Visualization of Host–Guest Interactions Between a Modified Nucleoside and Organic Moieties. Crystal Structures of 2′-Deoxy 5′-*O*-trityluridine and 2′-Deoxy 5′-*O*-tritylthymidine with Benzene, Toluene, Xylene, Trimethylbenzene, Cyclohexane and Water

D. PRAHADEESWARAN, S. KOLAPPAN, R. KRISHNAN and T. P. SESHADRI[*]
Department of Physics, Indian Institute of Science, Bangalore 560012, India

Abstract. This paper describes the crystal structures of 2′-deoxy 5′-*O*-trityluridine(5′-TU) and 2′-deoxy 5′-*O*-tritylthymidine (5′-TT) containing different organic moieties. There are two crystallographically independent nucleoside molecules present in the asymmetric units of all the structures. Uracil and thymine bases of the 2′-deoxy 5′-trityl uridine(5′-TU) and all the 2′-deoxy 5′-tritylthymidine structures are in an *anti* conformation with respect to their furanose rings. Thymine bases of molecules A and B form symmetric self pairs through N(3)—O(2) hydrogen bonds, whereas uracil bases are not engaged in hydrogen bonding between themselves. Ribose moieties of both molecules of 2′-deoxy 5′-trityithymidine with benzene and toluene are in the C(2′)-*endo* conformations while molecules A and B of 2′-deoxy 5′-tritylthymidine containing xylene, trimethylbenzene, cyclohexane and water are in the C(3′)-*endo* and C(1′)-*exo* conformations, respectively. Both ribose moieties of 5′-TU show C(3′)-*endo* puckering. The conformation about the C(4′)—C(5′) bond for all the 2′-deoxy 5′-tritylthymidine structures is g^+, contrasting with the g^- for the 5′-TU structure. Benzene and toluene molecules stack between TT base pairs, while xylene, trimethylbenzene and cyclohexane are oriented obliquely to the base pairs. 2′-Deoxy 5′-tritylthymidine containing toluene shows a type V C—H$\cdots\pi$ interaction between the methyl group of toluene and the thymine base. Remarkably, the 2′-deoxy 5′-tritylthymidine-containing xylene, trimethylbenzene, cyclohexane and water structures demonstrate a strong type I O—H$\cdots\pi$ interaction between the ribose O(3′) and the thymine base seen only in 1.25% of the structures. Molecular packing and hydrogen bonding are discussed.

Key words: modified nucleosides, conformation, DNA and RNA

---

[*] Author for correspondance.

1. Introduction

Nucleic acids are known to form two types of molecular complexes. In the first type the guest molecule is sandwiched between the nucleic acid base pairs of a duplex structure, whereas in the second type it stacks between the base pairs of a non-duplex structure. There are many examples of the first type involving the intercalation of planar acridine dyes between DNA base pairs [1, 6]. The stereochemistry of drug intercalation has been analyzed in detail. However, there are only very few examples of the second type such as ApU-9-amoniacridine [7], d(GPC)-actinomycin [8]. We wish to present the crystal structures of molecular complexes of 2′-deoxy 5′-trityluridine and 2′-deoxy 5′-O- tritylthymidine with various organic molecules. This work was carried out as part of our ongoing studies on nucleic acid constituents [9, 10].

2. Crystallization and Data Collection

5′-Trititylthymidine (5′-TT) purchased from Sigmal Chemical Co., USA was used for crystallization without further purification. Crystals of 5′-TT containing benzene (5′-TTB), toluene (5′-TTT) and water (5′-TTW) in its lattice were grown by liquid diffusion of the respective solvents into chloroform and chlorobenzene solutions of the compound. Crystals of 5′-TT with xylene (5′-TTX), trimethylbenzene (5′-TTTB) and cyclohexane (5′-TTCH) were grown by slow evaporation of chloroform solutions of the nucleoside containing the respective solvents and 2,4-pentanediol in nine well cavity plates. Crystals of 2′-deoxy 5′-O-trityluridine (5′-TU) were grown by diffusion of acetone into an aqueous solution of the compound. Unit cell dimensions were determined from a small set of about 10 low angle reflections ($\theta \leqslant 15°$) obtained from an automatic search on a CAD-4 diffractometer. They were subsequently refined using high angle reflections ($10° \leqslant \theta \leqslant 30°$). It was observed that 5′-TTB and 5′-TTT having very nearly the same unit cell parameters belong to the triclinic system, 5′-TTX, 5′-TTTB, 5′-TTCH and 5′-TTW belong to the orthorhombic, while 5′ TU belongs to the monoclinic system. CuK$_\alpha$ intensity data with Ni filter were collected for all crystals using $\omega - 2\theta$ scan mode up to $\sin \theta/\lambda = 0.62$ Å^{-1} except for 5′-TTCH as the diffraction pattern did not extend beyond 0.59 Å^{-1} due to the poor quality of the crystal. Intensities of only unique reflections were measured. Two reflections monitored periodically every 100 reflections showed less than 5% variation, indicating crystal and instrument stability. All data sets were corrected for Lorentz and polarization errors and empirical absorption corrections were also applied to them. It was anticipated from density measurements of the crystals that the asymmetric unit contained two nucleoside and two solvent (benzene, toluene) molecules are included in 5′-TTB and 5′-TTT while, two nucleoside and one solvent (xylene, trimethylbenzene and cyclohexane) molecules in 5′-TTX, 5′-TTTB and 5′-TTCH respectively. Although, 5′-TTW was crystallized in the presence of chlorobenzene, density measurements indicated the presence of three water molecules only. Density measurements indic-

ated that there are no solvent molecules in the 5′-TU structure. Crystal data and other crystallographic information are given in Table I.

3. Structure Determination and Refinement

Crystal structures of 5′-TTB, 5′-TTT, 5′-TTX and 5′-TU were solved independently by direct methods using SHELXS-86 [11]. The nucleoside coordinates of 5-TTX were used in the refinements of 5′-TTTB, 5′-TTCH and 5′-TTW as they all had very nearly the same cell parameters. Solvent molecules benzene, toluene, xylene, trimethyl benzene, cyclohexane and water oxygens in their respective structures were determined from difference Fourier maps computed after a few cycles of initial isotropic thermal parameter refinement using SHELEXL-93 [12]. Atoms of the cyclohexane molecule had higher thermal parameters and their bond distance and angles were found to be abnormal indicating thermal disorder. So they were restrained during the refinement cycles. The paucity of high angle data presented additional problems in the refinement of this structure. Refinements of other structures progressed without difficulty. Five strong peaks which could be assigned as water oxygens were detected in the difference Fourier map of 5′-TTW although only three were expected from density measurements. Temperature factors of all the water oxygens were found to be rather high on refinement and so they were considered to be disordered. Their occupancies and thermal parameters were refined alternately. Eventually, the sum of their occupancies turned out to be close to 3.0, in agreement with the density measurements. All the structures were subjected to anisotropic thermal parameter refinements after which the hydrogen atoms were located from difference maps. Some of the H atoms which could not be located from difference maps were fixed on the basis of geometrical criteria. The positional and thermal parameters of the H atoms located from difference Fourier maps and only the thermal parameters of the H atoms fixed geometrically were refined in the final cycles. The final R factors of the structures with H atoms and weighting function are 0.041, 0.046, 0.071, 0.075, 0.123, 0.085 and 0.055 for 5′-TTB, 5′-TTT, 5′-TTX, 5′-TTTB, 5′-TTCH, 5′-TTW and 5′-TU respectively.

4. Results and Discussion

The conformation of the nucleoside molecules are shown in Figure 1. Important torsion angles are listed in Table II.

