Hydrogen-Bonded Interactions in the Systems
\( L\)-Cysteine - \( H_2\text{SeO}_3 \) and \( L\)-Cysteine - \( H_2\text{SeO}_4 \): A DFT Study

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ABSTRACT

Using the density functional theory method at the B3LYP/6-31G(d,p) level of theory, the formation of hydrogen-bonded complexes of \( L\)-cysteine with selenious and selenic acids has been studied. In both cases of selenium-containing acids, the complexes occur preferably by cysteine carboxylic group, therewith the enthalpy of formation values consist from \(-19\) to \(-21\) kcal/mol, and free energy from \(-6\) to \(-9\) kcal/mol. Probably, the initial act of interaction in the system hydroxyl-containing selenium compound - \( \alpha\)-amino acid, proceeding with mutual orientation of the reactants molecules and intermolecular hydrogen bonds formation, serves as a prerequisite for the thiol group capability of participating in the subsequent stages (including more completed transformations) of biologically important reactions.

Keywords: Amino Acids, B3LYP, Complexation, Cysteine, Density Functional Theory, Hydrogen Bond, Selenic Acid, Selenious Acid

INTRODUCTION

The position of selenium in the Periodic table between the metals and the nonmetals makes selenoproteins ideal catalysts for many biological redox transformations (Jacob, Giles, Giles, & Sies, 2003). Sulphur and selenium occur in proteins as constituents of the \( \alpha\)-L-amino acids cysteine, methionine, selenocysteine, and selenomethionine. Recent research underscores that these amino acids are truly exceptional. Unlike any other amino acid, the “redox chameleon”
cysteine can participate in several distinct redox pathways, including exchange, electron, atom, and radical transfer reactions (Giles, Giles, & Jacob, 2003). Cysteine-based redox processes can change not only the chemical properties (e.g., reductive-oxidative and metal-binding activity), but also the biological activity (Jacob, Holme, & Fry, 2004). Recent studies on the redox behaviour of cysteine residues in peptides and proteins have dramatically changed our perspective of the amino acids' role in biocatalysis, intracellular redox sensing and cell signalling. Cysteine proteins are therefore able to act as “redox switches”, to sense concentrations of oxidative stressors and unbound zinc ions in the cytosol, to provide a “storage facility” for excess metal ions, to control the activity of metalloproteins, and to take part in important regulatory and signaling pathways (Giles, Watts, Giles, Fry, Littlechild, & Jacob, 2003).

Cysteine and methionine are the only amino acids in proteins that undergo reversible oxidation/reduction under biological conditions and, as such, provide a means for control of protein activity, protein-protein interaction, protein trafficking, and protein-DNA interaction. Hydrogen peroxide and other reactive oxygen species (ROS) provide a mechanism to oxidize signaling proteins. However, oxidation of sulphur-containing side chains of cysteine and methionine by ROS can result in oxidation states of sulphur (e.g., sulphinate, sulphonate, sulphone) that are not reducible under biological conditions. Thus, mechanisms for oxidation that protect against over-oxidation of these susceptible residues and prevent irreversible loss of activity would be advantageous. The study (Jones, Go, Anderson, Ziegler, Kinkade, & Kirlin, 2004) shows that the cysteine/cystine couple provides a means to oxidize proteins without direct involvement of more potent oxidants.

Selenium has been increasingly recognized as an essential element in biology and medicine. Its biochemistry resembles that of sulphur, yet differs from it by virtue of both redox potentials and stabilities of its oxidation states. Selenium can substitute for the more ubiquitous sulphur of cysteine and as such plays an important role in more than a dozen selenoproteins (Besse, Siedler, Dierks, Kessler, & Moroder, 1997; Jacob, Maret, & Vallee, 1999).

Bioavailabilities of selenium in living organisms depends on the nature of selenium-containing species, on the selenium oxidation state. Thus, the results obtained in (Yoshida et al., 2005) indicate that the main selenium species in the mushroom Lentinula edodes enriched with selenite or selenate is selenomethionine bound to protein or selenate bound to polysaccharides in the cell wall, respectively.

The isomorphous character of chalcogen analogues of amino acids in peptides and proteins allows the selenium- and tellurium-containing amino acids to be exploited for production of heavy metal mutants of proteins and thus to facilitate the phasing problem in x-ray crystallography. In addition, selenocysteine has been recognized as an ideal tool for the production of selenoenzymes with new catalytic activities. Moreover, the fully isomorphous character of disulphide replacement with diselenide is well suited to increase the robustness of cystine frameworks in cystine-rich peptides and proteins and for the de novo design of even non-native cystine frameworks by exploiting the highly negative redox potential of selenols (Moroder, 2005).

The prerequisite for such deeply proceeding chemical transformations of α-amino acids caused by selenium-containing compounds could be a definite mutual orientation of the reactants molecules, and even a further formation of complexes between the reacting agents. The above items elucidation is possible using the contemporary methods of quantum chemistry (Pankratov, 2007).

The purpose of the present work is quantum chemical study of principal feasibility of complexation on the L-cysteine interaction with selenious and selenic acids.

Computations were carried out by means of the DFT method (Koch & Holthausen, 2001) using the PC GAMESS series software (Granovsky, 1993). Within the SCF, the hybrid B3LYP functional, which combines the three-parameter exchange functional by Becke
An Efficient Algorithm for Automating Classification of Chemical Reactions into Classes in Ugi’s Reaction Scheme
www.igi-global.com/article/efficient-algorithm-automating-classification-chemical/68017?camid=4v1a