

NOP-Targeted Peptide Ligands

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Abstract

The nociceptin/orphanin FQ (N/OFQ)-N/OFQ peptide (NOP) receptor system is widely distributed at both the peripheral and central level where it modulates important biological functions with increasing therapeutic implications. This chapter wants to provide a comprehensive and updated overview focused on the available structure–activity relationship studies on NOP receptor peptide ligands developed through different rational approaches. Punctual modifications and cyclizations of the N/OFQ sequence have been properly combined furnishing potent NOP selective ligands with different pharmacological activities (full and partial agonists, pure antagonists) and enhanced metabolic stability in vivo. The screening of peptide libraries provided a second family of NOP ligands that have been successfully optimized. Moreover, recent findings suggest the possibility to

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M.-C. Ko, G. Caló (eds.), *The Nociceptin/Orphanin FQ Peptide Receptor*, Handbook of Experimental Pharmacology 254, https://doi.org/10.1007/164_2018_198 apply different multimerization strategies for the realization of multi-target NOP/opioid receptor ligands or tetrabranched N/OFQ derivatives with extraordinarily prolonged duration of action in vivo. The diverse approaches led to the identification of important pharmacological tools along with drug candidates currently in clinical development such as Rec 0438 (aka UFP-112) for the treatment of overactive bladder and SER 100 (aka ZP120) for the clinical management of systolic hypertension.

Keywords

Nociceptin/orphanin FQ · NOP · Peptide ligands · SAR studies

1 Introduction

Nociceptin/orphanin FQ (N/OFQ; FGGFTGARKSARKLANQ, see Fig. 1) shows significant similarities in the primary sequence with other endogenous peptides of the opioid family of which dynorphin A can be considered its closer analogue (Calo' and Guerrini 2013). Nevertheless, due to its unique structure, N/OFQ is unable to interact with classical opioid receptors (MOP, DOP, and KOP), as well as opioid peptides are unable to bind the N/OFQ peptide (NOP) receptor. Typically, the first four N-terminal residues of the heptadecapeptide sequence of N/OFO (FGGF) represent the "message" domain responsible for NOP activation, while the "address" fragment is composed of the last C-terminal residues (7-17) and promotes NOP binding affinity and receptor selectivity (Calo' et al. 2013; Mustazza et al. 2018). The central dipeptide Thr⁵Gly⁶ constitutes a hinge region between message and address sequences. The message tetrapeptide of N/OFQ is clearly superimposable to the canonical YGGF N-terminus of mammalial opioid peptides. Thus, the simple Tyr¹/Phe¹ replacement is fundamental for N/OFQ selectivity being able to preclude NOP/opioid receptors cross activation (Calo' et al. 2013). A series of crystallographic studies performed with NOP (Thompson et al. 2012) and classical opioid receptors (Wu et al. 2012; Manglik et al. 2012; Granier et al. 2012) in complex with specific antagonists suggested that the Phe¹ phenyl ring of N/OFQ would face a hydrophobic region of the receptor binding pocket while the phenolic function of Tyr¹ in opioid peptides would be involved in a hydrogen bond network with the conserved His residue present in position 52 of TM VI of opioid receptors.

Truncation studies on N/OFQ indicated the exclusive possibility to shorten the C-terminal portion up to the identification of N/OFQ(1–13) as the minimal active sequence (Calo' et al. 1996; Dooley and Houghten 1996). Moreover, C-terminal amidation proved to reduce the susceptibility to carboxypeptidases of both N/OFQ and N/OFQ(1–13) (Guerrini et al. 1997). It has to be remarked that, according to NMR studies, the C-terminal "address" portion of N/OFQ would assume a typical alpha helix conformation in physiological conditions (Orsini et al. 2005; Tancredi et al. 2005). This region is characterized by the presence of two couples of Arg-Lys dipeptide units at 8–9 and 12–13 positions, which are important for the affinity/ selectivity of the peptide because of the capability to promote the α -helix bioactive





motif as well as to interact with negative residues in the second extracellular loop of the NOP receptor (Daga and Zaveri 2012).

Advances in the pharmacology and medicinal chemistry of the N/OFQ-NOP system have been recently reviewed by different authors (Toll et al. 2016; Mustazza et al. 2018; Zaveri 2016). This chapter wants to provide a comprehensive and updated overview focused on SAR studies on NOP receptor peptide ligands that have been thus far developed following different rational approaches.

