Interactions of Water with Mono- and Diamino Derivatives of *N*,*N*′-Dimethyluracil

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Molecular structures of mono- and diamino derivatives of *N*,*N*′-dimethyluracil and their complexes with water are investigated by ab initio quantum chemical methods at the MP2/6-31G(d,p) level of theory. The results of the calculations demonstrate that the formation of the N···H−O hydrogen bonds with participation of the nitrogen atom of the amino group in the *N*,*N*′-dimethyl-5,6-diaminouracil complex with water is caused by the intrinsic properties of this substituent. An analysis of the geometries and water−amine interaction energies for different monohydrates of mono- and diamino derivatives of *N*,*N*′-dimethyluracil indicates that the formation of this H bond requires the presence of the neighboring proton donor group. The energy of the N···H−O hydrogen bonds depends on a degree of conjugation between the lone pair of the nitrogen atom and the π system of the rest of the molecule. In the case of amino derivatives of uracil, the weakest conjugation is observed for the substituent at the C(5) atom. Therefore, the N···H−O hydrogen bond is formed by this amino group. A comparison of the amine−water interaction energies and the relative stability of isomeric monohydrates allows for the conclusion that the formation of such nonstandard hydrogen bonds is the most favorable way for interactions of 1,2-diamines with water and other proton donors.

Introduction

Hydrogen bonding plays a very important role in determining both the structure and function of various biological molecules.[1] In particular, the hydrogen bonds are responsible for the formation of the secondary structure of nucleic acids because of the existence of adenine−thymine and guanine−cytosine Watson−Crick base pairs. In this case, conventional N−H···O hydrogen bonds are considered to include the imido and amino groups of nucleobases as donors of proton.[2−4]

However, it was recently suggested[5] that amino groups in DNA bases can also be a proton acceptor. An analysis of crystallographic data[6−8] and theoretical calculations[9−12] reveals the possibility of close contacts between the nitrogen atom of the amino group and the hydrogen atom of the hydroxy or other amino groups in the crystals of DNA and various oligonucleotides. On the basis of these results, it was concluded that interactions between amino groups may play a role in the twisting of base pairs and in recognition of nucleosides.[5,13] However, all of these data were obtained for macromolecules in the solid state. Therefore, it is not clear if this intrinsic property of the amino group or the formation of such hydrogen bonds is forced by crystal packing and steric strain in the macromolecule.

The possibility for the existence of N···H−O bonds was considered by Smets et al.[14,15] for monohydrated complexes of 4-aminopyridine, 4-aminopyrimidine, and *N*,*N*-1-trimethylcytosine. However, the applied matrix-isolated FT-IR technique does not allow for a definite conclusion concerning the presence of such complexes. More clear evidence concerning the existence of this type of hydrogen bond was obtained from a microwave investigation of aniline−water[16] and aniline−methanol[17] complexes. It was demonstrated that hydrogen bonds between the amine and a proton donor were rather strong, and the amino group acted as a proton acceptor. A recent investigation of the aniline dimer ion by electronic and vibrational spectroscopy[18,19] results in the conclusion that neutral and ionic moieties of this complex are bonded by the N···H−N hydrogen bond.

The most clear evidence of the existence of the N···H−O hydrogen bonds is provided by X-ray diffraction study of the monohydrate of *N*,*N*′-dimethyl-5,6-diaminouracil. Two independent crystallographic studies[20,21] demonstrate that the amino group at the C(5) atom forms a weak hydrogen bond with the water molecule (the N···H distance is 2.29 Å). The second amino group is not involved in such interactions. However, it is not yet clear what is the role of crystal packing in the formation of this hydrogen bond.

In the present paper, we perform a quantum-chemical investigation of complexes of water and mono- and diamino derivatives of *N*,*N*′-dimethyluracil. We demonstrate that the ability to form this type of hydrogen bond is an intrinsic property of the amino group.

