

Synthesis and conformational analysis of a series of galactosyl enkephalin analogues showing high analgesic activity

J.L.Torres, H.Pepermans^{1,2}, G.Valencia, F.Reig, J.M.García-Antón and G.Van Binst¹

Laboratory of Peptides, CID–CSIC, Jordi Girona 18–26, 08034 Barcelona, Spain, and ¹Eenheid Organische Chemie (ORGC), Vrije Universiteit Brussel, Pleinlaan 2, B-1050 Brussels, Belgium

²Present address: Unilever Research Laboratories, O.Van Noortlaan 120, 3133 AT Vlaardingen, The Netherlands

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Two galactosyl derivatives of [DMet²,Pro⁵] enkephalinamide (compound 1), namely [DMet²,Pro⁵] enkephalin [*N*^{1,5}-β-D-galactopyranosyl] amide (compound 2) and *O*^{1,5}-(β-D-galactopyranosyl) [DMet²,Hyp⁵] enkephalinamide (compound 3) have been synthesized. Such glycosylpeptides have been shown to be extremely potent analgesic agonists. The conformational analysis of these three compounds in DMSO-d₆ solution has been carried out using two-dimensional NMR methods. Both the parent compound (1) and the β*N*-galactosyl derivative (2) show similar NMR parameters which are consistent with fairly rigid β-strands at both the N-terminus and C-terminus, connected by a glycine residue that displays a mixture between multiple conformational states. Thus, although the β*N*-galactosyl derivative (2) has been shown to be significantly more potent than the parent compound (1) in the tail immersion and paw pressure tests of analgesia, no correlation can be established between the conformation of (1) and (2) in DMSO and the difference in analgesic activity. In contrast, important conformational differences with respect to (1) and (2) have been detected in the β*O*-galactosyl derivative (3). In this case, only one of the likely conformations for (1) and (2) are consistent with the experimental data. These data show that the position of the galactose residue in compound (3) causes Gly³ to lose flexibility leading to a more rigid folded conformation. Such a change in conformation could be related to the difference in analgesic activity between (2) and (3).

Key words: glycosyl peptides/enkephalin analogues/analgesic peptides/conformational analysis/two-dimensional NMR

Introduction

There is increasing evidence that the carbohydrate moieties of glycopeptides and glycoproteins play an important role in their biological activity and selectivity. It has become widely accepted that exposed sugar residues of glycoproteins or glycolipids serve as determinants for receptor recognition. In this sense, carbohydrate residues linked to proteins have been reported to be involved in such crucial processes as cell growth and cell differentiation (Olden *et al.*, 1985) and infection (Ofek *et al.*, 1978). It has also been found that different mammalian receptors exhibit a considerable and

specific affinity for either D-glucose or D-galactose containing glycoproteins (Ashwell and Harford, 1982; Lunney and Ashwell, 1976). Considering that this selection mechanism might hold for many analogous glycoproteins and for mammals in general (Ashwell and Morell, 1974), the incorporation of sugar moieties could give an improvement of the selectivity of pharmaceuticals towards different receptors.

In earlier papers we reported a considerable increase in analgesic activity after incorporation of D-glucose and D-galactose residues into enkephalins (Torres *et al.*, 1988; García-Antón *et al.*, 1987). These results encouraged us to further investigate the influence of the sugar moieties in the activity and selectivity of such glycopeptides. Thus, we have incorporated the same sugar moieties into different positions in the parent peptide.

In the present work we describe the synthesis of a series of potent analgesic galactosyl enkephalins. For comparative purposes we selected the same parent compound that we used before (Torres *et al.*, 1988; García-Antón *et al.*, 1987), [DMet²,Pro⁵] enkephalinamide (Bajusz *et al.*, 1977), (compound 1). This enkephalin analogue is a potent μ-selective agonist (Shaw and Turnbull, 1978) that shows a selectivity ratio μ/δ = 30. The galactosyl moieties have been incorporated into the fifth amino acid both via a β*N*-glycosyl linkage between the C-terminal proline and β-D-galactopyranosylamine to give [DMet²,Pro⁵] enkephalin [*N*^{1,5}-β-D-galactopyranosyl] amide (compound 2) and via β*O*-glycosyl bond formation between the hydroxyl group of hydroxyproline and β-D-galactopyranose to give *O*^{1,5}-(β-D-galactopyranosyl) [DMet²,Hyp⁵] enkephalinamide (compound 3). The schematic structures of both the *N*- and *O*-glycosyl enkephalin derivatives, as well as the parent compound, are shown in Figure 1.

The *in vivo* analgesic activity of these three compounds has been studied. Even though this material is due to be published elsewhere, we wish to summarize here some significant data related to the NMR data. The *O*-galactosyl derivative (3) is the most active of these analogues and one of the most potent *in vivo* opioid peptide agonists synthesized up to now. This galactosyl analogue has proved to be >50 000-fold more potent than morphine and 1000-fold more potent than the parent compound (1) in rats, in both the tail immersion and paw pressure tests of analgesia after intraventricular administration (10 animals) (Rodríguez *et al.*, 1989). Compound (2) is also a potent analogue but ~10 times less potent than compound (3) in the same test of analgesia (Rodríguez *et al.*, 1989). These significant results have led us to question whether any conformational changes could be related to such an important increase in analgesic activity induced by the sugar moieties of such glycosyl enkephalins.

The conformational properties of both naturally occurring enkephalins and their synthetic analogues have been widely studied by many authors using spectroscopic methods, X-ray

