

¹H AND ¹³C NMR STUDIES OF CONFORMATIONAL BEHAVIOUR OF LEU-ENKEPHALIN

C. GARBAY-JAUREGUIBERRY, B. P. ROQUES⁺ and R. OBERLIN

⁺*Département de Chimie Organique, ERA 613 CNRS, Université René Descartes, 4, Avenue de l'Observatoire, 75270 Paris, Cedex 06, France*

M. ANTEUNIS

Laboratory for NMR Spectroscopy, University of Gent, Krijgslaan 271, Gent B-9000, Belgium

S. COMBRISSE

Ecole de Physique et Chimie, 10, Rue Vauquelin, 75005 Paris

and

J. Y. LALLEMAND

ENS 24, Rue Lhomond, 75005 Paris, France

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1. Introduction

Since the isolation from brain tissues by Hughes et al. [1] of two pentapeptides (Met-enkephalin and Leu-enkephalin) which interact with opiate receptors, a number of other endogenous peptides have been shown to share this property [2].

All these compounds (except Leu-enkephalin) are fragments of β -lipotropin and have in common the Met-enkephalin 61–65 N-terminal part of this peptide.

We have recently studied by ¹H and ¹³C NMR the preferential conformation of Met-enkephalin in DMSO-*d*₆ solution [3,5]. Our results and those of Gibbons obtained independently [6] are in favour of a folded conformation (β_1 -turn) bearing a structural analogy between morphine and the N-terminal part of the peptide.

Many synthetic derivatives of enkephalins have been prepared and their affinities for opiate receptors tested [7–9]. Few structural modifications are allowed and decisive features for receptor interaction seem to be the presence and location of the aromatic side chains of the tyrosine and phenylalanine residues.

On the other hand the inactivation of enkephalins has been shown to take place through cleavage of the Tyr–Gly amide bond. From this knowledge, two groups [10,11] have prepared the D.Ala₂ Met-enkephalin which is an enzyme-resistant analog and elicits a potent long-lasting analgesia.

Compared to Met-enkephalin, the natural peptide Leu-enkephalin exhibits a lower affinity for opiate receptors in vitro [9].

In order to obtain informations about the structure activity-relationships between the two natural peptides, we have studied the preferential conformation of Leu-enkephalin in DMSO-*d*₆ by ¹H and ¹³C NMR.

2. Materials and methods

2.1. Synthesis of Leu-enkephalin

Large quantities of Leu-enkephalin were prepared by standard liquid-phase synthesis as previously described for Met-enkephalin [4] using L.Leu.OMe in place of L.Met.OMe. Leu-enkephalin (F : 216°C) was purified by crystallization (MeOH/H₂O – 9/1).

Table 1
Chemical-shifts and J -coupling in Leu-enkephalin at 40°C

Residue	Shifts (ppm/TMS)				Coupling constants (J in Hz)				
	H_α	H_β	NH	Other	$^2J_{\alpha_1\alpha_2}$	$^3J_{\alpha\beta}$	$^2J_{\beta_1\beta_2}$	$^3J_{NH-H_\alpha}$	Other
Tyr ₁	3.5 _s	2.9		Arom. 7.0 H_m 6.7 H_o		5.0	13.5		$J_{o,m} = 8.5$
Gly ₂	3.5		8.4					~4.5 ^a (twice)	
Gly ₃	3.6		7.9		17.8 ^a			5.5–6 ^a (twice)	
Phe ₄	4.5	3.1	8.1	Arom.		4.0	13.8	8.5	
		2.8		7.2		9.5			
Leu ₅	4.1	1.5	7.9 _s	CH-(CH ₃) ₂ 1.6 0.9		12	14	7.8	$J_{CH-CH_3} = 6.5^b$ $J_{CH-H_{\beta 1}} = 5.5^b$ $J_{CH-H_{\beta 2}} = 7.5^b$

^aComputed values^bComputed values at 90°CChemical-shifts and J -coupling in Leu-enkephalin at 40°C

3.1.3. Determination of the preferential conformation of Leu-enkephalin

From the conformational angles determined in table 2 we can reject a γ -turn [19,20] involving the CO of Gly₃ and NH of Leu₅ for the profit of a β -turn.

