type of dissymmetric system. Hence 2R:3S:4S:5S:6Sapplies to I.

(10R:11S:12R:13R) Coupled with Known (2S:3R)VIIe. N.m.r. analyses on Va and its variants²² (cf. Chart I) disclosed the relative configuration ascribed to segment C-9, 10, 11, 12. Rotational properties in the V-series were consistent with a D-center at C-13, which provided the over-all D-galacto absolute configuration, as depicted.²³ This was confirmed via the alternate degradation route (Chart I), leading to known²⁴ (2S:3R)-2-acetamido-3-acetoxybutane (VIIe). Accordingly, specifications (10R:11S:12R:13R) are established in oleandomycin, completing the definition of all centers shown in I.25

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5.11; C-1, C-6 methylene, apparent doubled doublet at τ 6.08; OAc (4), τ 7.94 \pm 0.01; C-6 Me, τ 9.01; C-2 Me, τ 9.06; C-4 Me, τ 9.10. The shielding relationship of the specific C-methyl groups are com-patible with the configuration of P-1 but not P-2. All non-meso configurations at C-2,3,4 were also eliminated in these considerations (cf. ref. 1a).

(21) P-1 and P-2 represent known ABA types (cf. p. 28 and Chapters 5 and 14 in ref. 15) possessing predictable rotation and rotational shift following acetylation. The observed (+) for IIIc and (-) for IIId, and the (-) shift, are in accord with P-1; the opposite is expected for P-2

(22) N.m.r. (Vd in CHCl₃): C-9 H, τ 4.58 (J (9a,10a) = 9 c.p.s.); C-11 H, τ 5.26 (J (11a, 10a/11a, 12e): 11/5 c.p.s.); C-13 H, τ 6.17 (J (13, 12/13, Me) = 2.5/7 c.p.s.); C-9 OAc, C-11 OAc, τ 7.87, 7.89; C-13 Me, C-10 Me, C-12 Me, τ 8.79, 9.04, 9.11 (all J = 7 c.p.s.); C-10 H and C-12 H, complex splitting pattern.

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W. D. Celmer

Medical Research Laboratories, Chas. Pfizer & Co., Inc. Groton, Connecticut Received February 24, 1965

Macrolide Stereochemistry. II. Configurational Assignments at Certain Centers in Various Macrolide Antibiotics1

Sir:

This report reveals additional support for a thesis of predictable configurational uniformity among macrolide antibiotics. Occurrence of the same absolute configuration at anomeric centers, *i.e.*, α -L: β -D (cf. Klyne's rule^{2,3}), in various macrolide glycosides and revision of controversial specifications, *i.e.*, $(\beta-L)$,⁴ (2S:4R), (3R), (

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(2) W. Klyne, Biochem. J., 47, xli (1950).
(3) (a) T. Reichstein and E. Weiss, Advan. Carbohydrate Chem., 17, 65 (1962). (b) Klyne's rule (cf. pp. 98, 99 in ref. 3a), originally applied to steroid glycosides, is now regarded with an explicit 6-deoxypyranoside proviso to circumvent understandable exceptions involving D-glucosides (cf. ref. 3c,d). While the rule notably holds for oleandrose found in both macrolide and steroid glycosides (cf. Table I), it need not apply outside these fields. (c) R. Okazaki, T. Okazaki, J. L. Strominger, and A. M. Michelson, J. Biol. Chem., 237, 3025 (1962); S. Matsu-hashi, Federation Proc., 23, 170 (1964). (d) Nucleotide-bound 4-keto-6deoxy- α -D-glucose apparently serves as a common intermediate for both D- and L-6-deoxypyranosides in bacterial cell wall biosynthesis.³⁰ It follows that while still nucleotide-bound the "completed" ' sugars possess the same anomeric configuration, i.e., α -D- and β -L-; by invoking a common transferase mechanism involving net inversion, the resulting glycosides must occur as β -D- and α -L-, as observed and as empirically predicted by Klyne's rule.

The α -L: β -D Nature of Anomeric Centers. Table I covers cited and new assignments to anomeric centers in various macrolide^{1c,7-19} and pertinent^{3b} steroid^{3a,20,21} glycosides involving pyranosides of known⁷ 6-deoxyhexoses.