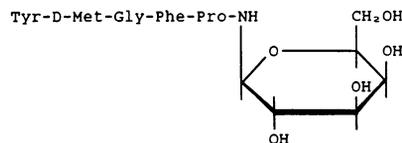
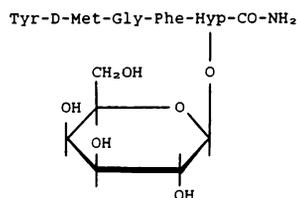
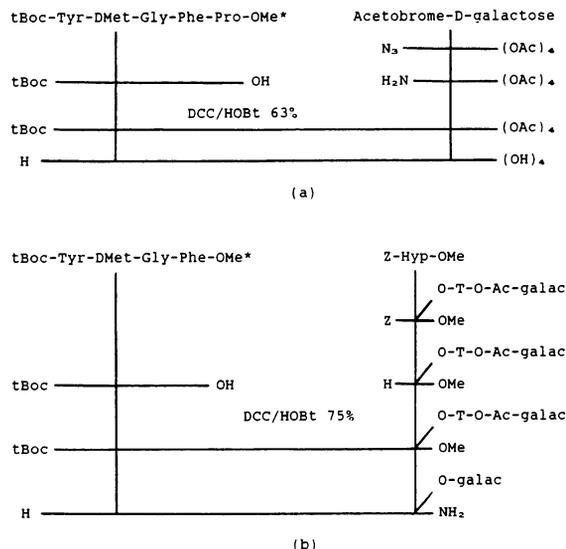
Tyr-D-Met-Gly-Phe-Pro-NH₂[DMet²,Pro³] enkephalin amide (1)[DMet²,Pro³] enkephalin [N^1 - β -D-galactopyranosyl] amide (2) O^1 - β -(β -D-galactopyranosyl)[D-Met²,Hyp³] enkephalin amide (3)

Fig. 1. Schematic structures of the parent compound (1) and the galactosyl derivatives (2) and (3).

crystallography and energy calculations (for reviews see Rapaka *et al.*, 1986; Schiller, 1984). Theoretical studies on low energy conformations of enkephalins indicate that both β -turns and extended forms are possible stable conformations in equilibrium (Loew and Burt, 1978; De Coen *et al.*, 1977; Wijne, 1980; Manavalan and Momany, 1981; Paine and Scheraga, 1985, 1986; Purisima and Scheraga, 1987). Experimental methods have also led to many different conclusions. Thus, several authors have detected folded conformations of enkephalins in DMSO or water solutions, mainly by NMR measurements (Garbay-Jaureguiberry *et al.*, 1976, 1980; Jones *et al.*, 1976; Momany, 1977), whereas some other authors find no proof for the existence of stable folded conformations in solution for such small peptides, neither from NMR data (Motta *et al.*, 1987; Higashijima *et al.*, 1979) nor from UV and circular dichroism data (Spirtes *et al.*, 1978). Nevertheless, Higashijima *et al.* (1979) pointed out the importance of ionization in the resulting conformation. They suggested that folded dipolar forms could be stabilized by head to tail interactions between the two charged ends of the peptide.

Most of these conformational analyses of enkephalins were based on 1D NMR measurements. For many years, the presence of folded conformations in solution has been mainly supported by both low temperature coefficients of NH chemical shifts and coupling constants. Modern NMR techniques allow the measurement of other spectroscopic parameters, in particular nuclear Overhauser effects (NOEs), which lead to more unequivocal conclusions. Such techniques have been successfully used in the determination of protein structures (Wüthrich, 1986). However, two problems hamper the application of NOE techniques to peptides of the size of enkephalins. Firstly their unfavourable $\omega_0\tau_0$



* Prepared following the stepwise liquid phase procedure by using mixed anhydrides (Isobutylchloroformate) as activated N-protected amino acids (Torres *et al.*, 1988).

Fig. 2. Synthesis of compounds (2) and (3). Glycosylation strategies.

values make it difficult to detect NOEs. This problem can be avoided either by changing the magnetic field strength or by increasing the solvent viscosity at low temperatures (Motta *et al.*, 1988). A different approach is to measure the NOEs in the rotating frame, for which no $\omega_0\tau_0$ condition yields zero NOEs (Bothner-By *et al.*, 1984). Secondly, the flexibility of small linear peptides causes them to show a wide number of conformations in solution and averages the measured conformation-dependent parameters, NOEs in particular (Jardetzky, 1980; Kessler *et al.*, 1988). In the present work we describe the conformational study of the new series of galactosyl enkephalins in DMSO- d_6 solutions using NOESY and ROESY experiments.

Results

Synthesis

Compounds (2) and (3) have been synthesized following different strategies. The best reaction pathways among those tested are shown in Figure 2. The preparation of (2) includes the βN -glycosylation of the pentapeptide tBoc-Tyr-DMet-Gly-Phe-Pro-OH (63% yield) (Figure 2a) whereas compound (3) was obtained by previous βO -glycosylation of protected hydroxyproline and subsequent incorporation of this galactosyl amino acid, after saponification, to the rest of the peptide fragment (Figure 2b). In this case two hydroxyl protecting groups on the sugar moiety have been used. The best chemical yields were obtained by using acetylated sugars instead of the bulkier benzyl derivatives. Thus in the coupling between O^1 -(2,3,4,6-tetra- O -acetyl- β -D-galactopyranosyl) hydroxyproline methyl ester and tBoc-Tyr-DMet-Gly-Phe-OH 75% yield was achieved compared to 29% using O^1 -(2,3,4,6-tetra- O -benzyl- β -D-galactopyranosyl) hydroxyproline methyl ester.

Conformational analysis

The conformation of (1), (2) and (3) in DMSO- d_6 was studied by ¹H-NMR at 270 MHz. All the signals were

Table I. The 270 MHz ^1H -chemical shifts of (1), (2) and (3) in $\text{DMSO-}d_6$

	Compound		
	(1)	(2)	(3)
Tyr NH_3^+	— ^a	— ^a	8.10
α	3.92	3.98	3.95
β_1	2.82	2.82	2.82
β_2	2.82	2.82	2.91
<i>ortho</i> H	6.96	6.96	6.96
<i>meta</i> H	6.62	6.65	6.65
DMet NH	8.57	8.62	8.58
α	4.25	4.26	4.33
β_1	1.70	1.72	1.76
β_2	1.55	1.58	1.61
$\gamma_{1,2}$	2.15	2.18	2.18
S- CH_3	1.95	1.98	1.96
Gly NH	8.13	8.20	8.18
α_1	3.65	3.68	3.70
α_2	3.50	3.55	3.52
Phe NH	8.19	8.12	8.15
α	4.65	4.67	4.66
β_1	3.00	2.98	3.04
β_2	2.68	2.73	2.71
aromatic H	7.15–7.27	7.15–7.27	7.15–7.27
Pro/Hyp α	4.18	4.31	4.27
β_1	1.92	2.00	2.17
β_2	1.74	1.94	1.95
γ_1	1.78	1.80	4.40
γ_2	1.78	1.80	
δ_1	3.56	3.62	3.82
δ_2	3.56	3.44	3.69
galac NH		8.25	
H1		4.65	4.17
H2		3.40	3.20
H3		3.30	3.25–3.30
H4		3.36	3.25–3.30
H5		3.30	3.25–3.30
H6		3.67	3.59

^aAt the current stage of the research it was not possible to assign neither hydroxyl chemical shifts nor Tyr NH_3^+ chemical shifts except for (3) in the latter case.

assigned by phase sensitive 2QF-COSY (Marion and Wüthrich, 1983) and Relayed-COSY (Weber and Müller, 1987) experiments. All assignments are listed in Table I.

