XIX SBQT
Simpósio Brasileiro de Química Teórica 2017
12 a 17/Nov, 2017, Águas de Lindóia/SP, Brasil

Conformational Analysis and pK_a Calculations of Glycine in Aqueous Solution

Diego Nascimento de Jesus, Neubi Francisco Xavier Junior, Cristiane Martins Cardoso,

Clarissa Oliveira da Silva, Glauco Favilla Bauerfeldt

Departamento de Química – Universidade Federal Rural do Rio de Janeiro

Abstract: Glycine is the simplest and perhaps the most important amino acid in general metabolism. Moreover, studies of the behavior of biomolecules in the interstellar medium (ISM) point out that glycine is found in solid phase, covered by icy mantle. The presence of water molecules seems to be essential for its survival [1]. In water solutions, glycine behaves as a zwitterionic specie and can be found in different protonation degrees: H_2Gly^+ ($HO_2CCH_2NH_3^+$), in low pH values; HGly ($^-O_2CCH_2NH_3^+$), in intermediate pH values and Gly^- ($^-O_2CCH_2NH_2$), in high pH values. The transitions from H_2Gly^+ to HGly and HGly to Gly^- occur at pH values equal to the corresponding pK_a values: $pK_{a,1}$ = 2.35 and $pK_{a,2}$ = 9.78 [2]. Although the zwitterion is the most abundant specie in physiological pH, the tautomerization is also possible and the HGly specie is better described as an equilibrium between the zwitterion ($^-O_2CCH_2NH_3^+$) and the neutral ($HO_2CCH_2NH_2$) forms [3]. Despite all the evidences and experimental knowledge about glycine and its related specie in aqueous solutions, a structural model considering all the possible geometries in condensed phase is still missing. This work aims to the description of the several stationary points related to the different species of glycine and to the selection of the lowest energy geometries. Such structural model is here validated through pK_a calculations and these geometries will finally be used to compose a model for the icy mantle and the possible surface reactions leading to the destruction of glycine in the ISM. In order to achieve the microscopic description of glycine's aqueous solution, theoretical calculations have been performed at the B3LYP level, adopting the 6-311++G(2d,2p) basis set. The presence of the solvent has been simulated through CPCM calculations, with Pauling atomic radii for building up the molecular cavity and explicitly including the solute cavitation energy and solute-solvent dispersion and repulsion interaction energies in the total energies. The choices for the CPCM method and Pauling radii have been done from previous test runs. As an isolated system, eight conformers are located for the neutral glycine. In aqueous solutions, the same number of the corresponding conformers is found, although the minimum energy conformer in solution is different from the lowest energy geometry in gas phase. An additional water molecule has been included as a microsolvation model for the neutral HGly form (HGly(ne).H_2O). For the zwitterion, only one conformer has been found and similarly, the inclusion of an addition water molecule allowed the microsolvation description of the zwitterionic specie (HGly(zw).H_2O). The standard Gibbs free energy difference for the tautomerization reaction, HGly(ne).H_2O →HGly(zw).H_2O, at the CPCM/B3LYP/6-311++G(2d,2p) level, is -6.84 kcal mol^{-1}, in good agreement with the

experimental value (-7.27 kcal mol^{-1}). Only one conformer has also been found for Gly^-, whereas three conformers have been located for the H_2Gly^+ specie and a microsolvated model for both has also been set by inclusion of an additional water molecule, forming the $Gly^-.H_2O$ and $H_2Gly^+.H_2O$ specie. The whole set of stationary points has been used for the calculation of the pK_a values, which have been determined based on two reference reactions: $H_2Gly^+.H_2O + MA \rightarrow MAH^+ + HGly(zw).H_2O$ (R1) and $HGly(zw).H_2O + A^- \rightarrow Gly^-.H_2O + HA$ (R2), where MA = methylamine, MAH^+ = methylamonium cation, A^- = acetate anion and HA = acetic acid. From the standard Gibbs free energy values for each reference reaction, the pK_a values have been determined: $pK_{a,1}$ = 1.31 and $pK_{a,2}$ = 9.41. The good agreement with the literature values suggest that the set of geometries located for each glycine form in aqueous solution is satisfactory and complete enough to provide a good description of the structure of this amino acid in the water environment.

Key-words: glycine, aqueous solution, tautomerization
Support: This work has been supported by CAPES

References:

[1] A. Pernet, J. Pilmé, F. Pauzat *et al*, Astronomy & Astrophysics, 552, A100 (2013)
[2] D. Voet, J. G. Voet, "Biochemistry" (2011), John Wiley & Sons, Inc.
[3] C. Kim, B. Park, H. Lee *et al*, Organic & Biomolecular Chemistry, Org. Biomol. Chem., 11, 1407. (2013)