4.1. CONFORMATION OF THE THYMINE AND URACIL BASES

Uracil and thymine bases in all the structures are planar. The conformation of the thymine and uracil bases with respect to their ribose moieties are *anti* as inferred from their torsion angles about the glycosyl bond shown in Table II. Purine bases adopt a *syn* conformation more often than pyrimidine bases. Thymine bases of

Table I. Crystal data

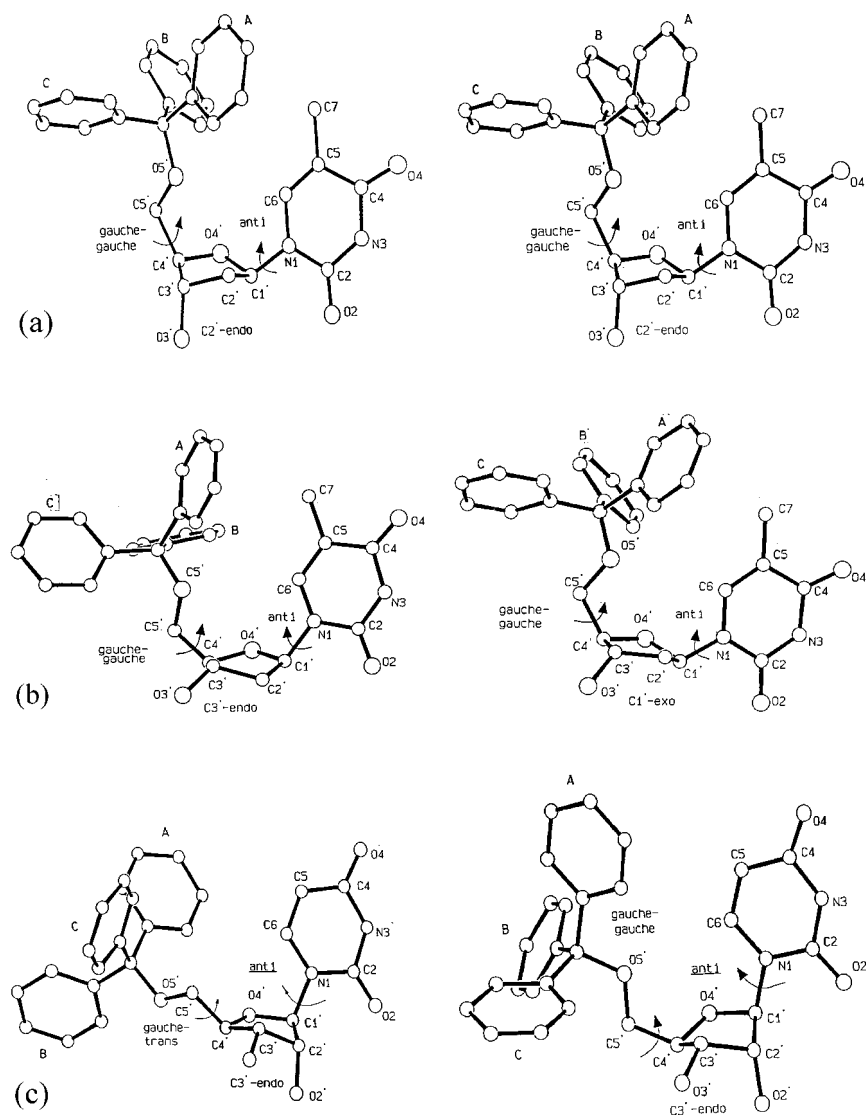| Compound	(1) Benzene	(2) Toluene	(3) Xylene	(4) Trimethylbenzene	(5) Cyclohexane	(6) Water	(7) Trityl uridine
Empirical formula $C_{29} H_{28} N_2 O5+$	C_6H_6	C_7H_8	$0.5C_8H_{10}$	$0.5C_9H_{12}$	$0.5C_6H_6$	$1.5H_2O$	$C_{28}H_{26}N_2O_6$
Molecular weight	562.3	576.3	590.7	604.7	562.3	514.2	486.5
Space group	$P1$	$P1$	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$	$P2_1$
Crystal Size (mm)	$1.0 \times 0.25 \times 0.25$	$1.5 \times 0.4 \times 0.4$	$0.4 \times 0.4 \times 1$	$0.8 \times 0.2 \times 0.1$	$0.5 \times 0.2 \times 0.1$	$1.0 \times 0.6 \times 0.4$	$0.6 \times 0.2 \times 0.1$
a (Å)	10.441 (2)	10.465 (2)	9.953 (2)	9.965 (3)	9.953 (3)	9.985 (2)	11.995 (3)
b (Å)	11.250 (3)	11.186 (3)	15.929 (4)	15.949 (3)	15.929 (3)	15.742 (2)	11.492 (3)
c (Å)	13.871 (3)	14.240 (3)	36.162 (6)	36.150 (6)	36.162 (7)	36.491 (5)	17.381 (2)
$\alpha°$	69.8 (2)	69.3 (2)	90.0	90.0	90.0	90.0	90.0
$\beta°$	87.7 (2)	87.3 (2)	90.0	90.0	90.0	90.0	92.6 (1)
$\gamma°$	81.8 (2)	81.5 (2)	90.0	90.0	90.0	90.0	90.0
V (Å^3)	1515.8	1542.2	5733.2	5745.4	5733.2	5735.8	2393.4
Z	2	2	8	8	8	8	4
$D_{calc.}$ (g cm^{-3})	1.25	1.28	1.36	1.38	1.24	1.17	1.36
$D_{meas.}$ (g cm^{-3})	1.24	1.27	1.37	1.39	1.25	1.19	1.35
μ cm^{-1}	6.3	6.1	8.2	6.2	6.4	6.7	9.0
Ranges of hkl	$-10 \leqslant h \leqslant 12$	$-12 \leqslant h \leqslant 11$	$0 \leqslant h \leqslant 12$	$0 \leqslant b \leqslant 12$	$0 \leqslant h \leqslant 11$	$0 \leqslant h \leqslant 8$	$0 \leqslant h \leqslant 14$
	$-12 \leqslant k \leqslant 13$	$-12 \leqslant k \leqslant 13$	$0 \leqslant k \leqslant 19$	$0 \leqslant k \leqslant 19$	$0 \leqslant k \leqslant 17$	$0 \leqslant k \leqslant 8$	$0 \leqslant k \leqslant 14$
	$0 \leqslant l \leqslant 16$	$0 \leqslant l \leqslant 17$	$0 \leqslant l \leqslant 44$	$0 \leqslant l \leqslant 44$	$0 \leqslant l \leqslant 40$	$0 \leqslant l \leqslant 45$	$-21 \leqslant l \leqslant 21$
Data collection mode	$\omega–2\theta$	$\omega–2\theta$	$\omega–2\theta$	$\omega–2\theta$	$\omega–2\theta$	$\omega–2\theta$	$\omega–2\theta$
Number of reflections collected	5987	6056	5679	5759	4676	6052	5202
Number of observed unique reflections	5508 $Fo \geqslant 4\sigma(F)$	5717 $Fo \geqslant 4\sigma(F)$	5122 $Fo \geqslant 3\sigma(F)$	3912 $Fo \geqslant 3\sigma(F)$	2844 $Fo \geqslant 3\sigma(F)$	4475 $Lo \geqslant 2\sigma(L)$	4943 $Fo \geqslant 3\sigma(F)$
$\sin\theta/\lambda$ Å^{-1}	0.62	0.62	0.61	0.61	0.59	0.62	0.62
R	0.041	0.046	0.071	0.075	0.123	0.085	0.055
wR	0.121	0.132	0.076	0.072	0.343	0.307	0.060