2 Structure-Activity Relationship Studies on N/OFQ-Related Peptides

2.1 Linear N/OFQ Derivatives

The key structural modifications applied to N/OFQ sequence for generating useful NOP peptide ligands have been summarized in Fig. 1. Phe¹ is one of the most essential residues for NOP binding/activation/selectivity (Calo' et al. 2013). The saturation of the Phe¹ benzyl moiety (Cha¹) and the replacement of Phe¹ with a Leu¹ are highly tolerated while Ala¹ derivatives are essentially inactive. In addition, the inversion of the configuration of Phe¹ (D-Phe¹) abolished the activity. This suggests that a bulky and lipophilic side chain at the first residue is required while aromaticity is not mandatory for receptor binding. The N-terminal residue seems to be of key relevance for ligand efficacy if considering that the reduction of the peptide bond between Phe¹ and Gly² [Phe¹ Ψ (CH₂-NH)Gly²] or the shift of the benzyl side chain to the N-terminal nitrogen (Nphe¹) led to partial agonism (i.e., [F/G]N/OFQ(1-13) NH₂) or antagonism (i.e., [Nphe¹]N/OFQ(1–13)-NH₂), respectively (see Table 1) (Calo' et al. 2013; Toll et al. 2016). Of note, a significant loss of selectivity over opioid receptors was observed when Phe¹ has been replaced with Tyr¹ that was even more evident with the introduction of a 2,6-dimethyltyrosine (Dmt) residue at the same position (Molinari et al. 2013). This led to the identification of [Dmt¹]N/OFQ (1-13)-NH₂ and [Dmt¹]N/OFQ-NH₂ as mixed NOP/opioid agonists with an interesting potential as innovative spinal analgesics. In contrast, the replacement of Phe¹ with an amino phosphonate moiety in N/OFQ(1-13)NH₂ resulted in low potency though NOP selective agonists (Todorov et al. 2012).

Unlike other opioid ligands, N/OFQ is particularly sensitive to substitutions at the Gly^2 - Gly^3 dipeptide spacer. X-ray analysis (Thompson et al. 2012) and docking studies (Daga and Zaveri 2012) confirmed the importance of both the composition and length of the Gly^2 - Gly^3 unit that imposes the right distance between Phe¹ and Phe⁴ and confers high conformation flexibility. This allows the N-terminal nitrogen atom of the message tetrapeptide to establish an ionic interaction with the Asp¹³⁰ of the NOP receptor (Toll et al. 2016). Different substitutions have been also performed at the Phe⁴ residue that is critical for NOP binding/activation (Guerrini et al. 2001). Noteworthy, the potency of the endogenous peptide was significantly enhanced with the introduction of electron withdrawing moieties (especially a fluorine atom) at the para-position of the Phe⁴ phenyl ring (Guerrini et al. 2001; McDonald et al. 2002).

	Human NOP			Mouse NOP		
		Functional		Functional		
		potency		potency		
	Binding	[³⁵ S]	a 24			
	affinity	GTPγS	Ca ²¹	mVD	Reference	
NOP agonists	p <i>K</i> _i	pEC ₅₀	pEC ₅₀	pEC ₅₀		
N/OFQ	9.91	8.75	9.54	7.47	McDonald et al. (2003), Camarda et al. (2009), and Toll et al. (2016)	
N/OFQ(1-13)-NH ₂	10.24	9.28	9.30	7.40	McDonald et al. (2003), Camarda et al. (2009), and Toll et al. (2016)	
[Dmt ¹]N/OFQ(1– 13)-NH ₂	10.59	9.46	8.94	ND	Molinari et al. (2013) and Cerlesi et al. (2017)	
[(pF)Phe ⁴]N/OFQ (1–13)-NH ₂	9.40	9.55	nd	8.19	Guerrini et al. (2001) and McDonald et al. (2002)	
[Arg ¹⁴ Lys ¹⁵]N/OFQ	9.49	9.85	9.56	8.93	Okada et al. (2000), Rizzi et al. (2002a), and Camarda et al. (2009)	
UFP-112	10.55	10.55	9.05	9.24	Arduin et al. (2007) and Camarda et al. (2009)	
NOP partial agonists	pK _i	pEC ₅₀	pEC ₅₀	pEC ₅₀		
[F/G]N/OFQ(1–13)- NH ₂	9.27	8.05	8.03	Slight transient effect	Wright et al. (2003) and Camarda et al. (2009)	
UFP-113	10.26	9.73	7.97	Variable effects	Arduin et al. (2007), Camarda et al. (2009)	
NOP antagonists	pK _i	pA ₂	pA ₂	pA ₂		
[Nphe ¹]N/OFQ(1– 13)-NH ₂	8.39	7.33	6.29	6.04	McDonald et al. (2003), Camarda et al. (2009), and Calo' et al. (2000)	
UFP-101	10.24	8.85	7.66	7.29	McDonald et al. (2003), Camarda et al. (2009), and Calo' et al. (2002)	

