

Interaction between nano silver and bacteria: modeling approach

Noha M. Sabry¹, Sahar Tolba², Fagr Kh. Abdel-Gawad¹, Samah M. Bassem¹, Hossam F. Nassar³, Gamila E. El-Taweel¹, Aly Okasha⁴, Medhat Ibrahim⁴

¹Environmental Research Division, Centre of Excellence for Advanced Science, National Research Centre, 33 El-Bohouth St., 12622 Dokki, Giza, Egypt

²Department of Microbiology, Faculty of Science, Ain Shams University, Cairo, Egypt

³Environmental Sciences and Industrial Development Department, Faculty of Postgraduate Studies for Advanced Sciences (PSAS), Beni-Suef University, Beni-Suef, Egypt

⁴Spectroscopy Department, National Research Centre, 33 El-Bohouth Str. 12622 Dokki, Giza, Egypt

*corresponding author e-mail address: medahmed6@yahoo.com

ABSTRACT

A model molecule for bacteria is simulated in this work to study the mechanism of interaction between bacteria and silver nanoparticles. B3LYP/LANL1DZ quantum mechanical model was utilized to calculate the total dipole moment, HOMO/LUMO band gap energy and molecular electrostatic potential. Results indicated that silver in the form of Ag.6H₂O interacts through hydrogen bond of both active sites of COOH and NH₂. The interaction could take place as adsorb state or complex state. The complex interaction led to the release of OH groups. Both interactions increased the reactivity which could result in further interaction with the surrounding environment. Both total dipole moment and HOMO/LUMO band gap energy indicated that the interaction throughout NH₂ is more probable in comparison with that through COOH.

Keywords: B3LYP/LANL1DZ, silver nanoparticles, protein, bacteria, total dipole moment, band gap energy, electrostatic potential.

1. INTRODUCTION

Early in 1959, the concept of nanotechnology was introduced [1]. This concept was subsequently followed by the establishment of the term “nanotechnology” which is referring to the engineering of different materials on the nano-scale level [2]. Nowadays, the materials in nanoscale are widely applied owing to their unique properties [3-5]. The biological activity of nano-scale materials dedicates them for many applications. Silver nanoparticles (AgNPs) show antibacterial activity [6], owing to their unique physical, chemical and biological characteristics and high surface area, which increases their specific biological activity to volume ratio [7-9]. It is stated that AgNPs show a bactericidal effect against several types of bacteria [10-12]. The potential impacts of AgNPs against several kinds of bacteria were reviewed [13]. Among their contradictory effects, AgNPs were found to be helpful to maintain the microbial community diversity in activated sludge [14]. Some bacteria such as *Pseudomonas aeruginosa* show great intrinsic antibiotic resistance which limits some effective antibiotics, but AgNPs have potential effects and could prevent infections of such bacteria due to its antibacterial activity [15]. Although the applications of AgNPs as biologically active

nanomaterials have abundantly increased, alongside nano gold, the mechanism of interaction is still not fully known [16-17]. These findings resulted in many research studies reporting that AgNPs, among some other nano-scale materials, are considered as non-traditional antimicrobial agents [18-20]. Recently, the interaction between ZnO and bacteria is described as coordination between hydrated metal oxides and active sites of the protein [21]. Molecular modeling and/or molecular modeling with molecular spectroscopy are tools for understanding the mechanism of interaction in many biological systems [22-25].

Molecular modeling with different levels of theory is needed to understand the mechanism of interaction between nano-scale materials and bacteria. Accordingly, molecular modeling calculations at B3LYP/LANL1DZ are utilized to study the mechanism of interaction between AgNPs and bacteria. A model amino acid molecule is chosen as a building block for protein structure representing bacteria. The interaction is described in terms of three important physical parameters, namely total dipole moment (TDM), HOMO/LUMO band gap energy and molecular electrostatic potential (ESP).

2. EXPERIMENTAL SECTION

All the studied structures are calculated with Gaussian 09 [26] program at Spectroscopy Department, National Research Centre, Egypt. B3LYP/LANL1DZ [27-29] model is utilized to

calculate TDM, HOMO/LUMO band gap energy and mapping molecular ESP.

