Crystal Structure of *N*(6),*N*(6)-Dimethyladenine Dihydrate

Tor Dahl

Institute of Mathematical and Physical Sciences, University of Tromsø, P.O. Box 953, N-9001 Tromsø, Norway

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The title compound crystallizes in the monoclinic space group *Pn* with cell dimensions $a = 3.885(2)$, $b = 15.545(4)$, $c = 7.994(2)$ Å, $\beta = 95.79(3)°$. The structure was refined to $R = 0.042$ for 886 observed reflections. The *N*(6),*N*(6)-dimethyladenine molecules are in the usual N(9)-H tautomeric form. They are stacked in infinite columns with an interplanar distance of 3.458(3) Å, and, unlike many closely related adenine derivatives, with a considerable degree of molecular overlap.

The protonation of the *N*(6),*N*(6)-dimethyladeninium ion has been shown to be different in three different crystalline compounds.[1-3] A possible relationship between the position of protonation and the stacking of the ions has been discussed. In contrast, most other substituted adeninium ions investigated so far are protonated in one and the same manner.[4] Neutral adenine derivatives usually crystallize as N(9)-H tautomers, but the N(7)-H tautomeric form has also been observed.[5]

Cell dimensions found from preliminary investigations of *N*(6),*N*(6)-dimethyladenine (DMA) dihydrate indicate that the DMA molecules form stacks with a considerable degree of molecular overlap, as distinct from *N*(6)-methyladenine and many other adenine derivatives, where there is very little molecular overlap in the stacks.[6]

The main purposes of the present investigation were to study the H positions and the proton affinity of the N atoms, and if possible, to explain the unusual molecular overlap in the stacks.

Experimental

Colourless, plate-shaped crystals were obtained by evaporation from a solution of DMA in methanol. The crystal used for structure determination had the dimensions $0.7 \times 0.1 \times 0.5$ mm, approximately along the *a*-, *b*- and *c*-axis, respectively.

The cell parameters and X-ray intensities were measured on an Enraf-Nonius CAD4 diffract-ometer using CuKα radiation ($\lambda = 1.5418$ Å). The cell parameters were determined from the setting angles of 25 reflections. The intensities were collected by an ω/2θ scan at a rate in ω of $0.7-2.9°\text{min}^{-1}$. No intensity reduction of the standard reflections during the data collection was observed. For the structure determination, the 887 reflections with $I > 2\sigma(I)$ were used. Corrections were made for Lorentz and polarization effects and also for absorption, using an empirical method.[7]

Crystal data

N(6),*N*(6)-Dimethyladenine dihydrate, $C_7H_9N_5 \cdot 2H_2O$; F.W. = 199.21, Space group *Pn* (No. 7, cell choice 2)[8], $a = 3.885(2)$, $b = 15.545(4)$, $c = 7.994(2)$ Å, $\beta = 95.79(3)°$, $V = 480.3(3)$ Å^3, $Z = 2$, $D_x = 1.38$, $D_m = 1.40$ g cm^{-3} (flotation), μ (CuKα) = 8.90 cm^{-1}.
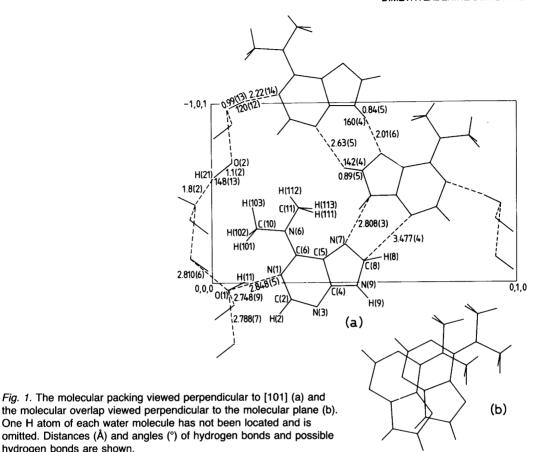
Structure determination and refinement

From a Patterson map and successive Fourier syntheses all non-H atoms could be located. From a difference map all H atoms were found, except one H atom of each water molecule. These two H atoms were not included in the refinement. In the last part of the least-squares refinement, positional parameters for all other atoms and thermal parameters (anisotropic for non-H atoms and isotropic for H atoms) were re-

Table 1. Positional parameters and equivalent or isotropic temperature factors (Å^2). $U_{eq} = 1/3 \sum_i \sum_j U_{ij} a_i^* a_j^* \mathbf{a}_i \mathbf{a}_j$ cos α_{ij}. Standard deviations in parentheses.

