

Van der Waals Interactions in Aromatic Systems: Structure and Energetics of Dimers and Trimers of Pyridine

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Full geometry optimizations at the dispersion-corrected DFT-BLYP level of theory were carried out for dimers and trimers of pyridine. The DFT-D interaction energies were checked against results from single-point SCS-MP2/aug-cc-pVTZ calculations. Three stacked structures and a planar H-bonded dimer were found to be very close in energy (interaction energies in the range from -3.4 to -4.0 kcal mol $^{-1}$). Two T-shaped geometries are higher lying, by about 1 kcal mol $^{-1}$, which is explained by the more favorable electrostatic interactions in the stacked and H-bonded ar-

rangements. The DFT-D approach has proved to be a reliable and efficient tool to explore the conformational space of aromatic van der Waals complexes and furthermore provides interaction energies with errors of less than 10–20% of ΔE . Comparisons with previous results obtained by using only partially optimized model geometries strongly indicate that unconstrained optimizations are mandatory in such weakly bonded low-symmetry systems.

1. Introduction

Noncovalent interactions of aromatic systems are of great importance in biological systems, such as DNA and proteins (e.g., see refs. [1,2] and references therein), and in supramolecular chemistry.^[3] Bonding and structure of these aggregates are mainly determined by a complicated interplay between van der Waals (vdW, also called dispersion) and electrostatic (ES) interactions. At shorter intermolecular distances exchange-repulsion (ER) contributions, which stem from the Pauli principle, dominate forces. The ES and ER contributions can already be described accurately at the Hartree–Fock (HF) level of theory, whereas vdW interactions represent pure electron-correlation (EC) effects.^[4] It is now also clear that common Kohn–Sham density functionals, which treat electron correlation only in an approximate manner, cannot describe vdW interactions (e.g., see refs. [5–7] and references therein). On the other hand, it is well established that Møller–Plesset perturbation theory (MP2),^[8] the mostly widely applied ab initio approach for weakly bound complexes, tends to overestimate the interaction energies and to underestimate intermolecular distances.^[9–11] More sophisticated methods based on coupled-cluster theory^[12] [e.g., CCSD(T) and QCISD(T)] are computationally infeasible with reasonably large atomic orbital (AO) basis sets already for medium-sized systems.^[5] Recently, one of us introduced an empirical correction scheme for DFT calculations (termed DFT-D^[7]) that accounts for vdW interactions by pairwise additive C_6/R^6 potentials. Calculations with this very efficient method have shown promising results for a wide variety of weakly bonded systems^[7,13] (for related methods see, e.g., ref. [14–16]).

A well-examined example of aromatic vdW complexes is the benzene dimer. According to recent high-level ab initio calculations,^[10,17–19] the so-called T-shaped and parallel-displaced structures are found to be lowest in energy (interaction energies of about -2.7 to -3.0 kcal mol $^{-1}$ ^[18,19]) and their energy dif-

ference is less than 0.1 kcal mol $^{-1}$. Although the benzene dimer is an important benchmark system, it must be regarded as an insufficient model for aromatic interactions in biosystems, where mostly substituted or heteroaromatic species (e.g., phenols, DNA bases) occur. Thus, the straightforward next step towards a basic understanding and accurate modeling of such systems is the pyridine dimer (for a recent study on substituted benzene–benzene complexes, see ref. [20]). Due to the lower symmetry of pyridine (C_{2v}), more possible orientations exist, even when only stacked dimers are considered. Moreover, it is to be expected that the large monomer dipole moment (2.19 D^[21]) and thus a delicate interplay between vdW and ES effects will strongly influence the shape of the structures. This view is supported by a single-crystal X-ray study on pyridine^[22] that reported a surprisingly complex orthorhombic structure belonging to the $Pna2_1$ space group with 16 molecules (arranged in four layers) in the unit cell. A theoretical study^[23] in which several hypothetical structures were examined by minimizing the lattice energy by distributed multipole analysis concluded that the experimentally observed structure is only metastable. The simulation resulted in structures with pairs of parallel-displaced pyridine rings that have more negative lattice energies than the experimental phase. A recent theoretical study^[24] that appeared shortly before completion of our work investigated several pyridine dimer and trimer structures at the DFT-B3LYP and MP2 levels of theory. The authors

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used frozen monomer geometries in subsequent single-point calculations on the complexes. They also assumed highly symmetric structures of these complexes and only varied the intermolecular distances. Minima were found at 3.6 Å for all stacked structures and 3.0 and 3.4 Å for T-shaped structures. Our calculations that are based on full geometry optimizations without any a priori symmetry restrictions yield structures with different intermolecular orientations, shorter intermolecular distances, and stronger binding. The substantial deviations from the outcomes presented in ref. [24] and the success of the newly developed DFT-D and SCS-MP2 methods for such a complex system prompted us to report more conclusive results on pyridine oligomers here.

