

POLYENE ANTIFUNGAL ANTIBIOTICS :

α AND β GLYCOSIDIC STRUCTURES IN LUCENSOMYCIN AND NYSTATIN

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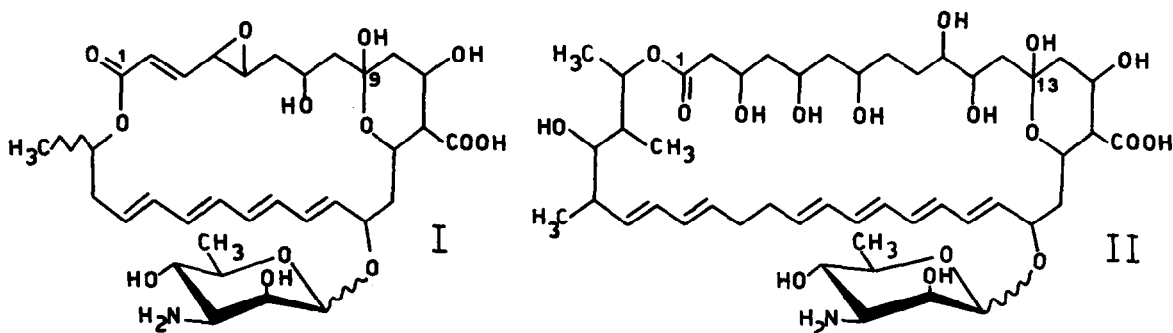
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Antifungal antibiotics lucensomycin (I) and nystatin (II), present in their structures an amino sugar (mycosamine: 3-amino-3,6-dideoxy-D-mannose) glycosidically linked to the macrocyclic aglycone.¹



The ¹³C-NMR spectra (25.2 MHz, DMSO-d₆, t=33 °C) show, in the region around 100 ppm from TMS, which is characteristic for hemiketal and acetal C atoms, ^{1,2,3} signals at 95.8, 96.2, 96.3 ppm for I,⁴ and at 96.6, 97.4 ppm for II. In the fully coupled ¹³C-NMR spectrum of I, the resonance at 96.3 ppm can be assigned to the quaternary 9-C. In turn signals at 96.2 and 95.8 can be associated with the 1'-C of the mycosamine, thus showing the existence of two types of acetal C atoms. In a similar way in II, the peak at 96.6 ppm results from the overlap of two resonances, one of them belonging to the 13-C and the other, as well as that at 97.4 ppm, can be assigned to the anomeric carbon of the mycosamine. The measured J_{1'C-1'H} values show that the resonance at 96.2 ppm in I (J=165 Hz) is due to a carbon bearing an equatorial proton, while those at 95.8 in I and 96.6 in II (J=158 Hz) are due to C atoms bearing axial protons.⁵ These values fit well, in fact, Bock's correlation between the

orientation of the anomeric protons and anomeric coupling constants (169-171 Hz for equatorial protons and 158-162 Hz for axial ones), which has proved to be valid^{6,7} for free pyranoses and for glycopyranosides.

To ascertain the correct stereochemistry of the amino sugar, nystatin (II) has been hydrolysed and the mycosamine has been isolated as the N-carbobenzyloxy derivative (III);⁸ the resulting mixture of the α and β anomers has been used as a conformational model for the mycosamine in antibiotics I and II. The ¹³C-NMR spectrum of III shows two signals for the α and β anomeric carbons at 94.0 and 93.2 ppm and the corresponding $J_{1'C-1'H}$ values are 170 and 159 Hz respectively. Moreover ¹H-NMR (270 MHz, DMSO-d₆ and pyridine-d₅, t=29 °C) indicate that both the anomers of III have the same conformation; the ³J_{H-H} (α anomer: $J_{12}=2.1$, $J_{23}=3.0$, $J_{34}=11.0$, $J_{45}=9.4$ Hz; β anomer: $J_{12}=2.6$, $J_{23}=2.8$, $J_{34}=10.5$, $J_{45}=9.3$ Hz) are in fact only compatible with a ⁴C₁ conformation but not for example with an inverted chair ¹C₄,⁹ less likely also because of steric interactions of bulky groups. The similarity of $J_{1'C-1'H}$ for III and the amino sugar glycosidically linked to the macrolides in I and II is therefore strongly suggestive of α and β configurations at the anomeric centres in these two antibiotics. Furthermore analysis of the $J_{1'C-1'H}$ values suggests that whereas the β anomer maintains the ideal chair conformation when linked to the macrolide backbone, the α is somewhat distorted.¹⁰ The measured α/β ratios, deduced from the relative intensities of the peaks concerned, change with the nature of the aglyconic residue: the α anomer is 55% in I, but drops to 20% in II. These percentages are however only indicative because these antibiotics are natural blends of different natural active constituents¹¹ and the technique itself (¹³C-NMR-FT) suffers from relatively large uncertainties in quantitative determinations.

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