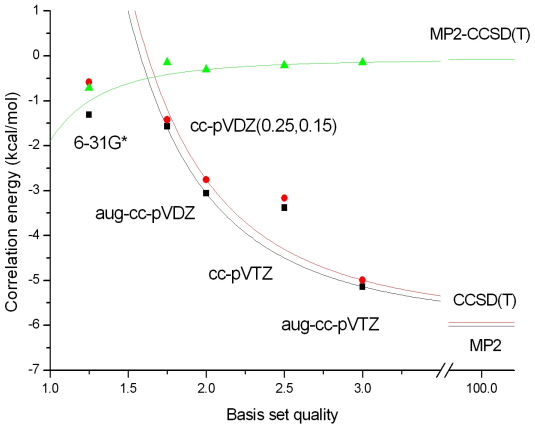

Figure 2

1. M. Fayereisen, G. Fitzgerald & A. Komornicki, *Chem. Phys. Lett.*, **208** (1993), 359.
2. R. Ahlrichs, M. Bär & M. Häser, *Chem. Phys. Lett.*, **162** (1989), 165.
3. A. Halkier, T. Helgaker & P. Jörgensen, *Chem. Phys. Lett.*, 302 (1999), 437-446.
4. P. Hobza & J. Šponer, *Chem. Phys. Lett.*, **288** (1998), 7-14.

POTENTIAL ENERGY SURFACES OF GUANINE - CYTOSINE BASE PAIR AND RELATED TAUTOMERS: MOLECULAR DYNAMICS AND AB INITIO STUDY

Martin Kabeláč and Pavel Hobza

J. Heyrovský Institute of Physical Chemistry, Academy of Sciences of the CzechRepublic and Center for Complex Molecular Systems and Biomolecules, Prague, Czech Republic. E-mail: martin.kabelac@jh-inst.cas.cz

Introduction:

The structure of DNA is determined among other factors by interactions between nucleic acid (NA) bases: guanine (G) , cytosine (C), adenine (A) and thymine (T). A theoretical study of the interaction is important for understanding of stabilizing forces in DNA and RNA. The interaction of NA bases in a vacuum in now being studied in experimental laboratories [1-4] and a knowledge of the potential energy surfaces is essential for an interpretation of experimental results. This information can be obtained by performing correlated *ab initio* calculations in combination with molecular dynamics/quenching technique (MD/Q) [5-6].

Methods:

1. *Molecular dynamics/ quenching calculations* were carried out in the NVE canonical ensemble (Constant number of particles, volume and energy) employing Cornell *et al.* AMBER force field [7], which gives results comparable with *ab initio* data [8]. Due to comparable stability of several cytosine and also guanine tautomers, all possible combinations of these tautomers should be considered. Only the most stable (stabilization energy higher than 18 kcal/mol) and populated (population greater than 5%) structures of base pairs were taken for further *ab initio* calculations.

2. *Ab initio calculations*. The geometries, interaction and tautomerization energies of base pairs were determined on RI-MP2 level employing TZVPP (5s3p2d1f/ 3s2p1d) basis set.

Results:

In all cases planar H-bonded structures are the most stable and most populated ones. The T-shaped and stacked structures are about several kcal/mol less stable (typically 5-10 kcal/mol) than the structure of the global minimum and will not be probably detectable by experimental technique.

Among all possible combinations of tautomers the highest stability shows canonical Watson-Crick (WC) structure (-26.9 kcal/mol) followed by the same binding pattern with N7 keto tautomer of guanine Also other binding patterns of ketoguanine-ketocytosine tautomers are very stable. The structures of other combinations of tautomers are usually less stable (about 4-5 kcal/mol) than the WC pair, including ketoguanine-enolcytosine structure observed in the experiment [2]. An exception is an enolguanine - ketocytosine nonplanar structure with surprisingly high stability (-25.3 kcal/mol), but due to unfavorable geometry and stability of the enolguanine tautomer itself, this structure will not be probably detectable.

Summary:

We have presented a powerful technique for scanning of potential energy surfaces of nucleic acid base pairs, which can be used for analysis of experimental results. It is demonstrated that the use of standard procedure based on chemical feeling and experience is not sufficient and several mainly unusual structures can be omitted.

***Acknowledgement**: This work was supported by grant No. LN00A032 to the Center for Complex Molecular Systems and Biomolecules, from MSMT of the Czech Republic.*

1. E. Nir, C. Janzen, P. Imhof, K. Kleinermanns, M.S. de Vries, *Phys. Chem. Chem. Phys.*, **4** (2002) 732-739.
2. E. Nir, C. Janzen, P. Imhof, K. Kleinermanns, M.S. de Vries, *Phys. Chem. Chem. Phys.*, **4** (2002) 740-750.
3. S. Carles, F. Lecomte, J. P. Schermann, C. Desfrançois, *J. Phys. Chem. A*, **104** (2002) 10662-10668
4. I. Galetich, S. G. Stepanian, V. Shelkovsky, M. Kosevich, Y.P. Blagoi, L. Adamowicz, *J. Phys. Chem. A*, **104**, (2000) 8965-8971.
5. M. Kabeláč, P.Hobza, *J. Phys. Chem.B*, **105** (2001), 5804-5817.
6. M. Kabeláč, P. Hobza, *Chem. Eur. J.*, **7** (2001) 2067-2074.
7. W. D. Cornell, P. Cieplak, C. I. Bayly, I. R. Gould, K. M. Merz, D. M. Ferguson, D. C. Spellmeyer, T. Fox, J. W. Caldwell, P. A. Kollmann, *J. Am. Chem. Soc.* ,**117** (1995) 179-5197.
8. P. Hobza, M. Kabeláč, J. Šponer, P. Mejzlík, J. Vondrášek; *J. Comp. Chem.*, **18** (1997) 1136-1150.