Theoretical Study of Electronic Properties and Geometric of Theophylline Using Molecular Dynamics Car-Parrinello

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INTRODUCTION

Theophylline (1,3-dimethyl-7H-purine-2,6-dione) is a dimethylxanthine with similar molecular structure to other methylxanthines such as caffeine and theobromine. Theophylline is an alkaloid and can be found in existing plants in various regions of the world. Theophylline has several pharmacological actions of therapeutic applications. Relaxes smooth muscle, bronchial muscle, stimulate the central nervous system stimulates the heart muscle and kidney acts producing diuresis. Theophylline is one of spasmogens release inhibitors more effective among xanthine. It is found as the main component of prescription medications for the treatment of chronic obstructive pulmonary disease (COPD) and asthma treatment. [1, 2]

METHODS

The structural data of the molecule were conducted at Quantum ESPRESSO program package, which carried out the simulation of the molecular dynamics of Car-Parrinello.[3] Calculations were made to a value of 400.000 steps. To maintain adiabaticity system a μ fictitious mass of 400 u.a which proved effective during the whole simulation of dynamic vacuum was used. To reduce the calculation for the electronic subsystem, the pseudopotential ultrasoft Vanderbilt, together with plane waves. The temperature of the ionic subsystem was kept constant using the Nosé-Hoover thermostats to 300 K. The temperature used was the statistical ensemble NVT.

RESULTS AND DISCUSSION

The Map of molecular electrostatic potential and the structural data were also calculated using Density Functional Theory using the theory level B3LYP/6-311++G(2d,p). The interatomic bond distances with greater variations were: H15-C12, C7-N3, C9=O2, C7-O1 e C13-H17 with relative error, in relation the results with DFT of 1,849 %, 1,598%, 1,480%, 1,482% e 1,809% respectively. The interatomic angles with greater variations were: H14-C12-H16, C12-N3-C9 e H17-C13-N4 with relative error 1,320%, 1,259% and 1,435% respectively. The largest variations of these bond lengths and angles are due possibly to the fact that atoms are more electronegative regions and then it can be assumed that such interaction is outside the full domain of the functional.

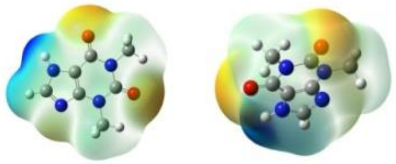

Figure 1. Map electrostatic potential molecular

CONCLUSIONS

The results of the molecular dynamics simulation of Car-Parrinello in theophylline led to obtaining the geometrical values for the distance and angles entres atoms of the molecule. It is observed good agreement between the theoretical results values obtained by DFT. These results allow an interesting study about possible interactions of theophylline in a solvent such as water.

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