Method of Calculation

The molecular structures of molecules **1**−**5** and their complexes with water were fully optimized using the second order of the closed shell restricted Møller−Plesset perturbation theory[22] with the standard 6-31G(d,p) basis set. Hessian calculations were performed to establish the nature of the stationary points found by geometry optimization. Vibrational frequencies were calculated at the same level of theory, within the harmonic approximation, using analytical second derivatives

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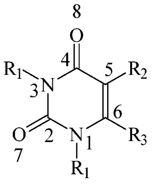


1 R_1=R_2=R_3=H
2 R_1=Me, R_2=R_3=H
3 R_1=Me, R_2=NH_2, R_3=H
4 R_1=Me, R_2=H, R_3=NH_2
5 R_1=Me, R_2=R_3=NH_2

for isolated molecules **1**−**5** and numerical second derivatives for hydrated complexes. No imaginary frequencies were found. All calculations were performed using the Gaussian 98 program.[23]

An analysis of the electron density distribution was carried out within Bader's "Atoms in Molecules" (AIM) approach[24] using a wave function obtained at the same level of theory.

Results and Discussion

A comparison of the geometry of *N,N′*-dimethyl-5,6-diaminouracil **5** and unsubstituted uracil **1** demonstrates the significant changes in the bond lengths and angles within the pyrimidine ring (Table 1). It was previously suggested[20] that this deformation is caused by the presence of two strong electron-donating substituents at the C═C double bond. However, a recent DFT study[25] of methylated uracil demonstrates that the replacement of the hydrogen atoms in uracil by a methyl group results in an expansion of the ring due to changes in the bond angles. To distinguish the influence of methyl and amino groups, we have calculated the geometry structure of *N,N′*-dimethyluracil **2** and its monoamino derivatives **3** and **4**.

An analysis of the geometry of molecules **1**−**5** demonstrates that the deformation of bond angles within the pyrimidine ring results from the presence of methyl groups which is in agreement with a previous conclusion.[25] However, we also found some changes in bond lengths which were not detected by the DFT method. In particular, a notable elongation of both carbonyl bonds (Δl = 0.011−0.013 Å) and a shortening of the C(4)−C(5) bond (Δl = 0.01) is observed. Such deformation of the geometry of the pyrimidine ring are retained also in the amino derivatives **3**−**5**.

The presence of amino groups results in changes in bond lengths within the six-membered ring. The characteristics of these changes are determined by the position of a substituent at the C(5)═C(6) double bond. In the case of compound **3**, the shortening of the N(1)−C(2) and N(3)−C(4) bonds and the elongation of the C(2)−N(3), C(6)−N(1), and C(4)−C(5) bonds indicate a weakening of conjugation within the pyrimidine ring. This agrees well with the antiaromatic character of the cyclic π system in uracil.[26] The presence of an electron-donating substituent results in a further decrease in the degree of aromaticity in the conjugated system and partial disruption of the $\pi-\pi$ interactions between the different parts of the ring.

A different situation is observed for the 6-amino derivative **4**. The trans configuration of the substituent with respect to the C(4)═O(8) carbonyl group creates favorable conditions for effective $\pi-\pi$ interactions between these fragments. This assumption is confirmed by the significant shortening of the C(4)−C(5) bond and by the elongation of the C═C double bond (Table 1). Also a decrease in the C−NH_2 bond as compared to **3** is observed. However, the length of the carbonyl bond remains almost unchanged.

TABLE 1: Selected Geometrical Parameters of Isolated Molecules 1−5

	1	2	3	4	5
Bond Lengths, Å					
N(1)−C(2)	1.396	1.393	1.379	1.404	1.399
C(2)−N(3)	1.385	1.391	1.400	1.383	1.384
N(3)−C(4)	1.414	1.416	1.393	1.416	1.414
C(4)−C(5)	1.460	1.450	1.459	1.437	1.438
C(5)−C(6)	1.350	1.351	1.357	1.361	1.368
C(6)−N(1)	1.376	1.373	1.387	1.382	1.381
C(2)−O(7)	1.217	1.230	1.233	1.231	1.231
C(4)−O(8)	1.219	1.230	1.238	1.233	1.237
C(5)−N			1.399		1.429
C(6)−N				1.390	1.382
Bond Angles, deg					
N(1)−C(2)−N(3)	112.7	114.8	114.5	115.0	115.6
C(2)−N(3)−C(4)	128.4	126.2	126.0	126.0	125.8
N(3)−C(4)−C(5)	113.3	114.4	115.7	114.7	114.7
C(4)−C(5)−C(6)	120.0	120.1	119.0	120.8	120.7
C(5)−C(6)−N(1)	121.9	122.2	121.7	121.2	121.0
C(6)−N(1)−C(2)	123.7	122.3	123.1	122.2	122.0
N(1)−C(2)−O(7)	122.8	121.0	122.1	121.2	122.1
N(3)−C(4)−O(8)	120.4	120.0	121.3	119.4	121.4
C(6)−C(5)−N			125.3	−	118.3
C(5)−C(6)−N				123.3	121.3
$\sum NH_2$ (at C(5))[a]			334.2	−	322.2
$\sum NH_2$ (at C(6))[a]				337.9	336.2
Torsion Angles, deg					
N(1)−C(2)−N(3)−C(4)	0.0	0.0	0.1	−1.3	−0.3
C(6)−N(1)−C(2)−N(3)	0.0	0.0	1.9	3.0	2.6
N−C(5)−C(6)−N					−6.8

[a] Sum of bond angles at the nitrogen atom of the amino group.

