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Update on melatonin receptors: IUPHAR Review 20

Correspondence Ralf Jockers, Inserm, U1016, Institut Cochin, 22 rue Méchain, 75014 Paris. E-mail: ralf.jockers@inserm.fr

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Ralf Jockers^{1,2,3}, Philippe Delagrangé⁴, Margarita L. Dubocovich⁵, Regina P. Markus⁶, Nicolas Renault⁷, Gianluca Tosini⁸, Erika Cecon^{1,2,3} and Darius P. Zlotos⁹

¹Inserm, U1016, Institut Cochin, Paris, France, ²CNRS UMR 8104, Paris, France, ³University Paris Descartes, Paris, France, ⁴Institut de Recherches Servier, Croissy, France, ⁵Department Pharmacology and Toxicology, Jacobs School of Medicine and Biomedical Science, University at Buffalo (SUNY), Buffalo, USA, ⁶Institute of Biosciences, University of São Paulo, São Paulo, Brazil, ⁷Inserm UMR 995, LIRIC, UFR Pharmacie, Lille, France, ⁸Neuroscience Institute and Department of Pharmacology and Toxicology, Morehouse School of Medicine, Atlanta, GA, USA, and ⁹Department of Pharmaceutical Chemistry, The German University in Cairo, New Cairo City, Cairo, Egypt

Melatonin receptors are seven transmembrane-spanning proteins belonging to the GPCR superfamily. In mammals, two melatonin receptor subtypes exist - MT₁ and MT₂ - encoded by the *MTNR1A* and *MTNR1B* genes respectively. The current review provides an update on melatonin receptors by the corresponding subcommittee of the International Union of Basic and Clinical Pharmacology. We will highlight recent developments of melatonin receptor ligands, including radioligands, and give an update on the latest phenotyping results of melatonin receptor knockout mice. The current status and perspectives of the structure of melatonin receptor will be summarized. The physiological importance of melatonin receptor dimers and biologically important and type 2 diabetes-associated genetic variants of melatonin receptors will be discussed. The role of melatonin receptors in physiology and disease will be further exemplified by their functions in the immune system and the CNS. Finally, antioxidant and free radical scavenger properties of melatonin and its relation to melatonin receptors will be critically addressed.

Abbreviations

AD, Alzheimer's disease; ADHD, attention-deficit/hyperactivity disorder; ASDs, autism spectrum disorders; fMLP, N-formyl-l-methionyl-l-leucyl-l-phenylalanine; FPG, fasting plasma glucose; HD, Huntington's disease; IOP, intraocular pressure; MS, multiple sclerosis; MTR, melatonin receptor; NREM, non-rapid eye movement; PD, Parkinson's disease; QR2, quinone reductase 2; REM, rapid eye movement; SCN, suprachiasmatic nucleus; T2D, type 2 diabetes

Tables of Links

TARGETS
GPCRs^a
5-HT _{2C} receptor
β ₂ -adrenoceptor
A _{2A} adenosine receptor
GPR50
MT ₁ receptor
MT ₂ receptor
Voltage-gated ion channels^b
Ca _v 2.2 channels
Transporters^c
GLUT1
Enzymes^d
CaMKII
ERK1

LIGANDS		
6-Chloromelatonin	CIFEA	[³ H]-melatonin
5-HEAT	Difluoroagomelatine	Ramelteon
6-Hydroxymelatonin	[¹²⁵ I]-DIV880	S22153
2-(indolin-1yl)-melatonin	Dopamine	S24014
2-Iodomelatonin	EFPPEA	S24773
2-[¹²⁵ I]iodomelatonin	fMLP	S26131
2-Methoxy-α,β-didehydro-agomelatine	GR 128107	S26284
5-Methoxyluzindole	GR 196429	Tasimelteon
4P-PDOT	(Hydroxymethylphenyl) agomelatine	TNF
[¹²⁵ I]-SD6	IIK7	TIK 301
[¹²⁵ I]-S70254	isoamyl agomelatine	UCM 454
AAE-M-PBP amine	K185	UCM 765
Agomelatine	Luzindole	UCM 793
BOMPPA	MCA-NAT	UCM1014
cAMP	N-acetyl-serotonin	
CBOBNEA	Melatonin	

These Tables list key protein targets and ligands in this article which are hyperlinked to corresponding entries in <http://www.guidetopharmacology.org>, the common portal for data from the IUPHAR/BPS Guide to PHARMACOLOGY (Southan *et al.*, 2016) and are permanently archived in the Concise Guide to PHARMACOLOGY 2015/16 (^{a,b,c,d}Alexander *et al.*, 2015a,b,c,d).

Introduction

The hormone melatonin is mainly produced by the pineal gland following a circadian rhythm, with high levels during the subjective night. Melatonin can also be produced by extra-pineal sites like the retina, the gastrointestinal tract and the innate immune system. This hormone regulates a variety of physiological and neuroendocrine functions in mammals through activation of two GPCRs, the MT₁ and MT₂ receptors. Both receptors are typically coupled to G_{i/o}-type proteins and the MT₁ receptor is coupled, in addition, to G_q-type proteins. In humans, the *MTNRIA* gene encoding MT₁ is located on chromosome 4q35.1 and the *MTNR1B* gene encoding MT₂ on chromosome 11q21-q22.

This article will review and discuss recent updates by the melatonin receptor subcommittee of the International Union of Basic and Clinical Pharmacology (IUPHAR) database (<http://www.guidetopharmacology.org/GRAC/FamilyDisplayForward?familyId=39>), which include the development of new MT receptor ligands, radioligands and structural perspectives of the MT receptors. The discovery of MT receptor dimers with physiological function *in vivo* as well as genetic variants and mutants of MT receptors will be discussed as they provide a new dimension to understand MT receptor pharmacology and function. An update on the latest results obtained with MT receptor knockout (KO) mouse models will be provided. Among the many physiological effects of MT receptors, we chose to focus on those of the immune system and the CNS. At the end of the review, MT receptor-independent effects, including

antioxidant and free radical scavenger properties of melatonin, will be critically addressed.

For more complete or other specific aspects of MT receptors, the reader is referred to other recent expert reviews (Jockers *et al.*, 2008; Dubocovich *et al.*, 2010; Markus *et al.*, 2013; Tosini *et al.*, 2014; Zlotos *et al.*, 2014; Liu *et al.*, 2016).

MT receptor ligands

MT₁ and MT₂ receptors share a high degree of sequence homology and bind both the natural ligand, melatonin, with high affinity. Important progress has been made in the development of synthetic MT receptor antagonists and agonists and subtype-selective ligands by diversifying the chemical scaffolds. Indeed, MT receptor ligands from different structural classes show distinct structure–activity relationships on native and recombinant MT receptors (Dubocovich *et al.*, 1997; Dubocovich *et al.*, 2010; Zlotos, 2012; Zlotos *et al.*, 2014). The methoxy group and the acetamido side chain of melatonin determine the intrinsic activity and the binding affinity, respectively, at both hMT₁ and hMT₂ receptors (Dubocovich *et al.*, 1997; Browning *et al.*, 2000; Audinot *et al.*, 2003). Replacement of the amide methyl group by ethyl and propyl substituents enhances affinity (Sugden *et al.*, 1995). Exchange of the indole ring by various aromatic scaffolds maintains high binding and agonist potency.