The $^3J_{\text{HN}\alpha}$ coupling constants were measured from 1D spectra and are given in Table II. $^3J_{\alpha\beta}$ coupling constants for Phe⁴ were also measured from 1D spectra (see Table V).

Amide chemical shifts, their temperature coefficients and the $^3J_{\text{HN}\alpha}$ coupling constants are listed in Table II. The values are independent of concentration within experimental error.

NOEs were measured using NOESY (Kumar *et al.*, 1980) and ROESY (Bothner-By *et al.*, 1984) experiments. For qualitative purposes ROESY was found to be better than NOESY since more NOEs were detected. Some different values of mixing times (τ_m) were tested (50–200 ms). A time of 100 ms was found to be optimal for (2), whereas for (1) and (3) a τ_m of 200 ms was used. ROESY data can

Table II. Chemical shifts, temperature coefficients and coupling constants of the NH protons

		Residue			
		D-Met ²	Gly ³	Phe ⁴	galac ⁶
δ (p.p.m.)	(1)	8.57	8.13	8.19	
	(2)	8.62	8.20	8.12	8.25
	(3)	8.52	8.18	8.15	
$\Delta\delta/\Delta T$ (p.p.b./K)	(1)	–3.0	–3.0	–4.5	
	(2)	–2.5	–3.0	–4.5	–4.5
	(3)	–5.5	–8.5	–4.5	
$^3J_{\text{HN}\alpha}$ (Hz)	(1)	7.9	5.8 ^a	8.4	
	(2)	7.8	6.1 ^a	8.4	9.1
	(3)	7.9	5.7 ^a	8.4	

^aBoth $^3J_{\text{HN}\alpha}$ measured were equal.

Table III. Intrarresidual NOEs observed by ROESY in $\text{DMSO-}d_6$

	Correlation ^a	Compound		
		(1)	(2)	(3)
Tyr $\text{NH}_3^+ - \alpha\text{H}$		–	–	++
Tyr $\text{NH}_3^+ - \beta\text{H}$		–	–	+
Tyr <i>ortho</i> H – αH		++	++	++
Tyr <i>ortho</i> H – βH		+	+	+
Tyr <i>meta</i> H – βH		–	+	+
Tyr $\alpha\text{H} - \beta\text{H}$		+	+	+
D-Met NH – αH		+	+	+
D-Met NH – $\beta_1\text{H}$				+
D-Met NH – $\beta_2\text{H}$		+	++	++
D-Met NH – γH		++	++	++
D-Met $\alpha\text{H} - \beta_1\text{H}$		++	++	++
D-Met $\alpha\text{H} - \beta_2\text{H}$		++	++	++
D-Met $\alpha\text{H} - \gamma\text{H}$		++	++	+++
Gly NH – $\alpha_1\text{H}$	D ₁		+++	–
Gly NH – $\alpha_2\text{H}$	D ₂		+++	+++
Phe NH – αH		+	+	+
Phe NH – $\beta_1\text{H}$			++	
Phe NH – $\beta_2\text{H}$		+	++	++
Phe $\alpha\text{H} - \beta_1\text{H}$		++	++	++
Phe $\alpha\text{H} - \beta_2\text{H}$		+	++	+
Pro $\alpha\text{H} - \beta\text{H}$		++	++	++
Pro $\gamma\text{H} - \delta\text{H}$		++	++	
Hyp $\gamma\text{H} - \beta\text{H}$				++
galac NH – H1			+	
galac NH – H2			++	

^aLetter correlates with ROESY cross-peaks in Figures 4 and 5 and with short distances in Figure 6.

be found in Tables III (intrarresidual NOEs) and IV (inter-residual NOEs).

Our proposal for the backbone conformation of (1), (2) and (3) is based on (i) measurements of the $^3J_{\text{HN}\alpha}$ coupling constants, (ii) the occurrence of NOEs as measured by ROESY and NOESY experiments and (iii) the solvent exposure as revealed by the temperature dependence of the NH chemical shifts.

Experimental data seem to be similar for both the N-terminus and C-terminus of the three compounds in contrast with the obtained parameters for Gly³.

DMet² and Phe⁴ show $^3J_{\text{HN}\alpha}$ values of ~ 8 Hz, which correspond to ϕ_i torsion angles around -90° or -150°

(Phe⁴) and +90° or +150° (DMet²) when the equation:

$${}^3J_{\text{HN}\alpha} = 6.4 \cos^2\Theta - 1.4 \cos\Theta + 1.9,$$

with $\Theta = |\phi - 60^\circ|$ (L-AA) or $|\phi + 60^\circ|$ (D-AA), is used

Table IV. Interresidual NOEs observed by ROESY in DMSO-*d*₆ solutions

	Correlation ^a	Compound			
		(1)	(2)	(3)	
				303 K	333 K
$\alpha_i\text{H}-\text{NH}_{i+1}$					
Tyr $\alpha\text{H}-\text{D-Met NH}$	A	+++	+++	+++	-
D-Met $\alpha\text{H}-\text{Gly NH}$	B	+++	+++	+++	+
Gly $\alpha_1\text{H}-\text{Phe NH}$	C ₁	+++	+++	-	-
Gly $\alpha_2\text{H}-\text{Phe NH}$	C ₂	+++	+++	+++	+
Pro $\alpha\text{H}-\text{galac NH}$			++		
$\beta_i\text{H}-\text{NH}_{i+1}$					
Tyr $\beta\text{H}-\text{D-Met NH}$		+	++	+	-
$\alpha_i\text{H}-\delta_{i+1}\text{H}$					
Phe $\alpha\text{H}-\text{Pro } \delta_1\text{H}$		+++	+++		
Phe $\alpha\text{H}-\text{Pro } \delta_2\text{H}$		+++	+++		
Phe $\alpha\text{H}-\text{Hyp } \delta_1\text{H}$	E ₁			+++	++
Phe $\alpha\text{H}-\text{Hyp } \delta_2\text{H}$	E ₂			+++	++
Others					
Hyp $\gamma\text{H}-\text{galac HI}$	F			+++	++

^aLetters correlate with ROESY cross-peaks in Figures 3–5 and with short distances in Figure 6.

