A} (V_b = 2 \text{ V})$	$\Delta I, \mu\text{A} (V_b = -1.5 \text{ V})$	$\Delta I, \mu\text{A} (V_b = -1 \text{ V})$	Amino acid
0.31	0.84	0.29	His
0.79	1.05	0.37	Ala
1.87	1.52	0.69	Asp
0.46	0.27	0.18	Tyr
Experimental graphene-based devices			
References	$I (\mu\text{A})$	Biomolecule	Detected biomolecule
[28]	0.05	Immunoglobulin Ig (G)	Protein
[29]	5	E. coli	Bacteria
[30]	4	DNA	Nucleic acids
[7]	10	DNA	
[31]	1	DNA	

tion) is clearly possible. The adsorption process was studied for four amino acids: His, Ala, Asp and Tyr. We report that $E_{\text{Tyr/grap}}^{\text{ads}} > E_{\text{His/grap}}^{\text{ads}} > E_{\text{Asp/grap}}^{\text{ads}} > E_{\text{Ala/grap}}^{\text{ads}}$, whereas $d_{\text{Asp/grap}}^{\text{ads}} > d_{\text{Ala/grap}}^{\text{ads}} > d_{\text{His/grap}}^{\text{ads}} > d_{\text{Tyr/grap}}^{\text{ads}}$. The values reported are typical of a strong physisorption.

A transfer of charge from the graphene to the molecules is generated due to the substrate-adsorbate interaction (graphene acts as a weak electronic donor). Local longitudinal and transverse dipoles are induced by the charge transfer toward the adsorbates. In order to evaluate the changes in electronic transport of graphene,

we sandwiched the adsorbed molecule between two graphene electrodes (drain-source). When the V_b applied is between -1 V and -2 V, the modeled device has high specificity and sensitivity for the amino acids His, Ala, Asp and Tyr. The theoretical values for the current are of the same order of magnitude as experimental measurements reported for graphene FET biosensors for other biomolecules. The results suggest the possibility to use a graphene-based biosensor for electrical detection of amino acids, with potential application for a protein sequencer.

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