Figure 1. Structures of 5′-TT and 5′-TU molecules A and B viewed approximately perpendicular to the bases showing their conformational features. (a) 5′-TTB; (b) 5′-TTX; (c) 5′-TU.

nucleoside molecules A and B form self pairs through an N(3)$\cdots$O(2) hydrogen bond with a propeller twist of 3.7° and 10.7° for the triclinic and orthorhombic structures, as shown in Figure 2. Base pairing in nucleic acid structures have been classified into six different types [13] from a database analysis. There are two symmetric and one asymmetric type pairings pertaining to thymines. Under this classification, 5′-TT belongs to the symmetric pairing similar to that observed in the structures of azido thymidine [14, 15] and *cis*-thymidine 3′–5′-cyclic methyl-

Table II. Selected torsion angles (°) for 5′-TT and 5′-TU with e.s.ds in parenthesis

Selected torsion angles	Triclinic		Orthorhombic		5′-TU	
	Molecule A	Molecule B	Molecule A	Molecule B	Molecule A	Molecule B
Base						
χ_{CN} = O4′—C1′—Ni—C2	−140.3(4)	−128.8(4)	−151.2(4)	−123.5(5)	−155.3(2)	−162.1(2)
Exocyclic bond						
ϕ_{oo} = O5′—C5′—C4′—O4′	−62.0(5)	−59.7(5)	−72.5(5)	−62.0(5)	71.4(5)	−66.8(3)
ϕ_{oo} = O5′—C5′—C4′—C3′	59.1(5)	61.1(5)	46.8(5)	58.9(5)	−171.4(2)	51.6(3)
C4′—C5′—O5′—C1T	169.8(4)	167.2(4)	172.3(4)	171.2(4)	−162.9(2)	−174.6(2)
Ribose						
C2′—C1′—O4′—C4′	−22.4(4)	−25.3(4)	−4.5(5)	−23.5(6)	10.4(3)	4.3(3)
O4′—C1′—C2′—C3′	36.3(4)	37.3(4)	−16.5(5)	25.9(6)	−30.7(3)	−29.1(3)
C1′—C2′—C3′—C4′	−35.2(4)	−34.2(3)	29.7(5)	−18.2(6)	38.1(2)	41.2(2)
C2′—C3′—C4′—O4′	22.9(4)	20.2(3)	−32.7(5)	5.0(6)	−33.2(2)	−40.1(2)
C3′—C4′—O4′—C1′	−0.68(4)	3.1(3)	24.0(5)	11.9(5)	14.6(3)	22.5(3)
Trityl moiety						
C5′—O5′—C1T—C10	151.1(4)	–	−172.0(4)	–	−159.5(3)	–
C5′—O5′—C1T—C20	31.5(5)	–	73.2(5)	–	84.7(3)	–
C5′—O5′—C1T—C30	−91.9(4)	–	−52.9(9)	−53.0(5)	−37.7(4)	–
C5′—O5′—C2T—C10	–	−176.3(3)	–	175.9(4)	–	−178.8(2)
C5′—O5′—C2T—C20	–	64.0(4)	–	57.6(5)	–	68.1(3)
C5′—O5′—C2T—C30	–	−60.5(4)	–	−66.7(5)	–	−58.4(3)
O5′—C1T—C10—C11	31.4(5)	–	−32.5(6)	–	−34.3(4)	–
O5′—C1T—C10—C15	−150.2(4)	–	150.6(5)	–	148.2(4)	–
O5′—C1T—C20—C21	−116.8(5)	–	−176.3(5)	–	−68.6(4)	–
O5′—C1T—C20—C25	61.8(5)	–	10.3(7)	–	107.5(4)	–
O5′—C1T—C30—C31	155.5(4)	–	−64.7(6)	–	177.5(3)	–
O5′—C1T—C30—C35	26.7(6)	–	110.5(6)	–	−0.9(5)	–
O5′—C2T—C10—C11	–	−23.6(5)	–	−31.3(6)	–	160.4(3)
O5′—C2T—C10—C15	–	158.5(4)	–	149.7(5)	–	−24.5(4)
O5′—C2T—C20—C21	–	97.5(5)	–	97.5(5)	–	88.2(4)
O5′—C2T—C20—C25	–	−79.9(5)	–	−84.2(6)	–	−84.2(4)
O5′—C2T—C30—C31	–	152.0(4)	–	−24.2(6)	–	30.6(4)
O5′—C2T—C30—C35	–	−31.7(5)	–	−156.3(5)	–	−156.5(3)

phosphate [16]. By contrast, uracil bases in the 5′-TU do not form hydrogen bonds between themselves in the lattice.

