

STRUCTURES OF  $\beta$ -AMINO ACIDS IN ANTIBIOTICS ITURIN A

Akira Isogai\*, Seiji Takayama, Shigeo Murakoshi<sup>†</sup> and Akinori Suzuki  
Department of Agricultural Chemistry, The University of Tokyo,  
Bunkyo-ku, Tokyo 113, Japan

<sup>†</sup>Kanagawa Horticultural Experimental Station, Ninomiya-machi,  
Kanagawa 259-01, Japan

**Summary:** An antibiotic iturin A was separated into several components (A-1~8) using HPLC and the structures of the  $\beta$ -amino acids of each component were established based on NMR and mass spectral analysis.

During our screening search for antibiotics against phytopathogenic fungi, we isolated a peptidal substance produced by a *Bacillus* species and tentatively termed 10W. Physicochemical studies on 10W revealed that it was identical with iturin A<sup>1)</sup>, which is a mixture of homologous cyclic peptide composed of each one mole of a lipophilic  $\beta$ -amino acid, glutamine, tyrosine, proline and serine, and three moles of asparagine. The structures of two main components have been proposed as I-a and b by Peypoux *et al*<sup>2-5)</sup>.

However, results of our preliminary studies on the antibiotic were not coincident with the proposed structures. Therefore, we attempted to carry out a complete characterization of the structures of each component of iturin A.

An antibiotic 10W was a mixture of homologous peptides and separated into eight components using HPLC on ODS (Nucleosil 5C<sub>18</sub>) with acetonitrile-10mM ammonium acetate (2:3) as in Fig.1-a, while iturin A gave seven peaks in the chromatogram as in Fig.1-b and each of them corresponded to 10W-2~8. Though the contents of each component were slightly different between these two antibiotics, two abundant components of iturin A were evidently identical with 10W-2 and 4. Therefore, hereafter 10W-1~8 are called iturin A-1~8, respectively.

The mass spectra of each component of iturin A obtained with FAB ionization system showed homologous M+H ion peaks at  $m/z$  1029 for iturin A-1, 1043 for A-2, 1057 for A-3, A-4 and A-5, 1071 for A-6 and A-7, and 1085 for A-8. The mass spectra of the N-acetyl methyl ester of the lipophilic amino acids of iturin A-2 and A-4 isolated from the hydrolyzate by solvent extraction were identical with the published data of the same derivatives of C<sub>14</sub>- and C<sub>15</sub>- $\beta$ -amino acids of iturin A, respectively<sup>3)</sup>.

After being partially hydrolyzed, iturin A-2 afforded a mixture of oligopeptides, among which were identified Glu-Pro, Tyr-Asp, Ser-C<sub>14</sub>- $\beta$ -amino acid, Glu-Pro-Asp and Ser-C<sub>14</sub>- $\beta$ -amino acid-(Asp, Tyr).

In the <sup>13</sup>C-NMR spectra methyl carbons of aliphatic long chain compounds

usually resonate nearly at  $\delta$  14 ppm for normal-type compounds, 23 ppm for iso-type, and 11 and 19 ppm for anteiso-type compounds<sup>6)</sup>. The  $^{13}\text{C}$ -NMR spectrum of N-acetyl methyl ester of  $\text{C}_{14}$ - $\beta$ -amino acid of iturin A-2 showed only one aliphatic methyl signal at  $\delta$  14.1 ppm, indicating that this  $\beta$ -amino acid is not of iso-type but of normal structure. The other signals<sup>7)</sup> were well coincident with those of long chain aliphatic compounds<sup>6)</sup>. Thus the structure of  $\text{C}_{14}$ - $\beta$ -amino acid of iturin A-2 should be 3-amino-tetradecanoic acid.

The above mentioned chemical shifts of the derivative of the isolated  $\beta$ -amino acid were very similar to those in the whole peptide, suggesting that those did not shift due to any steric effects in the peptide.

