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Nucleosides, Nucleotides and Nucleic Acids

Publication details, including instructions for authors and subscription information: http://www.informaworld.com/smpp/title~content=t713597286

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Vivian Cody^a; Thomas I. Kalman^b

^a Medical Foundation of Buffalo, Inc., New York, Buffalo ^b Department of Medicinal Chemistry, School of Pharmacy, State University of New York at Buffalo, New York, Amherst

To cite this Article Cody, Vivian and Kalman, Thomas I.(1992) 'Conformation Analysis of Two Anti-HIV Nucleoside Analogues 2',3'-Dideoxy-3'-fluorocytidine and Its N⁴-Dimethylaminomethylene Prodrug Derivative', Nucleosides, Nucleotides and Nucleic Acids, 11: 2, 731 - 738

To link to this Article: DOI: 10.1080/07328319208021737 URL: http://dx.doi.org/10.1080/07328319208021737

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CONFORMATIONAL ANALYSIS OF TWO ANTI-HIV NUCLEOSIDE ANALOGUES 2',3'-DIDEOXY-3'-FLUOROCYTIDINE AND ITS N4-DIMETHYLAMINOMETHYLENE PRODRUG DERIVATIVE#

Vivian Cody* and Thomas I. Kalman+

*Medical Foundation of Buffalo, Inc., 73 High Street, Buffalo, New York 14203

*Department of Medicinal Chemistry, School of Pharmacy, State University of New York at Buffalo, Amherst, New York 14260

ABSTRACT. Crystal structure analysis of 2',3'-dideoxy-3'-fluorocytidine (1) and its prodrug derivative, N^4 -dimethylaminomethylene-2',3'-dideoxy-3'-fluorocytidine (2), active anti-HIV nucleoside analogues, reveals that both structures adopt an anti conformation about the glycosyl bond. The furanose ring is C2'-endo for (2) and C2'-endo/C1'-exo and C2'-endo/C3'-exo for the two independent molecules of (1), respectively.

A prototype anti-HIV prodrug, \underline{N}^4 -dimethylaminomethylene-2',3'-dide-oxy-3'-fluorocytidine (NSC-614989), was designed and synthesized, as a representative of one of a rationally selected series^{1,2}. The introduction of a proper substituent at the exocyclic NH_2 group of the parent deoxycytidine analogue (3'-F-ddC, $C_9H_{12}N_3O_3F$,1) lead to an increase in lipophilicity³ of the resulting \underline{N}^4 -dimethylaminomethylene-2',3'-dideoxy-3'-fluorocytidine (DDFC, $C_{13}H_{16}N402F$,2). The kinetics of the spontaneous hydrolysis of the side chain was determined and a feasible mechanism involving two distinct intermediates was established³. In the CEM cell line, complete protection against HIV was achieved by 6 μ M 2, without any cytotoxicity up to 200 μ M, the highest concentration tested. Protection of CEM cells from HIV mirrored the lowering and elimination of p24 antigen levels¹⁻³. Prodrug 2 and its congeners represent an active, non-cyctotoxic series having real therapeutic potential. Due to

^{*}Dedicated to the memory of Prof. Tohru Ueda

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TABLE 1. Crystal data for 2',3'-dideoxy-3'-fluorocytidine (1) and \underline{N}^4 -dimethylaminomethylene-2',3'-dideoxy-3'-fluorocytidine (2).

Molecular Formula Molecular Weight Crystal System Space group Cell Dimensions	(1) C ₉ H ₁₂ N ₃ O ₃ F 229.22 Triclinic P1	(2) C ₁₃ H ₁₆ N402F 279.30 Orthorhombic P2 ₁ 2 ₁ 2 ₁
a (Å) b c α(°) β	6.973(1) 7.315(1) 10.5987(1) 95.15(1) 107.84(1) 104.38(1)	10.453(1) 14.865(2) 8.6967(6) 90.0 90.0 90.0
Z V(ų) D _c (Mg/mm³) Crystal Size (mm) Radiation (Å) μ(cm⁻¹)	2 490.3(1) 1.55 0.2x0.4x0.5 0.71069 1.23	4 1351.29(2) 1.37 0.3x0.5x0.6 0.71069 0.98
T(K) R (%) wR hkl range reflections	3.1 3.4 -1 <h<10,-10<k<10 -14<1<14 2239</h<10,-10<k<10 	294 5.6 5.2 -1 <h<15,-1<k<21 -1<l<13="" 2020<="" td=""></h<15,-1<k<21>
Est. unit wt Max Δ/σ Δ/ρ_{max} (eÅ ⁻³) Δ/ρ_{min} (eÅ ⁻³)	0.367 0.00 0.24 20	0.669 0.00 0.48

