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SHORT REPORT

A New 6-deoxy-talopyranoside derivative with antibacterial and radical-scavenging activities from *Streptomyces* sp. HDSJ4

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Abstract: Chemical investigation of the secondary metabolites from a *Streptomyces* sp. strain yielded two compounds (**1** and **2**), including an undescribed 6-deoxy-talopyranoside derivative, designated strepyranin A (**1**). The structure of strepyranin A was unambiguously established based on comprehensive spectroscopic analyses, including 1D and 2D NMR spectra, together with HRESIMS data. Compound **1** was assayed for its antibacterial and radical-scavenging activities. Bioassays revealed that strepyranin A (**1**) exhibited weak antibacterial activity against *Pseudomonas aeruginosa* and *Streptococcus pneumoniae*, with minimum inhibitory concentration (MIC) values of 64 μg/mL and 128 μg/mL, respectively, and moderate DPPH radical-scavenging activity with an RSA of 36.4%.

Keywords: Talopyranoside derivative, endophytic *Streptomyces*, secondary metabolites, antibacterial activity, radical-scavenging activity

1 Actinobacterial Source

Streptomyces sp. HDSJ4 strain was isolated from the bark of *Taxus chinensis* sampled off Lijiang, Yunnan. Taxonomic identification of this isolate was accomplished via sequence analysis of the 16S ribosomal DNA. The resultant 16s rDNA sequence was submitted to GenBank with the accession code PZ631066. Furthermore, the strain was deposited at the Marine Ecology Research Center, Shandong Marine Resource and Environment Research Institute (Yantai, China) for long-term preservation.

2 Previous Studies

Plant-derived actinomycetes have attracted sustained research interest as a valuable source of bioactive secondary metabolites in recent decades (Wu et al., 2009). Living inside plant tissues or *Taxus* hosts, these endophytic actinomycetes evolve intimate symbiotic relationships with their hosts and adapt to special plant internal micro-niches (Zhao et al., 2011; Parel & Khare, 2026). Shaped by the unique internal microenvironment of plant tissues, they possess distinctive metabolic pathways and can produce diverse natural products that are structurally analogous to host-derived bioactive compounds, including taxanes, polyketides, alkaloids and terpenoids with remarkable pharmacological potential (Hassan et al., 2023; Waheed et al., 2026; Yu et al., 2025). Among these microbes, *Streptomyces* strains are particularly prominent. Genomic mining and chemical investigations have revealed that endophytic actinomycetes abundant silent biosynthetic gene clusters (Cunliffe & Rutledge, 2026; Lasch et al., 2026). Such strains are capable of generating cytotoxic, antimicrobial and anti-inflammatory metabolites, and are regarded as promising alternative microbial resources for sustainable acquisition of high-value lead compounds (Jose et al., 2021). As part of our ongoing research program targeting novel bioactive secondary metabolites from actinobacterial strains, two distinct metabolites, designated compounds **1** and **2**, were isolated from the fermentation broth extract of the marine actinobacterium *Streptomyces* sp. HDSJ4. The present work comprehensively describes their purification workflow, complete structural characterization, and bioassays.

3 Present Study

The actinobacterial strain *Streptomyces* sp. HDSJ4 was revived and cultured on potato dextrose agar (PDA) plates at 25°C for 3 days. Once the agar surface was completely covered by actinobacterial mycelia, cylindrical agar discs were sterilely punched from the plates using a disinfected cork borer. The obtained agar inocula were subsequently transferred into rice-based solid fermentation substrates. The fermentation system was distributed into 120 separate 1000 mL Erlenmeyer flasks, each preloaded with 100 g rice

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and 80 mL sterile distilled water. Static cultivation of the inoculated flasks was carried out at ambient temperature for 30 days. Upon completion of the fermentation process, the fermented solid matrix was subjected to repeated exhaustive extraction with ethyl acetate (EtOAc); three independent EtOAc extraction cycles were implemented in total. All organic-phase fractions collected from extractions were pooled and concentrated via vacuum rotary evaporation, affording 285 g of crude actinobacterial extract.