Table 1 In vitro biological activity of N/OFQ-related peptide ligands

 $[^{35}S]$ GTPγS: $[^{35}S]$ GTPγS binding in membranes from CHO cells expressing the human NOP; Ca²⁺: calcium mobilization in CHO cells coexpressing the human NOP and the Gα_{qi5} chimeric protein; mVD electrically stimulated mouse vas deferens; pEC₅₀: agonist potency; pA₂/pK_B: antagonist potency; UFP-112: [(pF)Phe⁴Aib⁷Arg¹⁴Lys¹⁵]N/OFQ-NH₂; [F/G]N/OFQ(1–13)-NH₂: [Phe¹Ψ(CH₂-NH)Gly²]N/OFQ(1–13)-NH₂: UFP-113: [Phe¹Ψ(CH₂-NH)Gly²(pF)Phe⁴Aib⁷Arg¹⁴Lys¹⁵]N/OFQ-NH₂; UFP-101: [Nphe¹Arg¹⁴Lys¹⁵]N/OFQ-NH₂

A series of N/OFQ(1–13)-NH₂ analogues in which the Thr⁵ residue was substituted with both natural and nonnatural amino acids has been recently investigated (Guerrini et al. 2015). These analogues behaved as NOP full agonists with highly variable potency thus suggesting that Thr⁵ would contribute to the binding to the receptor more than to its activation. Yet, neither the size of X⁵ side chain nor its lipo/hydrophilic nature and hydrogen bond capability seemed of significant relevance for receptor binding. In particular, the simple removal of the side chain hydroxyl function of Thr⁵ ([Abu⁵]N/OFQ(1–13)-NH₂) determined a substantial preservation of NOP activity.

The effect of various modifications of the C-terminal motif of N/OFQ and N/OFQ (1-13)-NH₂ has been also investigated (Calo' et al. 2013). Notably, a highly potent NOP agonist was obtained when a third Arg-Lys couple was introduced at the 14–15 positions of the native peptide sequence (Okada et al. 2000). [Arg14Lys15]N/OFO displayed indeed higher binding affinity (threefold) and potency (17-fold) compared to N/OFQ. Similar results have been achieved with the introduction at the same positions of different combinations of positively charged residues such as Lys-Arg, Lys-Lys, and Arg-Arg (Okada et al. 2008). On the contrary, when a single positive residue was introduced in either 14 or 15 position, a moderate enhancement of binding and biological activity was observed. In addition, with the aim to investigate the importance of the C-terminal secondary structure, both alpha helix inducers (Aib, alpha-aminoisobutyric acid) and breakers (Pro) have been alternatively introduced at key positions of the address domain (Zhang et al. 2012; Tancredi et al. 2005). Aib⁷, Aib¹¹, and Aib¹⁵ peptide derivatives were significantly more potent than the native ligand. On the other hand, Pro⁵, Pro⁶, Pro⁷, and Pro¹¹ substitutions severely compromised the activity of the endogenous peptide.

Finally, Thr⁵ or Ser¹⁰ have been scrutinized as possible glycosylation sites of N/ OFQ-related peptides (Biondi et al. 2006; Arsequell et al. 2011). These investigations agree in the identification of Ser¹⁰ as preferred anchoring point for a monosaccharide unit. Of the reported compounds, [Ser¹⁰-O- α -D-GalNAc]-N/OFQ exhibited a pK_i value of 8.42 in competition binding experiments with similar affinity as N/OFQ (Arsequell et al. 2011). A NMR analysis performed in membrane mimicking environments indicated that, unlike for Thr⁵ derivatives, Ser¹⁰ glycosylated analogues exist prevalently as linear α -helix motifs that are supposed to interact in a more favorable binding pose with the NOP compared to folded structures.

Some of the chemical modifications of the N/OFQ sequence described above have been profitably combined in the search for potent NOP peptide ligands with different pharmacological activities spanning from full agonists (N/OFQ(1–13)-NH₂, [(pF)Phe⁴]N/OFQ(1–13)-NH₂, [Arg¹⁴Lys¹⁵]N/OFQ, UFP-112) to partial agonists ([F/G]N/OFQ(1–13)-NH₂, UFP-113) and antagonists ([Nphe¹]N/OFQ (1–13)-NH₂, UFP-113). The structures and the in vitro pharmacological profile of these molecules at the human and murine NOP receptor are reported in Table 1.

