Crystal and Molecular Structure of 1,7-Dimethylguanosine Iodide

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Summary The prominent feature of the packing arrangement in 1,7-dimethylguanosine iodine is the sandwiching of the iodine atom by the bases.

METHYLATED nucleosides have been isolated from a variety of DNAs and RNAs. Their presence appears to impart special characteristics to the nucleic acids in which they are present and in all probability makes them species specific (for a review, see ref. 1).[1] In order to assess the effects of alkylation on the secondary structure of the nucleic acids, *X*-ray studies on the alkylated nucleosides and the nucleotides should be quite helpful. Here we report the crystal structure of the "modified" nucleoside 1,7-dimethylguanosine iodide (DMGI).

Orthorhombic crystals of DMGI, $C_{12}H_{18}N_5O_5I$, were obtained from aqueous solution by evaporation. The crystal data are: space group $P2_12_12_1$, $a = 7{\cdot}277(1)$, $b = 12{\cdot}553(2)$, and $c = 17{\cdot}282(2)$ Å, $Z = 4$, $D_c = 1{\cdot}847$ g cm^{-3}. Intensities (2θ 0—120° gave 1738 unique reflections of which 1692 were observable) were measured on a GE XRD-6 diffractomer by the stationary-crystal stationary-counter method using filtered Cu-K_α radiation. The structure was solved by Patterson and Fourier methods, and refined by block diagonal least-squares. The present R index, is 15%. Though the accuracy of the structure is relatively low (e.s.d.s. are 0·02 Å and 1° in bond lengths and angles respectively), the conformation and the packing of the molecules are felt to be noteworthy.

The bond distances and the angles of DMGI are quite similar to those found for *NN*-dimethylguanosine (DMG)[2] and guanosine dihydrate, forms A (GA) and B (GB)[3] with a few expected exceptions. The internal angles at N(1) and N(7) are significantly larger in DMGI, as a result of the extra-annular methyl groups on these atoms. Such differences have been noted in other purine and pyridine bases.[4–6]

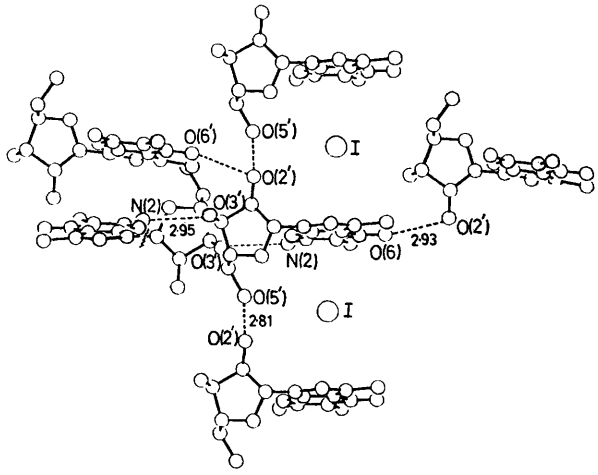

FIGURE 1. The packing arrangements in 1,7-dimethylguanosine iodide.

The torsion angle χ_{CN} about the glycosidic bond[7] is $-112°$, corresponding to the *syn*-conformation of the base in relation to the sugar. A similar value of this torsion angle was found for DMG ($-104°$).

The conformational resemblance between DMGI and DMG is also observed in the sugar residue. The furanose ring in both structures exhibits a puckering with C(2) *endo* and C(3) *exo*. The torsion angles[7,8] describing the sugar are as follows: τ [C(1)–O(1)'] $-13°$, τ [C(1)'–C(2)'] 30°, τ [C(2)–C(3)'] $-37°$, τ [C(3)–C(4)'] 31°, τ [C(4)–O(1)] $-12°$, ϕ_{oo} 49° (g) and ϕ_{oc} 165° (τ).

The principal features of the packing arrangement are shown in Figures 1 and 2. The intermolecular contacts which have all the characteristics of hydrogen bonding are: O(2)'–(H) · · · O(6), O(5)'–(H) · · · O(2)', N(2)–(H) · · · O(3)', and N(2)–(H) · · · I. There appears to be no intramolecular and inter-base contacts which can be interpreted as hydrogen bonds.

The bases of DMGI are arranged almost perpendicular to the *a* axis of the crystal; the normals to their planes make a 9° angle with the axis. The separation between the base planes is 7·17 Å. An iodide atom lies approximately midway between these purine rings; "sandwiched" between them. The closest intermolecular contact of the iodine [aside from the N(2) hydrogen bond] are with the atoms comprising the imidazole portion of a "sandwiching" base. Some of these contacts are shorter than normal van der Waals contacts. The increased charge density in the imidazole ring resulting from N(7) methylation is no doubt responsible for the observed "sandwiched" effect. Somewhat analogous type base–halogen interactions have been observed in the structures of guanosine hydrobromide[9] and 5'-methylammonium-5' deoxyadenosine iodide monohydrate.[10]

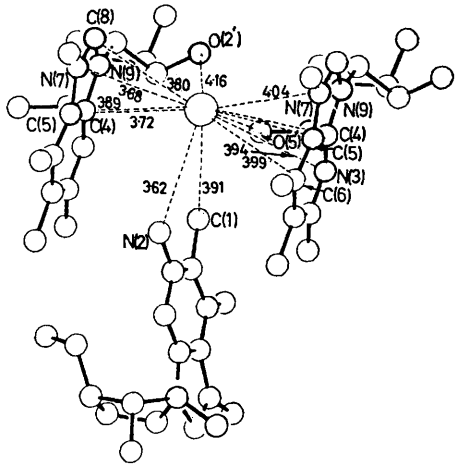

FIGURE 2. The arrangement of atoms round the iodine atom in 1,7-dimethylguanosine iodide, distances in Å; O(5)' · · · I 3·75; C(4) · · · I 3·64; C(5) · · · I 3·68; C(9) · · · I 3·95.

Parallel stacking of purine bases is a dominant force behind the stabilization of the nucleic acid structure.[11] A dramatic effect on the secondary structure can be brought about by alkylation of the N(7) position of guanosine as shown by the present findings. The ability of many agents some being anticancer and others mutagenic, to alkylate at this site has been demonstrated in a number of studies.[12]

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