(Pardi *et al.*, 1984). Since in proteins (L-amino acids) ϕ angles of all residues except glycine have been reported to be in the range -30° to -180° (Richardson, 1981), both of the angles obtained for each amino acid are possible. Nevertheless, the detection of the similarly intense NH- αH , NH- $\beta_1\text{H}$ and NH- $\beta_2\text{H}$ ROESY cross-peaks both in DMet² and Phe⁴ leads to ϕ_i angles around $+150^\circ$ and -150° , respectively, since $\phi_2 = +90^\circ$ and $\phi_4 = -90^\circ$ are not consistent with NH- αH NOEs (Sherman *et al.*, 1987). In addition, the strong Tyr $\alpha\text{H}-\text{DMetNH}$, DMet $\alpha\text{H}-\text{GlyNH}$ and either Phe $\alpha\text{H}-\text{Pro}\delta_1\text{H}$ and Phe $\alpha\text{H}-\text{Pro}\delta_2\text{H}$ or Phe $\alpha\text{H}-\text{Hyp}\delta_1\text{H}$ and Phe $\alpha\text{H}-\text{Hyp}\delta_2\text{H}$ interresidual ROESY cross-peaks indicate that $\psi_1 \approx \psi_4 \approx +120^\circ$ and $\psi_2 \approx -120^\circ$ in the three compounds and Pro $\alpha\text{H}-\text{galacNH}$ NOE leads also to $\psi_5 \approx +120^\circ$ in (2) (Billeter *et al.*, 1982). The ϕ_i and ψ_i torsion angles obtained are consistent with the existence of two fairly rigid β -structures involving on one hand Tyr¹ and DMet² and on the other hand Phe⁴ and Pro⁵, extended to the galactose moiety in (2).

Following the Karplus equation given previously (Pardi *et al.*, 1984) and the Bystrov curves for glycol residues (Bystrov, 1976) the measured ${}^3J_{\text{HN}\alpha_1\alpha_2}$ vicinal coupling constants of Gly³, around 6 Hz, lead to $\phi_3 \approx +30^\circ$ or -30° for the three compounds. These torsion angles are consistent with the detection of NH- $\alpha_1\text{H}$ but not NH- $\alpha_2\text{H}$ NOEs, and NH- $\alpha_2\text{H}$ but not NH- $\alpha_1\text{H}$, respectively. The observation of both NOEs in (2) (ROESY cross-peaks D₁, D₂ in Table III and Figure 4) is then incompatible with the ${}^3J_{\text{HN}\alpha}$ data and indicates conformational heterogeneity. In contrast, only the NH- $\alpha_2\text{H}$

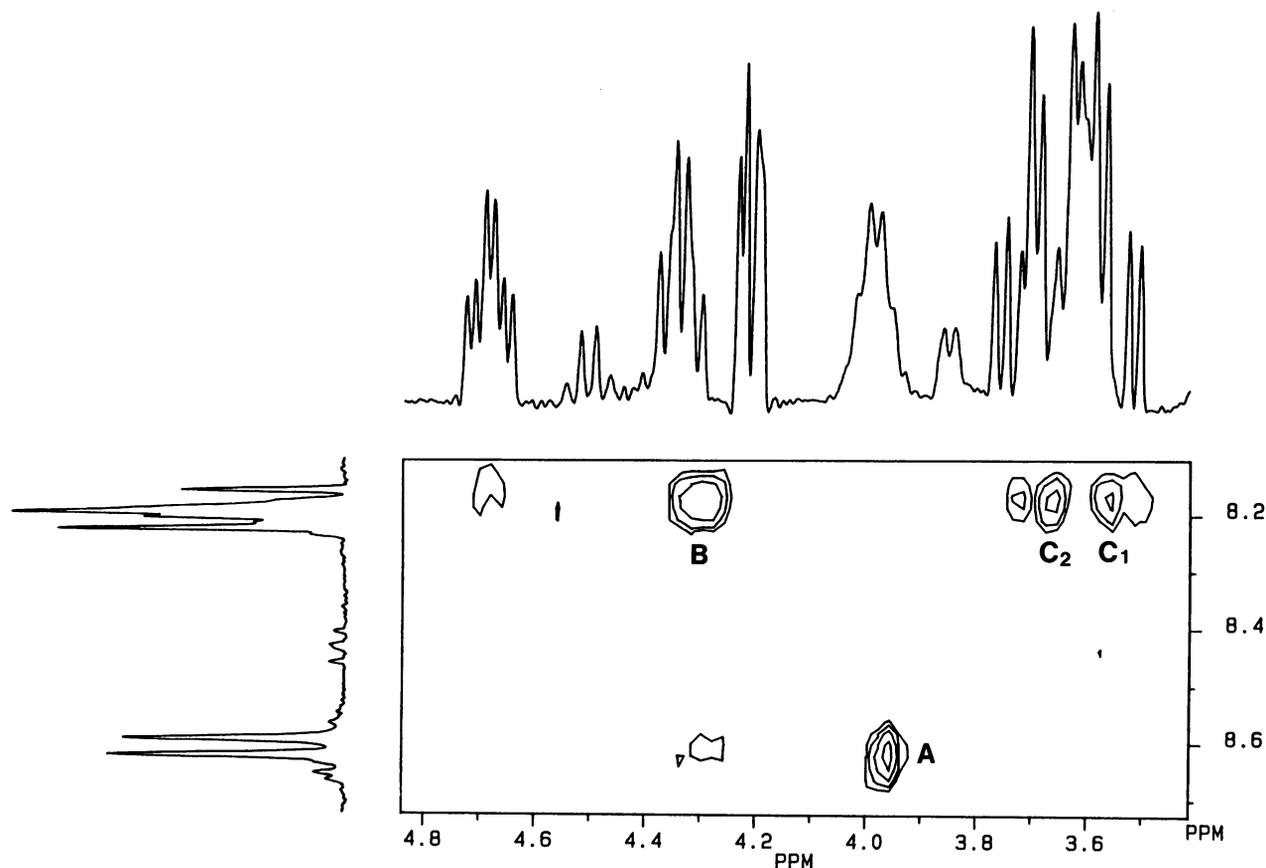


Fig. 3. ROESY spectrum of compound (1) in DMSO-*d*₆. NH- αH extensions where (A) Tyr $\alpha\text{H}-\text{DMet NH}$; (B) DMet $\alpha\text{H}-\text{Gly NH}$; (C₁) Gly $\alpha_1\text{H}-\text{Phe NH}$; (C₂) Gly $\alpha_2\text{H}-\text{Phe NH}$. 10 mM, 303 K, mixing time $\tau_m = 200$ ms. Negative levels are shown.