Either n.m.r.²² or molecular rotational difference² (m.r.d.) or both of these methods were employed for analyses. Reference data stem from evident or predictable properties in keeping with known (hexose)⁷ configuration²³ and preferred conformation²⁴ of the corresponding pyranoside in each case. The observed conformity suggests a biogenetic basis for Klyne's rule consistent with known ramifications of 6-deoxy sugar biosynthesis.^{1c,3e,d}

Coupling of New Specifications (2R:3S:4S:9S) in Dihydroerythromycin with Established $(8R:10R)^{5,10}$ and (xylo-C-2,3,4)^{6,25} in Erythromycin.²⁶ Confrontation in erythromycin of predictable $(2R:3S:4S)^{1b}$ and circumstantially derived $(2S:3R:4R)^{5,6}$ specifications prompted the following re-examination of established data. In recalling the isomeric pairs (A:B) of C_7 compounds (lactones, hydrazides, triols, cf. Chart I) derived from the nucleus of dihydroerythromycin by Gerzon, et al., 10 one need only consider I and II for A as well as III and IV for B, i.e., four sets of absolute configurational possibilities. However, it is now pointed out that a simple arithmetical process, 27, 28

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(25) In these laboratories, the n.m.r. spectrum (CDCl₃) of the known O-acetylanhydride of the meso-1,5-diacid corresponding to lactone-A (cf. ref. 10 and Chart I) showed J 10/10 c.p.s. at τ 4.93, i.e., J 3a,2a/ 3a,4a (x_1/b) ; cf. chemical proof in ref. 6. (26) Cf. ref. 5, 6, 10, 11, 27 for the over-all development of constitu-

tional and configurational relationships.

Table I. Anomeric Configurational Analyses

		N	.m.r.ª		
6-De	oxy sugars	Chem.	$J_{1,2},$	M.r.d., ^{<i>b</i>}	
Hexose ⁷	Glyoside	shift, τ	c.p.s.	ΔM_D	Conclusion
L-Oleandrose	Oleandomycin ⁸	(4.99)8	(3.5/1.0)8	(-263°) ⁸	(lit. α -L-) ⁸
	Oleandrin ²⁰			$(-263^{\circ})^{20}$	α-L-
L-Cladinose	Erythromycin-A ¹¹	5.05	4.0/1.0	(-297°) ¹¹	α- L-
	Erythromycin-B ¹²	5.08	4.0/1.0	$(-270^{\circ})^{12}$	α-L-
L-Mycarose	Magnamycin-A ⁹			(-389°) ^{98,b}	α-L-
	Tylosin ^{13,14}	4.90	2.5/<1	$(-269^{\circ})^{13}$	a-L-
	Spiramycins ⁷	4.90	2.0/<1		α-L-
	Leucomycins ⁷	4.90	2.0/<1		α-L -
L-Arcanose	Lankamycin ¹⁵			$(-524^{\circ})^{15}$	α-L-
D-Desosamine	Oleandomycin ⁸	(5.74)8	$(7.0)^8$	$(-80^{\circ})^{8}$	(lit. β-D-) ⁸
	Erythromycin-A ¹¹	(5.42)4	$(7.1)^4$	$(-34^{\circ})^{11}$	(lit. β -D-) ⁴
	Erythromycin-B ¹²	5.56	7.0	$(-52^{\circ})^{12}$	β- D -
	Narbomycin ⁷	5.67	7.0		β - D-
	PA 133-A,B ¹⁹	5.63	7.7		β- D -
D-Mycaminose	Magnamycin-A ⁹	(5.52)4	$(7.1)^4$		(lit. β-D-)4
	Tylosin ^{13,14}	5.40	7.0		β- D -
	Spiramycins ⁷	5.50	7.0		β - D-
	Leucomycins ⁷	5.48	6.5		β-D-
D-Mycosamine	Pimaricin ^{16,17}			$(-308^{\circ})^{17}$	β - D-
D-Mycinose	Chalcomycin ¹⁸	1. P. W.	$(7.1)^{18}$		$(lit. \beta-D-)^{18}$
-	Tylosin ^{13,14,18}	5.73	7.0	$(-98^{\circ})^{14}$	β-D-
D-Chalcose	Chalcomycin ¹⁸		$(7.1)^{18}$		$(lit. \beta-D-)^{18}$
	Lankamycin ¹⁵			$(-75^{\circ})^{15}$	β- D-
D-Oleandrose	Lanafolein ²¹			$(-60^{\circ})^{21}$	β-D-

^a All 6-deoxypyranosides in these cases evidently follow a preferred conformation correlated with series, *i.e.*, L(1C) and D(C1). Since all L-examples are also 2-deoxy sugars, their expected $J_{1,2}$ values follow accordingly, *i.e.*, α -L(1C): $J_{1e,2a} = 2.5$ -4.0, $J_{1e,2e} = <1$ -2.5 c.p.s.; β -L(1C): $J_{1a,2a} = 9.0$ -9.5, $J_{1a,2e} = 2.0$ -4.0 c.p.s. Only D-sugars possessing an axial proton at C-2 were examined, *i.e.*, β -D(C1): $J_{1a,2a} = 6.5$ -7.5 c.p.s.; α -D(C1): $J_{1e,2a} = 2.0$ -4.0 c.p.s. β -Culated from available [α]D data (cf. citations) where MD = [α]D × mol. wt./100 and Δ MD = MD of glycoside (or appropriate derivative) minus MD of the corresponding aglycone (cf. ref. 2). All given Δ MD values possessing correct sign and reasonable magnitudes compared to MD values known or predictable for the α -L(1C) or β -D(C1) pyranoside in question.