As for Met-enkephalin [3,4] we suggest a β_1 -bend

to be the lowest energy-chain reversal conformation for Leu-enkephalin. The angular parameters required for this type of bend [18] ($\phi_{i+1} = -60^\circ$, $\psi_{i+1} = -30^\circ$ and $\phi_{i+1} = -90^\circ$, $\psi_{i+2} = 0^\circ$) are satisfied when residues $i+1$ and $i+2$ are identified with Gly₃ and Phe₄. Consequently such a β_1 -turn does involve the

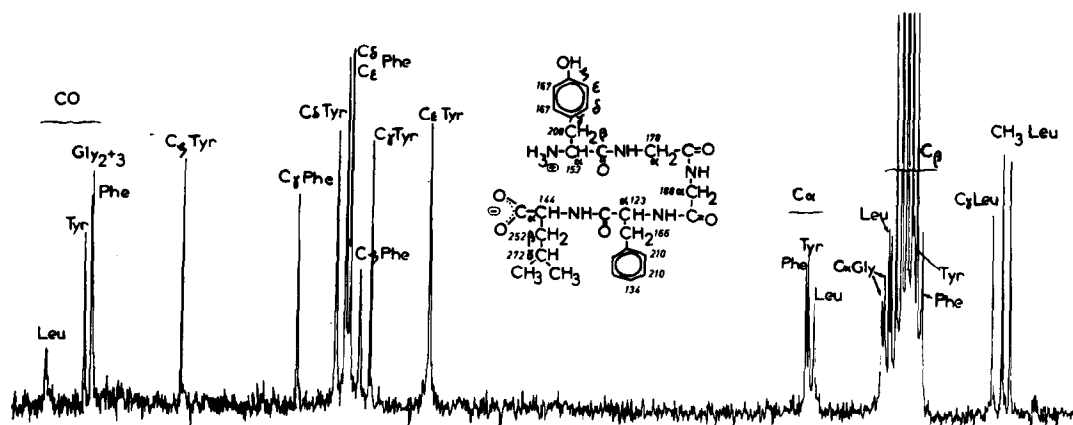


Fig.2. Plots of δNH (ppm) versus temperature ($^\circ C$).

Table 2
Conformational parameters in Leu-enkephalin at 40°C

Residue	θ°	ϕ°	ψ°	Rotamers population		
				<i>a</i>	<i>b</i>	<i>c</i>
Tyr			$\pm 60^a$	0.49 ^b	0.22 ^b	0.29
Gly ₂		+ 90	+ 30 and -60 to -120			
	± 30	+ 30	$\sim + 60$			
	± 120	- 60	$\sim - 30$			
		± 180	$\pm (60 \text{ to } 180)$			
Gly ₃	± 10	+ 50	+ 30 and -120			
	± 130	± 70	± 30 and -120			
		- 170	$\pm (60 \text{ to } 180)$			
Phe ₄	+ 150	- 90	0 \pm 30	0.63 ^b	0.10 ^b	0.27
	+ 210	- 150	-60 and 120 \pm 40			
Leu ₅	+ 145	- 85		$\sim 1.0^b$	$\sim 0.0^b$	~ 0.0
	+ 215	- 155				

^aMost probable value

^bThe attribution of rotamers 'a' and 'b' may be reversed if the signal locations for the β -protons pro *R* and pro *S* are opposite

Conformations quoted 'a', 'b' and 'c' are those with C β -C R bond antiperiplanar to respectively the carbonyl O=O, the peptide-NH and C α -H bond.

Gly₂, Gly₃, Phe₄ and Leu₅ residues with a hydrogen bond between the CO of Gly₂ and NH of Leu₅ in accordance with the small temperature variation for the NH of Leu₅. A $\beta_{II'}$ -type bend, although predicted [18,21] to be less energetically favoured than a type I cannot be rejected definitively because the values determined for Gly₃ and Phe₄ (table 2) are closed to those described in a $\beta_{II'}$ -type bend ($\phi_{i+1} = +60^\circ$, $\psi_{i+1} = -120^\circ$, $\phi_{i+2} = -80^\circ$, $\psi_{i+2} = 0^\circ$) with these residues at the *i* + 1 and *i* + 2 positions of the turn [18].

For the residues not included in the chain reversal we propose to take the values ($\phi_2 = 180^\circ$, $\phi_5 = -155^\circ$) for Gly₂ and Leu₅ which favour a final folded structure with a head-to-tail interaction between NH₃⁺ and COO⁻ as proposed in Met-enkephalin [4].

The somewhat smaller temperature dependence of the NH of Gly₃ cannot be explained by a γ -turn between the CO of Tyr₁ and NH of Gly₃ because the ϕ , ψ values (table 2) are not in accordance with those required [19,20] for such a bend.

Except for Gly₂, the coupling constants are not largely modified by an increase of temperature indicating that the conformation of the backbone is well defined. At 80°C, the coupling constant $^3\text{JNH-CH}_2$ in Gly₂ becomes < 0.8 Hz. Nevertheless this decrease is not necessarily related to conformational changes. The exchange of the NH-proton following the NH₃⁺ of the first amino acid rises with temperature ($\tau < 1/J$) which prevents the existence of coupling constant [22,23].

The side-chain rotamer populations listed in table 2, show that for Tyr and Phe, the two possible *trans*-gauche rotamers are favoured but like in Met-enkephalin the others have significant populations. On the opposite in the residue Leu only one *trans*-gauche rotamer around χ_1 is populated.