Computational Methods

All calculations were performed on a parallel LINUX PC cluster using the TURBOMOLE 5.6 program suite.^[25] The DFT-D approach^[7] was used with the BLYP^[26,27] density functional. The resolution of identity (RI) approximation^[28,29] was employed for all DFT and MP2 calculations, and the corresponding auxiliary basis sets were taken from the TURBOMOLE basis set library.^[30] If not mentioned otherwise, all structures were fully optimized at the DFT-D level without any symmetry constraints (resulting higher symmetries are reported, however) by using a AO basis set of valence-triple- ζ quality with two sets of polarization functions (2d (C, N), 2p (H), denoted as TZV2P).^[31] The optimizations were started from various (unsymmetrical) initial dimer arrangements so that we could be sure to present here the true lowest minima on the potential energy surface. Subsequent single-point calculations were carried out with Dunning's correlation-consistent augmented polarized triple- ζ basis set (aug-cc-pVTZ). We also applied the SCS-MP2 model,^[17] a recently introduced improved version of standard Møller-Plesset perturbation theory in which the correlation energy is partitioned into parallel- and antiparallel-spin components which are separately scaled. It provides significantly improved energetics compared to standard MP2 for a wide variety of chemical systems, often reaches QCISD(T) accuracy, and also corrects for the systematic overestimation by MP2 of vdW interactions in unsaturated systems.^[17,32,33] All MP2, SCS-MP2, and QCI interaction energies (ΔE) were corrected for basis set superposition error (BSSE) by the counterpoise (CP) method^[34] (the small BSSE effects in the case of DFT-D, which are typically < 5% of ΔE , were absorbed into the empirical potential^[7]).

To evaluate the quality of the SCS-MP2 and DFT-D methods for our problem we performed additional QCISD(T)^[35] calculations for a typical structure. The dimer **1** with C_{2h} symmetry (see Figure 1) was used. Because QCISD(T) calculations are computationally demanding they are limited to the aug-cc-pVDZ basis set. It is known from the literature, however, that the basis-set dependence is very similar for MP2 and QCI calculations, so that the QCISD(T)/aug-cc-pVDZ values together with SCS-MP2 basis-set increments can be taken as the most reliable reference value. The results are listed in Table 1. The CP-corrected MP2 and SCS-MP2 interaction energies ΔE are approximately 0.5 kcal mol⁻¹ lower for the triple- ζ compared with those with the double- ζ basis set. This difference (and also the BSSE) diminishes for the triple- and quadruple- ζ basis-set pair to 0.1 kcal mol⁻¹, which yields estimated complete basis set limits of -5.9 and -4.0 kcal mol⁻¹ at the MP2 and SCS-MP2 levels, respectively. The QCISD(T) and SCS-MP2 values differ by only 0.3 kcal mol⁻¹, while the MP2 value is too low by about 2 and the

Table 1. Interaction energies ΔE [kcal mol⁻¹] for the stacked (C_{2h}) pyridine dimer **1**. The molecular geometry was optimized at the DFT-D-BLYP/TZV2P level of theory. Counterpoise-uncorrected values are given in parentheses

Method	ΔE		
	aug-cc-pVDZ	aug-cc-pVTZ	aug-cc-pVQZ
MP2	-5.2 (-8.4)	-5.7 (-6.9)	-5.8 (-6.3)
SCS-MP2	-3.4 (-6.6)	-3.8 (-5.1)	-4.0 (-4.5)
DFT-D	- (-3.3)	- (-3.1)	- (-3.1)
QCISD	-2.1 (-5.0)	-	-
QCISD(T)	-3.1 (-6.4)	-	-

