the type of linkage and the angle at the bridge atom, a chain with any required degree of polymerization could be generated, with any desired values of ϕ's and ψ's between the residues. This program enables one to generate a polymer chain, which could be nonhomogeneous in terms of the conformational angles (ϕ, ψ). Figure 10 depicts the mycodextran chain so generated, in which the (ϕ_n, ψ_n) at two of the α-1→3′ linkages along the chain has been chosen from area II. The figure shows that the perturbation at two adjacent linkages is sufficient to achieve the folding. The segments of the chain on either side of the fold are about 11 Å apart.

The packing of chains and the question of chain polarity in the unit cell must await the obtaining of superior X-ray data than were available to the writers.

Conclusions

Biopolymers of the mycodextran type, *i.e.*, with a regular copolymeric structure, are common both in plant and bacterial systems. The possible number of such regular molecular types based on permutations among the commonly occurring sugars, the glycosidic linkage type, and linkage configuration is exceedingly large. So far researchers have concentrated on homopolysaccharides, and this is only the second alternating copolysaccharide whose crystalline conformation is reported.[32] Nevertheless, the combined X-ray and conformational analysis approach as described herein would seem to offer the potential to derive the reference conformation which is the most likely candidate for being the maximum population state in the living system. It remains to be seen whether interaction with proteins, particularly in the enzyme–substrate complex, always involves this conformer or something closely akin. In the lysozyme–chitin case,[33] the conformation of the polysaccharide closely resembles that of the crystalline substrate. Mycodextranase rapidly degrades mycodextran to a tetramer,[34] which is the crystalline repeating unit. Subsequent hydrolysis is much slower and only proceeds to the disaccharide, nigerose. Furthermore, while the enzyme is specific for the α-1→4 link in mycodextran, it does not attack the same linkage in amylose. It has been suggested that enzyme action on polysaccharide substrates is dictated by the structure of the glycosyl moiety that becomes the reducing end unit of the product liberated.[35] If the maltose conformation in crystalline mycodextran is the same as in amylose, as we conclude, then it is clear that at least a glycosyl disaccharide conformation (α-1→3 unit in this case) is involved in triggering the enzyme action as has been suggested by the enzymologists[34] and would seem to be confirmed by the conformational data of this paper.

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Communications to the Editor

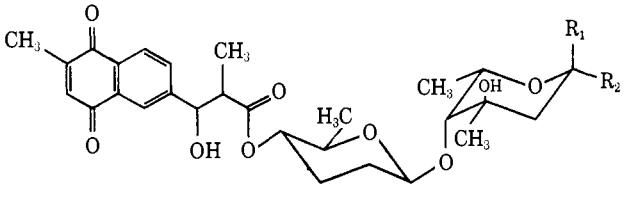
Axenomycins. I. The Structure of Chromophore and Sugar Moieties

Sir:

Axenomycin A, B, and D represent the major components of a new group of closely related antibiotics which are produced by *Streptomyces lysandri n. sp.* and have a complex structure containing a macrocyclic lactone, two sugar residues, and a 1,4-naphthoquinone chromophore. They have activity against plateworms and yeasts. We report here the structure of the chromophore and sugar moieties of axenomycin B, which are common to all the components of this group.

Axenomycin B, a neutral, crystalline substance, $C_{78}H_{126}O_{30}$ (mol wt 1530 (calcd 1542);[1] λ_{max}(MeOH) 250, 256, and 267 nm; $\nu_{quinone}$ 1665 cm^{-1}), on chromic acid oxidation[2] afforded 2-methyl-1,4-naphthoquinone-6-carboxylic acid[3] (methyl ester, mp 160°), identified by direct comparison with a synthetic specimen prepared from 2-methyl-6-naphthoic acid,[4] thus revealing the substitution of the naphthoquinone chromophore.