Substitutions at the two-position with a halogen or a phenyl group generate agonists with ~10-fold increased binding affinity. The majority of non-selective MT₁–MT₂ receptor ligands, including drugs used in humans, for example,

ramelteon [Rozerem®, (Kato *et al.*, 2005; Mini *et al.*, 2007; Rawashdeh *et al.*, 2011)], agomelatine [Valdoxan®, (de Bodinat *et al.*, 2010)] and tasimelteon [Hetlioz®, (Rajaratnam *et al.*, 2009; Lavedan *et al.*, 2015)], are agonists (Figure 1). Ramelteon and tasimelteon are MT receptor selective, while agomelatine is also an antagonist at the 5-HT_{2C} receptors, a pharmacological property believed to contribute to its antidepressant action. The therapeutic effects of approved drugs acting on hMT₁ and/or hMT₂ receptors as agonists were recently reviewed (Liu *et al.*, 2016). Other non-selective MT receptor agonists include 6-chloromelatonin, 6-hydroxymelatonin, 2-iodomelatonin, GR 196429 (Dubocovich *et al.*, 1997; Browning *et al.*, 2000;

Audinot *et al.*, 2003), UCM 793 (Rivara *et al.*, 2007) and 2-methoxy- α,β -didehydro-agomelatine (Morellato *et al.*, 2013). This latter ligand shows the highest affinity for hMT₁ (K_i = 0.03 nM) and hMT₂ (K_i = 0.07 nM) receptors and ~3500-fold greater potency than melatonin in the melanophore aggregation assay. TIK 301 (Mulchahey *et al.*, 2004) acts also as an antagonist at the 5-HT_{2C} and 5-HT_{2B} receptors (Landolt and Wehrle, 2009). 5-HEAT has a unique pharmacological profile acting as a full agonist at the hMT₁ receptor and antagonist at the hMT₂ receptor (Nonno *et al.*, 2000). EFPPEA, a high-affinity hMT₁ (K_i = 0.062 nM) and hMT₂ receptor (K_i = 0.420 nM) agonist, decreases the percentage of wakefulness and increases the percentage of slow wave

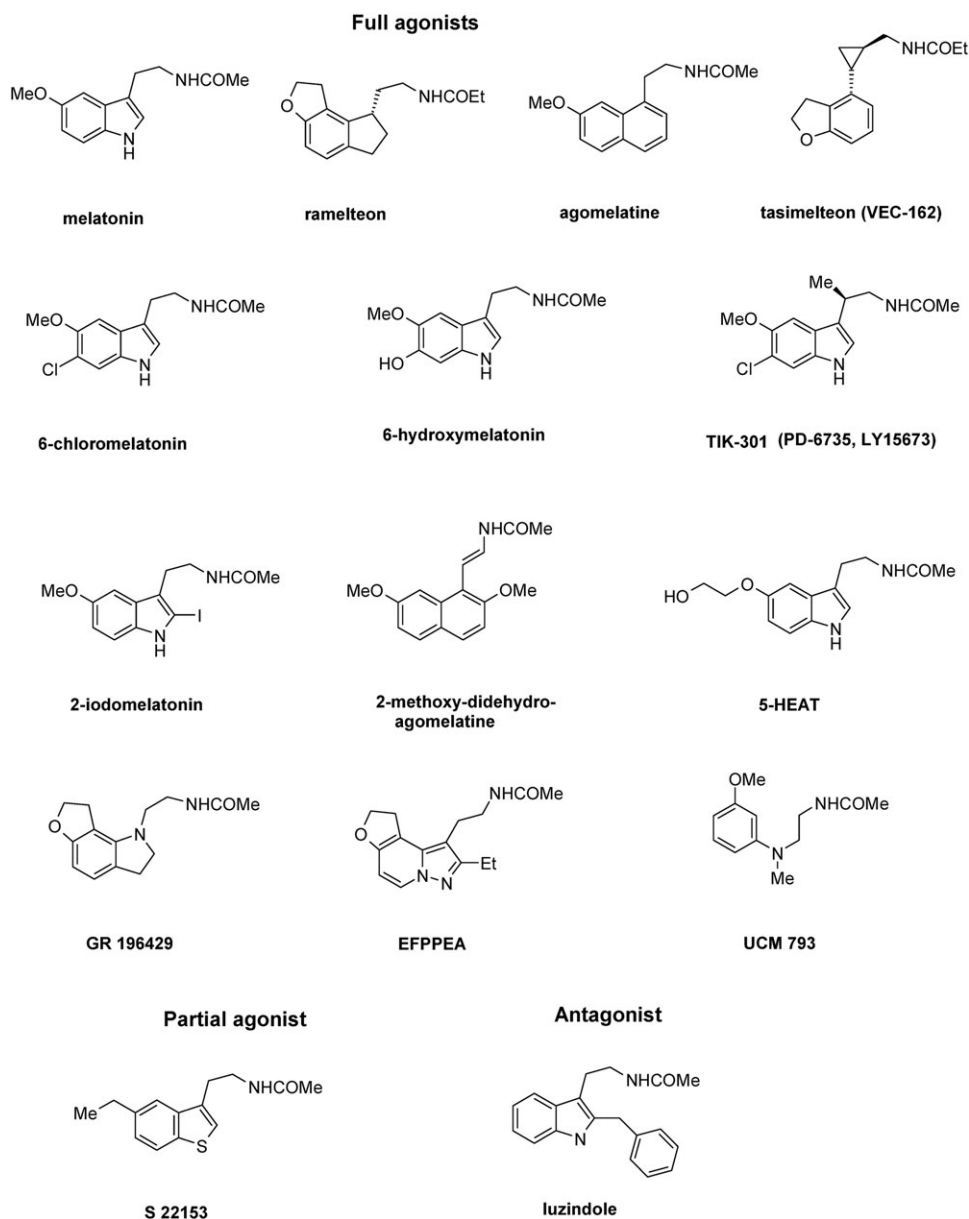


Figure 1

Structures of non-selective MT₁/MT₂ receptor ligands. 5-HEAT, 5-hydroxyethoxy-*N*-acetyltryptamine; EFPPEA, ethyl-furo-pyrazolo-pyridine-ethyl-acetamide.

sleep in cats (Koike *et al.*, 2011). The competitive MT receptor antagonist luzindole lacks the methoxy group, which led to the suggestion that this group is necessary for intrinsic activity (Dubocovich, 1988). Similarly, S22153 acts as a partial agonist (Audinot *et al.*, 2003). Luzindole, with a 15- to 25-fold higher affinity for hMT₂ than for hMT₁ receptors, is widely used for pharmacological characterization of functional MT receptors (Dubocovich *et al.*, 1997; Dubocovich *et al.*, 1998; Browning *et al.*, 2000; Dubocovich *et al.*, 2010).

A ligand is considered selective for a specific receptor type when its affinity or potency is at least 100-times higher than that for the other(s) receptor types in the family (Dubocovich *et al.*, 2010). This concept holds true for *in vitro* studies where ligand concentrations can be easily adjusted. However, ligand selectivity might be more difficult to reach *in vivo*, in the body fluids reaching the receptors. Depending on ligand dose and pharmacokinetics, concentrations could easily raise to levels activating both receptors (e.g. MT₁ and MT₂ receptors). This is particularly of concern for melatonin and synthetic MT receptor ligands activating receptors at picomolar concentrations (Dubocovich *et al.*, 1997; Browning *et al.*, 2000; Audinot *et al.*, 2003). Therefore, caution should be taken when interpreting selective MT receptor activation *in vivo* using MT receptor-selective ligands, unless pharmacological selectivity or lack of it, is confirmed by KO models with deletion of each receptor type.