2.2 Cyclic N/OFQ Derivatives

As mentioned above, different approaches including circular dichroism (CD) and NMR spectroscopy have been applied with the aim to elucidate the bioactive conformation of N/OFQ(1–17)-NH₂, N/OFQ(1–13)-NH₂, and related peptides (Lohman et al. 2015). These studies consistently suggest that the 7–17 address domain of N/OFQ would rather assume an amphipathic α -helical conformation in the binding pocket of NOP receptor thanks to a motif in which the positive Arg-Lys couples are regularly spaced by Ala residues. However, the α -helicity of linear N/OFQ analogues is irrelevant in aqueous medium making these compounds particularly subjected to the action of serum peptidases (Lohman et al. 2015). For these reasons, different efforts have been made in the design of proper C-terminal cyclization strategies that could promote water-stable α -helix motifs thus improving peptidase resistance and in vivo potency and duration of action of N/OFQ analogues.

As largely known, the addition of cysteine residues to peptides makes them prone to cyclization via the formation of intramolecular disulfide bridges. Following this approach, a small series of cyclic analogues of N/OFO(1-13)-NH₂ has been reported in 2001 (Ambo et al. 2001). These compounds came from the cyclization of either the N-terminal or the C terminal region of N/OFO thanks to the addition/replacement of Cys residues at key positions of the parent peptide sequence. Any cyclization involving the N-terminal part led to a complete loss of activity. On the other hand, the cyclization of the C-terminal portion led to potent derivatives especially when the disulfide linkage was introduced between the positions 10–14 where a serine and a leucine residue were replaced by two cysteines, respectively. Cyclo[Cys¹⁰,Cys¹⁴]N/ $OFQ(1-14)-NH_2$ (compound 1, Fig. 2) can be considered the first example of constrained N/OFQ-related peptide whose receptor affinity (pIC₅₀ = 9.91), potency $(pEC_{50} = 8.36)$, and efficacy were comparable to those of the native peptide (Ambo et al. 2001). In an attempt to identify a cyclic antagonist, Kitayama et al. reported in 2003 the synthesis of the Nphe¹ derivative of compound 1 (Kitayama et al. 2003) that however suffered from a severe reduction of NOP affinity.

As an alternative to the disulfide bridge strategy, a few N/OFQ cyclic analogues with side chain to side chain lactam linkage have been firstly reported by Charoenchai et al. (2008). Of this series, the cyclo-peptide **2** (cyclo[D-Asp⁷,Lys¹⁰] N/OFQ(1–13)NH₂, Fig. 2) showed subnanomolar binding affinity and high potency for the NOP receptor ($pK_i = 9.57$, $pEC_{50} = 8.80$). The usefulness of the

- 1: Phe-Gly-Gly-Phe-Thr-Gly-Ala-Arg-Lys-Cys-Ala-Arg-Lys-Cys-NH₂ 2: Phe-Gly-Gly-Phe-Thr-Gly-DAsp-Arg-Lys-Lys-Ala-Arg-Lys-NH₂ 3: Phe-Gly-Gly-(4F)Phe-Thr-Gly-Lys-Arg-Lys-Ser-Asp-Arg-Lys-Lys-Lys-Asn-Gln-Asp-NH₂
- 4: Nphe-Gly-Gly-(4F)Phe-Thr-Gly-Lys-Arg-Lys-Ser-Asp-Arg-Lys-Lys-Lys-Asn-Gln-Asp-NH2

Fig. 2 Structures of selected cyclic analogues of N/OFQ

lactamization strategy was later confirmed by Harrison et al. who performed multiple cyclizations of the address domain of N/OFQ(1–17)-NH₂ (Harrison et al. 2010) each involving the minimum number of residues that span a canonical α -helix (five amino acids). In the latter case, cyclizations were combined with strategical substitution of the message sequence intended to enhance ligand potency (i.e., (pF)Phe⁴) or induce antagonist activity (i.e., Nphe¹). The study resulted in the identification of the highly potent NOP agonist **3** (Fig. 2) with picomolar potency (pEC₅₀ = 10.40) in vitro and significantly higher and longer lasting antinociceptive activity in vivo in comparison with unconstrained peptides (Harrison et al. 2010). With the same approach, the potent NOP antagonist **4** (pIC₅₀ = 8.12) was discovered (Fig. 2). CD spectroscopy highlighted that constrained analogues of this series adopted α -helical conformation even in aqueous phosphate buffer where all the investigated unconstrained analogues exhibited minimal helicity. In addition, lactame derivatives showed longer half-life in human serum (Lohman et al. 2015).