QCISD value is too high by about 1 kcal mol⁻¹ (similar behavior is found for the benzene dimer^[10,18]). From these results it is clear that SCS-MP2 is a very accurate method for structures of this type and that standard MP2 as used in ref. [24] should be avoided. Taking the extrapolated SCS-MP2 result and correcting for the difference with respect to QCISD(T) at the aug-cc-pVDZ level leads finally to an estimated ΔE of about -3.7 kcal mol⁻¹. Compared to this reference value, the DFT-D method yields slightly too weak binding but can, however, still be considered as quite accurate (at least when compared to, for example, standard MP2). Note further that all applied methods yield monomer dipole moments between 2.13 and 2.34 D that compare well with the experimental value of 2.19 D.^[21]

2. Results

Our study included seven dimer and two trimer complexes of pyridine (Figure 1). Structures **1–4** are similar to that of the parallel-displaced benzene dimer. They differ in the relative ori-

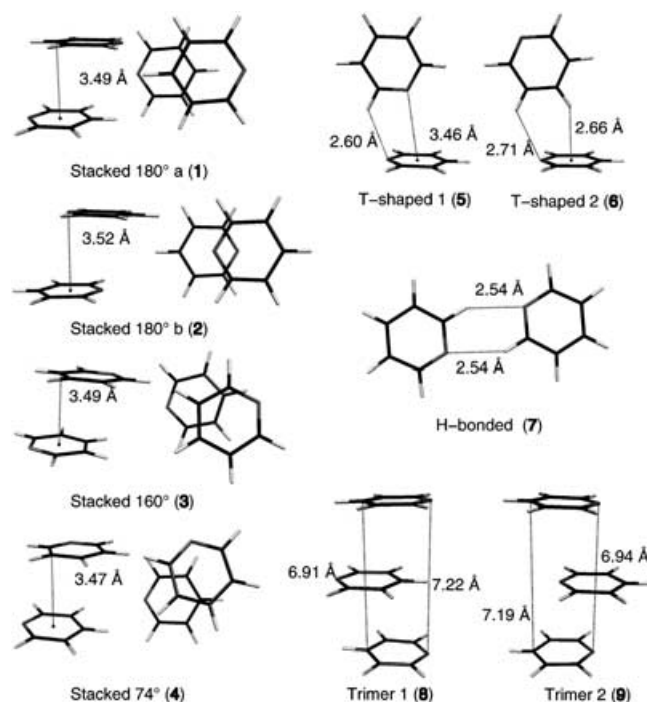


Figure 1. Optimized DFT-D-BLYP/TZV2P structures of the investigated pyridine complexes.

entation of the rings, which can be described best by the dihedral angle spanned by the center of each ring and the two nitrogen atoms. Geometry optimizations resulted in four different minima with rotational angles of 180, 180, 160, and 74°. The two 180° forms differ in the relative displacement of the monomers with respect to each other, that is, in **1** one carbon atom is above the midpoint of the other ring, while a nitrogen atom is located here in **2**. Most of the stacked structures are slightly bent away from a perfectly parallel orientation (by about 3°). For a T-shaped bonding motif two local minima were found. In **5** the nitrogen atom of the upper molecule points towards the center of the lower ring, whereas in **6** it is directed towards the other side, more resembling the T-shaped structure of benzene. Compared to the T-shaped structures reported in ref. [24], for which the authors assumed a perpendicular arrangement of the two N–C₄ axes, our full geometry optimizations yield structures in which one pyridine molecule is rotated by about 30° to form an additional N...HC interaction. The last dimer examined in our study is the hydrogen-bonded complex **7**.

For the trimers, two geometrical arrangements were considered. The monomers of both structures are arranged similarly to dimers **1** and **2** in such a way that the dipole moments of the neighboring monomers adopt an antiparallel orientation. In trimer **1** (**8**) the C₄ carbon atoms point towards the center, whereas in trimer **2** (**9**) the nitrogen atoms of the individual monomers are located above or below the center of the neighboring ring.

The results of the DFT-D optimizations are given for important geometrical variables in Figure 1 (Cartesian coordinates for all structures are supplied as Supporting Information), while the interaction energies for DFT- and MP2-based methods are gathered in Table 2. The results of a DFT energy decomposition analyses and Hartree–Fock, MP2, and SCS-MP2 correlation contributions to the interaction energies can be found in the Supporting Information.