Numerous ligands with high selectivity for hMT₂ over hMT₁ receptors have been identified (Zlotos *et al.*, 2014). MT₂ receptors possess a lipophilic pocket close to the N1–C2 binding region of melatonin, which is absent in MT₁ receptors (Rivara *et al.*, 2005). Accordingly, most MT₂ receptor-selective ligands bear a flexible bulky hydrophobic substituent in a position equivalent to C2 or N1 of melatonin (Figure 2). The tetrahydroquinoline analogue UCM1014 is the most potent MT₂ receptor-selective ligand reported to date. It shows picomolar binding affinity ($K_i = 0.001$ nM) at hMT₂ receptors, >10 000-fold selectivity over hMT₁ receptors and full agonist profile in the GTP γ S test (Spadoni *et al.*, 2015). Other agonists with approximately 800-fold hMT₂ receptor selectivity are BOMPPA (Hu *et al.*, 2010; Heckman *et al.*, 2011; Chan *et al.*, 2013; Hu *et al.*, 2013) and CIFEAA (Koike *et al.*, 2011). In imprinting control region mice, CIFEAA reentrainment effects to a new light/dark cycle indicate the involvement of MT receptors in the regulation of chronobiotic activity (Koike *et al.*, 2011). The dose of CIFEAA used in this study most likely reached micromolar concentrations, which would activate both MT₁ and MT₂ receptors, precluding any conclusion about the specific receptor type involved in the regulation of chronobiotic processes. Similarly, doses of the MT₂ receptor-selective antagonist 4P-PDOT (90 μ g/mouse s.c.) used to block the melatonin-mediated phase advance of circadian activity rhythms in mice (Dubocovich *et al.*, 1998) may have resulted in micromolar circulating 4P-PDOT concentrations hence blocking both MT₁ and MT₂ receptors.

Two moderately selective MT₂ receptor ligands, the agonist I1K7 (Faust *et al.*, 2000) and the partial agonist UCM 765 (Rivara *et al.*, 2007), have been used to examine the role of each MT receptor type in the modulation of sleep architecture. UCM 765 promoted non-rapid eye movement (NREM) sleep in rodents, and this effect was blocked by the MT₂

receptor antagonist 4P-PDOT (Ochoa-Sanchez *et al.*, 2011). In contrast, the non-selective MT₁–MT₂ receptor agonist UCM793 decreased sleep onset without having an effect on NREM sleep maintenance suggesting that dual MT₁ and MT₂ receptor agonistic activity accounts for the effect on sleep onset, whereas selectivity for MT₂ receptors has an additional effect on NREM sleep maintenance. I1K7 was also reported to reduce NREM sleep onset latency and transiently increase the time spent in NREM sleep in rats without altering rapid eye movement (REM) sleep latency or the amount of REM sleep (Fisher and Sugden, 2009).

Among the hMT₂ receptor-selective partial agonists GR 128107, 5-methoxyluzindole, S 24014, S 24773 (Dubocovich *et al.*, 1997; Audinot *et al.*, 2003) and isoamyl agomelatine, the latter shows the highest affinity ($K_i = 0.01$ nM) and selectivity (7200-fold) (Ettaoussi *et al.*, 2012). 4P-PDOT, an hMT₂ receptor-selective antagonist with 300- to 1500-fold higher affinity for hMT₂ receptors, is still considered the gold standard for pharmacological characterization of MT receptors (Dubocovich *et al.*, 1997). Other MT₂ receptor-selective antagonists, such as K185 (Sugden *et al.*, 1999; Faust *et al.*, 2000), UCM 454 (Rivara *et al.*, 2005) and 2-(indolin-1yl) melatonin (Zlotos *et al.*, 2009), display ~100-fold higher affinity for hMT₂ receptors. For (hydroxymethyl)phenyl agomelatine, the affinity for hMT₂ receptors is 750-times higher than for hMT₁ receptors (Poissonnier-Durieux *et al.*, 2008).

Discovery of MT₁ receptor-selective ligands remains a challenge, and only few compounds with preference for hMT₁ receptors have been reported (Zlotos *et al.*, 2014). Ligands preferentially binding to these receptors reach maximally 100-fold selectivity, and, when investigated, this selectivity is significantly reduced in functional *in vitro* studies (Figure 3). A common structural feature conferring MT₁ receptor selectivity is a bulky, hydrophobic ether replacing the methoxy group. The first hMT₁ receptor-selective agents were obtained by connecting two agomelatine units via their ether oxygen by (CH₂)₃- and (CH₂)₄-linker to give S 26131 (antagonist) and S 26284 (partial agonist), both displaying ~100-fold selectivity (Audinot *et al.*, 2003; Descamps-Francois *et al.*, 2003). A similar approach led to the UCM 793 dimer with 100-fold hMT₁ receptor selectivity and partial agonist activity (Spadoni *et al.*, 2011). Monomeric ligands, such as CBOBNEA (Mesangeau *et al.*, 2010), and AAE M PBP amine (Rivara *et al.*, 2012) are partial agonists showing similar ~100-fold selectivity for hMT₁ receptors. *N*-acetyl-*O*-phenoxypropyl serotonin is a full agonist obtained by exchange of the methoxy group of melatonin with an *O* (CH₂)₃Oph moiety. Although it shows only 10-fold binding preference toward hMT₁ receptors, its MT₁–MT₂ receptor binding ratio and hMT₁ receptor affinity were higher than that for the MT₁ receptor-selective reference compound S 26131 that was retested under the same experimental conditions (Markl *et al.*, 2011). A 140-fold MT₁ receptor selectivity could be attained by introduction of two fluorine atoms into the *N*-acetyl group of agomelatine. The resulting difluoroagomelatine shows high hMT₁ receptor binding ($K_i = 0.03$ nM) and is a non-selective MT₁–MT₂ receptor full agonist (Ettaoussi *et al.*, 2012). Very recently, tetrafluoro S26131, the difluoroacetamide analogue of S 26131, has been reported to show higher affinity and selectivity toward hMT₁ receptors than the parent ligand (Zlotos *et al.*, 2015).

