ADRIAMYCIN (14-HYDROXYDAUNOMYCIN), A NOVEL ANTITUMOR ANTIBIOTIC

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We report herein the structural elucidation of adriamycin, an antitumor antibiotic which has been compared favourably with clinically useful daunomycin in the experimental chemotherapy studies. 1,2

Adriamycin, $C_{27}H_{29}O_{11}N$, must have the same anthraquinone chromophore and glycoside structure as does daunomycin, ³ on the basic of spectroscopic data and of formation, on acid hydrolysis, of a red aglycone, adriamycinone, and of the aminosugar, daunosamine. ¹ Adriamycinone, $C_{21}H_{18}O_9$, m.p. 223-224°, $[\alpha]_D^{23} + 188°$ (c 0.1, dioxane), one OCH₃, hydroxyl (3440 cm⁻¹), carbonyl (1727 cm⁻¹), and chelated quinone (1615 cm⁻¹) absorptions in the infrared, shows ultraviolet and visible spectra superimposable on those displayed by the parent glycoside and by daunomycinone (I), ³ thus indicating the same type of substitution of the anthraquinone system as in I. Upon acetylation with acetic anhydride and pyridine, adriamycinone gives a pentaacetate $C_{31}H_{28}O_{14}$, m/e 624 (M), m.p. 166°, [α] $_D^{23} - 94°$ (c 0.1, CHCl₃), phenolic (1775 cm⁻¹) and alcoholic (1740 cm⁻¹) acetate bands, no hydroxyl absorption in the infrared. When treated with hydrogen bromide in acetic acid, adriamycinone gives a product whose visible spectrum (λ_{max} 467, 497, 521, 537 mµ in CHCl₃) is identical to that shown by bisanhydrodaunomycinone. This indicates the presence of two (and only two) hydroxyls on the aliphatic ring of the anthracyclinone system in adriamy-cinone. ^b) The fifth hydroxyl should therefore be placed on the acetyl side chain as in **I**.

Comparison of the mass spectra of daunomycinone and adriamycinone shows a similar fragmentation pattern (scheme 1), strongly supporting structure II for the latter compound. The 60 Mc n.m.r. spectrum (CDC1₂) of adriamycinone pentaacetate shows five sharp

a) Centro del C.N.R. per lo studio delle sostanze organiche naturali.

b) An additional hydroxyl group on the said ring would be revealed by a substantially different visible spectrum of the dehydration product [see (3), and references cited therein].

Scheme 1



singlets at δ 2.01 (6 H, two aliphatic OAc), 2.13 (3 H, aliphatic OAc), 2.40 (3 H, aromatic OAc), 2.48 (3 H, aromatic OAc), 3.95 (3 H, aromatic OCH₃). Four protons in the range 1.8-3.75 are attributed to CH₂-8 and CH₂-10. A quartet centered at δ 4.83 (2 H, J gem. 16.5 c.p.s.) is consistent with the presence of the COCH₂OAc group. A double doublet at δ 6.35 (1 H, J_{H-7,H-8} \sim 5, J_{H-7,H-8} \sim 1.5 c.p.s.) indicates the C-7 benzylic CHOAc. Three aromatic protons appear as a complex multiplet at δ 7-8.

Hydrogenolysis of adriamycin (III) with Pd/BaSO₄ in methanol gives daunosamine and 7-deoxyadriamycinone (IV), $C_{21}H_{18}O_8$, m.p. 253-255°, m/e 398 (M), 380 (M-H₂O), 349 (M-H₂O-CH₂OH), 339 (M-COCH₂OH), carbonyl (1727 cm⁻¹) and chelated quinone (1615 cm⁻¹) bands, tetraacetate (acetic anhydride and pyridine) $C_{29}H_{26}O_{12}$, m/e 566 (M), m.p. 186-188°, $\left[\alpha\right]_{D}^{23} - 6^{\circ}$ (c 0.1 dioxane). The 60 Mc n.m.r. spectrum (CDCl₃) of this tetraacetate shows, <u>inter alia</u>, two aliphatic OAc at § 2.05 and 2.18, the CH₂-14 quartet at § 4.88, and the absence of the C-7 benzylic CHOAc signal described above. The structure of IV proves the position of the glycosidic linkage at C-7 as in III.

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C.D. curves have been employed for establishing stereochemical relationships among anthracycline derivatives. ⁴ The stereochemistry at C-7 and C-9 in adriamycin is proved to be identical [i.e. 7(S), 9(S)] to that of daunomycin ⁵ by comparison of their C. D. curves, clearly demonstrating the same configuration at the said centers. The absolute configuration at C-1' in III is deduced to be (R), i.e. α -glycoside, from the identity of the optical rotations of adriamycin and daunomycin, ⁶ and of adriamycinone and daunomycinone, ⁶ suggesting the same optical contribution of the daunosamine moiety in the two glycosides. This is in agreement with general observations on the stereochemistry of the glycosidic linkage of a given carbohydrate inside a restricted class of natural glycosides, as in Klyne's rule and its extensions, ⁷ and it is also supported by biogenetic arguments. ⁸

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