Atom	x	y	z	U_{eq} or U_{iso}
N(1)	0.3360	0.2249(2)	0.1400	0.0556(8)
C(2)	0.4636(11)	0.2604(2)	0.0059(5)	0.0588(9)
N(3)	0.5401(10)	0.3406(2)	−0.0237(4)	0.0539(7)
C(4)	0.4740(10)	0.3915(2)	0.1056(5)	0.0455(7)
C(5)	0.3392(10)	0.3651(2)	0.2530(4)	0.0449(8)
C(6)	0.2702(9)	0.2768(2)	0.2690(5)	0.0470(7)
N(6)	0.1455(9)	0.2397(2)	0.4033(4)	0.0581(8)
N(7)	0.3021(10)	0.4373(2)	0.3540(5)	0.0517(7)
C(8)	0.4140(11)	0.5011(2)	0.2668(5)	0.0528(8)
N(9)	0.5162(9)	0.4776(2)	0.1172(4)	0.0485(7)
C(10)	0.0790(14)	0.1482(3)	0.4030(6)	0.0731(12)
C(11)	0.0697(12)	0.2891(13)	0.5491(5)	0.0649(10)
H(2)	0.528(12)	0.216(3)	−0.073(7)	0.077(12)
H(8)	0.390(12)	0.556(3)	0.294(7)	0.069(11)
H(9)	0.609(10)	0.513(3)	0.057(6)	0.058(10)
H(101)	0.294(14)	0.114(4)	0.384(6)	0.088(14)
H(102)	−0.111(13)	0.121(4)	0.307(7)	0.091(14)
H(103)	−0.057(29)	0.136(7)	0.499(16)	0.165(37)
H(111)	0.300(14)	0.337(5)	0.581(9)	0.114(18)
H(112)	0.037(16)	0.259(4)	0.624(10)	0.106(20)
H(113)	−0.073(15)	0.333(4)	0.505(8)	0.088(13)
O(1)	0.2163(19)	0.0548(2)	0.0147(6)	0.1225(17)
H(11)	0.08(4)	0.108(8)	0.024(21)	0.23(5)
O(2)	0.6725(19)	0.0687(3)	0.7683(7)	0.1268(20)
H(21)	0.75(5)	0.009(14)	0.700(23)	0.30(8)

Table 2. Bond distances (Å), uncorrected and corrected for librational motion, and bond angles (°) for non-hydrogen atoms. Standard deviations in parentheses.

Distance	Uncorrected	Corrected	Angle	
N(1)−C(2)	1.344(4)	1.348	C(6)−N(1)−C(2)	118.4(2)
C(2)−N(3)	1.309(4)	1.312	N(1)−C(2)−N(3)	130.1(3)
N(3)−C(4)	1.347(4)	1.353	C(2)−N(3)−C(4)	110.9(3)
C(4)−C(5)	1.398(3)	1.403	N(3)−C(4)−C(5)	126.2(3)
C(5)−C(6)	1.407(4)	1.412	N(3)−C(4)−N(9)	127.2(3)
C(6)−N(6)	1.351(4)	1.355	C(5)−C(4)−N(9)	106.7(2)
C(6)−N(1)	1.354(4)	1.360	C(4)−C(5)−C(6)	117.0(2)
C(5)−N(7)	1.397(4)	1.403	C(4)−C(5)−N)7)	108.7(2)
N(7)−C(8)	1.311(4)	1.315	C(6)−C(5)−N(7)	134.3(2)
C(8)−N(9)	1.348(3)	1.354	C(5)−C(6)−N(1)	117.4(2)
N(9)−C(4)	1.349(4)	1.354	C(5)−C(6)−N(6)	125.2(3)
N(6)−C(10)	1.445(5)	1.449	N(1)−C(6)−N(6)	117.5(2)
N(6)−C(11)	1.450(4)	1.456	C(6)−N(6)−C(10)	119.8(3)
			C(6)−N(6)−C(11)	122.0(3)
			C(10)−N(6)−C(11)	118.2(3)
			C(5)−N(7)−C(8)	103.9(2)
			N(7)−C(8)−N(9)	114.2(3)
			C(8)−N(9)−C(4)	106.5(2)

