X-RAY ANALYSIS OF MONOSODIUM CYTIDINE-5′-DIPHOSPHOETHANOLAMINE: $C_{11}H_{19}N_4O_{11}P_2Na.7H_2O$

We report here the molecular structure of monosodium salt of cytidine-5′-diphosphoethanolamine (CDP-ethanolamine) (Fig. 1) as determined from a three-dimensional single crystal X-ray analysis. CDP-derivatives play an important role in phospholipid metabolism. CDP ethanolamine, in particular, takes part in the biosynthesis of cephalin. The present study is in continuation of our X-ray analysis of nucleotide coenzymes (Viswamitra *et al.*[1]; Viswamitra *et al.*[2]).

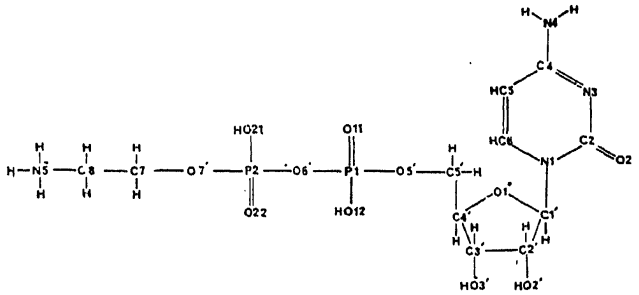

FIG. 1. Atom numbering scheme for CDP-ethanolamine molecule.

The monosodium salt of CDP ethanolamine (obtained from Boehringer Mannheim) is readily soluble in water giving neutral solution. Needle-shaped crystals of the compound were obtained from water-acetone solutions as in the case of nucleotide coenzymes[1, 2]. The crystal data were initially obtained from X-ray photographs and later refined on a Kappa-axis CAD-4 diffractometer.

$a = 6{\cdot}946$ Å, $b = 12{\cdot}503$ Å, $c = 28{\cdot}264$ Å,
$Z = 4$, $D_m = 1{\cdot}61$ gcm^{-3}, $D_{cal} = 1{\cdot}61$ gcm^{-3},
Space group: $P2_12_12_1$, $\lambda = 1{\cdot}5418$ Å.

The crystal (size $1{\cdot}95 \times 0{\cdot}15 \times 0{\cdot}025$ mm^3) mounted inside a Lindemann glass capillary along with a trace of mother-liquor was used for intensity data collection on the diffractometer. The reflections, 1454 in number, were retained as the observed ones out of a total of 2070 on the criterion that $I > 1{\cdot}5\sigma(I)$.

Structure Solution and Refinement

The structure was solved by direct methods using MULTAN (Main *et al.*[3]) followed by difference Fourier syntheses. Positional and the anisotropic thermal parameters were refined using structure factors least square techniques. The final R-factor for 1454 reflections was 10·4%.

Comments

The orientation of the base about the glycosidic N1–C1′ linkage is *anti* (C6–N1–C1′–O1′ = 62·8°). The ribose exhibits the uncommon C1′ *exo*–C2′ *endo* conformation. About the exocyclic C4′–C5′ and C5′–O5′ bonds the molecule has the usual *gauche*–*gauche* and *trans* conformations respectively (O1′–C4′–C5′–O5′ = − 66·3°, C3′–C4′–C5′–O5′ = 55·6°, C4′–C5′–O5′–P1 = 175·7°). The pyrophosphate has the characteristic staggered conformation (Fig. 2).

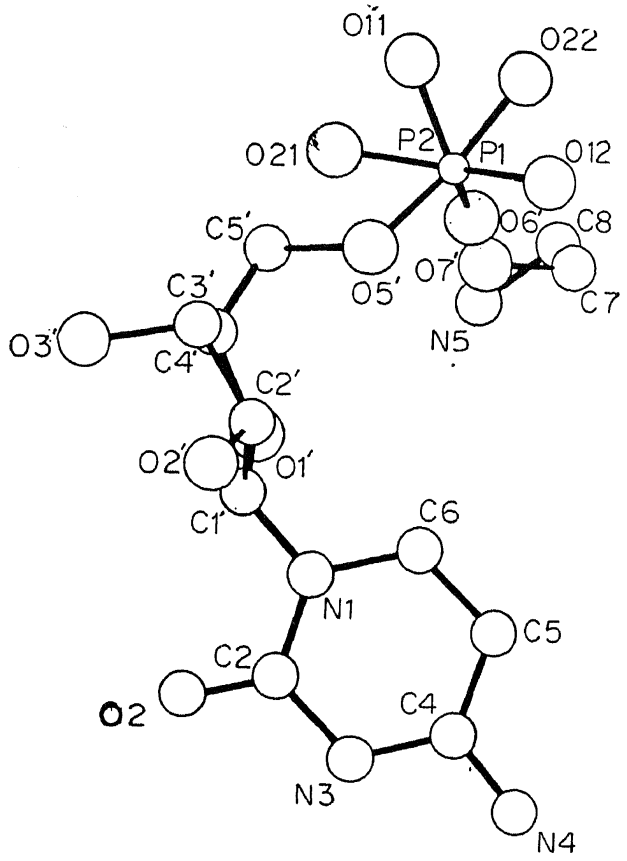

FIG. 2. View of the molecule down P1–P2 vector.

The bond lengths of the bridging oxygen O6′ to the two phosphorus atoms are different: P1–O6′ = 1·59 Å (0·01), P2–O6′ = 1·62 Å (0·01). Most of the torsion angles are similar to those of CDP–choline[1]. However, the torsion angle about P2–O7′ bond (− 102·7°) is significantly different from the corresponding angle in CDP–choline (71·3°) and this brings about a slightly extended structure for the former as compared to the highly folded one in the latter (Fig. 3). The intramolecular non-bonded N5···O7′ distance is 2·74 Å as a result of the *gauche* conformation about the C7–C8 bond (O7′–C7–C8–N5 = − 54·3°). The Na^+ ion is coordinated by five ligands from three indepedent CDP-ethanolamine molecules and does not link the base and the phosphate chain of the same molecule (Fig. 4). The distances of these ligands from Na^+ range from 2·20 Å to 2·45 Å. In the extended crystal structure the bases are not stacked. Three water molecules per nucleotide coenzyme have been presently identified. In the extended crystal structure the water molecules link up the phosphate and ethanolamine of the neighbouring molecules related by a 2_1-screw axis through hydrogen bonds. Details of the study will be published elsewhere.