Methanol was used to reconstitute the crude fermentation extract, followed by homogeneous mixing with normal-phase silica gel. Subsequent evaporation to eliminate all methanol solvent yielded dry sample powder for chromatographic loading. Primary separation of the crude sample was achieved through normal-phase silica gel column chromatography with a stepwise elution gradient of petroleum ether–acetone at volumetric ratios of 20:1, 5:1 and 1:1. The collected eluate fractions (petroleum ether/acetone, 1:1) were further purified using reversed-phase silica gel column chromatography. A linear methanol–water ($MeOH/H_2O$) gradient elution system was utilized herein, in which the volumetric percentage of methanol was progressively elevated from 20% to 100%. This separation procedure ultimately generated nine distinct subfractions designated Fr. 1 to Fr. 9. Fr. 4 ($MeOH/H_2O$, 1:1) was further separated by PTLC (CH_2Cl_2/MeOH, 15:1) and Sephadex LH-20 (MeOH) resulting in compounds **1** (4.1 mg) and **2** (7.5 mg) (Figure 1).

*Strepyranin A (**1**)*: Colorless oil; $[\alpha]_D^{20}$ = +10.1 (*c* = 0.1, MeOH); ^1H (500 MHz) and ^{13}C (125 MHz) NMR data, see Table 1; HRESIMS: *m/z* 265.1290 $[M + H]^+$ (calcd for $C_{11}H_{21}O_7$, 265.1287).

Antimicrobial activity assay: The antibacterial activity of the tested samples was evaluated against three common pathogenic bacteria in humans, including *Pseudomonas aeruginosa*, *Salmonella typhi* and *Streptococcus pneumoniae*, using a two-fold serial dilution method (Ghoneim et al., 2026; Yan et al., 2026). Briefly, the bacterial stock suspensions were diluted with Mueller-Hinton broth (MHB) to a final inoculum concentration of approximately 5×10^5 CFU/mL (Pu et al., 2026). The test samples were initially dissolved in dimethyl sulfoxide (DMSO) and subsequently subjected to two-fold serial dilution to obtain working concentrations ranging from 2560 to 2.5 μg/mL. For the in vitro antibacterial assay, 5 μL of serially diluted sample solution and 95 μL of prepared bacterial suspension were added into each well of a 96-well flat-bottom microplate, yielding final sample concentrations spanning 128 to 0.125 μg/mL. After incubation at 37°C for 24 h, the minimum inhibitory concentration (MIC) of each sample was determined as the lowest concentration that completely suppressed visible bacterial growth. Chloramphenicol and pure DMSO were used as the positive and negative controls, respectively, in all assays.

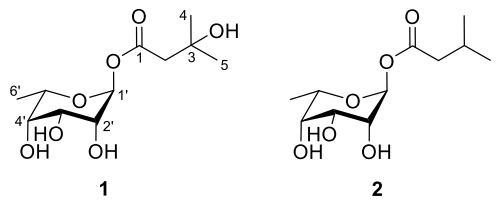


Figure 1. Chemical structures of compounds **1** and **2** isolated from *Streptomyces* sp. HDSJ4

Radical-scavenging activity assay (DPPH): The DPPH radical scavenging activity was evaluated based on a previously described method developed by reported method (Park et al., 2024; Yen et al., 2025), with appropriate modifications. A 0.2 mM DPPH stock solution was freshly prepared using methanol as the solvent, while all test samples were dissolved and gradient-diluted with methanol to obtain working solutions. For the reaction assay, 100 μL of each sample solution was mixed thoroughly with 150 μL of the prepared DPPH stock solution in a 96-well microplate. In this work, the final concentration of strepyranin A (**1**) in the reaction system was 40 μM. The microplate was tightly wrapped with aluminum foil to avoid light exposure and incubated at room temperature for 60 min to complete the reaction. After incubation, the absorbance of each reaction mixture was recorded at 517 nM using a microplate reader. Ascorbic acid was selected as the positive control for this assay system.