Chart I. Dihydroerythronolide Degradation Products^a: Absolute Configurational Considerations

A Series ^{a,b} Origin			B Serie Origi	es ^{a, c}		
C-1	\mathbf{R}_1	R1	C-11	-	R_1	R_1
2	H—C—CH₃	CH;CH	10	CH,-	CH	CH ₃ H
3	но-с-н	H—Ç—OH	9	HO-	-ĊH	H-C-OH
4	H-C-CH3	CH ₃ —C—H	8	H—	-CCH,	H-C-CH ₃
5	$\mathbf{C}\mathbf{H}_2$ \mathbf{R}_2 I	CH_2 —FII	R ₂ 7		$CH_2 - R_2$ III	${_{C}}H_{2}$ R $_{2}$ IV
Lactones Hydrazides Triols Model Syster	R_1 CO $CONHNH_2$ CH_2OH CH_2OH $R_1: R_2 = CO-O)^d:$	R₂ −−−−O OH OH	cf. A: A: A:		cf. B: B: B:	MD +81° +12° -21°(III = IV)
R ₁	R	1	R ₁	R	L ₁	
H-C-0	OCH ₃ CH ₃ O-C	—Н (сн,осн	CH₃O—C	с—н	CH ₃ H
CH ₃ O—C	H H—C	—OCH₃ (CH₄O—C—H	HC	C—OCH3	CH_2
HC0	OCH_3 CH_3O-C	—Н	H-C-OCH3	HC	C—OCH3	CH_3
CH_2	$-R_2$	$H_2 - R_2$	$CH_2 - R_2$	Ċ	$H_2 - R_2$	
$\frac{MD}{-7.6^{\circ}}$		6°	VII +68°	VI -27	II 76°	IX +44°e
a Cf ref 10 b Cf ref 6.25 c Cf ref 5 d Cf ref 30 c Cf footnote 21 in ref 10						

Cf. ref. 10. *Cf.* ref. 6, 25. \circ Cf. ref. 5. ^a Cf. ref. 30. *e Cf.* footnote 21 in ref. 10.

involving consideration of hydrazides $A\!:\!B$ and model compounds, leads to I:III as the sole set for A:B.29

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(29) The sign and expected magnitude of molecular rotational contribution from α and γ centers in the hydrazides I, II, III, IV are derived as follows: (α) From (+)(S) IX, [M]D +44°; (γ) from (-)(*R*:*R*) triol, i.e. III, = IV, $[M]D - 10.5^{\circ}$. It follows that the arithmetical sum of rotational contribution (RC) from α , β , and γ centers must equal the observed [M]D in each hydrazide case, i.e. (A = -74°) and (B = +12°). Knowing the sign and reasonable magnitude of RC at α and γ , their net sign and value (N) can be approximated in all possibilities. Thus, in I (N = -55°), II (N = $+55^{\circ}$), III and IV (N = $+33.5^{\circ}$). Each pair of possibilities is then tested with consistent signs for the RC of the unknown β center, *i.e.*, for I:III (a) if $-55^{\circ} + \beta = -74^{\circ}$ then $+33.5^{\circ} + \beta = +12^{\circ}$ or (b) if $-55^{\circ} - \beta = -74$ then $+33.5^{\circ} - \beta =$ +12. Expression (a) is untenable while (b) leads to reasonable sign and values for the RC of the β center, *i.e.*, -19° in I and -21.5° in II. It turns out that all other sets of possibilities receiving like inspecThis conclusion is substantiated by MD correlations involving lactones A:B and models³⁰ (cf. V with I and VII with III in Chart I). The above specifications then follow.²⁶

tion become disqualified due to their untenable arithmetic. Now, knowing only the sign of RC at all centers, it is possible to check the magnitude of apparent RC from the α center, e.g., since $-\alpha - \beta - \gamma$ = -74 then $+\alpha - \beta - \gamma = +12$, i.e., $\alpha = 43^{\circ}$ (cf. 44° for IX). (30) (a) A. K. Bose and B. G. Chatterjee, J. Org. Chem., 23, 1425