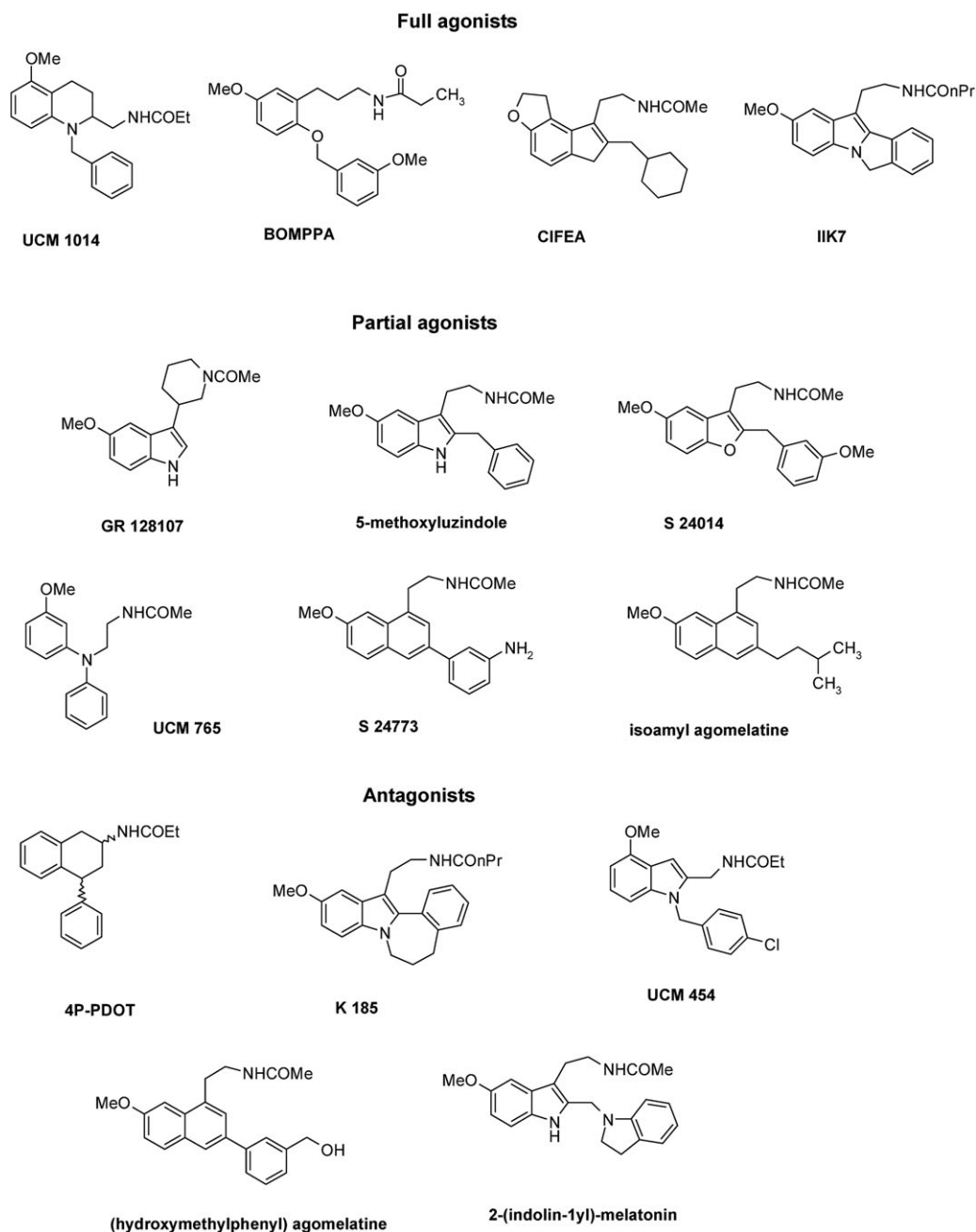


Figure 2

Structures of MT₂ receptor-selective ligands. BOMPPA, benzyloxy-methoxyphenyl-propylamide; CIFEA, cyclohexylmethyl-indenofurane-ethylacetamide; 4P-PDOT, 4-phenyl-2-propionamidotetralin.

In summary, while numerous ligands selective for the MT₂ receptor subtype are available, discovery of ligands with at least >100-fold selectivity for MT₁ receptors remains a challenging task. None of the MT₁ receptor-selective ligands has been tested *in vivo*. Future progress on the elucidation of the structure of MT receptors will hopefully foster the discovery of such ligands. The MT₁-MT₂ non-selective receptor antagonist luzindole and the MT₂ receptor-selective antagonists 4P-PDOT are still considered the gold standards for pharmacological characterization of MT receptors.

Radioligands – update

Radioactive- and fluorescent-labelled ligands are indispensable tools for the pharmacological characterization of GPCRs. A major breakthrough in the field of MT receptor research was the labelling of 2-iodomelatonin with ¹²⁵I at carbon 2 resulting in a high-affinity radioligand with high specific activity (Vakkuri *et al.*, 1984) for use in the localization (Vanecek, 1988) and pharmacological characterization of MT receptors in tissues (Dubocovich and Takahashi, 1987). The radioligand, 2-[¹²⁵I]iodomelatonin (2-[¹²⁵I]-IMLT), has

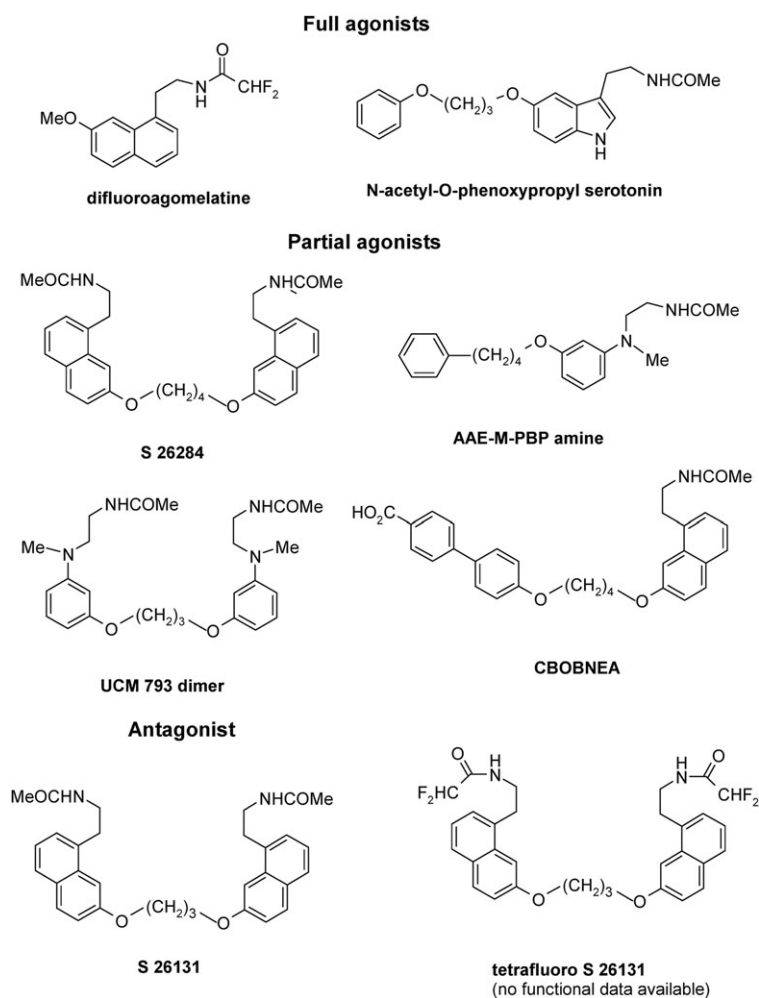


Figure 3

Structures of MT₁ receptor-selective ligands. CBOBNEA, carboxybiphenyloxy-butoxy-naphthalene-ethylacetamide; AAE-M-PBP amine, acetylaminoethyl-methyl-phenylbutoxyphenyl-amine.

been extensively used as a high-affinity radioligand for both MT₁ and MT₂ receptors, and was until recently the only available radioligand for the characterization and localization of melatonin binding sites in native tissues (Figure 4). Studies performed with [³H]-melatonin ([³H]-MLT) established the pharmacological profile of the human recombinant MT₁ and MT₂ receptors, as being identical to that established using 2-[¹²⁵I]-IMLT as a radioligand. However, due to the rather low specific activity of this [³H]-MLT, its use to characterize and/or localize melatonin sites in tissues with low MT receptor density is limited (Browning *et al.*, 2000).

