



A CYCLIC HEPTAPEPTIDE FROM VACCARIA SEGETALIS

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Abstract—A new cyclic heptapeptide, segetalin E, cyclo(-Gly-Tyr-Val-Pro-Leu-Trp-Pro-), has been isolated from the seeds of Vaccaria segetalis and the structure elucidated by extensive two-dimensional NMR methods and chemical degradation.

INTRODUCTION

As part of our continuing study of cyclic peptides from higher plants [1-2], we have investigated several cyclic peptides from Vaccaria segetalis, named segetalins which have oestrogen-like activity [3-5]. In addition, a conformational form of segetalin A analysed by NMR and computational methods have also been reported [6]. The seeds of Vaccaria segetalis have been used to activate blood flow and promote milk secretion. Furthermore, it is commonly used to treat amenorrhea and breast infections in China [7]. Further chromatographic purification of an ethyl acetate-soluble fraction of V. segetalis led us to isolate a new cyclic heptapeptide, named segetalin E (1). This paper deals with the isolation and structural elucidation of 1.

RESULTS AND DISCUSSION

The concentrated methanol extract of the seed of Vaccaria segetalis was extracted with ethyl acetate, followed by 1-butanol. The ethyl acetate phase was successively separated by silica gel column chromatography with a gradient system (CH₂Cl₂-methanol) and was subjected to HPLC on an ODS column with 37% CH₃CN containing 0.05% TFA to furnish a new cyclic heptapeptide, segetalin E (1, 0.004% yield), together with segetalins A-D (segetalin A: cyclo(-Gly-Val-Pro-Val-Trp-Ala-); segetalin B: cyclo (-Gly-Val-Ala-Trp-Ala-); segetalin C: cyclo (-Gly-Leu-His-Phe-Ala-Phe-Pro-); segetalin D: cyclo (-Gly-Leu-Ser-Phe-Ala-Phe-Pro-)] [3, 5].

The FAB-mass spectrum of 1 gave an $[M+1]^+$ at 813 and the molecular formula, C₄₃H₅₆N₈O₈, which

was permitted by HR-FAB mass spectrum, indicating

20 degrees of unsaturation, was established. Because the IR absorption bands (3310 and 1635 cm⁻¹) characteristics of amino and amide carbonyl groups indicated 1 to be a peptide, it was subjected to the standard amino acid analysis, which implied the presence of 1 mol each of Gly, Tyr, Leu, Val, and 2 mol of Pro. The 1H NMR spectrum in pyridine-d₅ indicated five amide NH signals between δ 8.42 and δ 9.95, and an indole NH signal at δ 12.12. The ¹³C NMR spectrum revealed seven carbonyl signals, which were involved in amide linkage. Analyses of the aromatic region of the 'H and ¹³C NMR spectra provided evidence for an indole ring system, indicating Trp. From the molecular formula and from ¹H and ¹³C NMR data, it became evident that 1 was a cyclic peptide. Complete assignments for the ¹H and 13 C NMR resonances in pyridine- d_5 (Table 1), were accomplished using combination of two-dimensional NMR experiments such as HMQC [8] and PFG-HMBC [9] spectra. The stereochemistry of each amino acid was confirmed to be all L-configuration by Marfey's derivation, followed by HPLC analysis [10].

The HMBC analyses suggested the seven amino acid sequence presented in structure 1. Two segments, Pro-Gly-Tyr-Val and Pro-Leu-Trp were assigned by two bond ¹H-¹³C correlations as follows; NH (Gly1)/CO (Pro7), NH (Tyr2)/CO (Gly1), NH (Val3)/CO(Tyr2), and NH (Leu5)/CO (Pro4), NH (Trp6)/CO (Leu5) (Fig. 1). Two structural units analysed by the HMBC correlations could be combined by ROE enhancements around two Pro residues in a phase-sensitive ROESY spectrum [11]. The ROE cross-peaks between Val3-H α and Pro4-H α , and between Trp6-H α and Pro7-H δ supported connectivities across Val3-Pro4 and Trp6-Pro7, respectively. Additional ROE correlations such as Tyr2-H α /Val3-NH, Leu5-NH/Trp6-NH, and Pro7-H α / Gly1-NH supported the above sequence and the structure of 1 was determined to be cyclo(-Gly-Tyr-Val-Pro-Leu-Trp-Pro-). A through-space interaction between

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Table 1. ¹H and ¹³C NMR signal assignments of segetalin E (1) in pyridine-d₅