3 Structure-Activity Relationship Studies on N/OFQ-Unrelated Peptides

Dooley et al. have reported in 1997 the first examples of peptide ligands of the NOP receptor featuring an amino acid sequence totally unrelated to that of N/OFQ (Dooley et al. 1997). This study originated from the screening of a large peptide combinatorial library and resulted in the identification of a small series of positively charged hexapeptides reflecting the general structure Ac-RYY(R/K)(I/W)(R/K)-NH₂. The functional profile of such compounds evaluated in three different assays (stimulated $[^{35}S]$ GTP γ S binding and inhibition of forskolin-stimulated cAMP in cells expressing the recombinant human NOP, and the electrically stimulated mouse vas deferens bioassay) revealed a partial agonist behavior. One of the most representative member of this class namely Ac-RYYRWR-NH₂ (see Table 2) was later employed in photoaffinity labeling studies with the aim to determine its binding domain on the NOP receptor (Bes and Meunier 2003). Interestingly, these studies indicated that N/OFQ and hexapeptides interact with the NOP receptor in distinct, although partially overlapped, regions and this could be the reason of their diverse pharmacological activities. Of this series, Ac-RYYRWR-NH₂ showed the highest efficacy in inhibiting cAMP accumulation (75% versus 84% for N/OFO), while the analogue Ac-RYYRWK-NH₂ (Table 2) exhibited lower maximal effect (58%). This suggests that the higher basicity of Arg compared to Lys at the 6-position could contribute to promote NOP activation. Of note, it was found that the side chain of Arg/Lys⁶ can be replaced with shorter moieties (such as in Orn, Dab, or Dap) without significant loss of activity in vitro (Kasakov et al. 2010).

The negligible in vivo activity of Ac-RYYRWR-NH₂ prompted further efforts aimed at improving proteolytic resistance. The resulting SAR profile indicated the importance of each Arg residue to maintain high binding affinity while Tyr² and Tyr³ seem to be less essential residues, although at least one of these must maintain its

		U		11 0					
				HN NH2 NH O H O H O H O H O C C I III-BTD					
	A¢-RYYRW								
$H_{2}N + H_{N} + H_{$									
	Human NOP		Mouse NOP						
	Binding affinity	Functional potency	Functional potency ^a	Reference					
NOP partial agonists	pK _i	pEC ₅₀	pEC ₅₀						
Ac- RYYRWR- NH ₂	9.22	8.66 ^b 9.28 ^c	nd	Dooley et al. (1997)					
Ac- RYYRWK- NH ₂	9.15	8.68 ^b 9.28 ^c	8.07	Dooley et al. (1997) and Rizzi et al. (2002b)					
Ac-R-(3Cl) Y-YRWR- NH ₂	10.5	9.30 ^b	nd	Judd et al. (2004)					
ZP120 (SER100)	9.6	9.30 ^c 7.15 ^d	8.88	Rizzi et al. (2002b), Kapusta et al. (2005), and Camarda et al. (2009)					
NOP antagonists	pK _i	pA ₂ /pK _B	pA ₂ /pK _B						
Isovaleryl- RYYRIK- NH ₂	8.13	Inactive ^b	9.7	Li et al. (2008)					
III-BTD	7.62	7.89 ^b 7.49 ^c	6.57	Becker et al. (1999), Hashiba et al. (2001), McDonald et al. (2002), and Bigoni et al. (2000)					
5	7.46	6.52 ^b	nd	Halab et al. (2002)					
6	7.14	6.87 ^b	nd	Van Cauwenberghe et al. (2004)					

Table 2 Structures and in vitro biological activity of N/OFQ-unrelated NOP peptide ligands

pEC₅₀: agonist potency; pA₂/pK_B: antagonist potency ^amVD ^b[³⁵S]GTPγS ^ccAMP ^dCa²⁺