Having already pointed out the inability of standard DFT to describe vdW interactions, it comes as no surprise that DFT-BLYP fails to yield any bonding of the stacked and T-shaped

dimers and stacked trimers, as all the interaction energies are positive. Only H-bridged dimer **7** is weakly bound. With the DFT-D approach all interaction energies are negative. The differences between the results with the two AO basis sets (TZV2P vs aug-cc-pVTZ) are small and do not influence the relative stabilities of the different structures, so we restrict our discussion to the values obtained with the aug-cc-pVTZ basis set. With DFT-D the lowest energy structure ($\Delta E = -3.5$ kcal mol⁻¹) is hydrogen-bonded dimer **7**. The N...H distances are 2.54 Å (see Figure 1), which is about 0.1 Å shorter than in the ammonia dimer.^[7] Only 0.2 kcal mol⁻¹ less stable is the 160° dimer **3**, which is the best of all π – π complexes. The distance between the center of the lower ring and the nitrogen atom of the upper ring is 3.49 Å. The 180° dimer **1** shows almost the same intermolecular distance and is only slightly less stable than **3**. The 74° stacked structure **4** has an interaction energy of -3.1 kcal mol⁻¹ and is thus almost as stable as **1**. The next most stable isomer is one of the T-shaped complexes (**6**). The distance between the center of the lower ring and the nearest hydrogen atom of the upper ring is 2.66 Å, and the interaction energy is -2.9 kcal mol⁻¹. The other 180° dimer (**2**) is clearly less stable than the other stacked complexes ($\Delta E = -2.3$ kcal mol⁻¹). The second T-shaped complex (**5**) is the least stable of the investigated structures.

The results for the investigated trimer structures are very similar to those for the two stacked dimers in the sense that the trimer with exocentric nitrogen atoms (**8**) is energetically more stable than the structure with the nitrogen atoms above the ring center (**9**). The DFT-D interaction energy for **8** is -6.3 kcal mol⁻¹, and the CP-corrected SCS-MP2 calculation gives -7.5 kcal mol⁻¹, which is slightly more than twice the value of **1**. Structure **9** is much more weakly bound even though the intermolecular distances are almost identical to those of **8**. The DFT-D calculation yields -4.6 kcal mol⁻¹ and the SCS-MP2 calculation -5.6 kcal mol⁻¹ for ΔE .

A graphical comparison of the DFT-D, MP2, and SCS-MP2 interaction energies is presented in Figure 2. Conventional MP2 clearly overestimates binding. The CP-corrected MP2 values for the stacked dimers are approximately 2.5 kcal mol⁻¹ lower than

the DFT-D values. For the T-shaped forms this difference is reduced to 1.0 kcal mol⁻¹, and for the H-bonded system it is only 0.6 kcal mol⁻¹. All systems show a BSSE of only about 20% of the interaction energy, which is much less than that obtained in ref. [24] with the 6-311++G** AO basis. The agreement of the DFT-D with the SCS-MP2 results is much better. The differences for the stacked forms are only 0.5–0.7 kcal mol⁻¹, and those of the T-shaped complexes are less than 0.2 kcal mol⁻¹. This is in agreement with the results of ref. [7] that DFT-D-BLYP slightly

Table 2. Interaction energies ΔE [kcal mol⁻¹] of pyridine dimers and trimers with respect to the corresponding number of monomers. All geometries were optimized at the DFT-D-BLYP/TZV2P level of theory

Compound	Symmetry	DFT ^[a, b]	DFT-D ^[a]	Method DFT-D ^[c]	MP2 ^[d]	SCS-MP2 ^[d]
Dimers						
1 stacked 180° A	C _{2h}	+2.6	–3.2	–3.1	–5.7	–3.8
2 stacked 180° B	C ₁	+2.8	–2.4	–2.3	–4.4	–2.8
3 stacked 160°	C ₁	+2.5	–3.3	–3.3	–5.8	–4.0
4 stacked 74°	C ₂	+2.6	–3.1	–3.1	–5.6	–3.8
5 T-shaped 1	C _s	+0.8	–2.2	–2.1	–3.3	–2.2
6 T-shaped 2	C _s	+0.6	–3.0	–2.9	–4.2	–3.1
7 H-bonded	C _{2h}	–1.7	–3.7	–3.5	–4.1	–3.4
Trimers						
8 stacked 180°	C _{2v}	+5.4	–6.4	–6.3	–11.3	–7.5
9 stacked 180°	C _{2v}	+5.8	–4.7	–4.6	–8.8	–5.6

[a] TZV2P AO basis. [b] Pure DFT-BLYP without empirical dispersion correction. [c] aug-cc-pVTZ AO basis.

[d] Counterpoise-corrected aug-cc-pVTZ values.