Assignment	$\frac{\partial}{\partial_H}$ (int. mult, $J(Hz)$)	$\frac{^{13}\text{C NMR}}{\delta_{\text{C}}}$	Assignment	$\frac{^{1}\text{H NMR}}{\delta_{_{ ext{H}}}}$	13 C NMR $\delta_{\rm C}$
α	4.00 (1H, dd, 6.3, 16.8)	40.65	α	5.03 (1H, dd, 4.4, 8.2)	55.07
	4.15 (1H, dd, 6.3, 16.8)		β	2.00(1H, m)	40.05
NH	8.44 (1H, t, 6.3)		ŕ	2.17(1H, m)	
C=O		168.21	γ	1.83 (1H, m)	24.92
Tyr2			$\stackrel{\cdot}{\delta}$	0.90(3H, s)	20.60
α	5.12 (1H, ddd, 3.9, 7.5, 10.1)	54.70		0.96 (3H, d, 6.5)	22.39
β	3.09 (1H, dd, 3.9, 13.6)	35.98	NH	8.96 (1H, d, 8.2)	
	3.34 (1 <i>H</i> , <i>dd</i> , 10.1, 13.6)		C=O		172.07
γ		128.73	Trp6		
δ	7.24 (2H, d, 8.5)	130.19	α	5.29 (1H, ddd, 4,2, 6.3, 6.5)	52.76
arepsilon	7.01 (2H, d, 8.5)	115.19	$oldsymbol{eta}$	3.66 (1H, dd, 4.2, 15.0)	26,94
ζ		156.37	,	3.93 (1H, dd, 6.3, 15.0)	
NH	8.67 (1H, d, 7.5)		NH	8.42 (1H, d, 6.5)	
C=O	,	172.53	1(NH)	12.12 (1H, s)	
Val3			2	8.01 (1H, d, 2.2)	125.35
α	4.46(1H, dd, 5.0, 8.0)	58.77	3	, , ,	108.66
β	2.17 (1H, m)	29.68	4	8.22 (1H, d, 7.5)	118.40
γ	0.96(3H, s)	18.47	5	7.23 (1H, t, 7.5)	121.07
	1.09 (3H, d, 6.9)	18.51	6	7.21 (1H, t, 7.5)	118.74
NH	9.95 (1H, d, 5.0)		7	7.51 (1H, d, 7.5)	111.39
C=O		170.60	8	, , , ,	136.30
Pro4			9		128.31
α	4.95 (1H, d, 6.4)	60.98	C=O		171.03
β	1.83(1H,m)	30.12	Pro7		
	2.81 (1H, dd, 6.4, 11.8)		α	4.42 (1H, dd, 7.2, 9.3)	58.77
γ	1.75(2H, m)	21.54	β	2.07(1H, m)	28.37
δ	3.49 (1H, m)	45.57	<i>i</i> -	1.88 (1H, m)	
	3.78(1H, m)		γ	1.88 (1H, m)	25.20
C=O	• • •	170.43	,	1.59 (1H, m)	
			δ	3.28 (2H, <i>m</i>)	47.12
			C=O		171.54

Val3-H α and Pro4-H α is indicative of a *cis* peptide bond between Val3 and Pro4, which is also supported by the carbon resonances (δ 30.12 and δ 21.54) of β and γ in Pro4 [12], and the occurrence of a doublet

signal of H α in Pro4 has also been correlated the *cis* peptide bond [13]. Segetalin E showed moderate cell growth inhibitory activity against P-388 cells (IC_{50} 40 μg ml⁻¹).

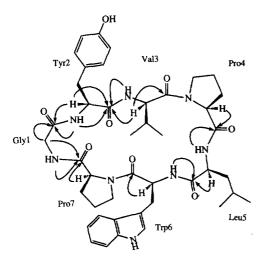


Fig. 1. Structure of segetalin E (1); arrows show some important HMBC correlations.