3. RESULTS SECTION

3.1. Building model molecules. Silver is proposed to be hydrated with 6 water molecules as shown in figure 1-a, to form silver hexahydrate (Ag.6H₂O). The model for protein structure is

indicated as shown in figure 2-a as amino acid monohydrate. The interaction between Ag.6H₂O and the model molecule of bacteria is supposed to take place through the hydrogen bonding of the

active site COOH or NH_2 . For the interaction between $\text{Ag}_6\text{H}_2\text{O}$ and protein, there are two schemes tried in this work. The first scheme is through weak interaction while the second one is through complex interaction. Both interactions took place between $\text{Ag}_6\text{H}_2\text{O}$ and H of COOH as indicated in figures 3 and 4, and H of NH_2 as indicated in figures 5 and 6 respectively. Figure 3 presents the optimized structure of amino acid monohydrate and $\text{Ag}_6\text{H}_2\text{O}$ through COOH as an adsorbed state. Figure 4 presents the optimized structure of amino acid monohydrate and $\text{Ag}_6\text{H}_2\text{O}$ through COOH as a complex. Figure 5 presents the optimized structure of amino acid monohydrate and $\text{Ag}_6\text{H}_2\text{O}$ through NH_2 as an adsorbed state. Figure 6 presents the optimized structure of amino acid monohydrate and $\text{Ag}_6\text{H}_2\text{O}$ through NH_2 as a complex state.

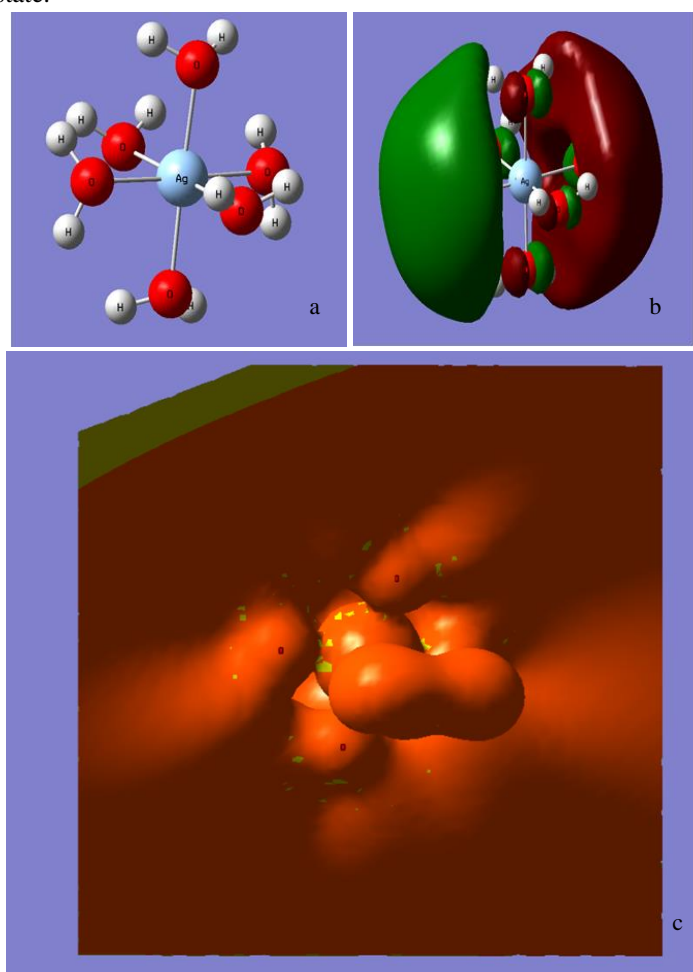


Figure 1. B3LYP/LANL1DZ optimized structure of a- $\text{Ag}_6\text{H}_2\text{O}$; b- HOMO/LUMO band gap energy of $\text{Ag}_6\text{H}_2\text{O}$ and c- Molecular electrostatic potential ESP of $\text{Ag}_6\text{H}_2\text{O}$.