its novel structural features, this class of compounds may show a favorable pharmacokinetic profile, including efficient penetration into the central nervous system, warranting its further study and <u>in vivo</u> evaluation.

X-ray crystallographic analysis was carried out on DDFC 2 and its parent compound 1. The results showed that the N^4 -side chain of 2 is coplanar with the pyrimidine ring; the glycosyl bond is anti, as preferred for pyrimidine nucleosides, and the furanose ring is C2-endo/C1' (3')-exo and C2'-endo for molecules 1 and 2, respectively.

MATERIALS AND METHODS

Samples of 1⁴ were converted to 2 employing a previously published procedure⁵ and recrystallized from aqueous ethanol. Crystal data for these compounds are listed in TABLE 1. Accurate cell dimensions were

TABLE 2. Atomic coordinates (X10⁴) and isotropic thermal parameters (Å²X10²) for 2',3'-Dideoxy-3'-fluorocytidine (1). Biso = $8/3\Pi^2$ $\Sigma_i\Sigma_j$ U_{ij} $a\star_i a\star_j$ a_ia_j

ATTOM	V/// ~\	Υ/Β(σ)	Z/C(σ)	BIS0*(σ)
ATOM	X/A(σ) 15272	20347	-3031	139(6)
N(1)				
C(2)	14804(5)	21798(5)	-3733(3)	1 . 1
N(3)	16095(5)	22657(5)	-4363(3)	1
C(4)	17830(5)	22129(5)	-4309(3)	*
C(5)	18308(6)	20609(5)	-3630(4)	• •
C(6)	16989(5)	19744(5)	-3024(4)	,
C(1')	13808(5)	19399(5)	-2[B8(4)	, ,
C(2')	12308(6)	17482(5)	-3201(4)	· _ ·
C(3')	11656(6)	16595(5)	-2113(4)	
0(1')	14982(5)	18971(4)	-1151(3)	
F(3')	10147(4)	17430(4)	-1869(3)	, ,
C(4'1)	14862(6)	15828(5)	-559(4)	• •
0(4'2)	15616(5)	15317(5)	-1601(3)	• • •
0(2)	13202(5)	22293(4)	-3732(3)	197(6)
N(4)	19077(5)	23052(5)	-4915(3)	163(7)
N(1*)	8964(5)	9073(4)	2874(3)	132(6)
C(2*)	9372(6)	7481(5)	3431(3)) 130(7)
N(3*)	7930(5)	6384(5)	3875(3)	137(6)
C(4*)	6090(5)	6774(5)	3721(3)	130(7)
C(5*)	5562(5)	8265(5)	3032(3)	147(7)
C(6*)	7036(5)	9389(5)	2643(3)) 145(7)
C(1'*)	10584(5)	10270(5)	2438(4)	147(7)
C(2'*)	10332(6)	9599(5)	972(4)) 171(8)
C(3'*)	11361(6)	11459(5)	602(4	185(8)
C(4/*)	10806(6)	12963(5)	1395(4)	
0(1/*)	10388(5)	12159(4)	2513(3	
F(3'*)	13573(5)	11793(4)	1081(3	
C(4'1*)	8853(6)	13443(5)	572(4	• • •
0(4'2*)	9444(5)	14508(5)	-381(3	
0(2*)	11057(4)	7155(4)	3502(3	, , ,
N(4*)	4760(5)	5722(5)	4223(3	` _ '
· · /	,		,	,,