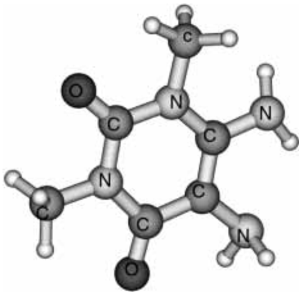


Figure 1. Structure of isolated molecule **5**.

In both molecules, the amino groups adopt a trigonal-pyramidal configuration (Table 1). The degree of pyramidality is slightly lower in **4**. This is caused by the more efficient conjugation between the lone-pair of the nitrogen atom and the π system of the pyrimidine ring as compared to **3**. It should be noted that the presence of an electron-donating substituent results in a deviation from planarity in the pyrimidine ring (Table 1).

The presence of two vicinal amino groups in molecule **5** causes the appearance of a strong steric repulsion between the hydrogen atoms of the substituents. This should enforce the significant deformation in the geometry of the amino groups. The essentially weaker conjugation between the lone pair of the nitrogen atom of the substituent at the C(5) atom and the π system of the C═C double bonds as compared to the second amino group causes drastic changes in the orientation of this substituent (Table 1, Figure 1). The amino group at the C(5) atom is arranged in such a way that the lone pair of the nitrogen atom lies almost in the plane of the pyrimidine ring and is oriented toward the hydrogen atom of a second amino group. On the basis of the distance between the N and H atoms (2.249 Å), one can assume the existence of a weak intramolecular hydrogen bond. However, topological analysis of the electron density distribution in molecule **5** does not reveal the presence of a (3, −1) bond critical point between these atoms. Therefore,

TABLE 2: Selected Geometrical Parameters (Å and deg) of Monohydrated Molecules 3−5

	3-W1	**3-W2**	**4-W1**	**4-W2**	**5-W1**	**5-W2**	**5-W3** calc	**5-W3** exper[10]
N(1)−C(2)	1.375	1.388	1.402	1.404	1.398	1.397	1.399	1.38293)
C(2)−N(3)	1.402	1.397	1.380	1.383	1.385	1.383	1.382	1.376(3)
N(3)−C(4)	1.390	1.399	1.422	1.417	1.408	1.415	1.407	1.401(3)
C(4)−C(5)	1.458	1.454	1.432	1.440	1.433	1.435	1.437	1.398(3)
C(5)−C(6)	1.362	1.355	1.365	1.359	1.373	1.371	1.371	1.38693)
C(6)−N(1)	1.386	1.375	1.387	1.379	1.379	1.383	1.387	1.386(3)
C(2)−O(7)	1.233	1.230	1.232	1.230	1.231	1.233	1.231	1.229(3)
C(4)−O(8)	1.243	1.237	1.234	1.232	1.246	1.238	1.240	1.245(3)
C(5)−N	1.390	1.429			1.429	1.430	1.435	1.428(3)
C(6)−N			1.379	1.401	1.377	1.376	1.375	1.331(3)
$\sum NH_2$ (at C(5))[a]	340.1	322.1			322.7	321.9	319.3	340.3
$\sum NH_2$ (at C(6))[a]			340.9	334.7	338.9	337.5	340.1	358.2
C(6)−C(5)−N−H	124.6	121.4			117.7	118.3	121.3	172.1
C(5)−C(6)−N−H			123.0	122.7	121.1	121.9	123.6	−169.9
N(1)−C(2)−N(3)−C(4)	−1.0	1.3	−0.9	−2.1	−0.9	1.0	1.0	3.6
C(6)−N(1)−C(2)−N(3)	−1.0	0.0	2.3	3.5	3.3	1.4	2.6	−0.8
N−C(5)−C(6)−N					−7.2	−6.6	−5.9	−3.3

[a] Sum of bond angles at the nitrogen atom of the amino group.

we should consider this N···H interaction only as an electrostatic attraction between two atoms with opposite charges. The presence of considerable steric strain also causes some twisting of the C(5)═C(6) double bond (the NH_2−C(5)−C(6)−NH_2 torsion angle is −6.8°). Similar results were obtained for hexaaminobenzene[27] where the value of the N−C−C−N torsion angle is 13.1°.