4.2. CONFORMATION OF THE DEOXYRIBOSE MOIETY

The conformation of the deoxyribose moieties of molecules A and B in 5′-TTB and 5′-TTT is C(2′)-*endo*, with the C(2′) atoms displaced by 0.59 and 0.61 Å from the best plane constituted by the remaining four atoms of the furanose ring on the same side of the C(5′) atom. In contrast, the deoxyribose moiety of molecule A
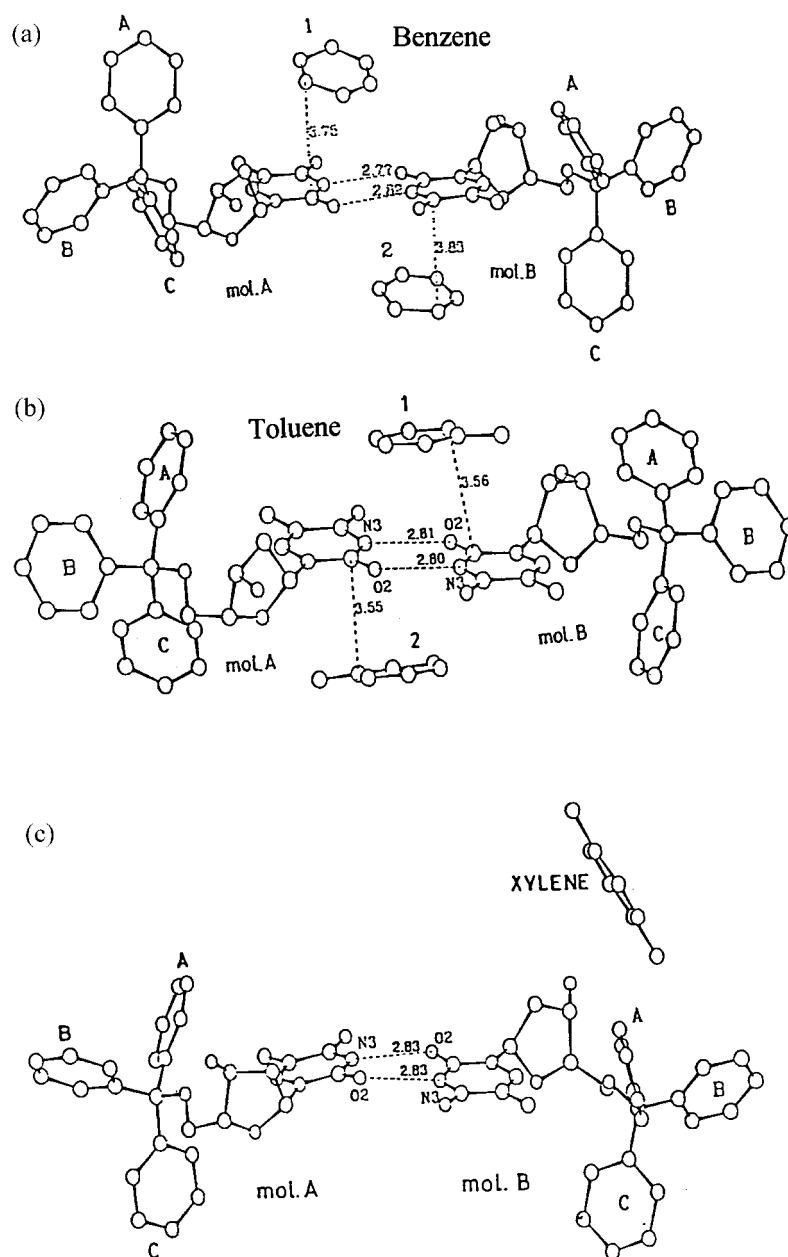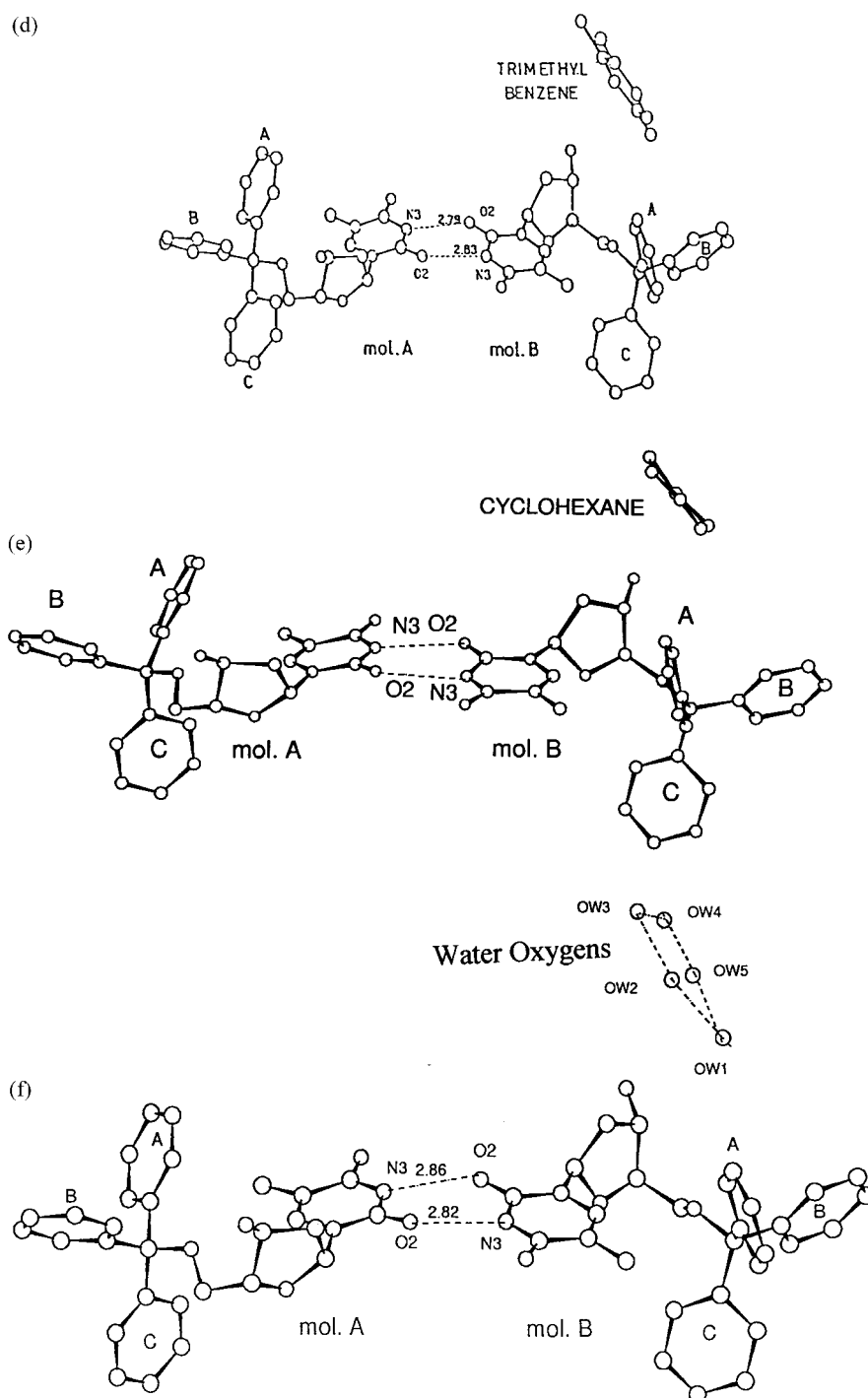
Figure 2.

(d)

TRIMETHYL
BENZENE

A

B

N3 2.79 O2
2.83
O2 N3

mol.A   mol.B

C

A

B

C

CYCLOHEXANE

(e)

A
B

N3 O2

O2 N3

C   mol. A   mol. B

A

B

C

Water Oxygens

OW3   OW4

OW5

OW2

OW1

(f)

A

B

N3 2.86   O2

2.82
O2   N3

C   mol. A   mol. B

A

B

C

Figure 2. An illustration showing the selfpairing between thymine bases through N(3)· · ·O(2)
hydrogen bonding; the stacking of benzene (a) and toluene (b) molecules on thymine pairs;
the oblique orientation of xylene (c), trimethylbenzene (d), cyclohexane (e) and the position
of water molecules (f).

of 5′-TTX, 5′-TTTB, 5′-TTCH and 5′-TTW in the orthorhombic structure shows C(3′)-*endo* puckering with the C(3′) atom displaced from the least squares plane formed by the remaining four atoms by 0.49 Å on the same side of C(5′) atom. While molecule B shows an unusual C(1′)-*exo* puckering with the C(1′) atom deviating by 0.37 Å on the opposite side of the C(5′) atom from the best plane. The conformation of the ribose moieties of molecules A and B of 5′-TU is C(3′)-*endo*, with the C(3′) atom displaced by 0.57 Å and 0.65 Å for A and B respectively from the planes constituted by the remaining four atoms on the same side of the the C(5′)-atom. It may be mentioned that C(2′) and C(3′) puckerings are commonly seen in nucleotides whereas the C(1′) puckering is observed very rarely in deoxynucleotides like 5′-dUMP Na_2 [17]

4.3. CONFORMATION ABOUT THE C(4′)—C(5′) BOND

The conformation about the C(4′)—C(5′) bond of both nucleoside molecules in all the 5′-TT structures is g^+ as seen from their torsion angles listed in Table II. In spite of the bulky trityl group covalently linked to the O(5′) atom the conformation is g^+ rather than g^- or t, where the trityl group will be turned away from the base reducing the steric hindrance between the trityl group and the thymine base. Contrastingly, the conformation of both 5′-TU molecules in the asymmetric unit is g^-.

4.4. CONFORMATION OF THE TRITYL GROUP

The torsion angles about the C(5′)—O(5′) bond for molecules A and B of 5′-TT are 172.3° and 171.2°, respectively, meaning that the trityl group is in the staggered form as in other trityl nucleoside structures [18]. Comparison of the torsion angles of both trityl groups shows that one of the rings is in a *trans* conformation while the other two are in *cis* conformations about the C(5′)—O(5′) bond. Also, the orientation of the phenyl rings of the trityl groups of molecules A and B are very nearly the same but their torsion angles differ by about 30°.