Van Cauwenberghe et al. (2004)

phenol group to sustain the agonist efficacy of the peptide (Kawano et al. 2002; Judd et al. 2004). Indeed, Ac-R-Phe(4-F)-Phe(4-F)-RWR-NH₂ ($pK_i = 8.82$) behaved as NOP antagonist while compound Ac-R-Tyr(3-Cl)-YRWR-NH₂ (Table 2) exhibited picomolar affinity for the NOP receptor with a functional profile of low efficacy partial agonist in different assays (Judd et al. 2004). Moreover, Trp⁵ was substituted with a series of nonnatural aromatic amino acids and the following biological investigation suggested that the indole moiety of the side chain at this position is not mandatory for biological activity (Carra' et al. 2005). Nevertheless, it was found that the fifth amino acid residue plays a crucial role in the modulation of agonist/ antagonist activity. Indeed an L-aliphatic/hydrophobic amino acid seems to favor antagonist activity, while a D-residue (especially D-Trp or a D-Arg) resulted in potent agonist activity (Ambo et al. 2007). More recently, Zamfirova et al. reported the synthesis and biological evaluation of a new series of congeners of Ac-RYYRWK-NH₂, modified at the 5-position with nonnatural tryptophan analogues (Zamfirova et al. 2013). This study highlighted the contribution of the 5-position to the modulation of selectivity over opioid receptors. Indeed, when a 5-methoxy β^2 -tryptophan residue was incorporated at the 5-position of Ac-RYYRWK-NH₂ a compound with higher affinity for opioid receptors than for NOP was obtained.

Other modifications of the original hexapeptide scaffold include the substitution of the N-terminal acetyl group that led in some cases to reduced or abolished intrinsic activity. In particular, the peptide pentanoyl-RYYRWR-NH₂ displays high NOP affinity ($pK_i = 9.89$) with barely measurable agonist activity (Judd et al. 2003). Furthermore, the compounds Isovaleryl-RYYRIK-NH₂ (Table 2) (Li et al. 2008) and Ac-Diaminobutyl-YYRWR-NH₂ (Judd et al. 2004) are examples of pure NOP antagonists obtained with modifications of the N-terminal residue. Arg¹ was also substituted with aminophosphonate moieties with a severe loss of NOP affinity and selectivity (Naydenova et al. 2010). The effect of modifications of the C-terminal portion of the hexapeptide scaffold has been explored as well. A reduction of ligand efficacy has been observed when the C-terminal amide moiety has been replaced by a primary hydroxyl function like in the NOP antagonist Ac-RYYRIK-ol (Kocsis et al. 2004; Gündüz et al. 2006). Noteworthy, the parent hexapeptide structure has been extended at the C-terminal position with an oligo-lysine frame in compound ZP120 (Ac-RYYRWKKKKKKK-NH₂, Table 2) developed by Zealand Pharma (Rizzi et al. 2002b). The (Lys)₆ sequence of this derivative would likely induce an α -helix conformation with consequent reduction of enzymatic vulnerability (Larsen 1999). The pharmacological profile of ZP120 (more recently known as SER100) has been extensively investigated both in vitro and in vivo consistently demonstrating its action as a potent and selective NOP partial agonist (Toll et al. 2016). This compound is of particular interest since SER100 is now in clinical development as innovative treatment for systolic hypertension (Kantola et al. 2017).

A screening of a synthetic combinatorial library of β -turn-constrained peptides resulted in the identification of the pseudohexapeptide III-BTD (Ac-Arg-DCha-BTD-DArg-D(pCl)Phe-NH₂, Table 2) as NOP antagonist with low binding selectivity over opioid receptors (Becker et al. 1999). Interestingly, the compound behaves as weak agonist toward all the three classical opioid receptors. The thiazolidinone bicycle inserted within the sequence of III-BTD as turn inducer has been later replaced with different azabicycloalkane amino acids in the search for more selective ligands (Halab et al. 2002). The introduction of a 6,6-bicyclic moiety (i.e., quinolizidine) in compound **5** determined the maintenance of NOP affinity with a significant improvement of selectivity especially over DOP receptors. However, at high concentration, **5** behaved as weak partial agonist at MOP and KOP receptors. Further SAR studies on this molecule focused on the importance of the Arg residues whose position, structure, and charge were modified (Van Cauwenberghe et al. 2004). This investigation resulted in the identification of the citrulline derivative **6** with slightly lower NOP affinity but improved potency and selectivity.

4 Bivalent NOP Peptide Ligands

With the aim to investigate the possible existence of NOP receptor homodimers, we recently reported a series of dimeric NOP ligands obtained by the linkage of two peptide or non-peptide pharmacophores with spacers of different length and chemical composition (Pacifico et al. 2017). A subset of homobivalent ligands have been obtained connecting the C-terminal portions of two N/OFQ(1–13) fragments chosen as pharmacophore units. The spacers varied from 18 to 32 atoms and were composed of Gly, Ala, β -Ala, Gaba, and Cys residues, in variable combinations. Neither ligand dimerization nor spacer length/composition seemed to affect agonist potency or efficacy. However, when low potency agonists, e.g., N/OFQ(1–12) and N/OFQ (1–11), were chosen as pharmacophores, dimerization resulted in total recovery of ligand potency. This effect of dimerization depends on the doubling of the C-terminal address sequence rather than the presence of an additional N-terminal message sequence or modifications of peptide conformation (Pacifico et al. 2017).

