

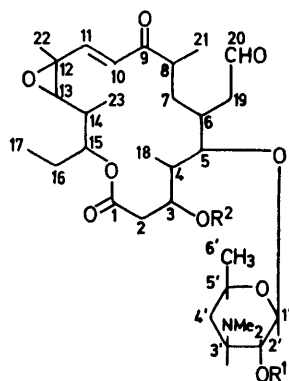
Structure of Rosamicin†, a New Macrolide from *Micromonospora rosaria*

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Summary Gross structure (1) has been assigned to the new macrolide antibiotic, rosamicin, on the basis of chemical and spectroscopic evidence.

FERMENTATIONS of *Micromonospora rosaria* sp. n. produce a new macrolide antibiotic, named rosamicin.¹ On the basis of chemical and spectroscopic data, structure (1), has been assigned to the new antibiotic.



- (1) $R^1 = R^2 = H$
 (2) $R^1 = COCH_3, R^2 = H$
 (3) $R^1 = R^2 = COCH_3$

Compound (1) was isolated by extraction¹ and was purified by crystallization from chloroform, m.p. 119–122°, $[\alpha]_D^{26} - 35^\circ$ (ethanol), λ_{max} (MeOH) 240 nm (ϵ 14,600), and analysed for $C_{31}H_{51}NO_9$. The i.r. spectrum indicated hydroxy (2.83 μ m), *N*-methyl (*ca.* 3.59 μ m), aldehyde (3.68 and 5.78 μ m), lactone (5.78 and 8.5 μ m) and conjugated ketone (5.90 and 6.15 μ m), while the n.m.r. spectrum (60 MHz, $CDCl_3$) exhibited bands at δ 0.9 (t, J 7 Hz, $-CH_2CH_3$), 1.45 (s, C- CH_3), 2.30 [s, 2(N- CH_3)], 4.25 [d, J 7 Hz, O-CH-(CH)O], 4.9 (ddd, $>CH-OC=O$), 6.54 [s, 2(C=CH)] and 9.72 p.p.m. (broad s, C-CH=O). In $(CD_3)_2CO$ the vinyl proton signal was resolved to an *AB* quartet, δ 6.43 and 6.87 p.p.m., J 16 Hz. The m.s. showed a molecular ion

peak at m/e 581 consistent with the empirical formula, and major fragmentations at m/e 563 ($M - 18$), 553 ($M - 28$), 407 ($M - 174$), 389 ($M - 174 - 18$), 174 and 158 (base peak). The latter two fragments are ascribed to a *D*-desosamine moiety in the molecule; hydrolysis of (1) with 6*N* hydrochloric acid afforded *D*-desosamine,² m.p. 85–87°, $[\alpha]_D + 15 \rightarrow + 50^\circ$ (water, 24 h), identical with an authentic sample (n.m.r., m.s.).

In view of the similarity of the physical properties of (1) and those of the macrolide antibiotic cirramycin A_1 ,³ a direct comparison of the mass spectra of the two compounds was carried out. Cirramycin A_1 showed a molecular ion peak at m/e 597 and fragmentations at m/e 579 ($M - 18$), 569 ($M - 28$), 407 ($M - 190$), 389 ($M - 190 - 18$), 190 and 174. The fragmentation patterns indicate that the aglycone in both compounds is the same, the difference being a desosamine moiety in (1) corresponding to a mycamnose moiety in cirramycin A_1 .[†]

Additional support for the structure of (1) was provided by its conversion into the 2'-monoacetate (2) [m.p. 116–121°, $[\alpha]_D - 25^\circ$ (ethanol), λ_{max} (MeOH) 240 nm (ϵ 14,000)] with one equivalent of acetic anhydride in acetone and into the 3,2'-diacetate (3) {m.p. 104–7°, $[\alpha] - 24^\circ$ (ethanol), λ_{max} (MeOH) 240 nm (ϵ 12,700), no residual hydroxy in the i.r.} with excess of acetic anhydride in pyridine. In the m.s., compound (2) had M^+ 623, with fragments at m/e 407 and 389 for the aglycone and at m/e 216 and 200 for 2-acetyl-desosamine, while compound (3) showed M^+ 665 and fragments at m/e 449 (acetyl aglycone) and 389 (449 – acetic acid) as well as at m/e 216 and 200.

Examination of the n.m.r. spectra of compounds (1), (2), and (3) [in $(CD_3)_2CO$] permitted assignment of the β configuration to the glycosidic linkage of desosamine ($J_{1,2}$ 7 Hz).^{2b} The point of attachment of the sugar moiety on the aglycone as C-5 followed from the acylation shifts and splitting patterns of H-3, H-5, and H-2'.

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† Formerly named rosaramicin.

‡ The structure of cirramycin A_1 is well founded on degradative studies.³

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