Three new iodinated radioligands have been recently characterized for use in the pharmacological characterization and localization of MT receptors (Figure 4). These radioligands are as follows: SD6 (*N*-[2-(5-methoxy-1H-indol-3-yl)ethyl]iodoacetamide), S70254 (2-iodo-*N*-2-[5-methoxy-2-(naphthalen-1-yl)-1H-pyrrolo[3,2-b]pyridine-3-yl]acetamide and DIV880 2-(2-[(2-iodo-4,5-dimethoxyphenyl)methyl]-4,5-dimethoxy phenyl) (Legros *et al.*, 2013; Legros *et al.*, 2016). [¹²⁵I]-SD6 has a similar pharmacological profile to that of 2-[¹²⁵I]-IMLT with the same affinity for MT₁ and MT₂

receptors. On the contrary, the two other radioligands [¹²⁵I]-S70254 and [¹²⁵I]-DIV880 show selectivity for MT₂ receptors with pK_d values of 9.6 and 9.7, respectively, in the absence of any specific binding to MT₁ receptors. All radioligands are agonists, either partial agonists ([¹²⁵I]-S70254, [¹²⁵I]-DIV880) or full agonists (2-[¹²⁵I]-IMLT, [¹²⁵I]-SD6, [³H]-MLT), which means that their K_d values depend not only on the affinity of the ligand for the receptor but also on the activation of the G protein in the ternary Ligand-Receptor-G protein complex.

The extensive pharmacological characterization of these three new radioligands in comparison with 2-[¹²⁵I]-IMLT and [³H]-MLT on membrane preparations from CHO-K1 cell lines stably expressing hMT₁ or hMT₂ receptors showed that [¹²⁵I]-S70254 and [¹²⁵I]-DIV880 mainly differ from 2-[¹²⁵I]-IMLT in their dissociation kinetics, which are faster for [¹²⁵I]-S70254 and [¹²⁵I]-DIV880 than for 2-[¹²⁵I]-IMLT (Legros *et al.*, 2016). Interestingly, [¹²⁵I]-SD6 labelled only approximately half of the binding sites detected with 2-[¹²⁵I]-IMLT in cells expressing hMT₁ receptors while comparable amounts were detected in cells expressing hMT₂

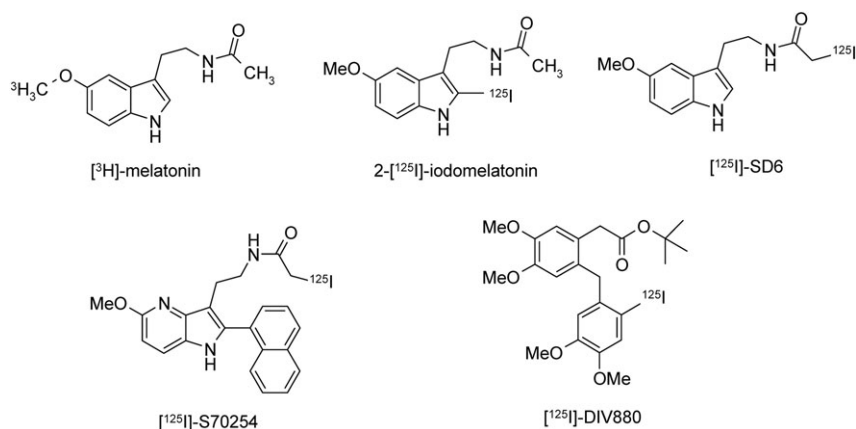


Figure 4

Structures of radioligands used to determine binding affinity for MT₁ and MT₂ receptors.

receptors (Legros *et al.*, 2013). This suggests the existence of different receptor subpopulations for hMT₁ receptors of which [¹²⁵I]-SD6 labels a more restricted number than 2-[¹²⁵I]-IMLT. In contrast, for hMT₂ receptors, similar subpopulations would be detectable by both radioligands. The nature of these receptor subpopulations is currently unknown but could be related to the differential engagement of hMT₁ receptors into complexes with different G proteins or β-arrestins following the binding of these agonistic radioligands. [¹²⁵I]-SD6 detected as 2-[¹²⁵I]-IMLT binding sites in sheep retinal membranes, while the MT₂ receptor-specific ligands [¹²⁵I]-S70254 and [¹²⁵I]-DIV880 failed to do so.

The MT₂ receptor-specific [¹²⁵I]-S70254 was successfully used for autoradiography studies in rat and sheep brain and retina slices (Legros *et al.*, 2016). A similar labelling pattern to 2-[¹²⁵I]-IMLT (detecting MT₁ and MT₂ receptors) was observed in several areas but also distinct labelling in others. Absence of labelling by [¹²⁵I]-S70254 in regions that are labelled by 2-[¹²⁵I]-IMLT can be explained by low (undetectable) MT₂ receptor levels. Absence of 2-[¹²⁵I]-IMLT labelling in regions labelled by [¹²⁵I]-S70254 could be due to the detection of different receptor complexes (see above).

Altogether, the new radioligands considerably expand the repertoire of pharmacological tools for MT receptors with the development of MT₂ receptor-specific radioligands and radioligands detecting distinct receptor populations revealing a previously unrecognized diversity. The availability of a radiolabelled antagonist would largely contribute in a better characterization of these different populations. Further advances can be expected from the development of fluorescent-labelled ligands.

Structural perspectives for MT receptors

Currently, crystal structures of MT₁ and MT₂ receptors are not available. Despite a sequence identity lower than 30% between MT receptors and the closest crystallized GPCRs, several three-dimensional (3D) models have produced some structural hypotheses for binding of (non)selective MT₁ and/or MT₂ receptor agonists (Table 1). According to site-directed mutagenesis data, most of these models corroborate the importance of both serine residues 3.35 and 3.39 in MT₁ as well as His5.46 in both MT₁ and MT₂ receptors.

Although His5.46 seems to be an anchoring residue for polar interactions with the methoxy or amide group of melatonin, only a few models of MT₁ receptors display a direct participation of serine residues in melatonin binding (Chugunov *et al.*, 2006; Farce *et al.*, 2008), which could be otherwise involved in an essential bending of helix 3 for binding site plasticity. Models take also into account several receptor–ligand interactions with amino acids conserved within GPCRs and known to play a role in aromatic switch activation (F5.47, W6.48).

Such homology modelling methods make predictions of flexible receptor regions difficult. Although not directly proven for MT receptors, E2 and I3 loops are known to be key features for ligand accessibility and G protein binding of GPCRs. Moreover, amino acid sequences of MT receptors show several singularities like the presence of a ^{3.49}NRV^{3.51} motif instead of the classical ^{3.49}DRY^{3.51} motif of other rhodopsin-like GPCRs. Another specificity is the replacement of the proline by an alanine residue in the conserved ^{7.49}NPXXY^{7.53} motif. Buried in the vicinity of the cytoplasmic surface, these marked differences are likely to affect receptor activation and/or signalling specificity of MT receptors rather than the ligand binding process.