Together with homobivalent ligands, a few examples of peptide-based bifunctional MOP/NOP agonists have been recently examined. This research area is of particular interest since molecules that are able to modulate multiple opioid receptors may result into novel opioid analgesics possibly with reduced side effects (Günther et al. 2018). In particular several recent studies demonstrated that the mixed NOP/opioid receptor agonist cebranopadol displays analgesic effects similar to morphine associated with reduced side effects (reviewed in Calo' and Lambert 2018). Moreover, the small molecule AT-121, with a bifunctional NOP/MOP agonist profile, has been shown to promote nonaddictive analgesia in nonhuman primates with potential as treatment for opioid abuse disorders (Ding et al. 2018).

As far as heterobivalent peptides are concerned, Kawano et al. obtained a first hybrid template linking dermorphin, as mu receptor agonist, to the NOP peptide ligand Ac-RYYRIK-NH₂ (Kawano et al. 2006). A synergistic effect was observed on both MOP and NOP binding potency when a relatively long spacer –Gly-Gly-Gly-Lys(Gly-Gly-)-NH₂ was incorporated between the pharmacophores. In fact, compound **7** (Fig. 3) exhibited picomolar affinities for the investigated targets (p K_i NOP = 10.33; p K_i MOP = 11.63); despite this, the chimeric compound did not show



8: H-Dmt-D-Arg-Aba-β-Ala-Arg-Tyr-Tyr-Arg-Ile-Lys-NH₂

Fig. 3 Structures of bifunctional NOP/opioid receptor peptide ligands

improved antinociceptive activity in vivo compared to the single peptides (Kawano et al. 2007). Dermorphin was also hetero-dimerized with the endogenous NOP agonist N/OFQ (Bird et al. 2016). The resulting compound showed in vitro the expected profile (i.e., the sum of that of the single monomeric components) but exhibited in vivo only weak antinociceptive properties.

More recently, Guillemyn et al. described chimeric compounds obtained through the linear combination of the N-terminal fragment H-Dmt-D-Arg-Aba- β -Ala-NH₂, as opioid pharmacophore, with different NOP peptide ligands at the C-terminal portion (Guillemyn et al. 2016; Lagard et al. 2017). Such hybrids were able to simultaneously activate opioid receptors and block NOP when evaluated in vitro. In this case, the merging strategy led to a slight loss of affinity toward both opioid and NOP receptors. Among the investigated compounds, the bifunctional peptide **8** (p*K*_i NOP = 7.38; p*K*_i MOP = 8.30, Fig. 3) elicited high and long lasting antinociceptive efficacy in vivo upon i.v. administration in mice. Of note, this molecule demonstrated higher analgesic efficacy in neuropathic pain models compared to morphine with limited effects on the respiratory function and reduced tolerance liability (Starnowska et al. 2017).

5 Tetrabranched NOP Peptide Ligands

Bracci et al. provided in 2003 the first evidences of the positive effect of N/OFO multimerization on its stability in plasma and serum (Bracci et al. 2003). A high efficacy chemical strategy for the synthesis of multi-branched peptides, the peptide welding technology (PWT), has been developed more recently (Calo' et al. 2018). This approach showed to significantly extend the typical short half-life of a series of peptides of therapeutic interest possibly because of a reduced proteolytic metabolism. The methodology is based on the thiol-Michael conjugation of three different tetra-maleimide functionalized cores (PWT1, PWT2, and PWT3; see Fig. 4) with four linear peptide monomers strategically functionalized with a cysteine residue. N/OFQ was employed in early studies to produce the first examples of PTW homotetravalent peptides (Guerrini et al. 2014). PWT-N/OFQ derivatives displayed higher binding affinity (threefold) for NOP than N/OFQ and comparable selectivity over opioid receptors (Rizzi et al. 2014). Moreover, PWT-derivatization of N/OFQ preserved its behavior as NOP full agonist in vitro with even improved potency. Interestingly, N/OFO clustering impacts also on the capability to discriminate between NOP/G protein and NOP/ β -arrestin 2 interaction. In particular, PWT2-N/ OFO displayed a significant bias toward G protein (Malfacini et al. 2015). Remarkably, PWT-N/OFQ derivatives showed enhanced potency (40-fold) compared to



Fig. 4 General structures of tetrabranched peptide ligands of the NOP receptor (PWT technology)

N/OFQ when evaluated in vivo for its inhibitory effects on mouse locomotor activity after supraspinal administration (Rizzi et al. 2014). Similar results, i.e., 40-fold higher potency than N/OFQ, were obtained investigating the spinal antinociceptive effects of PWT2-N/OFQ in neuropathic pain models in mice and in nonhuman primates (Rizzi et al. 2015).

