Supporting Information

for

Identification of cyclic depsipeptides and the dedicated synthetase from Hapsidospora

irregularis

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 Table S1. Determination of the absolute configuration of amino and hydroxyl acid moieties in 1-7.

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Table S3. The extracted signature sequences of the A domains of LACS.

Figure S1. HPLC analysis of the metabolites of *Hapsidospora irregularis* FERM BP-2511 in K2 broth (bottom) and K2 broth supplemented with 0.5% L-tyrosine (top) at 210 nm.

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Figure S29. ¹H NMR spectrum of **7** in CD₃OD.

Figure S30. ¹³C NMR spectrum of 7 in CD₃OD.

Figure S31. ¹H-¹H COSY NMR spectrum of **7** in CD₃OD.

Figure S32. HSQC NMR spectrum of 7 in CD₃OD.

Figure S33. HMBC NMR spectrum of **7** in CD₃OD.

Figure S34. Hydrolysis and purification procedure of compounds 2, 4, and 6.

Compound	Fragment after hydrolysis	Conc. (g/100 mL) Solvent		$[\alpha]_{\rm D}^{19}$			
1		1.00	Methanol	-97.8			
2		0.30	Methanol	-99.0			
	<i>N</i> -Me-L-Phe from 2A	0.095	6 N HCl	+21.1			
	3-AIB from 2A	0.10	6 N HCl	-16.0			
	L-Leu from 2B	0.15	6 N HCl	+15.7			
3		1.17	Methanol	-48.2			
4		0.25	Methanol	-68.0			
	<i>R</i> -HICA from 4B	0.06	1 N NaOH	+21.7			
	L-Val from 4B	0.09	6 N HCl	+27.8			
5		0.62	Methanol	-96.1			
6		0.50	Methanol	-46.0			
	S-HICA from 6A	0.23	1 N NaOH	-23.5			
	<i>R</i> -HICA from 6B	0.17	1 N NaOH	+21.8			
	L-Leu from 6B	0.19	6 N HCl	+16.9			
	L-Tyr from 6A	0.22	6 N HCl	-9.5			
7		0.34	Methanol	-52.9			
HICA = 2-hydroxy isocaproic acid; 3-AIB = 3-aminoisobutyric acid; Val = valine; Leu =							
leucine; Tyr	leucine; Tyr = tyrosine; <i>N</i> -Me-L-Phe = <i>N</i> -methyl-L-phenylalanine.						

Table S1. Determination of the absolute configuration of amino and hydroxyl acid moieties in **1-7** (recorded on a Rudolph Autopol IV polarimeter using a 10-cm microcell at 19 °C).

	Cell Identity (Ca ²⁺ Response as % positive control)							
Compound		HEK-293	HEK-293	HEK-293	HEK-293		BEAS-2B	
	LOBAR	TRPA1	TRPM8	TRPV3	TRPV4	HEK-293	TRPV1	BEAS-2B
1	2 ± 1	4 ± 6	19 ± 5	10 ± 3	1 ± 1	10 ± 2	20 ± 20	21 ± 7
2	N.D.	N.D.	1 ± 2	4.40 ± 0.06	1 ± 1	3 ± 3	1 ± 1	10 ± 2
3	0.6 ± 0.4	41 ± 9	7 ± 2	6 ± 3	5 ± 2	13 ± 4	1 ± 1	N.D.
		(p=0.008)						
4	N.D.	20 ± 10	3 ± 5	2 ± 2	2 ± 1	2 ± 3	N.D.	N.D.
5	4 ± 3	3 ± 7	14 ± 9	8 ± 2	2.6 ± 0.6	N.D.	3 ± 1	8 ± 2
6	37 ± 3	88 ± 6	21 ± 6	13 ± 3	1.5 ± 0.4	10 ± 4	8 ± 10	16 ± 6
	(p=0.001)	(p=0.0001)	(p=0.058)					
7	N.D.	1 ± 2	10 ± 6	5 ± 2	3.9 ± 0.6	N.D.	1 ± 2	N.D.

 Table S2. Ca²⁺ flux data for 1-7 in primary human lobar bronchial epithelial cells, HEK-293 TRP channel overexpressing cells, and BEAS-2B (immortalized human bronchial epithelial) cells.

Student's t-test, two-tailed p-value in parenthesis (n=3). Lobar cell response values were compared to the buffer only control. HEK-293 TRP-overexpressing cell response values were compared to the HEK-293 control value for the given compound. BEAS-2B TRPV1 cell responses were compared to the normal BEAS-2B response.

A domain of LACS	Signature sequence	Substrate
A_1	DIYYVSATAK	β-Alanine
A_2	GANLIGATVK	S-Leucic acid
A_3	DAHDIGAPIK	L-Leucine
A_4	DGLFIGIPVK	S-Leucic acid
A_5	DPWTYGAVVK	L-Phenylalanine

Table S3. The extracted signature sequences of the A domains of LACS.



Figure S1. HPLC analysis of the metabolites of *Hapsidospora irregularis* FERM BP-2511 in K2 broth (bottom) and K2 broth supplemented with 0.5% L-tyrosine (top) at 210 nm. 1-7: compounds **1-7**, A: cephalosporin P1, B: isocephalosporin P1, C: mixture of the tetramic acids Sch210971 and Sch210972. HPLC condition: Agilent 1200 HPLC instrument with an Agilent XDB-C18 column (5 μ m, 4.6 mm \times 250 mm), eluted with a gradient of acetonitrile-water (0-5 min: 5%, 5-40 min: 5–100%, 40-45 min: 100%) with 0.1% formic acid over 45 min at a flow rate of 1 mL min⁻¹.



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