NOE was detected in (3) (ROESY crosspeak D₂ in Table III and Figure 5) which accounts for the existence of only one of those ϕ_3 possibilities. Which ϕ_3 corresponds to this observation is not known without stereospecific assignment of $\alpha_1\text{H}$ and $\alpha_2\text{H}$. As far as the ψ_3 torsion angle is concerned, the strong Gly $\alpha_2\text{H}$ -PheNH (ROESY crosspeak C₂ in Table IV and Figure 5) and the absence of the Gly $\alpha_1\text{H}$ -PheNH sequential ROESY cross peak in (3) agree with $\psi_3 \approx +120^\circ$ or -120° . Again the lack of stereospecific assignment of $\alpha_1\text{H}$ and $\alpha_2\text{H}$ prevent a choice between ψ_3 values. Nevertheless, since GlyNH- αH and Gly αH -PheNH NOEs detected involve the same Gly αH , the only possible combinations for (ϕ_3, ψ_3) are $(+30^\circ, +120^\circ)$ and $(-30^\circ, -120^\circ)$. On the other hand, the

presence of two equally intense $\alpha\text{H}_i\text{-NH}_{i+1}$ for (1) (ROESY cross-peaks C₁, C₂ in Table IV and Figure 3) and (2) (ROESY cross peaks C₁, C₂ in Table IV and Figure 4) corresponds to $\psi_3=0^\circ$ which is energetically unfavourable. Considering the conformational heterogeneity at Gly³, the detection of NOEs involving both Gly αH is likely to be due to the co-existence of conformations with different ψ_3 . A possible combination would involve both conformations under consideration for (3).

Further restrictions can be introduced considering the conformation of the Phe⁴ side-chain (Table V). The data concerning compound (3) are consistent with a large population of the gauche (-) rotamer. In such a case, the conformation corresponding to $\phi_3 \approx +30^\circ$ and $\psi_3 \approx +120^\circ$ is clearly unfavourable and should be discarded. On the other hand, the data corresponding to (1) and (2) are more ambiguous. In that case, although $\psi_3 \approx +120^\circ$ should be also unfavourable, the consideration of all the significant

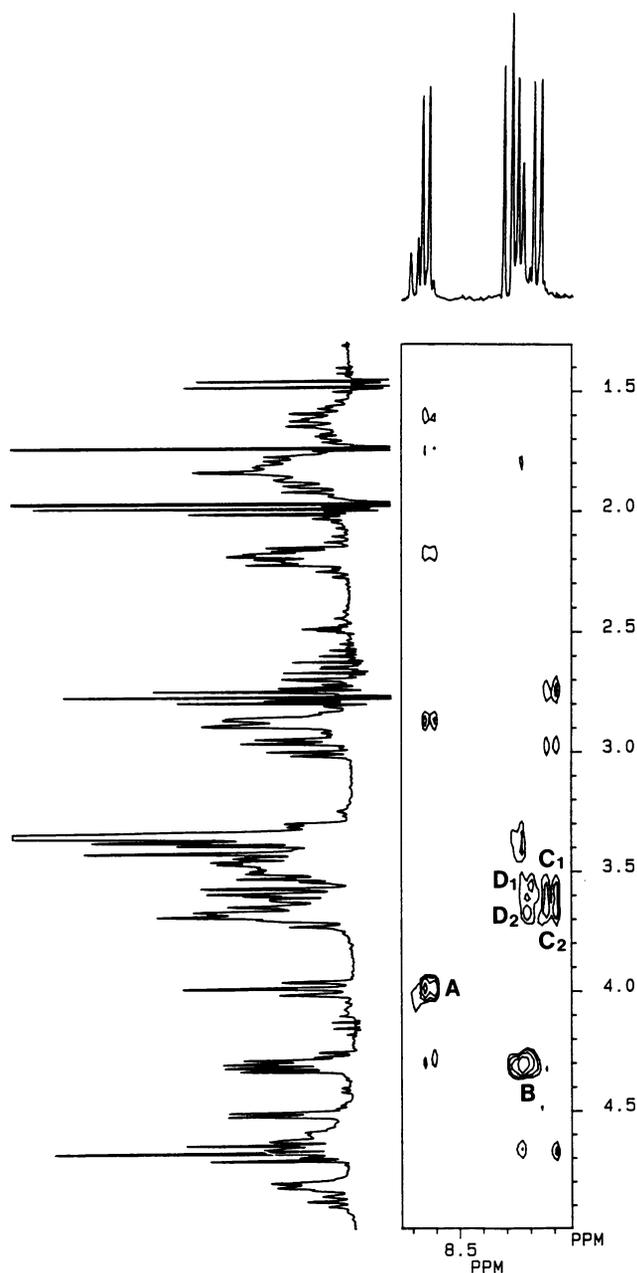


Fig. 4. ROESY spectrum of compound (2) in DMSO-*d*₆. NH- αH extensions where (A) Tyr αH -DMet NH; (B) DMet αH -Gly NH; (C₁) Gly $\alpha_1\text{H}$ -Phe NH; (C₂) Gly $\alpha_2\text{H}$ -Phe NH; (D₁) Gly NH- $\alpha_1\text{H}$; (D₂) Gly NH- $\alpha_2\text{H}$. 10 mM, 303 K, mixing time $\tau_m = 100$ ms. Negative levels are shown.