Methanolysis (0.05 *N* HCl at room temperature) of axenomycin B gave, in addition to axenolide,[5] **1a** (α-



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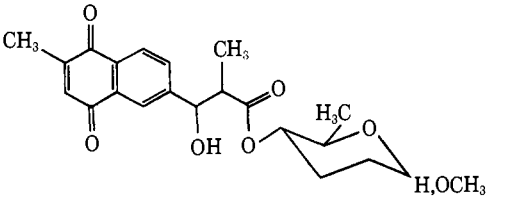

2

(1) Determined by the vapor pressure method.

(2) D. W. Mac Corquodale, L. C. Cheney, S. B. Binkley, W. F. Holcomb, R. W. Mc Kee, S. A. Thayer, and E. A. Doisy, *J. Biol. Chem.*, 131, 357 (1939).

(3) All the compounds have consistent elemental analyses and spectroscopic properties. Melting points, uncorrected, were taken at the Köfler hot stage. Unless otherwise stated optical rotations were measured in chloroform at 20°.

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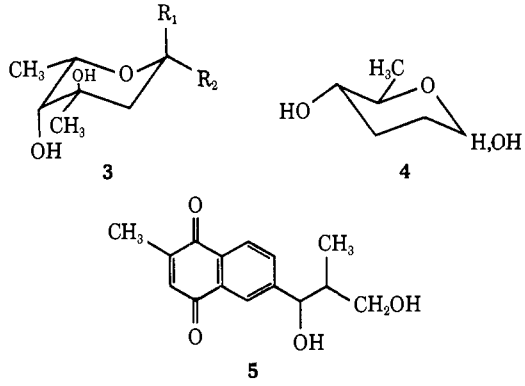
glycoside, R_1 = OMe, R_2 = H), $[\alpha]_D$ −27.7°; **1b** (β-glycoside, R_1 = H, R_2 = OMe), $[\alpha]_D$ +32°, $C_{29}H_{38}O_{10}$, mol wt 555[1] (calcd 546.7); **2** (3:1 mixture of α and β anomers), mp 114°, $[\alpha]_D$ +107°; and anomeric axenose methyl glycosides **3a** (α anomer, R_1 = OMe, R_2 =



3 **4** **5**

H, mp 101–103°, $[\alpha]_D$ −142°) and **3b** (β anomer, R_1 = H, R_2 = OMe, mp 122–123°, $[\alpha]_D$ +38°). **1a** and **1b**, $\nu_{CO\ ester}$ 1735 cm^{-1}, gave monoacetate (pyridine and Ac_2O) containing one hydroxyl not acetylatable. They were converted by further methanolysis to **2**, **3a**, and **3b**, whereas **1b** yielded **6** on alkaline saponification.

Compound **2**, *m/e* 402 (M), was saponified in methanolic 0.5 *N* NaOH to give, with concomitant decomposition of the chromophore, an anomeric mixture of methyl glycosides which were hydrolyzed with acid to the free sugar **4**, identified by direct comparison of the 2,4-dinitrophenylhydrazone (mp 156–157°, $[\alpha]_D$ −10° (*c* 0.28), pyridine) with an authentic sample of D-amicetose 2,4-dinitrophenylhydrazone.[6] On the other hand, reductive hydrolysis of **2** with excess $NaBH_4$ in aqueous MeOH, followed by air reoxidation, gave, together with D-amicetose methyl glycosides, the chromophore fragment **5** (*m/e* 260 (M), diacetate *m/e* 344 (M)). The structure of **5** was determined from pmr data. The pmr spectrum ($CDCl_3$) of **3b** shows signals at δ 1.28 (C-5 Me, d, J = 6.5 Hz), 1.34 (C-3 Me, s), 1.50–1.85 (C-2 protons, m, AB part of an ABX system), 1.77 (C-3 OH, s), 2.27 (C-4 OH, d, J = 10 Hz), 2.98 (C-4 H, dd, $J_{H,OH}$ = 10 Hz, $J_{4,5}$ < 1 Hz), 3.51 (CH_3O, s), 4.13 (C-5 H, dq, $J_{4,5}$ < 1 Hz, J_{H,CH_3} = 6.5 Hz), and 4.63 (C-1 H, dd, $J_{1,2ax}$ + $J_{1,2eq}$ = 12.5 Hz). The methyl glycosides **3a** and **3b** are not oxidized by periodate, thus revealing the trans orientation of the C-3 OH and C-4 OH. Configuration at C-3 was established by ir (CCl_4, 0.005 *M*) absorption at 3590 (sharp, free OH) and at 3530 cm^{-1} (broad, H-bonded OH) of the α anomer **3a**, indicating 1,3-diaxial interaction of C-3 OH and OMe.[7] On acid treatment **3a** and **3b** afforded the new sugar axenose (2,6-dideoxy-3-*C*-methyl-L-xylohexose), *m/e* 145 (M − OH), mp 111–112°, $[\alpha]_D$ at the equilibrium −28.5° (*c* 1, H_2O).[8]