3.2. Calculated physical parameters. In previous work, it is indicated that both TDM and HOMO/LUMO band gap energy are considered as indications for the chemical and biological reactivity of the chemical structure a given compound [30-31]. To describe a compound as reactive, its TDM is supposed to increase while its band gap energy is supposed to decrease.

Table 1 presents the B3LYP/LANL1DZ calculated TDM as Debye, HOMO/LUMO band gap energy as eV for the studied structures. Furthermore, HOMO/LUMO band gap energy for $\text{Ag}_6\text{H}_2\text{O}$; amino acid and the four model molecules of $\text{Ag}_6\text{H}_2\text{O}$ /amino acid interactions are indicated in figures 1-b, 2-b, 3-b, 4-b, 5-b and 6-b respectively.

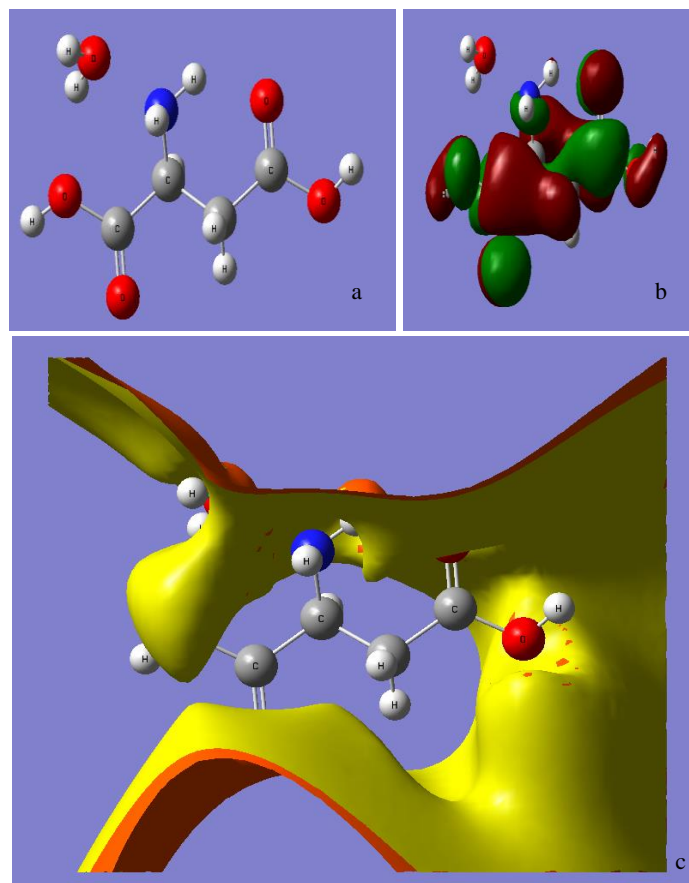


Figure 2. B3LYP/LANL1DZ optimized structure of a- amino acid monohydrate; b- HOMO/LUMO band gap energy of amino acid monohydrate and c- molecular electrostatic potential ESP of amino acid monohydrate.

