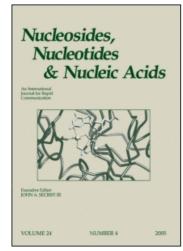
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Nucleosides, Nucleotides and Nucleic Acids

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

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To cite this Article Bailey, L. E. , García-Martin, M. L. , Stender, H. and Ball, G.(1999) 'Structural Studies of 5-Ethyl-2'-Deoxyuridine by Selective Pulse 1 H DPFGSE NOE Spectroscopy and PM3 Calculations', Nucleosides, Nucleotides and Nucleic Acids, 18: 4, 1067 — 1068

To link to this Article: DOI: 10.1080/15257779908041647 URL: http://dx.doi.org/10.1080/15257779908041647

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STRUCTURAL STUDIES OF 5-ETHYL-2'-DEOXYURIDINE BY SELECTIVE PULSE ¹H DPFGSE NOE SPECTROSCOPY AND PM3 CALCULATIONS.

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Abstract: The solution conformation of 5-ethyl-2'-deoxyuridine (EDU) has been calculated from the vicinyl proton-proton NMR coupling constants and nuclear Overhauser (NOE) distances using excitation sculpting of selective pulses (Double Pulsed Field Gradient Spin Echo NOE) at 500 MHz and molecular modelling (PM3) studies.

A structural study is reported on 5-ethyl-2'-deoxyuridine (EDU), a thymidine (dT) analogue with antiviral activity. The conformations in phosphate buffer saline solution (PBS) at pH 7.4 were inferred from the vicinyl proton-proton NMR coupling constants and nuclear Overhauser (NOE) distances using excitation sculpting of selective pulses (Double Pulsed Field Gradient Spin Echo NOE)¹ at 500 MHz and molecular modelling (PM3) studies. A pseudorotational equation of the form v_j = a_jv_{max} cos(P + 0.8 π (j - 2) was used to calculate the pseudorotational parameters of the deoxyribose ring². Analysis of the J-coupling constants measured from simulated spectra revealed that: (i) the C4'-C5' bond is primarily in the g+ conformation, to an extent of 55% for g+, 29% for t and 16% for g- at 310 K and (ii) the deoxyribose ring has a preference for a South-type (C2'-endo/C3'-exo) puckered conformation (approximately 64% at 310 K). The pseudorotational parameters of the South conformer are as follows: P=177 and v_{max} =35.

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TABLE 1. Solution and crystal structure conformations of EDU and dT.

PARAMETER	COMPOUND					
	Solution conformation				Crystal conformation	
	dT ⁴		EDU		dT ⁵	EDU ⁶
	N	S	N	S		
Exocyclic torsions:						
χ (O4'-C1'-N1-C2)	263.1° (anti)		111.2° (anti)		220° (anti)	70.9° (high anti)
% anti	77.8		73.5			
γ (O5'-C5'-C4'-C3')	59.7	60.8	59.7	60.8	172.9° (g-)	-46.8° (g+)
% g+ /g- / t	52.2; 18.1; 29.7		55.0; 16.3; 28.7			
Endocyclic torsions:						
v ₀ C4'-O4'-C1'-C2	-0.73	-8.01	-7.19	-12.54	-7.0°	-1.8°
v ₁ O4'-C1'-C2'-C3'	-27.34	30.72	-28.60	29.35	27.8°	-5.9°
v ₂ C1'-C2'-C3'-C4'	39.71	- 41.69	53.47	-34.95	-36.9°	9.9°
v ₃ C2'-C3'-C4'-O4'	-40.17	36.73	-57.92	27.20	33.1°	-10.8°
v ₄ C3'-C4'-O4'-C1'	25.28	-17.75	40.24	-9.06	-16.6°	8.8°
P ^(a)	19	185	25	177	187.5	27.2
$v_{\max}^{(b)}$	42	42	59	35	37.2	11.2
X ^(c)	0.37	0.63	0.36	0.64		
Sugar pucker	$^{3}T_{4}$	$^{2}T_{3}$	$^{3}T_{4}$	$^{2}T_{3}$	$_{3}T^{2}$ S	$^{3}T_{4}$ N
- -			C3'-endo/C2'-endo		C3'-exo	C3'-endo

⁽a) $\tan P = [(v_4 + v_1) - (v_3 + v_0)] / [2v_2(\sin 36^\circ + \sin 72^\circ)]$ (b) $v_{max} = v_2 / \cos P$ (c) Molar fraction.

The results reveal that another conformer with a North-type puckered conformation for the deoxyribose ring is also present in solution. (P=25, v_{max} =59). The characterization of the minor conformer must be regarded as an essential complement to the results of X-ray crystallographic analysis. One dimensional DPFGSE NOE measurements indicated a predominant *anti* conformation (73.5%)³.

It is concluded that the preferred conformation of 5-ethyl 2'-deoxyuridine in solution is in close agreement with the X-ray crystal structure.

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