*Molecule B

calculated from the least-squares analysis of 25 reflections for each crystal. Data were collected on a Nicolet P3V diffractometer using MoK a radiation. Both crystals were stable and showed no deterioration upon radiation. The data were corrected for Lorentz and polarization, but not for extinction or absorption effects. Both structures were solved by use of direct methods procedures using the programs MULTAN786 and NQEST7. Parameters were refined by full matrix least-squares techniques using anisotropic thermal parameters for the non-hydrogen atoms. Hydrogen atom positions were located in difference Fourier syntheses and refined isotropically. Atomic scattering factors were taken from the In-

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TABLE 3. Atomic coordinates (X10⁴) and isotropic thermal parameters (A²X10) for N^4 -Dimethylaminomethylene-2',3'-dideoxy-3'-fluorocytidine (2) Biso = $8/3 \pi^2 \Sigma_i \Sigma_j U_{ij} a *_i a *_j a_i a_j$

ATOM	X/A(σ)	Y/B(σ)	Z/C(σ)	BISO(σ)
N(1)	-597(3)	7906(2)	-2068(3)	30(1)
C(2)	183(4)	8572(2)	-1463(4)	33(1)
N(3)	-39(3)	8878(2)	-26(3)	32(1)
C(4)	-949(3)	8494(2)	840(4)	28(1)
C(5)	-1707(4)	7777(2)	286(4)	35(1)
C(6)	-1514(4)	7507(2)	-1195(4)	34(1)
C(1')	-367(3)	7620(2)	-3668(4)	31(1)
C(2')	540(4)	6822(2)	-3781(4)	35(1)
C(3')	49(3)	6327(3)	-5177(4)	37(1)
C(4')	-1370(3)	6555(2)	-5250(4)	30(1)
0(1')	-1543(2)	7346(2)	-4301(3)	34(1)
C(5')	-2237(4)	5818(2)	-4694(4)	35(1)
0(5′)	-1945(3)	5563(2)	-3149(3)	41(1)
F(3')	658(3)	6661(2)	-6491(3)	63(1)
0(2)	1077(3)	8869(2)	-2267(3)	50(1)
N(4)	-1230(3)	8815(2)	2283(3)	31(1)
C(41)	-438(3)	9423(2)	2827(4)	31(1)
N(42)	-681(3)	9867(2)	4116(3)	34(1)
C(421)	157(4)	10597(3)	4614(4)	42(1)
C(422)	-1859(4)	9706(3)	4976(5)	54(1)

ternational Tables for X-ray Crystallography⁸. All computations were performed on a VAX 8600 computer using the Nonius least-squares package. Positional parameters and isotropic thermal parameters for both structures⁹ are listed in TABLES 2 and 3.

RESULTS AND DISCUSSION

The molecular conformation and geometry of 1 and 2 are illustrated in FIG. 1 and 2, respectively, and their conformational parameters are defined in TABLE 4. These data show that the conformation in the two independent molecules of 1, and in 2, adopt an <u>anti</u> conformation, as usually observed in other pyrimidine nucleoside structures. The pucker of the furanose ring is defined by the pseudorotation parameter P and the degree of ring flattening¹³, ν_m . Although the values of ν_m normally cluster near 40°, that of 2 is significantly smaller, indicating a more flattened ring than in the two independent molecules of the parent nucleoside 1. The furanose ring is twist, C2'-endo/C1' or C3'-exo in 1 and C2'-endo in 2. The pseudorotation parameter P in these three mole-

FIG 1. Molecular conformation of 1 and 2 with their numbering schemes.

cules is in general agreement with the other nucleosides with anti-HIV activity^{14,15}. The conformation of the 5'-hydroxy oxygen is +sc with respect to the furanose ring in 1A and 2, and -sc in 1B.

Comparison of these structures with other related nucleosides (TABLE 4) reveals their overall conformational similarity. The orientation of the \underline{N}^4 -dimethylaminomethylene in 2 is $\underline{\text{cis}}$ to the cytosine N(3) as was also observed in the structure of \underline{N}^4 -aminocytidine, another \underline{N}^4 -substituted nucleoside (10). The conformation of ddC (11), which lacks 3'-F substitutent, is very different from those of 1 and 2. While the conformations of 1 and 2 are similar to one of the AZT conformers (12), the other is significantly different.