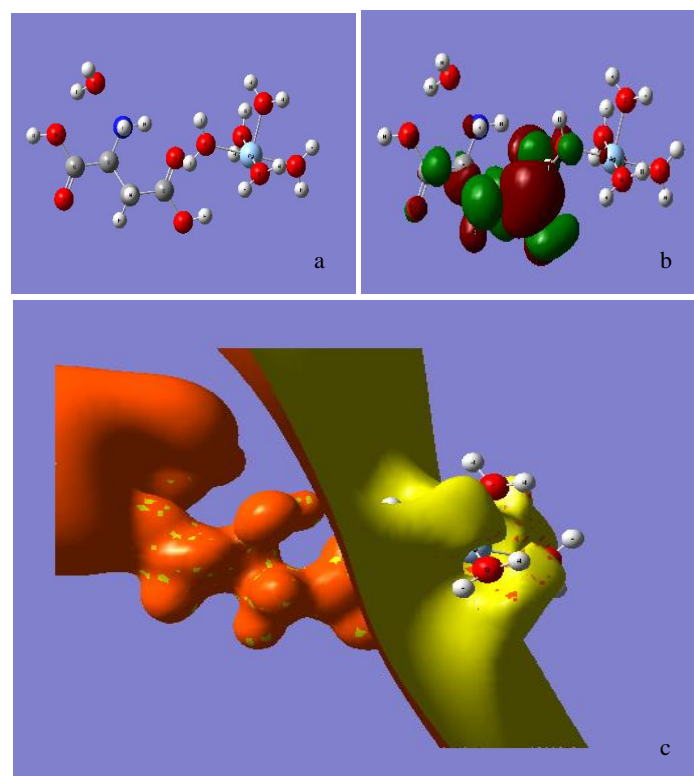


Figure 3. B3LYP/LANL1DZ optimized structure of a- amino acid monohydrate/ $\text{Ag}_6\text{H}_2\text{O}$; b- HOMO/LUMO band gap energy of amino acid monohydrate/ $\text{Ag}_6\text{H}_2\text{O}$ and c- molecular electrostatic potential ESP of amino acid monohydrate/ $\text{Ag}_6\text{H}_2\text{O}$. The interaction took place through COOH as adsorb state.

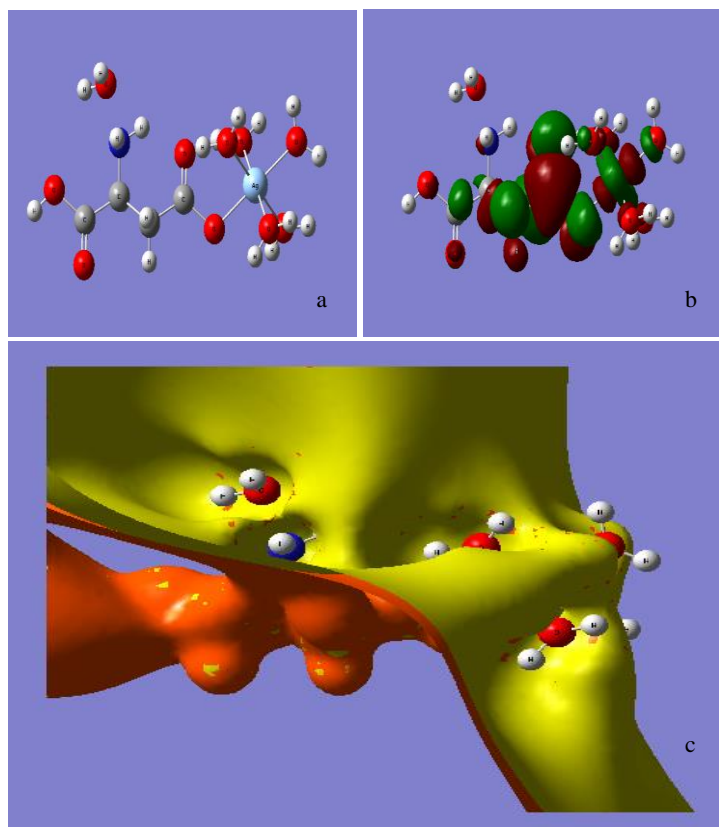


Figure 4. B3LYP/LANL1DZ optimized structure of a- amino acid monohydrate/Ag.6H₂O; b- HOMO/LUMO band gap energy of amino acid monohydrate/Ag.6H₂O and c- molecular electrostatic potential ESP of amino acid monohydrate/Ag.6H₂O. The interaction took place through COOH as complex.

