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# CRYSTAL AND MOLECULAR STRUCTURE OF 3'-O-ACETYL-2'-DEOXY-4-THIOTHYMIDINE

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#### 1. Introduction

When deoxy-4-thiothymidine-5'-triphosphate (ds  ${}^{4}$ TTP) was substituted for deoxythymidine-5'-triphosphate (dTTP) in the enzymatic synthesis of poly d (A-T) by DNA-polymerase the formation of poly d (A-s ${}^{4}$ T) could be demonstrated [1]. Poly d (A-s ${}^{4}$ T) was a poor primer for the synthesis of poly d (A-T) but did not serve as template if dTTP was replaced by ds ${}^{4}$ TTP. This different behaviour of poly d (A-s ${}^{4}$ T) and poly d (A-T) towards DNA-polymerase iniated a thorough investigation of the physical properties of deoxy-4-thiothymidine derivatives. In this paper the crystal and molecular structure of 3'-O-acetyl-2'-deoxy-4-thiothymidine is reported.

### 2. Materials and methods

Yellow prismatic crystals were obtained by slow evaporation of an aqueous solution of 3'-acetyl-4-thiothymidine. Space group and cell dimensions of these crystals were  $P2_12_12_1$  and a = 13.578 Å, b = 5.175 Å, c = 19.667 Å. The intensities of 1084 reflections were measured on a four circle diffractometer using Cu-radiation and corrected for geometrical factors but not for absorption. The structure was solved from a series of Patterson and Fourier syntheses and after several cycles of anisotropic least squares refinement a difference Fourier synthesis revealed the positions of all the hydrogen atoms. The final *R*-factor was 5.4%.

### 3. Results and discussion

In the figure, bond distances and angles within the molecule are given.

The geometrical data of the heterocycles are in reasonable agreement with the values found for 1methylthymine [2] and Ca thymdidilate [3]. The bonds C5-C6, C2-O2 and C-S of 1.333 Å, 1.211 Å and 1.673 Å length have double bond character. The arrangement of the atoms and substituents of the pyrimidine ring system is essentially planar except atom Cl', which is displaced by 0.124 Å from the plane.

The five membered deoxy-ribose ring is puckered with C2' endo (envelope form): C2' is 0.526 Å away from the best four atom plane. All the angles, dihedral angles and distances compare well with the corresponding values published for 5-fluoro-2'-deoxy- $\beta$ -uridine [4] except the bond length C3'-C4' which is increased by 0.05 Å. The conformation about the C4'-C5' and the C3'-O3' bond is gauche. The acetyl group is lying in a plane almost perpendicular to the deoxyribose ring.

The heterocycle of a nucleoside can take two preferred conformations with respect to the sugar moiety which are called syn and anti [5] depending upon the position of the oxygen atom O2 relative to the ribose, i.e. upon  $\tau_{\rm CN}$ , the dihedral angle C2'-C1'-N1-C6 [6]. In the syn conformation O2 is above or near the sugar residue and  $\tau_{\rm CN}$  is O to 180° whereas is the anti conformation O2 is away from the ribose and  $\tau_{\rm CN}$  is to -180°. In 3'-acetyl-4-thiothymidine CN is -63.7°, i.e. its conformation is anti.

This result is striking. 4-Thiouridine, an analogous molecule, crystallizes in syn conformation [7],  $\tau_{CN} = 139^{\circ}$ , but could be shown by NMR and ORD studies

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to exist in *anti* conformation [8] in aqueous solution. The reason for this conformational change of 4-thiouridine could be found in its peculiar crystal structure.

The 3'-acetyl-4-thiothymidine molecules are stacked along the crystallographic *b*-axis, the heterocycle being parallel to each other in a distance of 3.68 Å and tilted about 44.7° against the *b*-axis. The molecules are of hydrophobic character and there is only one hydrogen bond of 3.227 Å length from the sulfur to the O5'oxygen atom.

The molecules of 4-thiouridine are also arranged in stacks but the heterocycles are perpendicular to a crystallographic axis and 3.4 Å apart. They constitute a linear hydrophobic channel whereas the ribose moieties together with 1.5 molecules of water of hydration per nucleoside unit build up a hydrophilic channel.

The differences in the structures of 3'-acetyl-4-thiothymidine and 4-thioridine are *anti* conformation and hydrophobic character of the molecules for the first and *syn* conformation and the arrangement of hydrophobic-hydrophilic channels for the second structure. One could suspect that the conformational change from *anti* to *syn* depends upon the development of a hydrophobic-hydrophilic structure but we feel that some more data are needed to support that idea.

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