Such an orientation of the amino group at the C(5) atom results in the complete disruption of conjugation between the π system of the C═C double bond and the lone pair of the nitrogen atom. This is confirmed by the significant elongation of the C−N bond up to 1.429 Å and an essential increase in the degree of pyramidality in the substituent (Table 1). Therefore, changes in bond lengths within the pyrimidine ring in molecule **5** are very similar to those in **4** as mentioned above.

Thus, the results of the calculations demonstrate that the nitrogen atom of the amino group at the C(5) atom in **5** clearly has sp^3 hybridization. This considerably increases the proton-withdrawing ability of this atom and creates suitable conditions for the formation of an N···H−O hydrogen bond with a water molecule.

The optimization of the molecular structure of monohydrated *N*,*N*′-dimethyl-5,6-diaminouracil **5** with an initial geometry as is found in the crystal phase leads to the complex **5-W3** (Scheme 1) Unlike crystallographic data, the water molecule is located between two amino groups and forms two H bonds (Table 2, Figure 2a): a conventional N−H···O bond and an unusual N···H−O bond. In the crystal, two hydrogen bonds are also observed, but they form a water bridge between two different molecules of *N*,*N*′-dimethyl-5,6-diaminouracil **5**. Taking into account the geometrical characteristics (Table 2), one can suggest that the N···H−O hydrogen bond in complex **5-W3** is significantly stronger compared to the one observed in the crystal phase. Apparently, this is caused by a different location of the water molecule.

A comparison between the geometries of isolated molecule **5** and complex **5-W3** does not reveal considerable changes in the molecular parameters of structure **5.** The formation of the intermolecular hydrogen bonds results only in further differences in the pyramidality of the two amino groups (Table 3). A decrease in repulsion between these substituents which is manifested by a decrease in the N−C═C−N torsion angle should also be noted.

The pattern of H bonds found in **5-W3** is not unique for monohydrates of **5**. The results of the calculations reveal the existence of two other complexes of water with molecule **5** (Figure 2b,c). In the structure **5-W1**, water forms two conventional hydrogen bonds with the carbonyl and amino groups. This results in an elongation of the C(4)═O(8) bond up to 1.249 Å. It should be noted that the substituent at the C(5) atom retains its orientation (Figure 2b). Probably, an electrostatic interaction with other amino groups is more preferable. Therefore, the N−H···O bond in **5-W1** is relatively weak (Table 3). The **5-W2** complex is stabilized by a C−H···O hydrogen bond between the H atom of the methyl group and the oxygen of water and a conventional N−H···O bond. Both H-bonds formed are rather weak. This is confirmed also by the BSSE corrected values of the interaction energy between water and molecule **5** (Table 2). The highest interaction energy is predicted for the **5-W3** complex and the lowest for **5-W2**. This also agrees well with