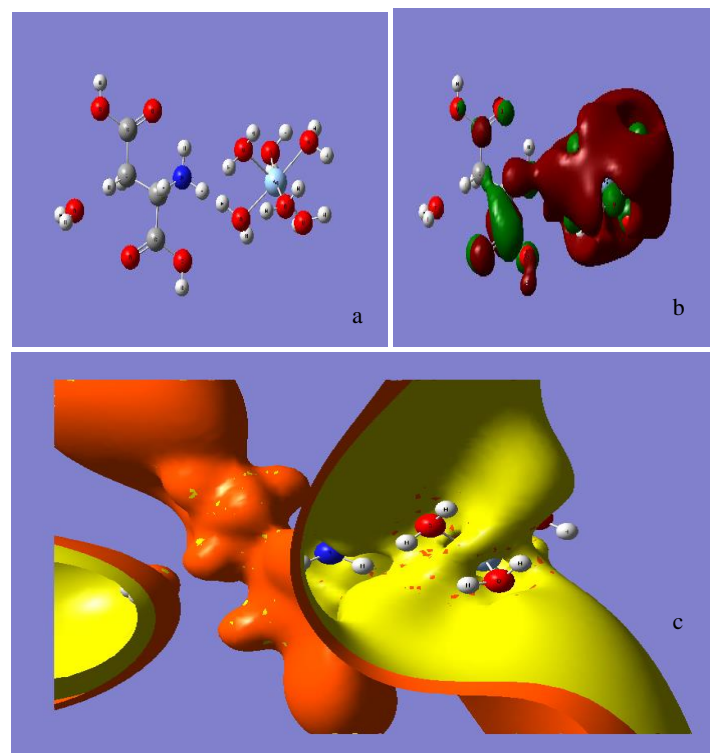


Figure 5. B3LYP/LANL1DZ optimized structure of a- amino acid monohydrate/Ag.6H₂O; b- HOMO/LUMO band gap energy of amino acid monohydrate/Ag.6H₂O and c- molecular electrostatic potential ESP of amino acid monohydrate/Ag.6H₂O. The interaction took place through NH₂.

As listed in table 1, Ag.6H₂O has a TDM of 1.2037 Debye and band gap energy of 1.0555 eV. Amino acid is hydrated with

one water molecule to form amino acid monohydrate which has a TDM of 1.4673 Debye and band gap energy of 2.0376 eV. As amino acid monohydrate and Ag.6H₂O are interacted as an adsorb state through COOH, the TDM is increased to 5.3929 Debye while the band gap energy is decreased to 0.6144 eV. The same interaction took place as a complex with the release of OH group. The TDM is increased to 9.2151 Debye while the band gap energy is 1.9100 eV. Although the adsorbed state shows a lower band gap energy, the complex state shows a higher TDM. This indicates that the two schemes could take place for the interaction through COOH.

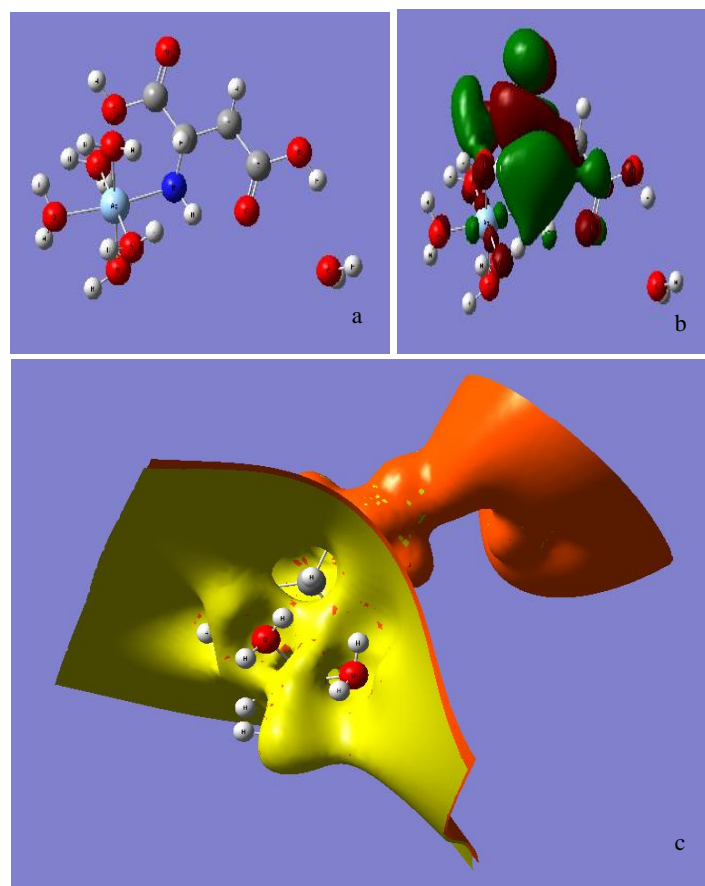


Figure 6. B3LYP/LANL1DZ optimized structure of a- amino acid monohydrate/Ag.6H₂O; b- HOMO/LUMO band gap energy of amino acid monohydrate/Ag.6H₂O and c- molecular electrostatic potential ESP of amino acid monohydrate/Ag.6H₂O. The interaction took place through NH₂ as a complex state.