The DPPH radical scavenging activity (RSA, %) was calculated via the following formula:

$$RSA\ (\%) = (1 - A_1/A_2) \times 100\%$$

where A_1 and A_2 refer to the absorbance of the sample group and the blank control group at 517 nM, respectively. All experiments were performed in triplicate, and the final results were presented as the mean ± standard deviation (SD).

Compound **1** was obtained in the form of a colorless oil, whose identity was established by comprehensive NMR and HRESIMS spectroscopic evidence. A prominent protonated molecular ion ($[M + H]^+$) was observed at m/z 265.1290 in its HRESIMS profile, in good agreement with the molecular formula $C_{11}H_{20}O_7$. The ^1H NMR spectrum (Figure S2

Table 1. ^1H (500 MHz) and ^{13}C (125 MHz) NMR data of compounds **1** and **2** (δ in ppm) in DMSO-d_6

Pos.	1		2	
	δ_C, type	δ_H (*J* in Hz)	δ_C, type	δ_H (*J* in Hz)
1	169.7, C		171.2, C	
2	48.6, CH_2	2.41, s	43.1, CH_2	2.22, m
3	68.6, C		25.7, CH	1.99, m
4	29.9, CH_3	1.20, s	22.5, CH_3	0.91, d (6.7)
5	29.8, CH_3	1.19, s	22.4, CH_3	0.90, d (6.7)
1′	94.8, CH	5.86, d (1.7)	94.8, CH	5.88, d (1.6)
2′	69.8, CH	3.55, m	69.8, CH	3.55, m
3′	65.5, CH	3.64, br s	65.5, CH	3.62, m
4′	72.4, CH	3.52, m	72.4, CH	3.52, m
5′	69.8, CH	3.90, q (6.3)	69.8, CH	3.86, m
6′	17.1, CH_3	1.11, d (6.4)	17.1, CH_3	1.11, d (6.5)
2′-OH		5.37, d (6.7)		5.37, d (6.8)
3′-OH		5.00, br s		5.00, d (6.4)
4′-OH		4.84, d (7.2)		4.85, d (7.1)
3-OH		4.65, s		

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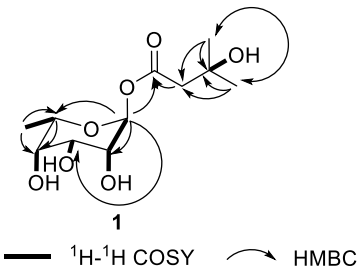


Figure 2. Key ^{1}H-^{1}H COSY and HMBC correlations of strepyranin A (**1**)

and Table 1) of **1** showed characteristic proton signals as follows: two singlet resonances for quaternary methyl groups at δ_H 1.20 (s, 4-CH_3) and 1.19 (s, 5-CH_3), one doublet methyl at δ_H 1.11 (d, J = 6.4 Hz, 6′-CH_3), and a set of sugar-derived protons consisting of one anomeric proton and four oxygen-substituted methine protons. Specifically, the glycosyl protons were observed at δ_H 5.86 (d, J = 1.7 Hz, 1′-CH), δ_H 3.55 (m, 2′-CH), δ_H 3.64 (br s, 3′-CH), δ_H 3.52 (m, 4′-CH), and δ_H 3.90 (q, J = 6.3 Hz, 5′-CH). In addition, four exchangeable hydroxyl protons were assigned at δ_H 5.37 (d, J = 6.7 Hz, 2′-OH), δ_H 5.00 (br s, 3′-OH), δ_H 4.84 (d, J = 7.2 Hz, 4′-OH), and δ_H 4.65 (s, 3-OH), while one methylene singlet was detected at δ_H 2.41 (s, 2-CH_2). The corresponding ^{13}C NMR and DEPT spectra (Table 1) yielded a total of 11 carbon resonances for compound **1**, which were classified into three methyl carbons, one methylene carbon, five methine carbons, and two quaternary carbons. Consistent with the deduced molecular formula, compound **1** possessed two degrees of unsaturation, which were ascribed to the presence of one ester moiety and one cyclic skeleton. Structural comparison indicated that compound **1** shared a high degree of structural similarity with isovaleryl 6-deoxy-α-L-talopyranoside (**2**) (Bitzer & Zeeck, 2006). The major structural discrepancy between the two compounds was substituent group located at the C-3 position. In the reported isovaleryl 6-deoxy-α-L-talopyranoside (**2**), the C-3 position was characterized as an oxygen-bearing methine carbon (δ 25.7, CH; δ 1.99, m), whereas this moiety was replaced by an oxygen-substituted quaternary carbon (δ 68.6, C) in compound **1**. This structural modification was further verified by key HMBC correlations from H-4 and H-5 to C-2 and C-3 in compound **1** (Figure 2). The full structure of compound **1** was further corroborated by diagnostic ^{1}H-^{1}H COSY and HMBC spectroscopic correlations. The observed ^{1}H-^{1}H COSY cross-peaks of H-1′/H-2′ and H-5′/H-6′ established the sequential proton connectivity within the sugar ring (Figure 2). Meanwhile, critical HMBC correlations from H-2 and H-1′ to C-1, from H-1′ to C-2′, C-3′ and C-5′, as well as from H-6′ to C-4′ and C-5′, further consolidated the skeleton connectivity of compound **1** (Figure 2). It should be noted that the intensities and peak shapes of these four hydroxyl proton signals in the ^{1}H NMR spectrum acquired in DMSO-d_6 are susceptible to variation, which is mainly caused by the water content in the solvent and the proton exchange rate.