SCHEME 1

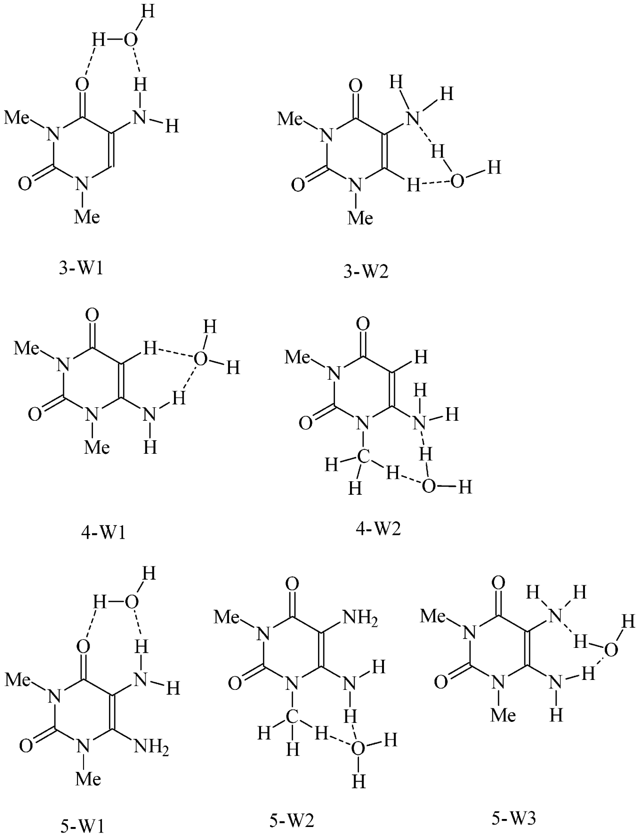


TABLE 3: Geometrical Parameters of the Hydrogen Bonds, BSSE Corrected Interaction Energy (E_{int}), and Related Stability (E_{rel}) of Monohydrated Complexes of Molecules 3−5

	3-W1	3-W2	4-W1	4-W2	5-W1	5-W2	5-W3
O−H···O(8) (Å)	1.928				1.908		
O−H···O(8) (deg)	152.3				163.3		
O···H−N (Å)	2.020		2.010		2.116	2.050	1.943
O···H−N (deg)	170.2		170.2		148.0	168.4	169.0
O···H−C(Me) (Å)				2.387		2.572	
O···H−C(Me) (deg)				161.8		140.5	
O−H···N (Å)		1.984		2.091			1.921
O−H···N (deg)		158.7		155.0			157.2
O···H−C(6) (Å)		2.307					
O···H−C(6) (deg)		133.9					
O···H−C(5) (Å)			2.649				
O···H−C(5) (deg)			133.1				
E_{int} (kcal/mol)	−11.41	−10.96	−9.1	−7.44	−11.73	−7.80	−13.43
E_{rel} (kcal/mol)	0	0.27	0	1.68	0.3	3.91	0

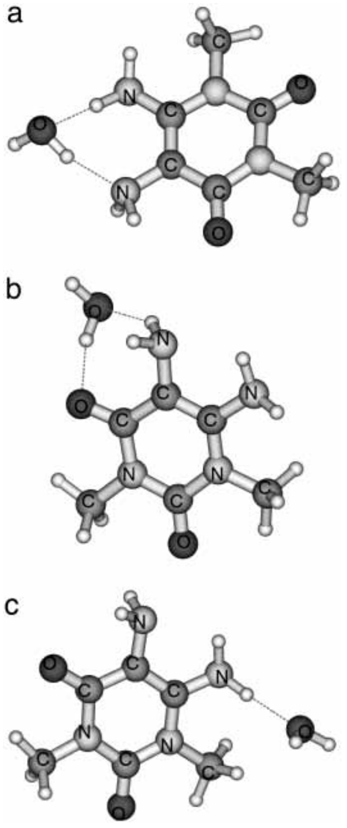


Figure 2. Structure of complexes of molecule **5** with water: (a) **5-W3**, (b) **5-W1**, (c) **5-W2**.

the relative energy of the isomeric complexes. The **5-W3** structure is the most stable (Table 3).

The results of calculations of monohydrated complexes of **5** allow for the assumption that the necessary condition for the existence of N···H−O hydrogen bonds is the absence of or the very weak conjugation between the lone pairs of the nitrogen atoms of the amino groups and the adjacent π system. This can explain why only the substituent at the C(5) atom of **5** forms such a bond. To test this assumption, we performed the search of all possible complexes between water and monoamino derivatives **3** and **4**. Only complexes where amino groups form H bonds were considered.

Two monohydrates were found in the case of **3** (Scheme 1). In the complex **3-W1**, water forms two conventional hydrogen bonds with the carbonyl and amino groups (Figure 3a). An interaction with the H_2O molecule does not significantly change the geometry of **3**. A decrease in the pyramidality of the amino group and a shortening of the C(5)−N bond (Tables 1 and 3) should be noted. This agrees well with the relatively weak character of the formed hydrogen bonds (Table 2).

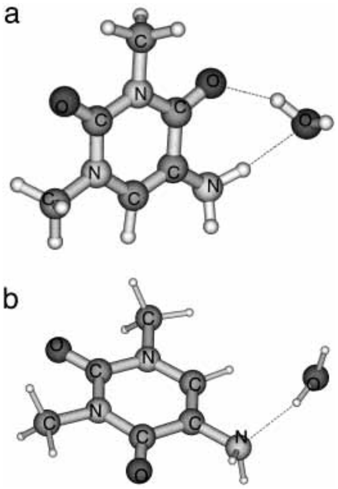


Figure 3. Structure of complexes of molecule **3** with water: (a) **3-W1** and (b) **3-W2**.