EXPERIMENTAL

General. IR and UV spectra were recorded on JASCO A-302 spectrometer and Hitachi 557 spectrophotometer, respectively. Optical rotation was measured with a JASCO DIP-4 spectrometer and $[\alpha]_D$ values are given in 10⁻¹ deg. cm² g⁻¹. FABMS and HRMS with a VG Autospec spectrometer. HPLC was performed with an Inertsil PREP-ODS column (20 mm i.d. \times 250 mm and 30 mm i.d. \times 250 mm, GL Science Inc.) packed with 10 μ m ODS. Peptide-containing fractions were traced by TLC on precoated TLC plated 60 F₂₅₄ (Merk) using a solvent system consisting of $CHCl_3/MeOH = 8.5:1.5$ in a saturated chamber. All NMR spectroscopy was carried out on a Varian Unity 400 spectrometer. The spectra were recorded at 300 K at a concn of 20 mg ml $^{-1}$ in pyridine- d_5 . The phasesensitive ROESY experiments were acquired with mixing times of 90 msec. The delay to optimize onebond correlations in the HMQC spectrum and suppress them in the HMBC spectrum was 150 msec and the evolution delay for long-range couplings in the HMBC spectrum was set to 90 msec.

Plant Material. The seeds of V. segetalis were purchased in Shanghai, the Peoples Republic of China in May, 1993. The botanical identification was made by Dr Zhi-Sheng Qiao, Department of Pharmacognosy, College of Pharmacy, Second Military Medical University, Shanghai, China. A voucher specimen has been deposited in the herbarium of the Tokyo University of Pharmacy and Life Science.

Extraction and isolation. The seeds of V. segetalis (5 kg) were extracted with hot MeOH × 3 to give a MeOH extract which was treated with EtOAc, n-BuOH and H₂O. The EtOAc sol. fraction (47 g), was subjected to silica gel CC using a CH₂Cl₂-MeOH gradient system (1:0-0:1). The fraction eluted by 15% MeOH was finally subjected to ODS HPLC with 37% CH₃CN containing 0.05% TFA solvent system to give segetalin E (200 mg) as colourless needles.

Segetalin E (1). Needles, mp 166–168° (from MeOH), $[\alpha]_D$ – 59° (c 0.40, MeOH); m/z 813 (Found: M⁺ + H, 813.4339. C₄₃H₅₇N₈O₈ requires, 813.4299); $\nu_{\rm max}$ (KBr)/cm⁻¹ 3310 (NH), 1635 (amide C=O) and 1516; $\lambda_{\rm max}$ (MeOH)/257 nm (ε 2400).

Amino acid analysis. Segetalin E (1 mg) was hydrolysed in 1 ml 6 M HCl in a sealed vial at 110° for 24 h. HCl was removed under red. pres., and residue was dissolved in 0.02 M HCl. Amino acids were determined by ion-exchange resin chromatography on a Hitachi L-8500 amino acid analyser with ninhydrin detection.

Absolute configuration of the amino acids. A soln of segetalin E in 6 M HCl was heated at 110° for 12 hr. After being cooled, it was concd to dryness. The residue was soluble in $\rm H_2O$ and treated with 1 - fluoro - 2,4 - dinitrophenyl - 5 - L - alanine amide (Marfey's reagent) and 1 M NaHCO₃ at 35° for 1 hr. After being cooled, 2 M HCl was added and then concd to dryness. This residue was subjected to HPLC (Lichrospher 100, RP-18 (10 μ m), Merck), 1 ml min⁻¹, detection 340 nm, solvent: 10–50% CH₃CN–50 mM triethylamine phosphate (TEAP) buffer.

Cytotoxic activity on P388 cells. The MTT (3 - [4,5 - dimethylthiazol - 2 - yl] - 2, 5 - diphenyltetrazolium bromide) colorimetric assay was performed in a 96-well plate. The blue formazan produced by the mitochondrial dehydrogenase of viable cells was measured spectrophotometrically. RPMI-1640 medium, $100~\mu l$, supplemented with 5% fetal calf serum and $100~\mu g$ ml $^{-1}$ kanamycin and containing mouse P388 leukaemia

cells $(3 \times 10^4 \text{ cells ml}^{-1})$ was added to each well. After overnight incubation $(37^\circ, 5\% \text{ CO}_2)$, 100, 30, 10, 3, 1, 0.3, and $0.1~\mu\text{g ml}^{-1}$ of sample solns were added to the wells and the plates were incubated for 48~hr. Then, $20~\mu\text{l}$ of MTT was added to each well and the plates were incubated for 4~hr. The resulting formazan was dissolved in $100~\mu\text{l}$ of 10% SDS containing 0.01~M HCl. Each well was mixed gently with a pipette for 1~or~2~min and the plate was read on a microplate reader (Tosoh MPR-A4i) at 540~nm. The $IC_{50}~(\mu\text{g ml}^{-1})$ value was defined as the concn of sample which achieved 50% reduction of viable cells with respect to the control.

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