The  $^{13}\text{C}$ -NMR spectrum of iturin A-4 showed two equivalent methyls at  $\delta$  23.0 ppm, indicating that the  $\text{C}_{15}$ - $\beta$ -amino acid of iturin A-4 is of iso-type and 3-amino-13-methyltetradecanoic acid. Chemical shifts in  $^{13}\text{C}$ -NMR spectra of terminal parts of  $\text{C}_{14}$ - and  $\text{C}_{15}$ - $\beta$ -amino acids in iturin A-2, A-3, A-4 and A-5 are summarized in Table 1, confirming that the structure of the  $\beta$ -amino acid in iturin A-3 is 3-amino-12-methyltetradecanoic acid and that the  $\text{C}_{15}$ - $\beta$ -amino acid in A-5 is 3-amino-pentadecanoic acid.

$^1\text{H}$ -NMR spectra of the above four components thus determined were clearly distinguishable from each others in their methyl regions; a 3H distorted triplet for a normal-type compound, a 6H doublet for an iso-type and a 6H multiplet due to triplet plus doublet for an anteiso-type compound.

$^1\text{H}$ -NMR spectra of the other minor homologs, iturin A-1, A-6 and A-7 and the mass spectra of the  $\beta$ -amino acids are shown in Table 1. All the structures of  $\beta$ -amino acids in iturin A components were established as in II-1~II-7 for iturin A-1~7, respectively. Iturin A-8 was deduced to have an anteiso-type  $\text{C}_{17}$ - $\beta$ -amino acid from the mass and  $^1\text{H}$ -NMR spectra, but it could be obtained too little to be fully characterized by  $^{13}\text{C}$ -NMR spectrum.

The data disclosed above and the reported ones on iturin A<sup>2)</sup> suggest the structures of iturin A-1~7 to be II-1~7.

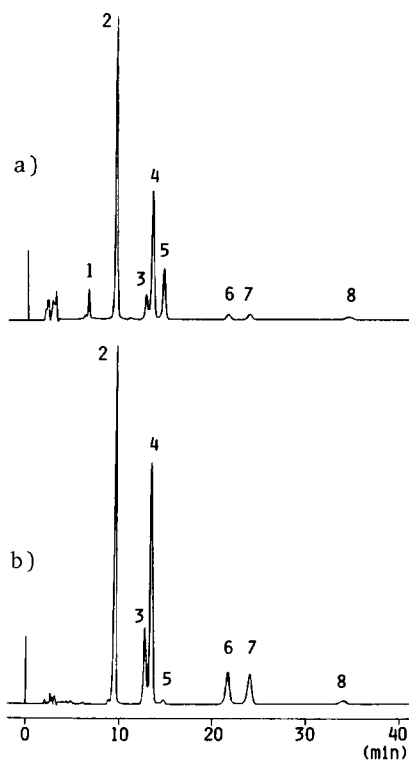


Fig.1. Chromatograms of the antibiotics on HPLC (ODS).

a) 10W, b) iturin A.



In recent years, Peypoux, Delcambe and their co-workers have studied the antibiotics belonging to iturin group, such as iturin C<sup>8)</sup>, mycosubtilin<sup>9)</sup>, bacillomycin L<sup>10)</sup> and bacillomycin D<sup>11)</sup>. All these antibiotics also have C<sub>14</sub> ~ C<sub>17</sub>- $\beta$ -amino acids. The structures of these  $\beta$ -amino acids should be reinvestigated because these have been determined in comparison with those of iturin A.

Acknowledgements. The authors thank Prof. F. Peypoux of Universite Claude Bernard for supplying a specimen of iturin A. They are also grateful to Mr. E. Yamauchi of JEOL Company Ltd. for measurement of FAB-mass spectra.

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- 6) "<sup>13</sup>C-NMR Spectroscopy" by E. Breitmaier and W. Voelter, 2nd ed., p. 131, Verlag Chemie, Weinheim, 1978.
- 7) Chemical shifts of the derivative were as follows (CDCl<sub>3</sub>):  
14.1 (C-14), 22.7 (C-13), 31.9 (C-12), 30.0 (C-6 ~ C-11), 26.2 (C-5),  
34.1 (C-4), 46.2 (C-3), 38.2 (C-2), 172.5, 169.7 (C-1, acetyl CO), 51.6 (OCH<sub>3</sub>), 23.4 (acetyl CH<sub>3</sub>).
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(Received in Japan 14 April 1982)