The Crystal and Molecular Structure of Tetrahydrofuranyluracil

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Crystals of the title compound, $C_8H_{10}N_2O_3$, are monoclinic, a = 11.554(5), b = 14.403(7), c = 5.092(3) Å, β = 100.64(4)° at 20 °C, space group $P^{2}{}_{1}/n$, Z = 4. Structure refined with least squares (1 507 reflections) at R 4.2%. The tetrahydrofuranyl ring has an *N*-conformation [C(3')*endo*–C(2')*exo*] with pseudorotation angle P 0.3° and $\phi_{max.}$ 37.3°. The uracil base has an *anti*-orientation (χ 15.4°) with respect to the five-membered ring. Two uracil rings at a distance of 3.37 Å, are perfectly stacked *via* a centre of symmetry.

THE *X*-ray study of the molecular structure of tetrahydrofuranyluracil (THFU) was undertaken in view of the conformational properties of THFU derivatives in solution described in the preceding paper.[1] Since THFU bears a structural resemblance to (deoxy)ribonucleosides this research is concomitant with our project on nucleic acid constituents.[2,3] The numbering of atoms of THFU is indicated in Figure 1. This notation differs slightly from the one given in the paper by Kruse *et al.*[1]

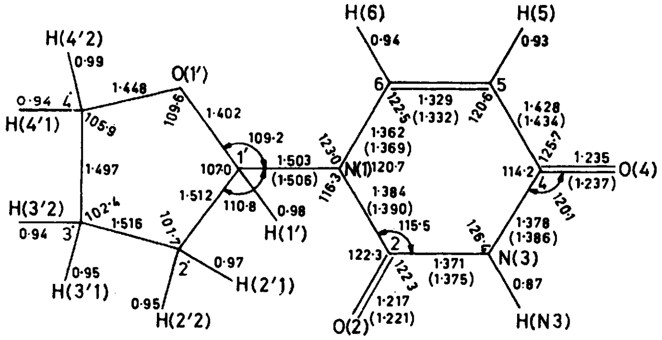

FIGURE 1 Numbering of atoms, intramolecular atomic distances, and valency angles of the molecule tetrahydrofuranyluracil. The numbers within parentheses refer to atomic distances corrected for rigid-body thermal motion.

Crystal Data.—$C_8H_{10}N_2O_3$, M = 182.2. Monoclinic, a = 11.554(5), b = 14.403(7), c = 5.092(3) Å, β = 100.64(4)° at 20 °C. Systematic absences ($h0l$ for $h + l$ odd and 0 k 0 for k odd) indicated space group $p^{2}{}_{1}/n$ (# 14). Assuming Z = 4 one obtains D_c 1.453 g cm^{-3}, confirmed by the analysis. Mo-K_α radiation, λ 0.710 69 Å, graphite monochromatized. Data collection on a three-circle diffractometer, using ω scan between θ 4 and 27.5°. The crystal with dimensions 0.55 × 0.51 × 0.28 mm was oriented along [1 0 0]. 3 738 Reflections were measured resulting in 1 909 symmetry-independent reflections. Discarding 330 reflections with $I < 2\sigma$ and 72 not observed ones a total of 1 507 reflections was available for the analysis. An absorption correction [μ(Mo-K_α) = 1.05 cm^{-1}] was not applied.

The structure was solved with direct methods using the program MULTAN [4] and refined with full-matrix least-squares to R 4.2 and R_w 4.3%. Details concerning the use of scattering, temperature, and reliability factors are mentioned elsewhere.[5] The heavy atoms were refined anisotropically, the hydrogen atoms isotropically with B values varying between 3.4 and 5.1 Å. The positional parameters and estimated standard deviations (e.s.d.s) of all atoms are given in Table 1. A list of structure factors as well as thermal parameters of the heavy atoms is deposited in Supplementary Publication No. SUP 22459 (7 pp).†