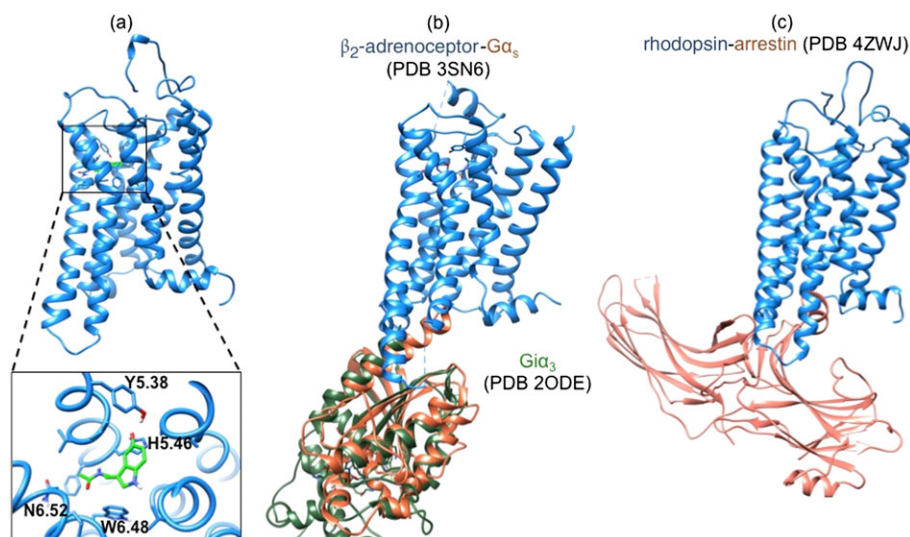
Whereas 3D models of MT receptors were up to now dedicated to the discovery and optimization of new efficient drugs, the next generation of 3D models should be expanded toward larger, multimeric systems and not be restricted to receptor monomers. Computation of the energy landscape of GPCRs by enhanced molecular dynamics simulations, together with NMR and X-ray studies, provided valuable molecular insights on the dynamics of ligand recognition, receptor activation and oligomerization (Johnston and Filizola, 2014). Depicting free energy landscapes of MT receptors should address biasing molecular dynamics simulations from the inactive apoform transiting toward the active trimeric L-R-Gi or L-R-arrestin forms of receptors (Figure 5). As ligands modulate these free energy landscapes (Provasi *et al.*, 2011; Dror *et al.*, 2013), *in silico* optimization of new efficient ligand structures could be explored by predicting its functional selectivity through arrestin or G_i-mediated pathways. These approaches also open the way for the exploration of homodimers and heterodimers, particularly MT₁/MT₂ and MT₁/GPR50 receptor complexes, as discussed in the following section.

Table 1

Summary of reported MT receptor homology models

Homology model	Crystal template	Binding amino acid	Reference
MT ₁ -ramelteon (non-selective agonist)	Inactive rhodopsin (Palczewski <i>et al.</i> , 2000)	Y175(E2), S182(E2), V5.43, <i>H5.46</i>	Uchikawa <i>et al.</i> , 2002
MT ₁ -agomelatine (non-selective agonist)	Inactive rhodopsin (Okada <i>et al.</i> , 2002)	L2.46, M3.32, <i>S3.35</i> , <i>S3.39</i> , <i>H5.46</i> , F5.47, P5.50	Voronkov <i>et al.</i> , 2005
MT ₁ -melatonin (non-selective agonist)	Inactive rhodopsin (Okada <i>et al.</i> , 2002)	L2.46, M3.32, <i>S3.35</i> , V3.36, <i>S3.39</i> , <i>H5.46</i> , F5.47, F6.44, W6.48, L6.51, N6.52, N7.49	Farce <i>et al.</i> , 2008
MT ₁ -2phenylmelatonin (selective agonist)	Active β_2 -adrenergic (Rasmussen <i>et al.</i> , 2011a,b)	M3.32, G3.33, Y5.38, <i>H5.46</i> , W6.48, L6.51, N6.52, Y7.39, A7.42, Y7.43	Rivara <i>et al.</i> , 2012
MT ₂ -2iodomelatonin (non-selective agonist)	Inactive rhodopsin (Okada <i>et al.</i> , 2002)	V5.42, <i>H5.46</i> , N6.52, L6.56, Y7.43	Mazna <i>et al.</i> , 2004
MT ₂ -UCM454 (selective antagonist)	Inactive rhodopsin (Okada <i>et al.</i> , 2004)	V3.36, I3.37, V3.40, Y183(E2), <i>H5.46</i> , F5.47, P5.50, I5.51, F6.44, W6.48	Rivara <i>et al.</i> , 2005
MT ₂ -melatonin	Inactive rhodopsin (Okada <i>et al.</i> , 2004)	L2.46, A2.49, <i>S3.35</i> , I3.37, <i>S3.39</i> , V5.42, V5.43, <i>H5.46</i> , F5.47	Voronkov <i>et al.</i> , 2005
MT ₂ -melatonin	Inactive rhodopsin (Okada <i>et al.</i> , 2002)	<i>S3.35</i> , V3.36, <i>S3.39</i> , V5.42, <i>H5.46</i> , W6.48, Y7.43	Chugunov <i>et al.</i> , 2006
MT ₂ -melatonin	Inactive rhodopsin (Okada <i>et al.</i> , 2002)	G3.33, V3.36, I3.37, N4.60, L4.57, T191(E2), Y5.38, <i>H5.46</i>	Farce <i>et al.</i> , 2008
MT ₂ -melatonin	Active rhodopsin (Scheerer <i>et al.</i> , 2008)	A3.29, V3.36, N4.60, <i>H5.46</i> , W6.48, L6.51	Zefirova <i>et al.</i> , 2011
MT ₂ -acylaminoethyl tetralin (selective partial agonist)	Active β_2 -adrenoceptor (Rasmussen <i>et al.</i> , 2011a,b)	M3.32, V3.36, N4.60, <i>H5.46</i> , W6.48, N6.52, Y7.43	Pala <i>et al.</i> , 2013

According to Ballesteros numbering, amino acids critical for ligand binding based on site-directed mutagenesis data (Conway *et al.*, 2001; Gerdin *et al.*, 2003; Kokkola *et al.*, 2003) are displayed in italic and bold.

**Figure 5**

Structures useful for the study of MT₁ receptor structure–function relationships. MT₁*-MLT (A) was derived from active forms of rhodopsin, β_2 -adrenoceptor and A_{2A} adenosine receptors (unpublished data, N.R.). Docking of melatonin (MLT) in the solvent-accessible cavity was achieved by energy relaxation by 300-ns molecular dynamics simulations. The structure of the MT₁*-MLT-Gi α_3 complex could be modelled on the basis of the sequence homology with the β_2 -adrenoceptor-G α_s structure (Rasmussen *et al.*, 2011b) and the homology between G α_s and Gi α_3 (Soundararajan *et al.*, 2008) (B) whereas the structure of the MT₁*-MLT-arrestin complex could be modelled based on the crystallized rhodopsin-arrestin complex (Kang *et al.*, 2015) (C).