Compound **1** lacks conjugated chromophores in its skeleton, consequently, no diagnostic Cotton effects were observed in its experimental ECD spectrum. Thus, TD-DFT ECD calculations could not be performed to support the assignment of its stereochemical configuration. Accordingly, the consistent NMR spectroscopic data between compound **1** and the previously reported isovaleryl 6-deoxy-α-L-talopyranoside (Table 1) confirmed the stereochemical configuration of the sugar moiety in compound **1**.

The antibacterial activity of strepyranin A (**1**) was assessed against three human pathogenic bacteria, including *P. aeruginosa*, *S. typhi*, and *S. pneumoniae*. As summarized in Table S1, compound **1** exhibited weak inhibitory activity against *P. aeruginosa* and *S. pneumoniae*, with MIC values of 64 μg/mL and 128 μg/mL, respectively. In contrast, Compound **1** displayed no noticeable inhibitory effect on the growth of *S. typhi* even at the highest tested concentration, with an MIC value > 128 μg/mL. In addition, the radical-scavenging activity of strepyranin A (**1**) was evaluated for radical scavenging activity. The result indicated that compound **1** displayed moderate antioxidant activity against DPPH radicals with the RSA value of 36.4% (Table S1). Although strepyranin A exhibited relatively weak bioactivity in our present assays, this 6-deoxy talopyranoside scaffold is still of interest. This unique glycoside skeleton can be regarded as a promising starting template for further structural modification, which may afford derivatives with improved bioactivity and help to develop potential lead molecules in future research.

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Author Contributions

Dongfang Yuan: Writing-original draft, Methodology, Investigation. Fei Miao: Validation and Data Curation. Shuo Sun: Formal analysis and Data curation. Yinyin Feng: Data analysis. Xiao Li: Writing-review & editing, Supervision, and Data curation.

Availability of Data and Materials

The authors declare that the data supporting the findings of this study are available within the paper and its Supplementary Information files. Should any raw data files be needed in another format they are available from the corresponding

author upon reasonable request. Source data are provided with this paper.

Ethics Approval

All bioassays in this work were conducted as in vitro biochemical tests with purified compound. No human subjects or live animals were included in the present study.

Artificial Intelligence (AI) Statement

The authors affirm that no Artificial Intelligence (AI) tools were employed in the preparation of this manuscript, which includes language editing, graphical abstract preparation, figure generation, or image editing.

Conflicts of Interest

The authors declare that they do not have any conflict of interests.

Supporting Information

Supporting information accompanies this paper on http://www.acgpubs.org/journals/records-of-natural-products.

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