4.5. INCLUSION OF AROMATIC SOLVENTS BETWEEN 5′-TT MOLECULES

Interestingly, both the benzene molecules present in the asymmetric unit are situated at about 3.8 Å between a pair of 5′-TT molecules A and B related by a cell translation along the 011 direction, as illustrated in Figure 3. A similar feature is also displayed by both toluene molecules in the 5′-TTT structure as depicted in Figure 3. The stacking arrangement of planar molecules had been classified into four types namely face-to-face, offset face-to-face, edge-in-angle and T-stacking [19]. The stacking of benzene and toluene between 5′-TT molecules in the triclinic lattice corresponds to the offset face-to-face type. The distance between the base pairs in the 5′-TTB and 5′-TTT structures is 8.2 Å, which is about 1.2 Å more
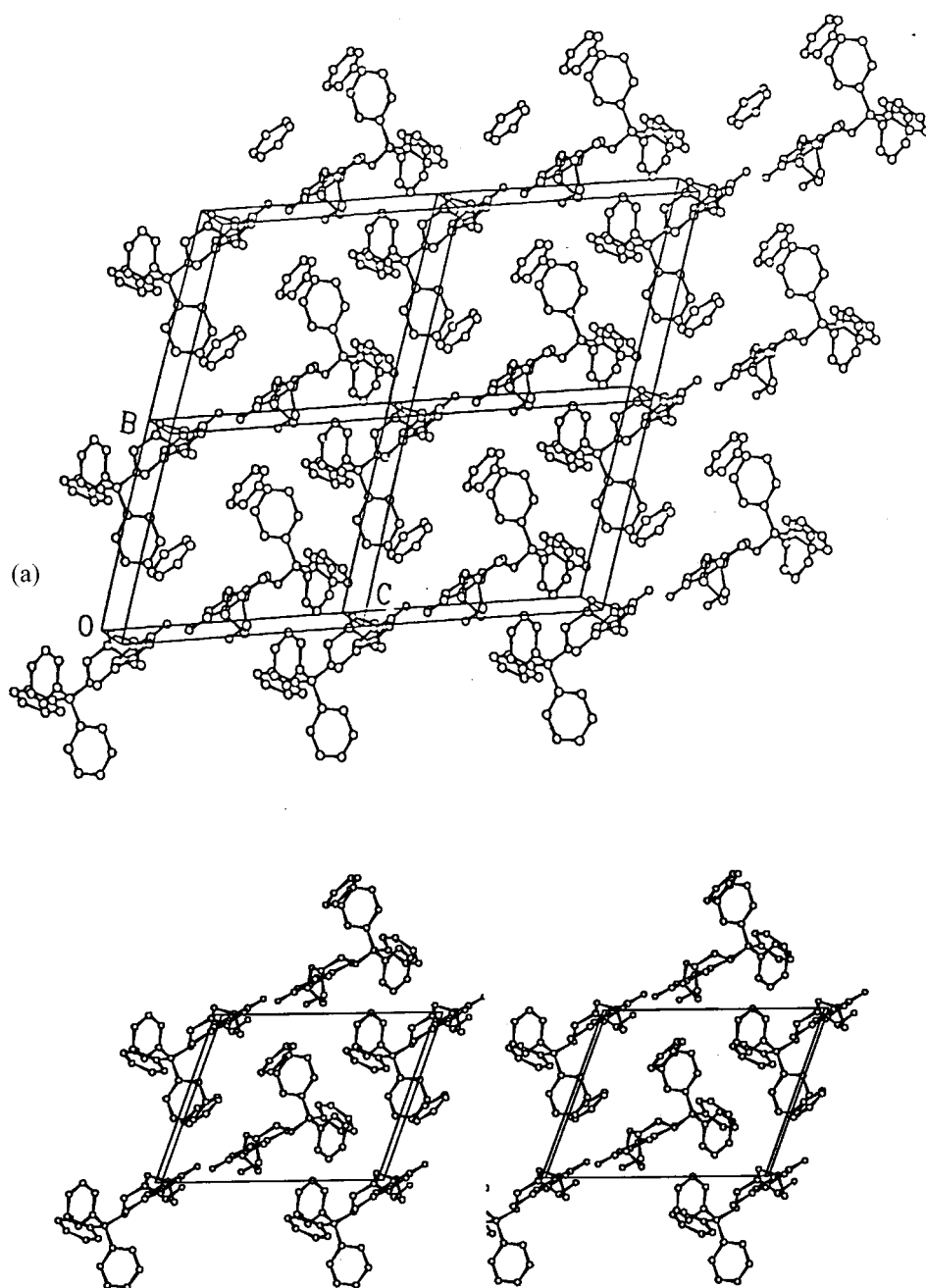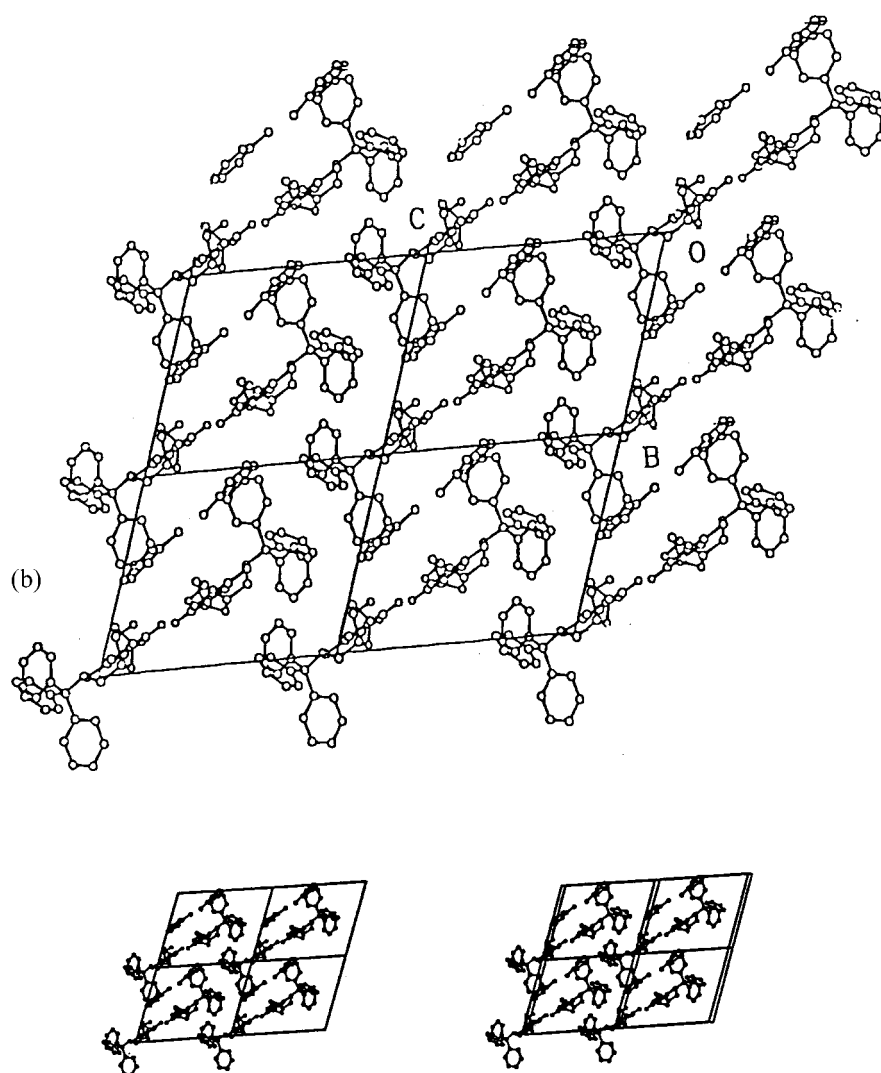
(a)

Figure 3.