MT receptor dimers

MT receptors are part of dynamic signalling complexes that contain proteins involved in receptor biosynthesis, export, signalling, desensitization, internalization and cytoskeleton modulation (Daulat *et al.*, 2007; Maurice *et al.*, 2008) (IntAct database, <http://www.ebi.ac.uk/intact/search/do/search?searchString=pubid:26514267>). The core of these complexes is often composed of receptor dimers, either homodimers of the same receptor or heterodimers composed of two different receptors (see Maurice *et al.*, 2011 and Ferre *et al.*, 2014). Initial observations have been made in 2002 in transfected HEK293 cells demonstrating the capacity of MT₁ and MT₂ receptors to form homodimers and heterodimers (Ayoub *et al.*, 2002) with MT₁/MT₂ heterodimers showing a pharmacological profile distinct from MT₂ homodimers (Ayoub *et al.*, 2004). Shortly after, MT₁ and MT₂ receptors were reported to form heterodimers with the orphan GPR50, which completely abolished the function of MT₁ receptors in MT₁/GPR50 heterodimers (Levoye *et al.*, 2006a). Sporadic reports on Western blots of endogenously expressed MT receptors in chicken astrocyte cultures (Adachi *et al.*, 2002) and *Xenopus* tectal cells (Prada *et al.*, 2005) further indicated the possible existence of MT receptor homodimers. However, the physiological relevance of these dimers remained largely unclear (Levoye *et al.*, 2006b) until 2013 when compelling *in vivo* evidence for the functional significance of MT₁/MT₂ heterodimers was obtained. In retinal photoreceptor cells, melatonin enhances the light sensitivity during the night. The phenotype of MT₁ receptor KO (MT₁^{-/-}) and MT₂ receptor KOs (MT₂^{-/-}) mice, the use of type-selective ligands and overexpression of a dominant negative form of MT₂ receptors in photoreceptor cells of transgenic mice indicated the exclusive involvement of MT₁/MT₂ heterodimers in this physiological effect of melatonin (Baba *et al.*, 2013). Interestingly, this effect was dependent on the activation of the G_q/PLC pathway by melatonin, an observation that could be confirmed *in vitro* in cells co-expressing MT₁ and MT₂ receptors.

Whether MT receptor heterodimers could become novel drug targets remains an open question. Recent evidence on the antidepressant agomelatine suggests this possibility (Kamal *et al.*, 2015). Previous studies showed that agomelatine is a high-affinity agonist for MT₁ and MT₂ receptors and an antagonist with moderate affinity for 5-HT_{2C} receptors (Audinot *et al.*, 2003; Millan *et al.*, 2003). Of note, the antidepressant effect of agomelatine involves both pathways in a synergistic manner (Racagni *et al.*, 2011). Formation of MT₂/5-HT_{2C} heterodimers was demonstrated in transfected HEK293 cells, and these heterodimers are targeted by agomelatine (Kamal *et al.*, 2015). Agomelatine behaved as a biased ligand, activating the G_i/cAMP pathway and antagonizing the G_q/PLC pathway. Whether the MT₂/5-HT_{2C} heterodimer participates in the antidepressant effect of agomelatine remains to be shown.

Formation of receptor dimers offers the possibility to design dimeric ligands targeting receptor dimers. Several dimeric ligands with two identical pharmacophores have been synthesized for MT receptors and their binding properties have been determined (Audinot *et al.*, 2003; Descamps-Francois *et al.*, 2003; Mesangeau *et al.*, 2010; Spadoni *et al.*, 2011; Journe *et al.*, 2014). Binding of the two

pharmacophores of these dimeric ligands to the two protomers of the same receptor dimer has been only shown in one study using a BRET approach (Journe *et al.*, 2014). Compounds linked through 22–24 atom spacers were able to bind to MT₁ and MT₂ receptor protomers in pre-existing homodimers and heterodimers and to induce conformational changes detected by BRET. Induction of receptor dimerization was not observed. The functional properties of these compounds remain to be studied. Taken together, the existence and physiological relevance of MT receptor dimers are increasingly recognized, but its functional role and pharmacological exploitation are still ongoing.

Genetic variants and mutants of MT receptors

The existence of many rare variants in the human population was discovered in recent genome sequencing programmes. The 1000 human genome project detected 38 million variants (Abecasis *et al.*, 2012) and 172 variants, including 46 non-synonymous variants, has been identified on average per GPCR in a population of 14 002 individuals (Nelson *et al.*, 2012; Karamitri and Jockers, 2014). Numerous variants have been identified in the *MTNR1A* and *MTNR1B* genes, encoding MT₁ and MT₂ receptors respectively. Here, only non-synonymous variants, modifying the amino acid sequence of the receptors, will be considered (Figure 6). Variants with altered receptor function can potentially participate in disease development. Ebisawa *et al.* (1999) were searching for variants in *MTNR1A* and *MTNR1B* genes in patients with circadian disorders. Two non-synonymous variants were identified in the *MTNR1A* gene (R54W, A157V) that were threefold and twofold more frequent in people with non-24 h sleep–wake syndrome (Table 2) (Ebisawa *et al.*, 1999). Due to the small sample size ($N = 22$), statistical significance was not reached.

Alteration of melatonin synthesis has been reported in autism spectrum disorders (ASDs) triggering the search for variants in *MTNR1A* and *MTNR1B* genes in 295 patients with ASD, 362 controls and 284 individuals from the human genome diversity panel (Chaste *et al.*, 2010). Six non-synonymous mutations were identified for *MTNR1A* and 10 for *MTNR1B* (Tables 2 and 3). The majority of these mutants showed altered receptor function. Particularly deleterious mutants were MT₁-I49N, which is devoid of any melatonin binding and cell surface expression, and MT₁-G166E and MT₁-I212T, which showed severely impaired cell surface expression and biased behaviour toward the ERK1/2 pathway. No significant difference in the prevalence of these mutations was found indicating that they do not represent major risk factors for ASD.

Four non-synonymous mutations were identified for *MTNR1A* and four for *MTNR1B* in a cohort of 101 individuals with attention-deficit/hyperactivity disorder (ADHD) (Tables 2 and 3); however, none of them was enriched in ADHD individuals as compared with the general population (Chaste *et al.*, 2011). The MT₁-Y170X nonsense mutation was only detected in one ADHD patient and introduced a premature STOP codon resulting in complete loss of receptor function.

MT receptor variants have been most extensively sought in studies focused on type 2 diabetes (T2D) based on the discovery of several frequent polymorphisms associated with