3.2. ^{13}C NMR chemical-shifts and T_1 relaxation times

Figure 3 shows the ^{13}C spectrum of Leu-enkephalin (0.1 M in DMSO-*d*₆/D₂O, 1/1) at 38°C. The assignments of all the ^{13}C -resonances were made by comparison with those of Met-enkephalin [5]. The experi-

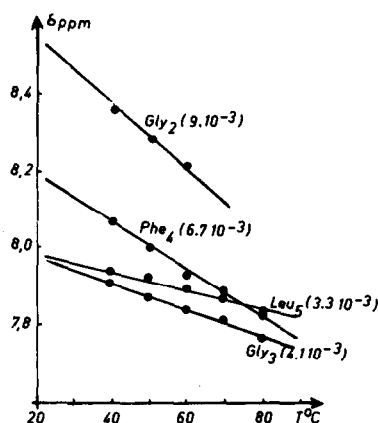
Fig.3. ^{13}C Spectrum of Leu-enkephalin.

Table 3
 ^{13}C Chemical-shifts and relaxation-time of Leu-enkephalin in DMSO- D_2O

Tyr	$\text{CH}\alpha$	55.2	0.143
	$\text{CH}_2\beta$	37.1	0.208
	$\text{C}\gamma$	126.1	1.5
	$\text{CH}\delta$	131.6	0.167
	$\text{CH}\epsilon$	116.6	0.167
	$\text{C}\zeta$	156.4	1.0
	C=O	171.9	1.5
Gly	$\text{CH}_2\alpha^a$	43.4	0.178
	C=O^b	170.9	2.0
Gly	$\text{CH}_2\alpha^a$	43.0	0.188
	C=O^b	170.8	1.7
Phe	$\text{CH}\alpha$	55.5	0.123
	$\text{CH}_2\beta$	38.1	0.166
	$\text{C}\gamma$	137.8	1.6
	$\text{CH}\delta$	129.4	0.210
	$\text{CH}\epsilon$	130.1	0.210
	$\text{CH}\zeta$	127.7	0.134
	C=O^b	170.6	0.9
Leu	$\text{CH}\alpha$	55.0	0.144
	$\text{CH}_2\beta$	42.2	0.253
	$\text{CH}\gamma$	25.5	0.272
	$\text{CH}_3\delta$	23.9	1.5
	$\text{CH}_3\delta$	22.6	1.7
	C=O	178.2	0.8

^{ab}These assignments may be reversed

mental data (δ , T_1) are reported in table 3. All the protonated ^{13}C exhibit a maximum NOE and thus their relaxation is only due to a dipole-dipole mechanism.

The T_1 -values for the CH_α of the backbone are of the same order and these results imply the same correlation time for the motions of all these carbons including those of the terminal residues. Phe₄ and Leu₅ side-chains have significant internal rotational freedom contrasting with that of Tyr₁-residue which exhibits no reorientation about its $\text{C}_\gamma\text{--C}_\zeta$ axis. All these results were found in Met-enkephalin [5] and the behaviour of Tyr has been attributed to a restricted motion with respect to the backbone and related to the mechanism of ligand-receptor interaction for this peptide [24].

In fact the smaller NT_1 -values of Tyr-residue were also found in the peptide precursors of enkephalin (to be published) and these results show that the T_1 measurements of Tyr should be interpreted with care in terms of conformational behaviour.

4. Conclusion

As shown by the NH temperature-dependence the conformational preference of the backbone of Leu-enkephalin is not as well defined as in Met-enkephalin.

In Leu-enkephalin it seems that the energy difference between at least two β -bends is small and there could exist a rapid equilibrium between these forms. However, in all cases it appears that Leu-enkephalin exhibits a highly folded structure as shown by the conformational preference of the Leu₅ side-chain which should not be restricted in a time averaged rotational conformation.

Many structural analogs of the enkephalin were prepared but it seems that the L.Tyr₁- and L.Phe₄-residues are essential for activity [7-9]. Thus the topological requirements between these aromatic rings are certainly of great importance particularly if the Phe-ring is involved in a folded part of the peptide. On the other hand, the replacement of Gly₂ by D.Ala₂ leads to a more active compound because it is not cleaved by the brain enzymes. The inactivation is easily obtained in the natural peptide by the relative freedom of the N.Tyr-Gly moiety. Due to the presence of many conformational rotamers for Tyr and Phe

side-chains, there may not be a simple relationship between the rotamers populations and the side-chain conformations at the receptor, although the *trans*-gauche rotamer of Tyr which presents the best geometrical analogy with morphine is also the most populated. Hence the differences in analgesic potencies between Met-enkephalin and Leu-enkephalin could be related to the life-time of the ligand-receptor complex but cannot be easily explained by our conformational study. Nevertheless such relationships between conformation and affinity for the receptor should be reinvestigated on the various classes of binding sites of enkephalins recently evidenced in rat-striatum [25,26].

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