Figure 3. An *a*-axis view of molecular packing in the triclinic lattice. (a) 5′-TTB; (b) 5′-TTT.

than that normally observed in intercalated drug–nucleic acid complexes. This type also resembles the pseudo intercalation of planar drug molecules between DNA base pairs [7, 8]. In addition, solvents like DMSO had been found to be located in the crystal lattice [20]. Besides this only a few drug complexes with nucleosides and nucleotides were reported earlier [21, 22]. Never before have nucleosides or nucleotides demonstrated the capability to form inclusion compounds in their crystal lattices. However, the ability of aromatic hydrocarbons to form inclusion compounds with organic hosts like cyclophane and ditritylurea is known [23-27]. Contrasting with benzene and toluene, guest molecules xylene, trimethylbenzene
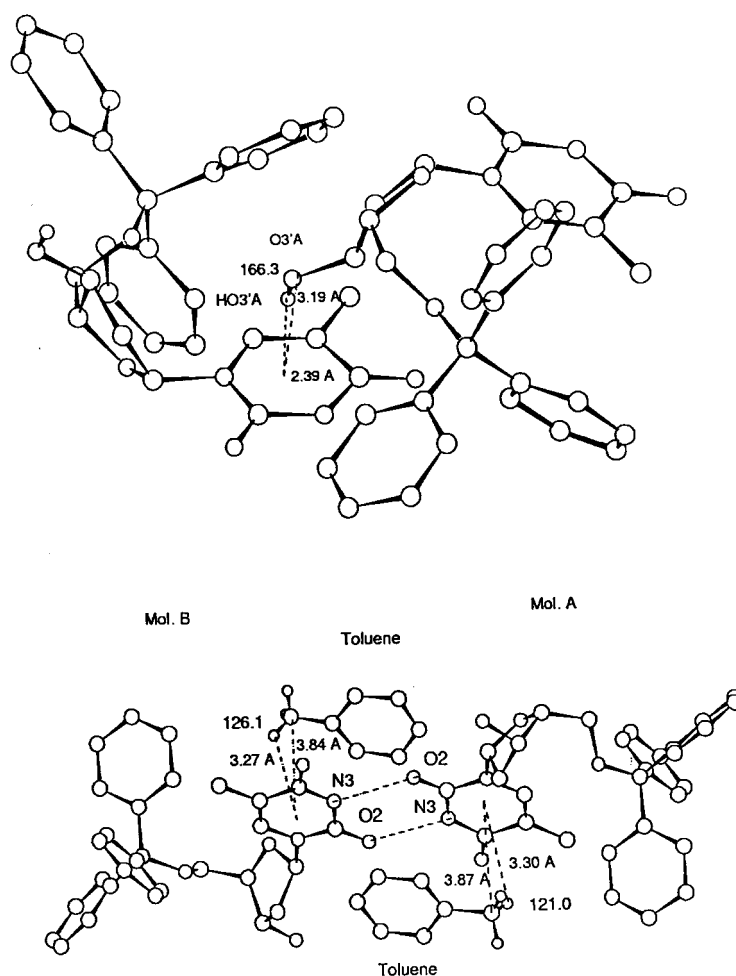
Figure 4. (Top) A figure illustrating the O—H· · · π interaction between O(3′A) and the thym-
ine base of the orthorhombic 5′-TT structures. (Bottom) Illustration of C—H· · · π interaction
between the methyl group of toluene and thymine base in the 5′-TTT structure.

and cyclohexane do not stack between T=T base pairs but are oriented at an angle
of about 70° in the orthorhombic lattice as shown in Figure 2. The distance between
the base pairs in these structures is 5.2 Å, significantly lower than that observed in
the 5′-TTB and 5′-TTT structures. This oblique orientation of xylene and trimethyl-
benzene with respect to the T=T base pairs could be due to the perturbation in the π
electron system of the aromatic rings due to the additional methyl groups present in
these molecules and non-planarity in the case of cyclohexane. None of these guest
molecules are involved in hydrogen bond interactions with the host molecules. In
significant contrast, 5′-TU does not accommodate guest molecules in its lattice.
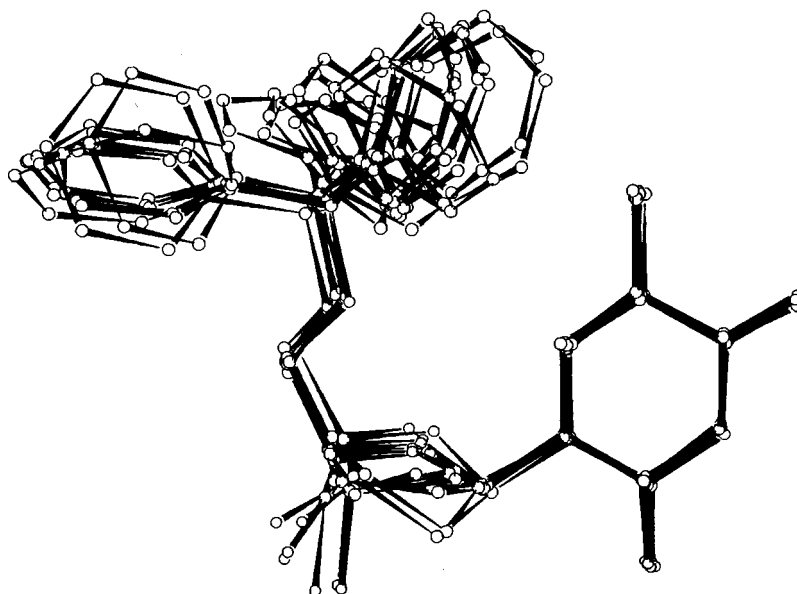
Figure 5. A superposition of 5′-TT molecules of all structures illustrating the conformational similarities of the base and furanose ring and variations in trityl group orientation.

4.6. HYDROGEN BONDING AND PACKING OF 5′-TT AND 5′-TU MOLECULES

Recently the combined theoretical and Cambridge crystallographic data base analysis of X—H$\cdots\pi$ interactions were reported by Melone et al. [28]. They have classified these interactions into six types based on their strength and geometry of approach. Remarkably, the 5′-TTT, 5′-TTB, 5′-TTCH and 5′-TTW structures demonstrate a strong O—H$\cdots\pi$ interaction between the ribose O(3′) and the thymine base as shown in Figure 4. The geometrical parameters of the interactions ($d_{\pi cH} = 2.39$ Å; $d_{\pi cO} = 3.19$ Å; $\theta = 78.4°$; $\alpha = 167.6°$; and $d = 0.48$ Å) are in agreement with the values of type I detected only in about 1.25% of the structures. It is rather surprising that it is only the host but not the guest molecules alone that participate in this interaction. In significant contrast to the orthorhombic structure, the triclinic 5′-TTT structure shows a C—H$\cdots\pi$ interaction between the methyl group of toluene and the thymine base. The geometrical parameters ($d_{\pi cH} = 3.30$, 3.27 Å; $d = 3.87, 3.84$ Å; $\theta = 72.8, 74.2°$; $\alpha = 121.0, 126.1°$; and $d = 0.98, 0.89$ Å) are in agreement with the values of type V reported to have been observed in 76.3% of the structures.