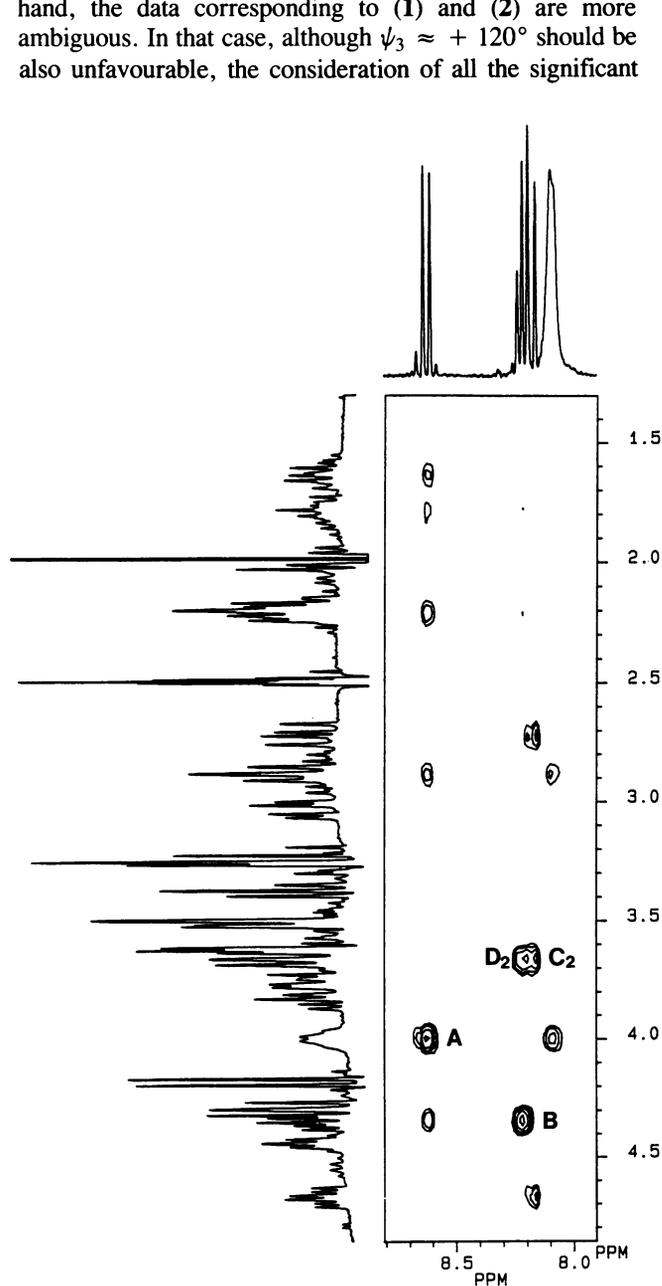


Fig. 5. ROESY spectrum of compound (3) in DMSO-*d*₆. NH- αH extensions where (A) Tyr αH -DMet NH; (B) DMet αH -Gly NH; (C₁) Gly $\alpha_1\text{H}$ -Phe NH; (C₂) Gly $\alpha_2\text{H}$ -Phe NH; (D₁) Gly NH- $\alpha_1\text{H}$; (D₂) Gly NH- $\alpha_2\text{H}$. 20 mM, 303 K, mixing time $\tau_m = 200$ ms. Negative levels are shown.

Table V. Data determining Phe⁴ side-chain conformation

	$^3J_{\alpha\beta 1}$ (Hz)	$^3J_{\alpha\beta 2}$ (Hz)	NOE _{αH-β1H}	NOE _{αH-β2H}	NOE _{NH-β1H}	NOE _{NH-β2H}
(1)	4.3	9.1	++	+	-	+
(2)	-	8.8	++	++	++	++
(3)	4.0	8.8	++	+	-	++

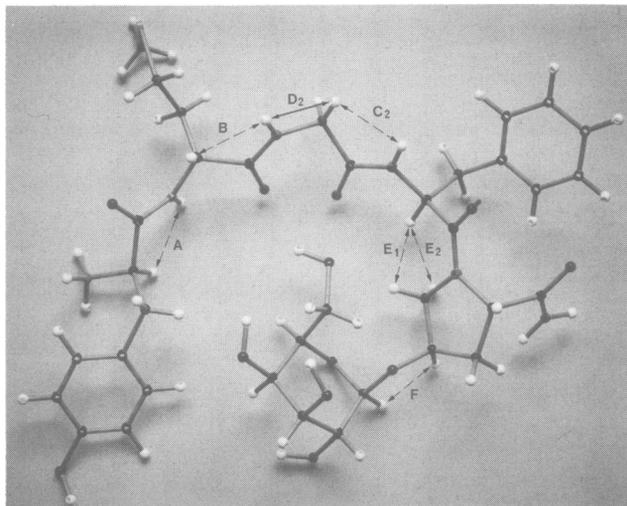


Fig. 6. Proposed conformation for compound (3). Solid arrows, short distances corresponding to intra-residual ROESY cross-peaks; broken arrows, short distances corresponding to inter-residual ROESY cross-peaks. Letters correlate with ROESY cross-peaks in Tables III and IV and Figure 5.

NMR data obtained in the present work does not allow us to discard any of the possible torsion angles.

In summary, the three compounds tested present two β strands connected to each other by a fairly flexible glycol residue at position 3. For compounds (1) and (2), experimental data are inconsistent with a single conformation of Gly³. In contrast, compound (3) seems to preferentially exist in a more rigid folded conformation in which $\phi_3 \approx -30^\circ$ and $\psi_3 \approx -120^\circ$ (Figure 6).

The temperature coefficients summarized in Table II show no evidence for hydrogen bonds involving the amide protons.

Furthermore, other experimental evidence has led us to suggest an explanation for the preferential existence of the proposed folded conformation in the β O-galactosyl analogue (3) and not in the β N-galactosyl analogue (2). Three strong NOEs detected even at 333 K, namely the previously mentioned Phe α H-Hyp δ_1 H, Phe α H-Hyp δ_2 H and Hyp γ H-galacH1 (ROESY cross peaks E₁, E₂ and F, respectively, in Table IV and Figure 5) prove that the C-terminus of (3) is an especially rigid part of the molecule compared with the N-terminus, since the rest of the sequential NOEs were weaker at high temperatures. In the proposed conformation for compound (3) (Figure 6) the hydroxyl groups in positions 4 and 6 of the galactosyl residue are faced to the carbonyl groups of DMet² and Gly³, respectively, so we suggest that such a conformation could be stabilized by hydrogen interactions between hydroxyl groups of galactose and carbonyl groups of the peptide backbone. Unfortunately, such a hypothesis cannot be supported by NOE data since all the non-exchangeable hydrogens of the galactosyl residue are too far from any hydrogen of the peptide moiety to show an observable NOE.