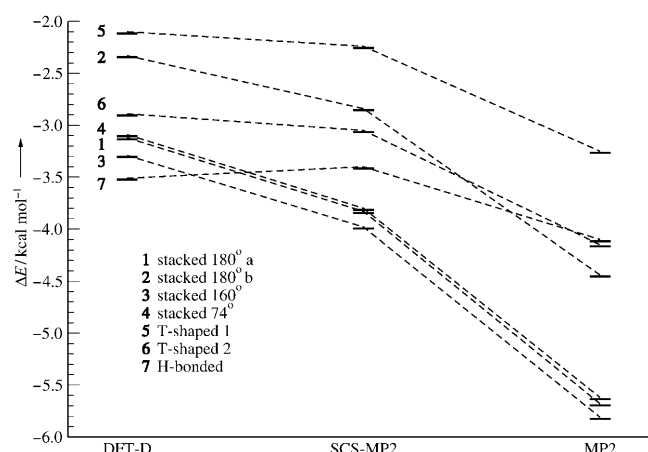


Figure 2. Energetic ordering of the pyridine dimer structures with DFT-D, SCS-MP2, and MP2 methods (aug-cc-pVTZ AO basis set).

favors saturated as opposed to π -stacking vdW interactions. The important energetic ordering of the different structures as computed with the three different methods is more clearly visible in Figure 2. With DFT-D the order of decreasing stability is $7 > 3 > 1 \approx 4 > 6 > 2 > 5$. This is maintained for SCS-MP2 with the exception that H-bonded dimer **7** is destabilized and now lies between **4** and **6**, that is, the nonsymmetrical stacked structure **3** is the global minimum at the SCS-MP2 level. This is in contrast to the results of ref. [24] where a structure similar to **1** was found to be best. Going from SCS-MP2 to MP2, **2** and **6** become even more strongly bound than **7** and interchange positions. A closer inspection of Figure 2 furthermore reveals that the differences between the applied methods are related to the type of binding involved. The dotted lines are parallel for all stacked (π - π bonded) dimers **1–4**. This also holds for the T-shaped (π -H bonded) structure, though the changes are smaller in this case.

Comparing the structures and energetics with the results from ref. [24] one can see three major differences. First, the structures obtained from unrestricted geometry optimizations in our study are separated by intermolecular distances that are about 0.1 Å shorter. Second, the CP-corrected MP2 interaction energies with comparable basis sets (6-311 + G** vs aug-cc-pVTZ^[36]) are lower for similar structures (e.g., $-5.7 \text{ kcal mol}^{-1}$ instead of $-4.0 \text{ kcal mol}^{-1}$ for **1**), and this indicates the importance of geometry optimization. Moreover, the T-shaped structures found here are bent by about 30°, even though optimization started from a perpendicular orientation with respect to the N-C4 axes, as proposed in ref. [24]. The corresponding interaction energies are about 2.0 kcal lower in our case. These observations lead us to the conclusion that the symmetry-restricted structures reported are very far from the true local minima with respect to the intermolecular orientations.

3. Conclusions

By means of full geometry optimizations at the dispersion-corrected DFT-BLYP level of theory, we predict five energetically close lying dimer structures of pyridine. The DFT-D interaction

energies were successfully checked against results from the SCS-MP2/aug-cc-pVTZ approach, which performs similarly to much more elaborate coupled-cluster methods. The DFT-D approach has proved to be a reliable and computationally fast tool to explore the conformational space of weakly bonded aromatic complexes. Comparisons with literature data strongly indicate that full geometry optimizations are mandatory in such weakly bonded low-symmetry systems. Over a wide range of different intermolecular orientations, the potential energy surface of the pyridine dimer seems to be quite flat, and this provides an explanation for the complicated X-ray structure and underlines the possibility for the coexistence of different phases in the solid state. By comparing similarly stacked structures of pyridine and benzene it is concluded that the electrostatic contribution of the permanent dipole moment to binding is about 1 kcal mol^{-1} (about 30% of the total ΔE). This leads to an increased relative stability of stacked over T-shaped structures, which are almost isoenergetic in benzene. The complexity of the system and the delicate balance of electrostatic and vdW contributions is further documented by the relatively high stability of the planar H-bonded structure, which lies only about $0.5 \text{ kcal mol}^{-1}$ above the best stacked form.

Keywords: ab initio calculations · density functional calculations · hydrogen bonds · pyridine dimer · van der Waals complexes

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