Hydrogen bond distances and angles in 5′-TTB and 5′-TTT are given in Table III. An a-axis view of the packing of 5′-TT molecules in the 5′-TTB and 5′-TTT structures is shown in Figure 3. The two 5′-TT molecules in the unit cell of the orthorhombic lattice are related by a pseudo-two-fold axis along the a axis. Also, 5′-TTB and 5′-TTT are isomorphous and a translation of 0.69, −0.69 and −0.57 Å along the a, b and c axes, respectively, of 5′-TTT gives the 5′-TTB coordinates.
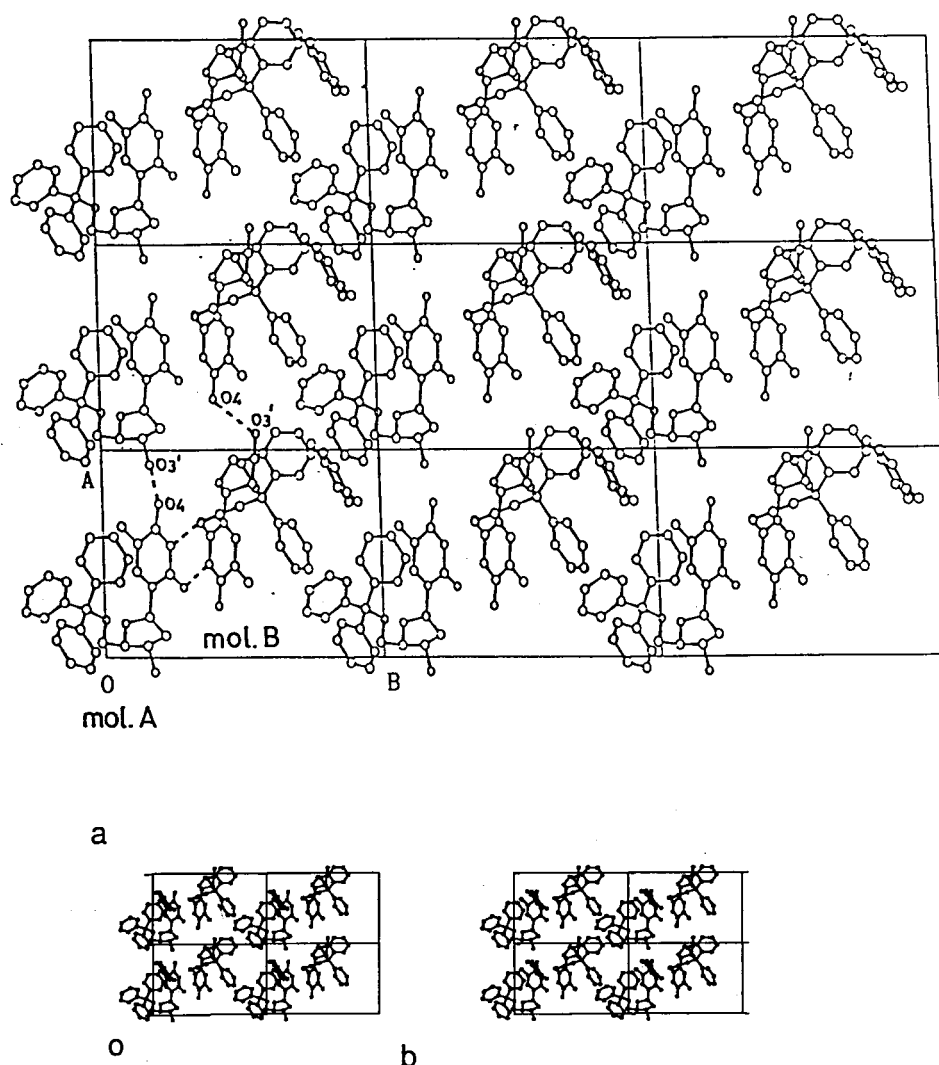
Figure 6. Packing of $5'$-TTX molecules in the orthorhombic lattice. Hydrogen bonds between the thymine bases and $O(3')$ and $O(4)$ atoms are shown in dotted lines.

A superposition of all $5'$-TT structures is shown in Figure 5, illustrating the degree of conformational similarity. It can be seen from Figure 3 that T=T base pairs are nearly perpendicular to the 011 plane. Trityl rings form columns along the b and c axes of the unit cell, respectively. Both phenyl rings B and C of molecule B form columns along the b-axis separated by a distance of 11.2 Å. Phenyl rings A and C of both molecules stacked along the 011 direction are oriented parallel to each other. All the dimers stack along the b-axis with solvent molecules between them as illustrated in Figure 3. The two crystallographically independent $5'$-TT molecules A and B in the asymmetric unit of the orthorhombic lattice are related
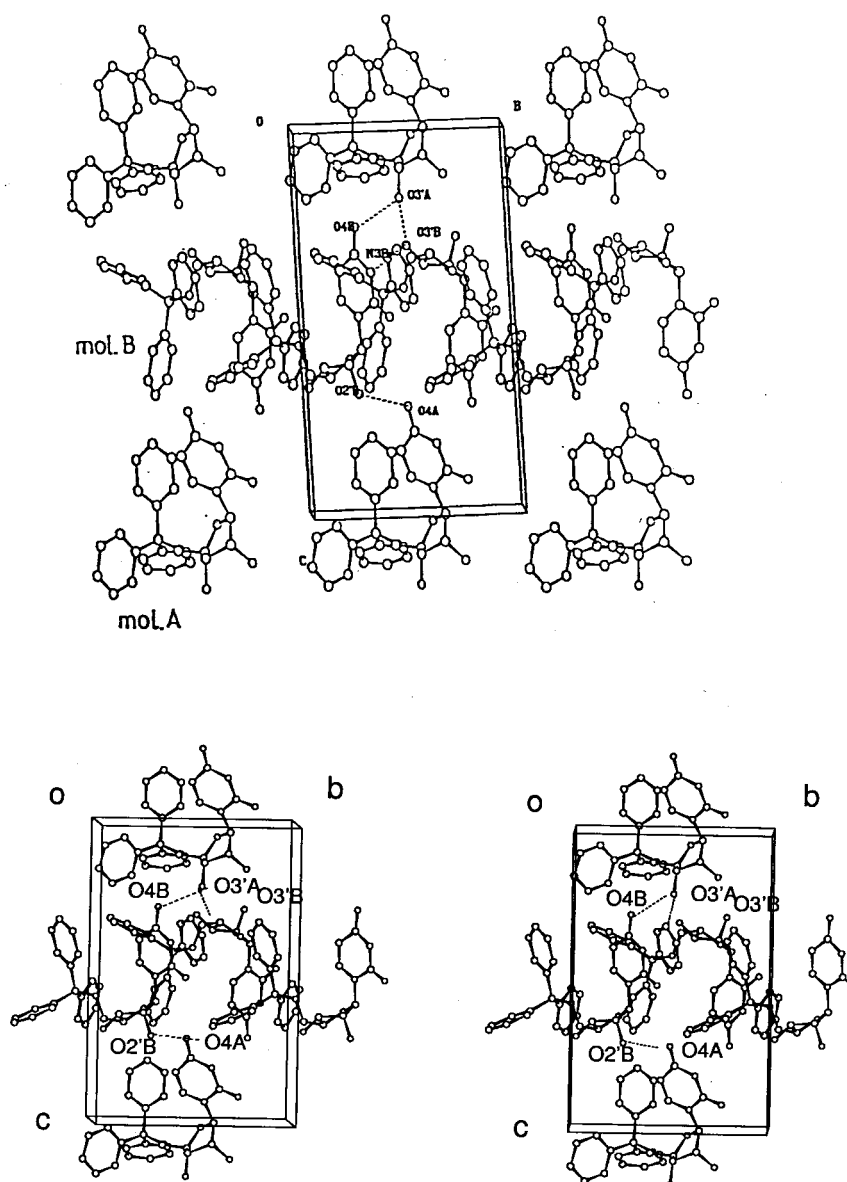
Figure 7. Packing of 5′ TU molecules viewed along the *a*-axis, showing the infinite chain formed by molecules A and B parallel to the *b*-axis which repeats along the *c*-axis.