TABLE 1

Fractional parameters of tetrahydrofuranyluracil. Estimated standard deviations in units of the last digit are given in parentheses

	x	y	z
C(1')	0.029 03(14)	0.267 67(11)	0.224 9(3)
C(2')	0.041 10(14)	0.359 18(11)	0.373 1(4)
C(3')	−0.077 30(15)	0.404 00(12)	0.269 5(4)
C(4')	−0.103 24(16)	0.372 57(12)	−0.015 5(3)
C(2)	0.051 45(12)	0.157 19(10)	0.597 5(3)
C(4)	−0.111 55(13)	0.058 21(10)	0.676 9(3)
C(5)	−0.183 54(14)	0.103 98(12)	0.456 6(4)
C(6)	−0.138 13(13)	0.168 17(11)	0.317 9(3)
O(1')	−0.046 94(10)	0.282 87(8)	−0.019 6(2)
O(2)	0.152 73(9)	0.183 19(8)	0.666 4(2)
O(4)	−0.144 27(10)	−0.003 53(8)	0.814 8(2)
N(1)	−0.023 20(10)	0.194 93(8)	0.379 8(2)
N(3)	0.003 54(11)	0.088 59(8)	0.730 5(3)
H(1')	0.103 1(14)	0.240 5(10)	0.193(3)
H(2'1)	0.104 8(16)	0.392 4(12)	0.316(4)
H(2'2)	0.059 7(14)	0.347 8(11)	0.561(4)
H(3'1)	−0.075 4(16)	0.469 7(14)	0.284(4)
H(3'2)	−0.134 2(14)	0.381 6(11)	0.365(3)
H(4'1)	−0.068 8(17)	0.412 3(12)	−0.126(4)
H(4'2)	−0.188 0(16)	0.363 9(12)	−0.085(3)
H(N3)	0.050 0(14)	0.064 3(11)	0.866(3)
H(5)	−0.261 9(16)	0.084 6(11)	0.412(3)
H(6)	−0.182 0(14)	0.198 8(11)	0.170(4)

DISCUSSION

The average e.s.d.s (corrected for errors in cell constants) are 0.002_3, 0.001_9, 0.002, and 0.01_8 Å for C–C, C–O, C–N, and C–H bonds respectively. The e.s.d.s of valency and torsion angles not involving hydrogen are *ca.* 0.1°. The intramolecular bond distances and valency angles are given in Figure 1. The numbers in parentheses refer to bond lengths in the uracil moiety corrected for rigid-body thermal motion according to the method of Cruickshank.[6] The rigid-body model was calculated according to the method of Schomaker and Trueblood.[7] The rigid body was less satisfactory for the tetrahydrofuranyl moiety. Therefore, the rigid-body correction has been omitted for this part of the molecule. The numerical

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† For details of Supplementary Publications see Notice to Authors No. 7 in *J.C.S. Perkin II*, 1978, Index issue.

data concerning these calculations are also in SUP 22459.

TABLE 2

Selected torsion angles (°) of the tetrahydrofuranyluracil (D-form, or *R*-enantiomorph)

Notation	Designation	Angle (°)	Conformation
τ_0	C(4′)–O(1′)–C(1′)–C(2′)	11.6	*N*-type; ^2_3T
τ_1	O(1′)–C(1′)–C(2′)–C(3′)	−29.9	C(3′)*endo*–C(2′)*exo*
τ_2	C(1′)–C(2′)–C(3′)–C(4′)	35.9	*P* 0.3
τ_3	C(2′)–C(3′)–C(4′)–O(1′)	−30.2	$\phi_{\max.}$ 37.3°
τ_4	C(3′)–C(4′)–O(1′)–C(1′)	12.0	
χ	O(1′)–C(1′)–N(1)–C(6)	15.4	*anti*
	O(1′)–C(1′)–N(1)–C(2)	−166.3	
	C(2′)–C(1′)–N(1)–C(2)	76.1	
	C(3′)–C(2′)–C(1′)–N(1)	89.0	
	C(4′)–O(1′)–C(1′)–N(1)	−108.3	

The uracil moiety is slightly distorted and only planar within 0.04 Å. Comparison of the bond lengths in the uracil moiety (uncorrected for thermal motion) with average values tabulated by de Graaff *et al.*[3] shows a few interesting differences: the very large glycosidic bond C(1′)–N(1) (1.503 Å, average value 1.464 Å) and rather long carbonyl bonds C(2)–O(2) and C(4)–O(4) (1.217 and 1.235 Å; average value 1.208 and 1.223 Å). According to Lo *et al.*[8] there is a relationship between the *N*-glycosyl bond length and the value of the torsion angle N(1)–C(1′)–O(1′)–C(4′). Using their equation (2) we calculate the value 1.504 Å for the length of this bond.