The **3-W2** complex is stabilized by two nonstandard H bonds (Figure 3b). One of them is the N···H−O bond with the participation of the nitrogen atom of the amino group. The formation of this bond results in a change in the pyramidality and orientation of this substituent with respect to the C═C double bond. The lone pair of the nitrogen atom lies almost in the plane of the pyrimidine ring. This entails a disruption of conjugation between the substituent and the π system of the heterocycle. As a result, the C(5)−N bond is elongated up to 1.429 Å, and the sum of the bond angles at the nitrogen atom is decreased to 322.1° (Table 3). A shortening of the N(1)−C(6) bond is also observed.

It should be stressed that the interaction between water and **3** in complex **3-W2** is only slightly weaker than in the case of **3-W1**. The difference in values of the BSSE corrected interaction energy is about 0.5 kcal/mol. This indicates that the energetic characteristics of the N···H−O and C−H···O bonds in **3-W2** are comparable with the conventional hydrogen bonds O···H−O and N−H···O in complex **3-W1** (Table 2). The difference in interaction energy correlates well with the relative stability of the monohydrates. The **3-W1** complex possesses a slightly lower energy (Table 3).

Two complexes of **4** with water are also revealed (Scheme 1). In the case of **4-W1**, water forms conventional N−H···O and nonstandard C−H···O hydrogen bonds with the amino group (Figure 4a). This results in a flattening of the amino group and a shortening of the C(6)−N bond (Table 2). The **4-W2**

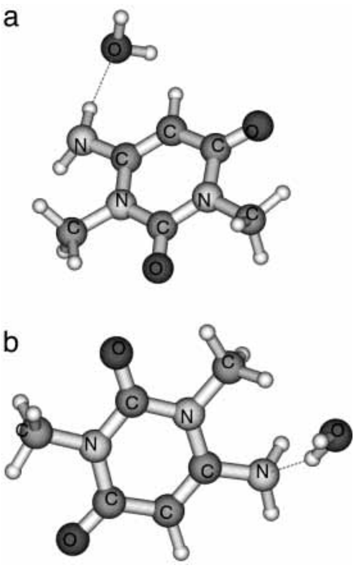


Figure 4. Structure of complexes of molecule **4** with water: (a) **4-W1** and (b) **4-W2**.

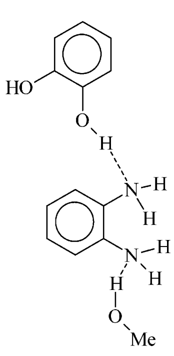
TABLE 4: Geometrical Parameters of the N···H−O Hydrogen Bonds Formed by Amino Groups in the Crystal Phase

comp	N···H (Å)	N···H−O (deg)	ref
5-W3	2.29	170.7	20
6	1.893	168.8	29
6	1.955	164.3	29
7	1.736	170.6	30

complex is stabilized by two unconventional hydrogen bonds: N···H−O and C−H···O are formed with the participation of one of the hydrogen atoms of a neighboring methyl group (Figure 4b). This causes some increase in the pyramidality of the amino group and an elongation of the C(6)−N bond (Table 2). However, the smaller value of the interaction energy indicates a weaker character for these hydrogen bonds compared to **4-W1** (Table 3). Following this trend, the energy of the **4-W2** complex is greater by 1.68 kcal/mol.

A comparison of the geometry, interaction energy, and relative stability of monohydrated complexes of molecules **3**−**5** indicates that the existence of the N···H−O hydrogen bonds between amines and water is caused by the intrinsic properties of amino group. The formation of this type of hydrogen bond requires the presence of a neighboring proton donating group. This allows the water to form a second hydrogen bond which further stabilizes the complex. The absence of such a group in complexes **3-W1**, **4-W1**, and **5-W1** results in the formation of the conventional N−H···O bonds rather than N···H−O bonds. The energy of the hydrogen bonds should also depend on the conjugation between the amino group and the π system of the other part of the molecule. The interaction energy between water and amine **3** is significantly larger compared to **4**. The strongest bond was found in the case of the **5-W3** complex where both conditions occur.