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W. D. Celmer

Medical Research Laboratories, Chas. Pfizer & Co., Inc. Groton, Connecticut Received February 24, 1965

Macrolide Stereochemistry. III. A Configurational Model for Macrolide Antibiotics¹

Sir:

A model (cf. 1 and 2) is proposed as a vehicle of configurational thought in macrolide antibiotic problems² dealing with molecular structures, biogenesis, and mode of action. The model's nucleus can be specified as: 2-D, 3-L, 4-D, 5-L, 6-L, 8-L, 10-D, 11-L, 12-L, 13-D, or D-threo-L-gulo-L-ido-, or (2R:3S:4R:5S:6S:8R:10R:11S:12R:13R)-2,4,6,8,10,12-hexamethyl-3,5,11,13-tetrahydroxy-9-ketotridecanoic acid 1,13-lactone. A carbohydrate corollary states that any L- or D-6-deoxypyranoside substituent bears an α -L- or β -D-specification at the anomeric center (cf. 2). There are no provisions for predicting the configuration at other carbohydrate or at exo-macrocyclic asymmetric centers or the precise position of sugar substitution. The model operates on the premise that the absolute configuration ascribed to a given center is general and is not altered by "extra" oxygen substitution involving replacement of hydrogen at an asymmetric center in certain macrolide antibotics. This

Table I. Macrolide Specifica	tions
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of earlier^{1c,3} evidence for and concepts of a principle of configurational standardization among macrolide antibiotics. The model is tied with Gerzon's propionate rule,⁴ Klyne's glycoside rule,^{1b,5} and the total absolute

Aglycone centers — Anomeric centers – Anomeric centers						
Macrolide	Evident	Predicted	Evident	Predicted		
Oleandomycin (I)	$(2R:3S:4S:5S:6S:8R:10R:11S:12R:13R)^{a}$	Same	(β-D:α-L) ^b	Same		
Erythromycin-A (II)	$(2R:3S:4S)^c$ $(8R:10R)^d$ $(13R)^e$	Same and (5R:6R:11R:12S)	$(\beta-D)^{c,f}(\alpha-L)^{c}$	Same		
Erythromycin-B (III)	$(xylo-C-2,3,4)^{e,g}$	(2R:3S:4S:5R:6R:8R:10R:11S:12R:13R) (xylo-C-2,3,4) ^h	(β-D:α-L) ^c	Same		
Erythromycin-C (IV)	Cf. II	Cf. II		$(\beta$ -D, α -L)		
Lankamycin (V)	(galacto-C-10,11,12,13) ⁱ	(2R:3S:4R:5S:6S:8S:10R:11S:12R:13R) (galacto-C-10,11,12,13) ^h	$(\beta$ -D, α -L) ^c	Same		
Narbomycin (VI)	$(6S:8R)^{i}$	Same and $(2R:4R:5S:12R:13R)$	$(\beta-D)^c$	Same		
Methymycin (VII)	$(4S:6R)^{k}$	Same and $(2R:3S:10S:11R)$		(β-D)		
Neomethymycin (VIII)	$(4S:6R)^{l}$	Same and $(2R:3S:10R:11S)$		(β- D)		
Chalcomycin (IX)	$(4S:6S)^{m}$	Same and (5S:8S)	$(\beta - D, \beta - D)^m$	Same		
Picromycin (Xa)	$(4S:6R)^{n''}$	(2R:3S:4S:6R:10S:11R)		(β-D)		
Picromycin (Xb)	$((2R:4S)^n)$	(2R:4S:5S: R:1)S:11R)		(β-D)		

^a Cf. ref. 1a. ^b Cf. footnote 8 in ref. 1b. ^c Ref. 1b. ^d Cf. ref. 3e. ^e Ref. 4. ^f Cf. footnote 4 in ref. 1b. ^o Cf. footnotes 6, 11, and 27 in ref. 1b. ^h Cf. relative configuration. ⁱ W. Keller-Schierlein (private communication); cf. Helv. Chim. Acta, 47, 78 (1964). ⁱ Cf. ref. 3f. ^k Cf. ref. 3c. ⁱ Cf. ref. 3b. ^m Cf. footnote 18 in ref. 1b. ⁿ This follows from ref. 3a, b according to the assigned structures in each case (Xa, ref. 6 and Xb, ref. 7). ^o Cf. ref. 2.

extends the applicability range of the model in its otherwise self-evident constitution-configuration matching workings.

Derivation. The current model represents fruition

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