 $[Dmt^1]N/OFQ(1-13)-NH_2$ has been clustered into PWT cores with the aim to provide a potential example of a tetrameric ligand with mixed NOP and opioid receptor agonist properties (Cerlesi et al. 2017). PWT2- $[Dmt^1]N/OFQ(1-13)$ displayed reduced NOP affinity if compared to the linear peptide monomer, with a similar selectivity profile (NOP = MOP = KOP > DOP). In functional assays, this compound behaved as a G protein biased NOP/MOP dual agonist. In addition, the compound prompted antinociceptive effects following spinal administration in monkeys, with tenfold higher potency than $[Dmt^1]N/OFQ(1-13)-NH_2$ and longer lasting effects (Cerlesi et al. 2017).

PWT2 technology was also employed to synthetize a tetrabranched derivative of the NOP antagonist UFP-101 (see Table 1). PWT2-UFP-101 preserved the NOP antagonist pharmacological activity displaying a value of potency ($pA_2 = 8.58$) comparable to that of UFP-101 ($pA_2 = 8.32$). Of note, tetramerization of UFP-101 determined a significant reduction of selectivity over opioid receptors, particularly for the DOP. When evaluated in vivo in the mouse forced swimming test, PWT2-UFP-101 exhibited antidepressant properties with higher potency (nearly tenfold) compared with UFP-101. In line with the PWT derivatives described above, the onset of the in vivo effects of PWT2-UFP-101 was significantly delayed. Nevertheless, unlike other tetrabranched derivatives, the duration of action of PWT2-UFP-101 was similar to that of UFP-101. It has been speculated that the latter finding may be due to the presence of the unnatural amino acid residue Nphe at N-terminal portion of UFP-101 resulting in an intrinsic proteolytic resistance that cannot be further improved through the PWT approach (Calo' et al. 2018).

6 Concluding Remarks

Collectively the diverse approaches to the obtainment of NOP peptide ligands resulted in the identification of important tools with pharmacological profiles spanning from full and partial agonists to pure antagonist. Some of these ligands largely contributed to the elucidation of the physiopathology of the N/OFQ-NOP system and its translational potential to the pharmacological treatment of different diseases. Of note, some of the design and synthetic efforts described above also contributed to reduce significantly the known pharmacokinetic weaknesses of peptide molecules paving the way to the concrete option of employing NOP-targeted peptide ligands for clinical purposes. In this regard, the extensive SAR studies performed on the endogenous sequence of N/OFQ drove to the identification of the NOP full agonist UFP-112 that is now under clinical development by Recordati under the name Rec 0438. This compound is currently in Phase II studies as innovative treatment for overactive

bladder patients (ClinicalTrials.gov Identifier: NCT03482037). Furthermore, SER 100 (alias ZP120) distinguishes as the most advanced N/OFQ-unrelated peptide that reached phase II clinical studies aimed at assessing its safety and efficacy after subcutaneous administration in patients with systolic hypertension (Kantola et al. 2017). Finally, preclinical studies performed in rodents and nonhuman primates suggested that the spinal administration of NOP selective as well as of mixed NOP/opioid peptides could be of value for the treatment of chronic pain (Toll et al. 2016). A relevant contribution in this area might come from N/OFQ-related PWT derivatives whose spinal analgesic action last for more than one day from injection (Cerlesi et al. 2017; Rizzi et al. 2015). These kind of compounds together with technological advances of targeted intrathecal drug delivery systems may hopefully provide in the near future interesting options for the management of chronic pain patients.

Author Contributions DP, GC, and RG wrote the chapter and approved its final version.

Declaration of Interests DP has nothing to declare. GC and RG are inventors of the patent applications WO2006/087340 and U.S. Serial No. 14/782,578 covering UFP-112 and PWT derivatives of N/OFQ, respectively, and are among the founders of the University of Ferrara spin-off company UFPeptides s.r.l., the assignee of these patents.

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