Thus, one can conclude that the formation of the N···H−O bond in the crystal of *N*,*N*′-dimethyl-5,6-diaminouracil monohydrate does not result from only packing effects but is governed by the intrinsic properties of the amino groups in **5**. The formation of such hydrogen bonds is the most favorable mechanism for interactions between water and **5**. Moreover, one can assume that this pattern of H-bonds should be a general case for complexes of 1,2-diamines with water and other proton donation agents. The search within the Cambridge Crystal Structure Database[28] reveals two structures of complexes containing such H-bonds (structures **6** and **7**).[29,30]



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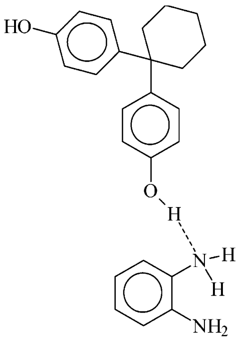

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In these cases, *ortho*-phenylenediamine forms the N···H−O hydrogen bonds with different alcohols. The geometrical characteristics of these bonds are listed in Table 4. It should be noted that in the crystal of **7** the second bond formed by water and alcohols is an intermolecular hydrogen bond. As follows according to Table 4, the N···H−O bonds in complexes **6** and **7** are significantly stronger compared to the crystal data for the monohydrate of *N*,*N*′-dimethyldiaminouracil. In the case of very strong interactions between the amino group and the proton donor, the transfer of hydrogen occurs. Such a situation was found for complexes of orthophenylenediamine with H_2S studied by X-ray diffraction.[31]

Conclusion

The results of the calculations demonstrate that the formation of N···H−O hydrogen bonds with the participation of a nitrogen atom from the amino group in the complex of *N*,*N*′-dimethyl-5,6-diaminouracil with water is caused by the intrinsic properties of this substituent. An analysis of the structure and the water−amine interaction energy for different monohydrates of mono- and diamino derivatives of *N*,*N*′-dimethyluracil indicates that the formation of this H bond requires the presence of a neighboring proton donor group. The energy of the N···H−O hydrogen bonds depends on the conjugation between the lone pair of the nitrogen atom and the π system of the rest of the molecule. In the case of amino derivatives of uracil, the weakest conjugation is observed for the substituent at the C(5) atom. Therefore, the N···H−O hydrogen bond is formed by this amino group. A comparison of amine−water interaction energies and the relative stability of isomeric monohydrates allows for the conclusion that the formation of such nonstandard hydrogen bonds is the most favorable mechanism for interaction of 1,2-diamines with water and other proton donors.

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References and Notes

(1) Saenger, W.; Jeffrey, G. A. *Hydrogen Bonding in Biological Structures*; Springer-Verlag: Berlin, 1991.

(2) Sponer, J.; Leszczynski, J.; Hobza, P. *J. Phys. Chem.* **1996**, *100*, 1965.

(3) Sponer, J.; Leszczynski, J.; Hobza, P. *J. Phys. Chem.* **1996**, *100*, 5590.

(4) Hobza, P.; Sponer, J. *Chem. Phys. Lett.* **1996**, *261*, 379.

(5) Luisi, B.; Orozco, M.; Sponer, J.; Luque, F. J.; Shakked, Z. *J. Mol. Biol.* **1998**, *279*, 1123.

(6) Shatzky-Swartz, M.; Arbuckle, N. D.; Eisenstein, M.; Rabinovich, D.; Bareket-Samish, A.; Haran, T. E.; Luisi, B. F.; Shakked, Z. *J. Mol. Biol.* **1997**, *267*, 595.

(7) Haromy, T. P.; Raleigh, J.; Sundaraligam, M. *Biochemistry* **1980**, *19*, 1718.

(8) Birnbaum, G. I.; Cygler, M.; Dudycz, L.; Stolarski, R.; Shugar, D. *Biochemistry* **1981**, *20*, 3294.

(9) Sponer, J.; Burcl, R.; Hobza, P. *J. Biomol. Struct. Dyn.* **1994**, *11*, 1357.

(10) Sponer, J.; Hobza, P. *J. Am. Chem. Soc.* **1994**, *116*, 709.

(11) Sponer, J.; Kypr, J. *Int. J. Biol. Macromol.* **1994**, *16*, 3.

(12) Sponer, J.; Leszczynski, J.; Hobza, P. *J. Biomol. Struct. Dyn.* **1996**, *14*, 117.