The hydrogen bonding pattern of molecule 1 is described in TABLE 5 and shows that all functional groups participate in a two dimensional network of hydrogen bond interactions, typical of nucleosides. In mole-

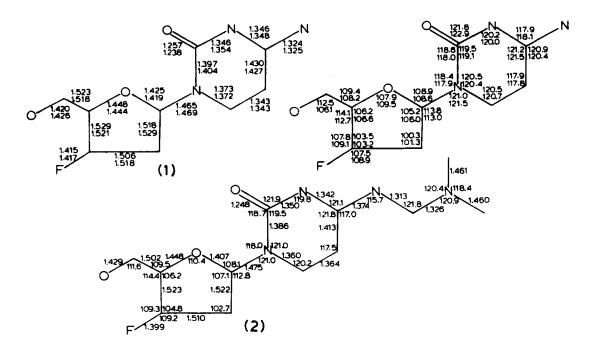


FIG. 2. Bond lengths and bond angles for 1 and 2, respectively. The two sets of values on 1 refer to molecule A and B respectively.

TABLE 4. Conformational comparison of some related pyrimidine nucleo-side analogues.

MOLECULE	N1-C1'A	Х°	Y°	v_m°	P°	Pucker	Ref
3'FddC 1A	1.465	-143.8	63.1	40	153	C2'-endo/C1'-exo	
1B	1.469	-153.1	-71.6	32	164	C2'-endo/C3'-exo	
DDFC (2)	1.475	-149.5	57.3	29	160	C2'-endo	
NH ₂ -Cyd A	1.490	-149.0	50.6	32	177	C2'-endo	(10)
В	1.477	-135.8	53.3	39	176	C2'-endo	(10)
ddC	1.485	-156.9	164.3	34	208	C3'-exo/C4'-endo	(11)
AZT(A)	1.460	-124.4	50.9	32	175	C2'-endo/C3'-exo	(12)
AZT(B)	1.502	-173.6	173.4	36	215	C3'-exo/C4'-endo	(12)

AZT-3'-azido-2',3'-dideoxythymidine; ddC, 2'-3'-dideoxycytidine; NH₂-Cyd, \underline{N}^4 -aminocytidine.

TABLE 5. Hydrogen bonding in (1) and (2)

	DA	D-H	HA	<d-ha< th=""></d-ha<>
(1)				
N(4)-H1N(3*)	3.021	0.89	2.15	170.0
-H2O(2)	2.977	0.90	2.12	159.8
0(5')-H0(2)	2.784	0.84	1.98	159.2
N(4*)-H1N(3)	2.987	0.86	2.13	172.6
-H20(2*)	2.937	0.86	2.10	166.0
0(5'*)-H0(5')	2.821	0.85	1.99	167.1
*Atoms in molecule B. (2)				
0(5')-H0(2)	2.701Å	0.96Å	1.76Å	163.2°

cule 2 there is only one intermolecular hydrogen bond interaction between O(5') and O(2) which is much stronger than the corresponding hydrogen bond in structure 1 due to the electron donating conjugated side chain in 2 which makes O(2) a much better hydrogen bond acceptor. This resonance effect is also reflected by changes in the cytosine ring geometry (FIG. 2).

Recently, a report appeared describing the crystal structure of 1. The data are in agreement with the results obtained in this independent work.

CONCLUSIONS

In both anti-HIV ddC derivatives 1 and 2, the 3'-F substituent alters significantly the overall conformation found in the unsubstituted ddC, but makes them resemble one of the two conformers of AZT, with similar sugar pucker and rotational angles. In prodrug 2, the presence of the conjugated \underline{N}^4 -substituent and the resulting resonance effect enhances the electron density at O(2), making it a stronger hydrogen bond acceptor. The \underline{N}^4 -side chain in 2 is coplanar with the pyrimidine ring and \underline{cis} to N(3) [\underline{syn} rotamer] due to steric interference by the H(5) in the opposite orientation.

ACKNOWLEDGEMENTS

This research was supported in part by funds from NIH grants CA- 34714 (VC) and AI-27251 (TIK).

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Received 9/12/91 Accepted 11/14/91