Discussion

The experimental NMR data presented are consistent with two β -strands (N-terminus and C-terminus) connected to each other by Gly³ for the three compounds tested. Both the parent compound [DMet²,Pro⁵] enkephalin amide (1), and the N^{1,5} galactosyl analogue [DMet²,Pro⁵] enkephalin [N^{1,5}- β -D-galactopyranosyl] amide (2) have been found to exhibit a similar conformational equilibrium with great flexibility at position 3. In contrast, O^{1,5}-(β -D-galactopyranosyl) [DMet²,Hyp⁵] enkephalin amide (3) shows a preferential folded structure.

As mentioned before, the N^{1,5}-galactosyl derivative (2) is significantly more potent than the parent compound (1) in rats, in both the tail immersion and paw pressure tests of analgesia after intraventricular administration. This difference in the analgesic activity of (1) and (2) cannot be related to any conformational change in DMSO solution since all the significant NMR parameters measured are very similar and consistent with a similar conformational equilibrium. Nevertheless, the increase in the analgesic activity of the O^{1,5}-galactosyl analogue (3) with respect to the N^{1,5}-galactosyl analogue (2) could be related to the adoption of the preferential folded conformation proposed in this work.

In conclusion, the introduction of a galactosyl moiety into the fifth residue of [DMet²,Pro⁵] enkephalinamide leads to an increase in analgesic activity of ~ 100 -times which is independent of the conformation of the molecule in DMSO solutions. Nevertheless, folded conformations seem to play an additional important role. In fact, when the galactosyl moiety is incorporated into another position in the same residue which allows galactose-peptide backbone interactions, a preferential folded conformation is detected. Such a conformational change could be related to an extra increment in analgesic activity of ~ 10 times.

Materials and methods

Synthesis

Thin layer chromatography was performed on silica gel plates (0.25 mm) from Merck. Spots were detected by reaction with ninhydrin or chlorine followed by toluidine solution. The sugar was detected by Orcinol-HCl. Amino acid analysis was performed in a Beckman 119 C instrument or a Biotronik LC 5001. All the solvents used were of analytical grade. They were distilled and stored over molecular sieves when necessary.

Microanalyses were performed by the Microanalytical Laboratory, Department of Biological Organic Chemistry, CID, Barcelona. FAB mass spectra were determined with a MS9-V6 updated system equipped with a VG-11 250 data system by the Laboratory of Mass Spectrometry, CID, Barcelona. An ion tech atom gun and a standard FAB source were used. The samples, dissolved in glycerol, were bombarded with 8 keV xenon atoms and the ions produced accelerated through 8 kV.

Isolation and purification of the protected glycosyl derivatives of the amino acids and peptides was carried out by flash chromatography, using Silica gel (40–63 μ m), 15 \times 2 or 15 \times 5 cm columns eluted with the appropriate solvent system at a flow rate of 5 cm/min.

The purity of the protected glycosyl amino acids and peptides was checked by reversed-phase HPLC [ODS, 5 μ m column, H₂O 0.05% trifluoroacetic acid (TFA):CH₃CN gradient elution from 9 to 100% CH₃CN at a linear rate of 3.5% CH₃CN/min] with detection by absorbance rationing measurements at several wavelengths.

2,3,4,6-tetra-O-acetyl- β -D-galactopyranosyl amine has been obtained from acetobromide-D-galactose according to the Bertho *et al.* (1932) procedure. The resulting product was characterized by ¹H-NMR. Melting point 137–139°C (literature value = 139°C).

Two different amino acid N-protecting groups have been used, benzyloxy-carbonyl (Z) and tert-butyloxycarbonyl (tBoc). Z groups were cleaved by hydrogenolysis in the presence of 10% palladium on charcoal (0.1 g/g) in

methanol. Removal of tBoc groups was achieved with TFA:CH₂Cl₂ (1:1) containing a few drops of 2-mercaptoethanol, 30 min at room temperature with a ratio of 10 ml acid-solvent mixture to 1 mmol of peptide or amino acid derivatives.

All optically active amino acids were of the L configuration with the exception of D-methionine, as indicated throughout the text.

¹H-NMR characterization of the final derivatives is not included in this experimental section.

βN-glycosylation. Synthesis of Tyrosyl, D-methionyl, glycyl, phenylalanyl, prolyl [*N*¹-β-D-galactopyranosyl] amide. Compound (2).

tBoc-Tyr-DMet-Gly-Phe-Pro-OH (0.750 g, 1.05 mmol) and 2,3,4,6-tetra-*O*-acetyl-β-D-galactopyranosylamine (0.36 g, 1.05 mmol) were dissolved in 20 ml of tetrahydrofuran (THF) at -20°C. 1-hydroxybenzotriazol (HOBt) (0.15 g) and two drops of 2-mercaptoethanol were added to the solution. *N,N*-dicyclohexylcarbodiimide (DCC) (0.21 g, 1.05 mmol) dissolved in 2 ml of THF was also added dropwise to the solution and the reaction mixture was kept at -20° for 1 h and then overnight at room temperature. The mixture was then filtered and the filtrate washed successively with 5% citric acid (3 × 20 ml), 5% sodium bicarbonate (3 × 20 ml) and water (3 × 20 ml). The organic layer was then dried over anhydrous Na₂SO₄ and the amorphous solid obtained after evaporation was purified by flash chromatography on silica gel using ethyl acetate:methanol (8:2) as eluent. Amino acid analysis: Tyr 0.94, D-Met 0.91, Gly 1.00, Phe 0.97, Pro 0.99. [α]₂₉₅²⁰ = 7.58°, [α]₂₅₅²⁰ = -26.06°, [α]₂₄₀²⁰ = -12.12°, [α]₂₃₅²⁰ = -38.18° (c = 0.32, methanol). ¹³C-NMR (20 MHz) (CDCl₃) 83.0 Cl galactose β anomer.