When amino acid monohydrate is interacted with Ag.6H₂O through NH₂ as adsorb state, the TDM measured 4.1538 Debye while the band gap energy measured 0.6746 eV. The interaction is then tried as a complex state in which the TDM slightly increased to 5.1691 Debye and the band gap energy also slightly increased to 0.7287 eV.

Table 1. B3LYP/LANL1DZ calculated total dipole moment as Debye, HOMO/LUMO band gap energy as eV for the studied structures.

| Structure | Total dipole moment | Band gap energy |
|--|---------------------|-----------------|
| Ag.6H ₂ O | 1.2037 | 1.0555 |
| Amino acid monohydrate | 1.4673 | 2.0376 |
| Amino acid monohydrate/Ag.6H ₂ O (COOH) adsorb | 5.3929 | 0.6144 |
| Amino acid monohydrate/Ag.6H ₂ O (COOH) complex | 9.2151 | 1.9100 |
| Amino acid monohydrate/Ag.6H ₂ O (NH ₂) adsorb | 4.1538 | 0.6746 |
| Amino acid monohydrate/Ag.6H ₂ O (NH ₂) complex | 5.1691 | 0.7287 |

Further confirmation for the interaction of the studied structures is needed, therefore the molecular ESP is calculated at the same level of theory.

It is stated that molecular ESP is displayed as the charge distribution revolving around a given structure in space. It is considered very important for describing then understanding both the electrophilic and nucleophilic attack sites for biological recognition [32]. Molecular ESP in this sense is considered as a tool necessary for the description of hydrogen bonding interactions [33].

The mapping of molecular ESP for Ag₆H₂O, amino acid and the four model molecules of Ag₆H₂O/amino acid interactions are indicated in figures 1-c, 2-c, 3-c, 4-c, 5-c and 6-c respectively. To describe the figures of ESP, the values of the ESP at the studied surface are represented by colors. Potential is increased according to the following increasing orders: red < orange < yellow < green < blue.

Blue is corresponding to the highest ESP energy and red indicates the lowest ESP energy [34]. In this sense as well, the intermediate colors represent intermediate ESP. As indicated in the mapping of ESP, the negative regions are mainly around the

oxygen which is considered as sites for electrophilic attacks. On the other hand, the positive region is localized over the silver indicating that these sites are the more probable for nucleophilic attacks. These data are in good agreement with those presented in the last section for both TDM and HOMO/LUMO band gap energy, suggesting that Ag₆H₂O is an active surface for interaction with protein throughout COOH and/or NH₂, with the interaction through NH₂ being the most probable. Data revealed that interaction between AgNPs and model molecule for bacteria increased indicating increasing the interaction with the surrounding molecules. If the interaction of AgNPs with bacteria is described as interaction with the active sites COOH and NH₂, the complex formation is blocking it, with the release of OH. Additionally, the adsorbed state inhibits the active site from making further interaction through it. While increasing TDM with decreasing band gap energy indicates that there is an increase in the ability of the structure for further interactions with the surrounding molecules. To understand this, it could be an indication for the possibility of degradation of protein as a result of future interactions with the surrounding media in the existence of water molecules.

4. CONCLUSIONS

Correlating both results, one can conclude that the interaction between silver and bacteria is more likely through the hydrogen bonding of NH₂ group. If the interaction is through complex state OH is released as a result of the interaction.

The TDM, HOMO/LUMO band gap energy, and molecular ESP results indicate that interaction between AgNPs and model molecule for bacteria increased the reactivity which may lead to

the possible degradation due to the high rate of interaction. This is indicated through the higher TDM, lower band gap energy and high surface area with unique surface properties based on active sites indicated by molecular ESP mapping. The possible degradation of the model molecule under the influence of AgNPs could be further verified in the future with another molecular modeling study.

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