The overall shape of the molecule (depicted in Figure 2) is almost planar. A number of torsion angles are given in Table 2. The furanoside ring is a nearly perfect half chair with a dyad running through O(1′) and the mid-point of bond C(2′)–C(3′). Using the notation of Altona and Sundaralingam[9] the angle of pseudorotation is *P* 0.3° and the maximum puckering angle is $\phi_{\max.}$ 37.3° for the D-form (*R*-enantiomorph). The conformation is of type *N* [C(3′)*endo*-C(2′)*exo*]. The orientation of the uracil ring with respect to the five-membered ring is *anti*(χ 15.4°).

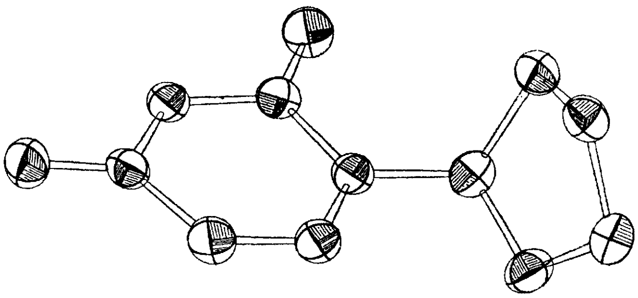

FIGURE 2 ORTEP projection of the molecule of tetrahydrofuranyluracil

Packing.—Figure 3 is an illustration of the crystal structure viewed in a projection along [0 0 1]. Two pyrimidine bases are nearly perfectly stacked *via* a crystallographic centre of symmetry at a mutual distance of 3.37 Å. Stacking of uracil molecules is rare. Apparently, in absence of solvating water or alcohol molecules base-stacking of uracil can be realised. The remaining interactions are hydrophobic. These contacts mainly consist of rather large H · · · H distances >2.56 Å. Each molecule THTU at *x,y,z* (I) is surrounded by 11 neighbours at $-\frac{1}{2}+x, -\frac{1}{2}-y, -\frac{1}{2}+z$ (II); $-\frac{1}{2}+x, -\frac{1}{2}-y, \frac{1}{2}+z$ (III); $-x, -1-y, -1-z$ (IV); $\frac{1}{2}+x, -\frac{1}{2}-y, -\frac{1}{2}+z$ (V); $-x, -1-y, -z$ (VI); $\frac{1}{2}+x, -\frac{1}{2}-y, \frac{1}{2}+z$ (VII); $x, y, -1+z$ (VIII); $-x, -y, -1-z$ (IX); $x, y, 1+z$ (X); $\frac{1}{2}-x, -\frac{1}{2}+y, -\frac{1}{2}-z$ (XI); and $\frac{1}{2}-x, \frac{1}{2}+y, -\frac{1}{2}-z$ (XII).

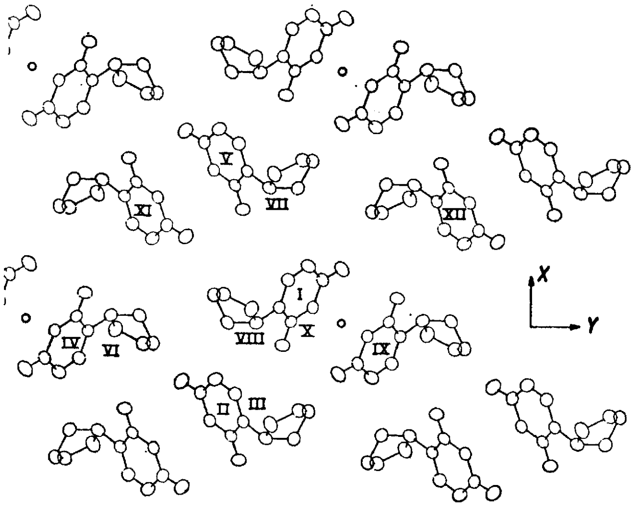

FIGURE 3 Crystal structure of THFU viewed in a projection along [0 0 1]

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