by a pseudo-two fold axis approximately perpendicular to the bases. They form self pairs through a N(3)—O(2) hydrogen bond as in the 5′-TTB and 5′-TTT structures. They pack as columns along to the (110) direction as depicted in the *c*-axis view (Figure 6) of the molecular packing. Each guest molecule is surrounded by eight 5′-TT molecules which are symmetry related. They form a cavity of dimensions

Table III. Hydrogen bonds with distances (Å) and angles (°)

X—H···Y	X—H	X···Y	H···Y	X–H···Y (°)	Symm
5′-TTB:					
N3A—H3A···O2B	0.91	2.784(6)	1.87	177(5)	1
N3B—H3B···O2A	1.04	2.817(4)	1.79	170(4)	1
C6A—H6A···O5′A	0.97	3.442(5)	2.51	159(4)	1
5′-TTT:					
N3A—H3A···02B	1.01	2.802(5)	2.04	171(7)	1
N3B—H3B···02A	0.95	2.818(5)	1.87	171(5)	1
C6A—H6A···O5′A	1.02	3.444(4)	2.45	163(4)	1
5′-TTX:					
N3A—H3A···O2B	1.10	2.797(1)	1.77	149(10)	1
N3B—H3B···O2A	0.80	2.841(1)	2.06	165(7)	1
O3′A···O4A	–	2.892(7)	–	–	2
O3′B···O4B	–	2.867(9)	–	–	2
C6B—H6B···O5′B	0.95	3.372(5)	2.49	154(8)	1
5′-TU:					
C6B—H6B···O5′B	0.94	3.365(4)	2.48	154(3)	1
N3A—H3A···O4B	0.92	2.863(3)	2.08	151(5)	3
O2′B—HO2′B···O4A	1.01	2.799(3)	2.21	158(4)	4
N3B—H3B···O3′B	0.86	2.761(2)	1.91	165(4)	5
O3′B—HO3′B···O3′A	1.01	2.650(2)	1.98	172(4)	6

Symmetry codes: 1. x, y, z; 2. $x − 1, y, z$; 3. $−x, y + 0.5, −z$; 4. $x, y, z + 1$; 5. $−x, y + 0.5, −z + 1$; 6. $−x, y − 0.5, −z + 1$.

14.2, 7.2 and 5.4 Å. The stacking arrangement between the host and guest molecule corresponds to the edge-in-angle type [19]. Interestingly, all the five water molecules in the 5′-TT structures are located in the vicinity of the ring of the trityl moiety and are also situated very close to that of xylene etc. Besides, the water molecules do not form any hydrogen bond with the nucleoside molecules. They form hydrogen bonds only among themselves.

Hydrogen bond distances and angles of 5′-TU are listed in Table III. N(3) of A molecule A and B forms hydrogen bonds with O(4B) and O(3′B) respectively. Ribose hydroxyl oxygens O(2′) and O(3′) of molecule B form a pair of hydrogen bonds with O(4A) and O(3′A) respectively, thereby establishing contacts with molecule A. O(2) and O(2′) of molecule A are not involved in any hydrogen bond formation. A notable feature of the structure is the formation of bifurcated C—H···O hydrogen bonds between C(6) and O(4′) and O(5′) of molecule B while C(6) of molecule A forms a hydrogen bond with O(4′) but not with O(5′) because O(5′) is turned away from the C(6) atom. The two crystallographically independ-

ent molecules A and B of 5′-TU pack as infinite columns along the *b*-axis which repeats along the *c*-axis as shown in Figure 7.

Acknowledgements

References

1. T. D. Sakore, S. C. Jain, C. C. Tsai, and H. M. Sobell: *Proc. Nat. Acad. Sci., U.S.A.* **74**, 188 (1977).
2. T. D. Sakore, B. S. Reddy, and H. M. Sobell: *J. Mol. Biol.* **135**, 763 (1979).
3. S. C. Jain, C. C. Tsai, and H. M. Sobell: *J. Mol. Biol.* **114**, 317 (1977).
4. S. C. Jain, K. K. Bhandary, and H. M. Sobell: *J. Mol. Biol.* **135**, 813 (1979).
5. B. S. Reddy, T. P. Seshadri, T. D. Sakore, and H.. M. Sobell: *J. Mol. Biol.* **135**, 787 (1979).
6. S. Neidle, G. Taylor, and M. Sanderson: *Nucl. Acids Res.* **5**, 4417 (1978).
7. N. C. Seeman, R. O. Day, and A. Rich: *Nature* **253**, 324 (1975).
8. F. Takusagawa, M. Dabrow, S. Neidle, and H. M. Berman: *Nature* **296**, 466 (1982).
9. G. S. Padjyar and T. P. Seshadri: *Nucleosides Nucleotides* **15**, 857 (1996).
10. D. Prahadeeswaran and T. P. Seshadri: *Acta Crystallogr.* **C55**, 389 (1999).
11. G. M. Sheldrick: SHELXS-86, *A Program for Crystal Structure Determination*, University of Göttingen, Germany (1986).
12. G. M. Sheldrick: SHELXL-93, *A Program for Crystal Structure Refinement*, University of Göttingen, Germany (1994).
13. C. C. Wilson: *Nucl. Acids Res.* **15**, 8578 (1987).
14. A. Camerman, D. Mastropaolo, and N. Camerman: *Proc. Natl. Acad. Sci., U.S.A.* **84**, 8239 (1987).
15. G. I. Birnbaum, J. Gieziewicz, E. J. Gabe, T. S. Lin, and W. H. Prusoff: *Can. J. Chem.* **65**, 2135 (1987).
16. W. G. Bentrude, A. E. Sopchik, G. S. Bajwa, W. N. Setzer, and G. M. Sheldrick: *Acta Crystallogr.* **C42**, 1027 (1986).
17. M. A. Viswamitra, T. P. Seshadri, and M. L. Post: *Nature* **258**, 542 (1975).
18. M. A. Capron, W. L. McEldoon, N. C. Baenziger, and D. F. Wiemer: *Acta Crystallogr.* **C50**, 291 (1994).
19. C. Seel and F. Vögtle: *Angew. Chem. Int. Ed. Engl.* **31**, 528 (1992).
20. S. M. Sharmila, T. P Seshadri, and M. A. Viswamitra: *Acta Crystallogr.* **C441**, 138 (1988).
21. P. Swaminathan, E. Westhoff, and M. Sundaralingam: *Acta Crystallogr.* **B38**, 5157 (1982).
22. H. M. Sobell, S. C. Jain, T. D. Sakore, and C. E. Nordman: *Nature* **231**, 200 (11971).
23. K. Odashima, A. Itai, Y. Iitaka, and K. Koga: *J. Org. Chem.* **50**, 4478 (1985)
24. K. Odashima, A.Itai, Y. Iitaka, and K.Koga: *J. Am. Chem.Soc.* **102**, 2504 (1980).
25. H. Hart, L. W. Lin, and D. L. Ward: *J. Am. Chem. Soc.* **106**, 4043 (1984).
26. H. Hart, L. W. Lin, and D. L. Ward: *J. Chem. Soc. Chem. Commun.* 293 (1985).
27. I. Goldberg, L. W. Lin, and H. Hart: *J. Incl. Phenom.* **2**, 377 (1984).
28. J. F. Malone, C. M. Murray, M. H. Charlton, R. Docherty, and A. J. Lavery: *Chem. Soc., Faraday Trans.* **93**, 3429 (1997).