(13) Juo, Z. S.; Chiu, T. K.; Lieberman, P. M.; Baikalov, L.; Berk, A. J.; Dickerson, R. E. *J. Mol. Biol.* **1996**, *261*, 239.

(14) Smets, J.; Adamowicz, L.; Maes, G. *J. Phys. Chem.* **1995**, *99*, 6387.

(15) Smets, J.; Destexhe, A.; Adamowicz, L.; Maes, G. *J. Phys. Chem. B* **1997**, *101*, 6583.

(16) Spoerel, U.; Stahl, W. *J. Mol. Spectrosc.* **1998**, *190*, 278.

(17) Haeckel, M.; Stahl, W. *J. Mol. Spectrosc.* **1999**, *198*, 263.

(18) (a) Nakanaga, N.; Chowdhury, P. K.; Ito, F.; Sugawara, K.; Takeo, H. *J. Mol. Struct.* **1997**, *413*−*414*, 205. (b) Vlieghe, D.; Sponer, J.; Van Meervelt, L. *Biochemistry* **1999**, *38*, 16443.

(19) Ohashi, K.; Inokuchi, Y.; Izutsu, H.; Hino, K.; Yamamoto, N.; Nishi, N.; Sekiya H. *Chem. Phys. Lett.* **2000**, *323*, 43.

(20) Shishkin, O. V.; Kolos, N. N.; Orlov, V. D. *Kristallographiya* **1997**, *42*, 293.

(21) Hueso-Urena, F.; Moreno-Carretero, M. N.; Low, J. N.; Masterton, A. G. *J. Mol. Struct.* **1997**, *435*, 133.

(22) Moller, C.; Plesset, M. S. *Phys. Rev.* **1934**, *46*, 618.

(23) Frisch, M. J.; Trucks, G. W.; Schlegel, H. B.; Scuseria, G. E.; Robb, M. A.; Cheeseman, J. R.; Zakrzewski, V. G.; Montgomery, J. A., Jr.; Stratmann, R. E.; Burant, J. C.; Dapprich, S.; Millam, J. M.; Daniels, A. D.; Kudin, K. N.; Strain, M. C.; Farkas, O.; Tomasi, J.; Barone, V.; Cossi, M.; Cammi, R.; Mennucci, B.; Pomelli, C.; Adamo, C.; Clifford, S.; Ochterski, J.; Petersson, G. A.; Ayala, P. Y.; Cui, Q.; Morokuma, K.; Malick, D. K.; Rabuck, A. D.; Raghavachari, K.; Foresman, J. B.; Cioslowski, J.; Ortiz, J. V.; Stefanov, B. B.; Liu, G.; Liashenko, A.; Piskorz, P.; Komaromi, I.; Gomperts, R.; Martin, R. L.; Fox, D. J.; Keith, T.; Al-Laham, M. A.; Peng, C. Y.; Nanayakkara, A.; Gonzalez, C.; Challacombe, M.; Gill, P. M. W.; Johnson, B. G.; Chen, W.; Wong, M. W.; Andres, J. L.; Head-Gordon, M.; Replogle, E. S.; Pople, J. A. *Gaussian 98*, revision A.7; Gaussian, Inc.: Pittsburgh, PA, 1998.

(24) Bader, R. W. F. *Atoms in Molecules: A Quantum Theory*; Oxford University Press: Oxford, 1990.

(25) Zhang, C. F.; Chen, X. J.; Yuan, Z. S.; Zhang, Z. J.; Xu, K. Z. *Chem. Phys.* **2000**, *256*, 275.

(26) Shishkin, O. V. *J. Mol. Struct.* **1998**, *447*, 1.

(27) Dixon, D. A.; Calabrese J. C.; Miller, J. S. *Angew. Chem., Int. Ed. Engl.* **1989**, *28*, 90.

(28) Cambridge Crystal Structure Database. Release December 2000.

(29) Goswani, S.; Mukherjee, R.; Nigam, G. D.; Chinnakali, K.; Fun, H.-K. *Acta Crystallogr.* **1998**, *C54*, 1647.

(30) Caira, M. R.; Horne, A.; Nassimbeni, L. R.; Okuda, K.; Toda, F. *J. Chem. Soc. Perkin Trans. 2* **1995**, 1063.

(31) Lindeman, S. V.; Struchkov, Yu. T.; Shishkin, O. V.; Desenko, S. M.; Lipson, V. V.; Orlov, V. D. *Acta Crystallogr.* **1993**, *C49*, 896.