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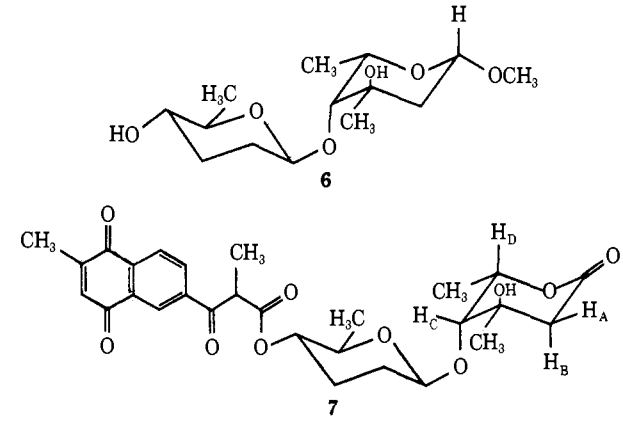
(8) Racemic 2,6-dideoxy-3-*C*-methyl-DL-xylohexose (DL-4-epimycarose) was obtained by synthesis.[9] The 3-*O*-methyl derivative of axenose (L-arcanose) is a component of the antibiotic lankamycin.[10]

Compound **6** (mp 148–150°, *m/e* 290 (M), $[\alpha]_D$



6 **7**

−120°) shows an axial glycosidic proton in the amicetose residue (pmr ($CDCl_3$) signal at δ 4.47, dd, $J_{1,2ax}$ + $J_{1,2eq}$ = 12 Hz), thus revealing the stereochemistry (β-glycoside) at this center. The pmr spectrum (DMSO-d_6)[11] shows two OH signals at δ 4.65 (amicetose C-4 OH, d, J = 5.0 Hz) and δ 4.53 (axenose C-3 OH, s). The above evidence fully agrees with structure **1**.

Additional support to this structure was provided by **7** (*m/e* 528 (M), ν_{OH} 3460, $\nu_{conj\ CO}$ 1700 cm^{-1}), obtained by mild chromic acid oxidation[2] of axenomycin B. The pmr spectrum ($CDCl_3$) of **7** shows, *inter alia*, signals at δ 1.51 (C-10 Me, d, J = 7.0 Hz), 2.43 and 2.64 (H_A, H_B, two d, $J_{A,B}$ = 17.5 Hz), and 4.92 (H_D, dq, $J_{D,Me}$ = 7 Hz, $J_{C,D}$ = 1.5 Hz).

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F. Arcamone,* W. Barbieri, G. Franceschi, S. Penco, A. Vigevani
Istituto Ricerche Farmitalia
20146 Milan, Italy

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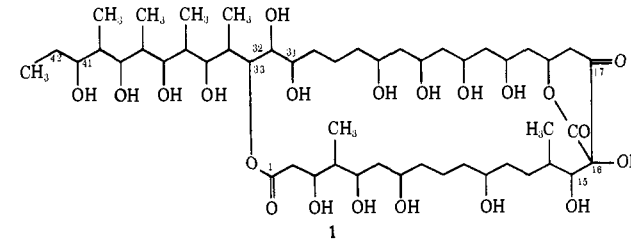
Axenomycins. II. The Structure of Axenolide

Sir:

Axenolide (**1**),[1] the aglycone of axenomycin B, is a



1

neutral, saturated, polyhydroxylated macrolide, C_{50}-

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