

COMMENTS

Comment on “Electron-Correlated Calculations of Electric Properties of Nucleic Acid Bases”

Pavel Hobza,^{*,†} Jiří Šponer,[†] and Jerzy Leszczynski[‡]

J. Heyrovský Institute of Physical Chemistry,
Academy of Sciences of the Czech Republic,
182 23 Prague 8, Czech Republic, and Department of
Chemistry, Jackson State University,
Jackson, Mississippi 39217

Received: February 19, 1997; In Final Form: June 22, 1997

It has been recently suggested by Johnson et al.¹ that our calculations² on DNA base pairs significantly underestimate base stacking. This speculation was based on an evaluation of the high-quality electrostatic properties of isolated nucleobases, namely, the finding that the standard basis sets of 6-31G* quality underestimate the vertical component of the Hartree–Fock (HF) polarizability by as much as 40% (in comparison with large basis set calculations).

The purpose of this comment is to show that the conclusion made in ref 1 is misleading.

First, there is not even a single value of base stacking energy reported in our papers obtained with the standard (energy-optimized) 6-31G* basis set. In all cases, we have used a modified 6-3G* basis set with diffuse (momentum-optimized, dispersion energy-optimized) d-polarization functions. Structures of H-bonded base pairs and trimers were optimized at the Hartree–Fock level using standard 6-31G* and 6-31G** basis sets. However, even in this case the subsequent MP2 interaction energy calculations were mostly carried out with the 6-31G basis set augmented by diffuse d-polarization functions. Nevertheless, in contrast to stacked complexes, for H-bonded complexes the diffuse polarization functions do not improve the interaction energy significantly. The diffuse d-polarization functions improve the electron correlation stabilization energy of the stacked dimers very significantly, by about 3 kcal/mol for the stacked cytosine dimer with respect to the standard 6-31G* basis set.

Second, and equally important, it is impossible to evaluate the accuracy of any procedure for calculations of the interaction energies on the basis of an evaluation of the monomer properties only as has been attempted by Johnson et al.¹

Let us now explain these two items in detail.

Choice of the Basis Set. It is well-known that the standard 6-31G* basis set underestimates significantly the polarizability and hence also the correlation interaction energy. We have written about it in all our reviews³ on intermolecular interactions and papers⁴ on DNA base pairs. Thus, instead of energy-optimized d-polarization functions, we used dispersion energy-optimized ones⁵ which are much more diffuse with an exponent of 0.25 for C, N, and O atoms. (The respective standard values are 0.8.) This modified 6-31G* basis set is mostly designated as 6-31G*(0.25).

Let us compare the polarizability and its perpendicular (zz) component for uracil (U), thymine (T), adenine (A), cytosine (C), and guanine (G) calculated with the standard 6-31G* and

diffuse 6-31G*(0.25) basis sets using the MP2/6-31G* (C_1) optimized geometries⁶ of bases. We obtained the following ratios of calculated HF polarizabilities with respect to those obtained with the large polarized basis set of Sadlej,⁷ reported in ref 1: the total polarizability, 81%, 83%, 80%, 82%, and 81% for U, T, C, G, and A with the 6-31G* basis set while the same numbers were 91%, 84%, 89%, 91%, and 89% with the 6-31G*(0.25) basis set. An even larger improvement has been found for the (zz) component of polarizability. The corresponding ratios provided by the 6-31G* basis set with respect to the Sadlej basis set were 58%, 67%, 58%, 61%, and 59% while for the 6-31G*(0.25) basis set the discrepancies were significantly reduced to 80%, 84%, 82%, 82%, and 80% for U, T, C, G, and A. It is clear from these data that the 6-31G*(0.25) basis set yields more accurate polarizabilities than the standard 6-31G* basis set. The 6-31G* basis set underestimates the total and vertical polarizabilities by about 19% and 39%, respectively, and the 6-31G*(0.25) basis set by about 11% and 18%. The vertical component of polarizability in our calculations is thus underestimated by about 20% (compared to the reference values¹), and not by 40%, as claimed in ref 1.

We admit that, in some parts of our papers, we are referring to the calculations simply at the MP2/6-31G* level, i.e., not stating explicitly that the diffuse polarization functions were used. However, at least the method section of our stacking papers^{2a,4a,c–e} explains this point so that no misunderstanding should arise when reading the papers properly. Nevertheless, in our recent paper, we address this issue once again in detail.^{4e}

Evaluation of Interaction Energy. Dispersion energy depends not only on the dipole polarizabilities but also on the quadrupole and higher polarizabilities. Further, other components of interaction energy are important. Therefore, accurate interaction energies are obtained only if higher contributions to the correlation interaction energy are considered. We have recently calculated⁸ H-bonding and stacking energies for model aromatic dimers including pyrimidine base pairs at the MP2 and CCSD(T) levels with various basis sets. For all H-bonded structures, the MP2 and CCSD(T) values were almost identical. However, for the aromatic stacked clusters, the MP2 method systematically overestimates the stabilization energies with respect to the CCSD(T) method.⁸ A similar observation has been made before for the benzene dimer and benzene...Ar clusters using larger basis sets⁹ and basically confirmed by a comparison with the experimental data. In addition (at least at the MP2 level), the aromatic stacking energies seem to converge rather fast with the size of the basis set.⁸ This means that the MP2/medium-sized (diffuse) basis set stabilization energies are close to the actual values for the aromatic stacked clusters and underestimate the intermolecular correlation stabilization for the H-bonded ones. We agree that even the latest CCSD(T) calculations do not represent the final ultimate accuracy; nevertheless, they are the most reliable values currently available. In view of these new data, we estimate that our MP2/6-31G*(0.25) base stacking energies are closer to the actual values than we have ever assumed before. The use of large basis sets recommended by Cybulski et al. would lead, at the MP2 level, to overestimation of dispersion stabilization. Consequently, the relative strengths of H-bonded and stacked DNA base pairs predicted by us² at the MP2/6-31G*(0.25) level may even be

* To whom correspondence should be addressed. e-mail: hobza@indy.jh-inst.cas.cz.

† J. Heyrovský Institute, Prague.

‡ Department of Chemistry, Jackson.

slightly biased in favor of the stacked pairs, i.e., in the opposite way than expected by Johnson et al.¹ It is very likely that our MP2/6-31G*(0.25) base pair stacking energies are close to the actual values and are not substantially underestimated as expected in ref 1.

References and Notes

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