

NOTES

IDENTIFICATION OF TAKACIDIN
AND ANTIBIOTIC U-0142 WITH
MONAZOMYCIN AND COMPARISON
OF TAXONOMIC PROPERTIES OF
THEIR PRODUCING ORGANISMS

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During the course of our investigation on the ionophorous antibiotics, we have recently determined the structure of monazomycin¹⁾ which is the first 48-membered lactone glycosidated with D-mannose to be isolated from the microbial sources. The mechanism of action of monazomycin on ion transport have been explained by the assembly of several monomers (approximately five) of the antibiotic in the form of pores or channels both in artificial and biological membranes.²⁾ Therefore, the antibiotic has aroused considerable interests in the field of molecular biology by its ability to alter ionic conductance or permeability across membranes. In this paper, we report the structural identification of two related antibiotics, takacidin^{3,4)} and antibiotic U-0142⁵⁾ and the morphological properties of their producing organisms.

The FD-MS spectra of takacidin and antibiotic U-0142 revealed characteristic ions at m/z 1,365 ($M+H$)⁺ and 1,387 ($M+Na$)⁺ suggesting the identity of these antibiotics with monazomycin (M.W. 1,364). Furthermore, their ¹H and ¹³C NMR spectra taken at 400 and 100 MHz, respectively, were completely superimposable with those of monazomycin (Table 1). Direct comparison of takacidin and antibiotic U-0142 with authentic monazomycin by silica gel TLC (CHCl₃ - MeOH - H₂O, 10 : 5 : 1 containing one drop of AcOH and BuOH - AcOH - H₂O, 3 : 1 : 1) showed the identical R_f values at 0.38 and 0.55, respectively. Consequently, takacidin and antibiotic U-0142 are confirmed to be identical with

Table 1. ¹³C NMR chemical shifts of monazomycin.*

Functionality	Chemical shift (ppm)
-COO-	175.3
-C=	146.3, 136.9
-CH=	134.8, 134.7, 134.5, 130.3×2, 123.1
-CH $\begin{matrix} \text{O-} \\ \diagdown \\ \text{O} \end{matrix}$	97.8
-CH-O-	82.8, 81.6, 80.8, 80.4, 78.3, 77.5, 76.0, 75.7, 74.7, 73.5, 73.3, 72.7, 72.3×2, 72.0, 71.8, 70.4, 69.8, 69.6, 69.0
-CH ₂ -O-	63.0
-CH-	42.9, 41.8, 41.7, 41.3, 41.2, 41.1, 39.9, 36.9, 36.8, 35.5
-CH ₂ -	43.3, 42.8, 41.8, 40.9, 39.0, 36.6, 36.0, 35.9, 35.3, 31.0, 30.34×2, 30.26, 28.5, 27.9, 27.3, 27.0, 26.8, 26.1
-CH ₃	17.5, 17.2×2, 16.9, 16.3, 13.3, 13.1, 11.9, 11.0, 10.8, 7.0×2

* The ¹³C NMR spectrum was measured in a CD₃OD solution. The chemical shifts were measured relative to CD₃OD and converted to TMS scale (CD₃OD=49.0 ppm).

monazomycin and their structure is depicted as shown in the Fig. 1.

The producing organisms of takacidin, antibiotic U-0142, and monazomycin were also compared according to the ISP method.⁶⁾ Monazomycin is produced by *Streptovorticillium mashuense** No. 3682-JTt₁,⁸⁾ while takacidin is produced by *S. griseovorticillatum** OEU722 (KCC S-0202),^{8,4)} and antibiotic U-0142 is produced by *Streptovorticillium* sp. KCC U-0142.

As shown in Table 2, the taxonomical properties of *S. mashuense* No. 3682-JTt₁ are in good agreement with those of the type culture of *S. griseovorticillatum* OEU722,⁹⁾ and distinct from

* According to BERGEY'S Manual (8th ed.)⁷⁾ *Streptomyces mashuensis*, which was originally reported as a monazomycin producing organism, is called hereafter *Streptovorticillium mashuense*. Similarly, *S. griseovorticillatus* which produces takacidin is called *S. griseovorticillatum*.

Fig 1. Structure of monazomycin.

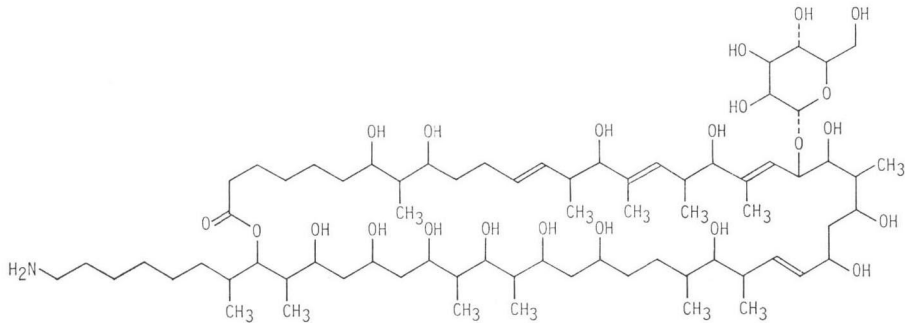


Table 2. Comparison of taxonomical characteristics.

	<i>S. mashuense</i> No. 3682-JT ₁	<i>Streptovercillium</i> sp. KCC U-0142	<i>S. griseovercillatum</i> KCC S-0202	<i>S. mashuense</i> ISP description
Spore chain	Umbelliverticilla	Umbelliverticilla	Umbelliverticilla	Umbelliverticilla
Spore surface	Smooth	Smooth	Smooth	Smooth
Color of colony	Red color-series	Red color-series	Red color-series	Red color-series
Reverse color	Not distinctive	Not distinctive	Not distinctive	Not distinctive
Color in media	No or trace of pinkish or yellowish	No or trace of pinkish or yellowish	No or trace of pinkish or yellowish	None
Melanoid pigment				
PYIA	—	—	—	+
TYB	—	—	—	+
TA	—	—	—	—
Starch hydrolysis	+	+	+	
Nitrate reduction	+	+	+	
Carbon utilization				
Good	Glucose, inositol	Glucose, inositol	Glucose, inositol	Glucose, sucrose, fructose
Fair	Fructose	Fructose	Fructose	Inositol
Trace or none	Arabinose, sucrose, xylose, rhamnose, raffinose, mannitol	Arabinose, sucrose, xylose, rhamnose, raffinose, mannitol	Arabinose, sucrose, xylose, rhamnose, raffinose, mannitol	Arabinose, xylose, rhamnose, raffinose mannitol

PYIA: Peptone - yeast extract - iron agar, TYB: tryptone - yeast extract broth, TA: tyrosine agar.

ISP description of *S. mashuense*.¹⁰⁾ Therefore, the producing organism of monazomycin must be renamed to *S. griseovercillatum*. The antibiotic U-0142 producing strain has the same properties as those of the type culture. Accordingly the strain, KCC U-0142, is identified with *S. griseovercillatum*. Thus, the three strains mentioned above, which were regarded as different species, are concluded to be identical.

We propose to call the antibiotic produced by *S. griseovercillatum*, monazomycin.

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