The cleavage of the protecting groups was carried out in two steps, TFA:CH₂Cl₂ (1:1) treatment for the elimination of the N-terminal tBoc group and NH₃:MeOH treatment for the cleavage of the acetyl groups. The resulting galactopyranosyl peptide was then purified by gel filtration on Sephadex G-25 and by semipreparative HPLC, C₁₈, solvent system H₂O-0.05% TFA:CH₃CN, isocratic mode elution 70:30, λ = 280 nm. Homogeneity was assessed by TLC and reversed-phase HPLC ODS 5 μm column, solvent system H₂O-0.05% TFA:CH₃CN 1 ml/min, gradient elution from 10 to 90% CH₃CN at a linear rate of 3.5% CH₃CN/min, 0.16 AUFS with detection by absorbance rationing measurements. Amino acid analysis: Tyr 0.95, D-Met 0.90, Gly 1.00, Phe 0.98, Pro 0.99. [α]₂₉₅²⁰ = 6.07°, [α]₂₅₅²⁰ = 28.21°, [α]₂₄₀²⁰ = 68.21°, [α]₂₃₅²⁰ = -63.93° (c = 0.32, methanol). ¹H-NMR ROESY, different intensity of galac N-1 and galac N-2 cross-peaks consistent with β anomer. FAB mass spectrometry: *m/z* 775 (*M* + 1).

βO-glycosylation. Synthesis of Tyrosyl, D-methionyl, glycyl, phenylalanyl, [*O*¹-β-D-galactopyranosyl] hydroxyprolinamide. Compound (3).

Z-Hyp-OMe (0.700 g, 2.5 mmol) was dissolved in 40 ml of dry benzene and 40 ml of nitromethane and heated under anhydrous conditions until about 15 ml of solvent had distilled off. To this solution a double equivalent amount of both 2,3,4,6-tetra-*O*-acetyl-α-D-galactopyranosyl bromide (2.056 g) and Hg(CN)₂ (1.286 g) were added in three portions: half of the given amounts at the beginning of the reaction and the rest in two equal portions after 2 and 3 h, respectively. The mixture was heated at 80°C for a total time of 4 h. The solution was then cooled and diluted with ether (80 ml) and filtered to eliminate the precipitated mercuric salts. The filtrate was then washed with water, dried over Na₂SO₄ and evaporated. The oily resulting mixture was submitted to flash chromatography on Silica gel (40-63 μm), 15 × 5 cm ID column eluted with hexane:ethyl acetate (3:7). ¹H-NMR (360 MHz, CDCl₃) *d* 4.35 *J*_{1,2} = 7.5 Hz H-1 β anomer.

After hydrogenolysis of the Z group, the incorporation of the resulting *O*₁-(2,3,4,6-tetra-*O*-acetyl-β-D-galactopyranosyl) hydroxyproline methyl ester to the tetrapeptide tBoc-Tyr-DMet-Gly-Phe-OH by the DCC/HOBt method and the purification of resulting protected galactosylated pentapeptide were carried out following the same procedure stated for compound (2).

The cleavage of the protecting groups and the C-terminal amide formation were also carried out in two steps, TFA:CH₂Cl₂ (1:1) treatment for elimination of N-terminal tBoc group and NH₃:MeOH (saturated at 0°C) treatment for the cleavage of acetyl groups and terminal amide formation from the methyl ester. The resulting galactopyranosyl peptide was then purified by gel filtration on Sephadex G-25 and semipreparative HPLC, C₁₈, solvent system H₂O-0.05% TFA:CH₃CN, isocratic mode elution 70:30, λ = 280 nm. Homogeneity was assessed by TLC and reversed-phase HPLC ODS 5 μm column, solvent system H₂O-0.05% TFA:CH₃CN 1 ml/min, gradient elution from 10 to 90% CH₃CN at a linear rate of 3.5% CH₃CN min, 0.16 AUFS with detection by absorbance rationing measurements. Amino acid analysis: Tyr 0.95, D-Met 0.90, Gly 1.00, Phe 1.05, Hyp 0.98. [α]₂₉₅²⁰ = 4.37°, [α]₂₅₄²⁰ = 0°, [α]₂₄₀²⁰ = 19.37°, [α]₂₃₅²⁰ = 9.69° (c = 0.32, MeOH). FAB mass spectrometry *m/z* 791 (*M* + 1), 813 (*M* + 23). ¹H-NMR (270 MHz, DMSO-*d*₆) ³*J*_{1,2} galac = 7.09 β anomer.

The parent compound (1) has been synthesized by coupling tBoc-Tyr-DMet-Gly-Phe-OH and H-Pro-OMe followed by deprotection and terminal amide formation.

Epimerization has been checked by gas chromatography on an enantioselective stationary phase (cyano ethyl-siloxane-L-valine-S-α-phenyl ethyl amide, Quirasil-valine). The extent of epimerization produced during each step in the synthesis of compounds (1-3) was not greater than 1%.

Conformational analysis

NMR spectra were recorded on a Bruker AM 270 spectrometer equipped with an Aspect 2000 computer running the DISN861 program. The obtained data were also processed with an Aspect 3000 computer running DISR87 or DISR88. For the conformational study the sample concentration was 10 or 20 mM in DMSO-*d*₆ (CEA 99.98%). Samples were degassed by several freeze-pump-thaw cycles. The types of 2D-NMR experiments carried out were phase-sensitive, double quantum filtered COSY (Marion and Wüthrich, 1983) and relayed COSY (Weber and Müller, 1987), NOESY (Kumar *et al.*, 1980) and ROESY (Bothner-By *et al.*, 1984).

All spectra were measured with a spectral width of 2703 Hz, covering the range 0.0-10.0 p.p.m.

The 1D spectra were measured with 8 K data. The interferograms were multiplied by a Gaussian function with LB = -3 and GB = 0.3, zero-filled to 16 K and Fourier transformed. The resulting spectra had a digital resolution of 0.3 Hz/point.

All the 2D spectra were measured in a phase-sensitive mode using TPPI (Marion and Wüthrich, 1983). In relayed COSY, the relay period amounted to 50 ms. Mixing times were 200-400 ms in NOESY and 50-200 ms in ROESY. In ROESY experiments the spin-lock field was 3.8 kHz, to minimize Hartman-Hahn effects (Bax and Davies, 1985).

All 2D spectra consisted of 256 or 512 interferograms of 1 K data. The interferograms were multiplied by a Gaussian function with LB = -3 and GB = 0.3 and Fourier transformed. The *t*₁-interferograms were multiplied by a sine bell function shifted by π/8, zero-filled to 1 K and Fourier transformed. The digital resolution in the resulting 512 × 512 W spectra was 5.3 Hz in both dimensions.

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