SUPPLEMENTARY MATERIAL

A new furan derivative from an endophytic *Aspergillus flavus* of *Cephalotaxus fortunei*

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Abstract: A new furan derivative named 5-acetoxymethylfuran-3-carboxylic acid(**2**), together with a known furan compound, 5-hydroxymethylfuran-3-carboxylic acid(**1**), were isolated from the fermentation of *Aspergillus flavus*, endophytic fungi in *Cephalotaxus fortunei*. The structures of **1** and **2** were elucidated by NMR, IR, UV and MS data, as well as compared with literature data. Compounds **1** and **2** exhibited potent antibacterial activity against *Staphylococcus aureus* with MIC values of 31.3 and 15.6 µg/mL, respectively. Compound **2** showed moderate antioxidant activity.

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Supplementary material S1: The NMR of compound **1** and **2**
 All the NMR data were given by Bruker Avance III-400

^1H -NMR of compound **1**

^{13}C NMR of compound **1**

¹H- and ¹³C NMR data of 2(DMSO-*d*₆)

Position	δ_C	δ_H	HMBC
2	140.06	8.10 (1H, s)	C-6, C-4, C-5,
3	145.69		
4	112.47	6.54 (1H, s)	C-7, C-3, C-5
5	161.72		
-COOH	173.62	9.29 (1H, s)	C-6, C-2
7	61.41	4.94 (2H, s)	C-4, C-5, C-8
8	169.54		
-CH ₃	20.73	2.11 (3H, s)	C-8

Values in δ (ppm)

¹H-NMR of compound 2

^{13}C NMR of compound 2

The main correlation in the HMBC of compound 2

The Model of conformation of 2

HSQC of compound 2

HMBC of compound 2

Supplementary material S2: The HR-ESI-MS of compound **2**

The (+)-HR-ESI-MS of compound **2**

The (-)-HR-ESI-MS of compound **2**

Supplementary material S3: The IR of compound **1** and **2**

IR of compound **2**

IR of compound **1**

Supplementary material S4: Strain identification of S19

Morphology diagram of endophytic fungi S19

The nucleotide sequence of S19 (without primer sequences)

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GGTTCCTAGCGAGCCCAACCTCCCACCCGTGTTTACTGTACCTTAGTTGCTTCGGCGGG
CCCCCATTTCATGGCCGCCGGGGGCTCTCAGCCCCGGGCCCGCGCCCGCCGGAGACA
CCACGAACTCTGTCTGATCTAGTGAAGTCTGAGTTGATTGTATCGCAATCAGTAAAAC
TTTCAACAATGGATCTCTTGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATAA
CTAGTGTGAATTGCAGAATTCCGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCC
TGGTATTCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCATCAAGCACGGCTTGT
GTGTTGGGTCGTCGTCCCCTCTCCGGGGGGGACGGGCCCCAAAGGCAGCGGCGGCAC
CGCGTCCGATCCTCGAGCGTATGGGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCG
CTTGCCGAACGCAAATCAATCTTTTTCCAGGTTGACCTCGGATCAGGTAGGGATACCCG
CTGAACTTAAGCATATCAATAAGCGGAGGAA
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System phylogenetic tree of strain S19 based 18S rDNA-ITS sequence