Fig. 1. The molecular packing viewed perpendicular to [101] (a) and the molecular overlap viewed perpendicular to the molecular plane (b). One H atom of each water molecule has not been located and is omitted. Distances (Å) and angles (°) of hydrogen bonds and possible hydrogen bonds are shown.

fined. As secondary extinction turned out to be important an isotropic extinction parameter was refined.[9] The strongest reflection, 101, seemed to be influenced mainly by other effects, causing systematic errors, and was left out of the refinement. The weights were computed from the expression

$$w = 499\, t_0(x) + 676 t_1(x) + 179 t_2(x)$$

where $t_n(x)$ is the Chebyshev polynomial and $x = |F_o|/|F_o\,(\mathrm{max})|$.[10] The final $R = 0.042$ and $R_w = [\Sigma w\,(F_o\text{-}F_c)^2/\Sigma/\;w\;F^2]^{1/2} = 0.055$. The maximum electron density in the final difference map is 0.21 e/Å³. Lists of observed and calculated structure factors and anisotropic temperature factors may be obtained from the author on request. The final positional parameters and U_{eq}/U_{iso} values are given in Table 1. Bond distances, uncorrected

and corrected for librational motion,[11] and bond angles are given in Table 1. The molecular packing is shown in Fig. 1.

Scattering factors were taken from Ref. 12. All calculations were performed on the VAX 8600 computer at the University of Tromsø. The computer programs used are included in the Oxford CRYSTALS package.[13]

Discussion

The DMA molecule is in the usual N(9)-H tautomeric form. No bond distances in DMA are significantly different from the corresponding distances in N(6)-methyladenine.[6] However, the angles C(6)-C(5)-N(7) and C(5)-C(6)-N(6) are 1.5(3)° and 3.1(4)°, respectively, larger than the corresponding angles in N(6)-methyladenine.[6] These differences both have the effect of increas-

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ing the distances from N(7) to C(11) and H(113) in the additional methyl group in DMA. These distances are 2.972(4) and 2.39(7) Å, respectively, which are considerably shorter than the van der Waals distances. No atoms of the ring system of DMA deviate significantly from a least-squares plane through these rings, and the distances of N(6), C(10) and C(11) from this plane are 0.023(3), −0.005(6) and 0.048(5) Å, respectively. The atoms C(6), N(6) C(10) and C(11) are coplanar.

The DMA molecules are stacked along [100] with an interplanar distance of 3.458(3) Å. The shortest interatomic distance between non-H atoms along the stack is that of 3.472(3) Å between C(4) and C(5). Several distances between methyl H atoms and atoms of the adjacent molecule in the stack are close to the van der Waals distance. In many crystal structures of adenine derivatives, N(6) is in contact with the imidazole ring of the adjacent molecule in the stack.[6] The molecular overlap in this structure (Fig. 1) is thus unusual not only with respect ot the degree of overlap. The unusual overlap seems to give an effective molecular packing and may thus be due to steric factors only, but it may also possibly indicate some important intermolecular interaction, e.g. between the C(6)-N(6) bond and the pyrimidine ring.

O(1) and O(2) have extremely large U_{11}-values, viz. 0.222(5) and 0.212(6) Å^2, whereas their other U_{ij}-values are not very different from those of the other non-H atoms. These results, the large U_{iso}-values of the water H atoms and the fact that only two such atoms were observed in the difference map indicate disorder in the orientation of the water molecules. The positions of the O atoms indicate that the unobserved H atoms are involved in hydrogen bonds between the water molecules (Fig. 1). The shape of the crystals shows that the hydrogen bonds which link the DMA molecules together through water molecules along [010] are weak compared to the hydrogen bonds along [101] and to the stacking interactions along [100]. This conclusion agrees well with the observed geometry of the intermolecular contacts. The N(9)−H(9)···N(7) bond is shorter than usually observed for this kind of hydrogen bond.[14] an even shorter N−H··bond of 2.739(8) Å has been observed between 6-histami-

nopurine molecules, which are in the N(7)−H tautomeric form.[5] There are no such short hydrogen bonds in the N(6)-methyladenine structure, which has a hydrogen bond system quite different from that of the DMA dihydrate structure.

This investigation shows that although DMA crystallizes in the same tautomeric form as N(6)-methyladenine, there are some striking differences between the intermolecular interactions in these compounds. A possible relationship between these differences and the distortions of the bond angles in DMA caused by the additional methyl group may be worth considering.

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