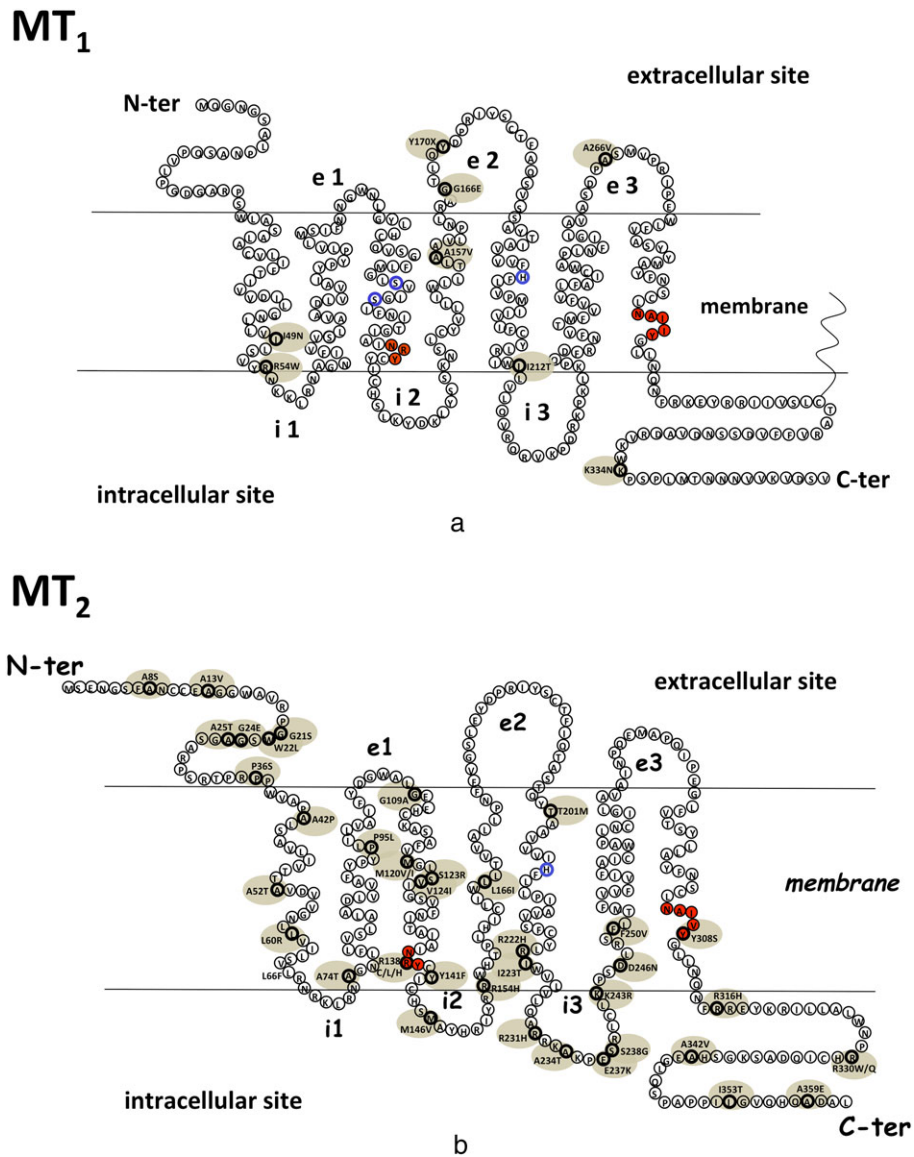


Figure 6

Distribution of non-synonymous MT₁ (A) and MT₂ (B) receptor variants identified in various human populations. Positions of variants are highlighted in light brown. Typical signatures of MT receptors such as the ³⁻⁴⁹NR_Y³⁻⁵¹ motif and the ⁷⁻⁴⁹NAXXY⁷⁻⁵³ motif are highlighted in red. Residues suspected to be directly involved in melatonin binding (S3.35 and S3.39 in MT₁ and H5.46 in both MT₁ and MT₂ receptors) are highlighted with a blue circle. The putative palmitoylation site at C314 is indicated in MT₁ receptors.

increased fasting plasma glucose (FPG) and T2D risk close to the *MTNR1B* gene in genome-wide association studies (Bouatia-Naji *et al.*, 2009; Prokopenko *et al.*, 2009). Sequencing of the coding region of the *MTNR1B* gene revealed six non-synonymous variants (G24E, L60R, V124I, R138C, R231H and K243R) of which none was associated with T2D risk. The common 24E variant was associated with increased body mass and decreased FPG (Andersson *et al.*, 2010), an observation that was not replicated in a later study (Bonfond *et al.*, 2012). Whereas only subtle changes in the capacity of G24E and V124I to activate a *GαΔ6q14myr* chimeric G protein, the L60R variant was completely inactive in transfected COS cells. A more extensive sequencing study discovered 40 non-synonymous variants in the coding region

of *MTNR1B* (Tables 2–4) (Bonfond *et al.*, 2012) of which 36 very rare mutants associated with T2D risk. Functional analysis of the 40 variants revealed intact cell surface expression for all variants. There was complete loss of melatonin binding in four very rare cases (A42P, L60R, P95L and Y308S) and partially and severely blunted signalling (*Gαq19* chimera and ERK1/2 activation) in one rare case (R138C) and nine very rare cases (W22L, A52T, A74T, R138H, R138L, L166I, R222H, R330W and I353T). Carriers of the 13 very rare loss-of-function variants showed increased T2D risk establishing a functional link between *MTNR1B* and T2D (see Karamitri *et al.*, 2013).

In conclusion, the genetic variability of the *MTNR1B* gene in terms of non-synonymous variants has now been well

Table 2Biologically important MT₁ receptor variants

Amino acid change	Type of variant	Description	Reference
I49N	Missense mutation	Rare variant identified in autism spectrum disorder patients, impaired cell surface expression, melatonin binding, cAMP inhibition and ERK1/1 activation	Chaste <i>et al.</i> , 2010
R54W	Missense mutation	Common variant identified in control population without obvious functional defect	Ebisawa <i>et al.</i> , 1999
A157V	Missense mutation	Common variant identified in control population without obvious functional defect	Chaste <i>et al.</i> , 2010; Ebisawa <i>et al.</i> , 1999
G166E	Missense mutation	Common variant identified in control population, impaired cell surface expression, reduced cAMP inhibition and ERK1/2 activation	Chaste <i>et al.</i> , 2010
Y170X	Nonsense mutation	Rare variant identified in attention-deficit hyperactivity disorder (ADHD) patient, premature STOP codon with impaired cell surface expression and cAMP inhibition	Chaste <i>et al.</i> , 2011
I212T	Missense mutation	Common variant identified in control population, impaired cell surface expression, cAMP inhibition and reduced ERK1/2 activation	Chaste <i>et al.</i> , 2010
A266V	Missense mutation	Common variant identified in control population with reduced ERK1/2 activation	Chaste <i>et al.</i> , 2010
K334N	Missense mutation	Rare variant identified in control population with reduced cAMP inhibition	Chaste <i>et al.</i> , 2010

Common [minor allelic frequency (MAF) >1%], rare (MAF 0.1–1%) variants.

defined and an association of very rare variants with T2D risk established. Less is known about the variability of the *MTNR1A* gene in terms of non-synonymous variants.

MT receptor mouse models – update

MT₁^{-/-} mice were created in the late 1990s followed by the generation of MT₂^{-/-} mice in 2003 (Liu *et al.*, 1997; Jin *et al.*, 2003). Studies using these mice have provided important insights on the role that MT receptors play in the modulation of many different biological functions. In MT₁^{-/-} mice, but not in MT₂^{-/-} mice, the inhibitory effect of melatonin on neuronal activity in the suprachiasmatic nucleus (SCN) is impaired suggesting the involvement of MT₁ receptors. In contrast, in SCN slices from MT₁^{-/-} mice melatonin (1–10 pM) phase shifts the peak of circadian rhythms of neuronal firing by approximately 3 h suggesting the involvement of MT₂ receptors (Liu *et al.*, 1997; Dubocovich *et al.*, 2005). Blockade of this effect using the MT₂ receptor-selective 4P-PDOT antagonist confirmed the latter conclusion shaping a pathway where MT₂ phase shifts the peak of neuronal firing through PLC-PKC signalling pathway (Mc Arthur *et al.*, 1997; Hunt *et al.*, 2001; Dubocovich *et al.*, 2005). Liu *et al.* (1997) reported that the phase shift of neuronal firing rhythms induced by 2-iodomelatonin (10 pM) was of smaller magnitude in the SCN slice from MT₁^{-/-} than in wild type (WT) mice suggesting a role for the MT₁ receptors in this response (see detailed discussion in Dubocovich, 2007). Together, these findings suggest a potential role for both MT₁ and MT₂ receptors in the phase shift of circadian rhythms of neuronal firing in the SCN slice *in vitro*. The use of MT₁^{-/-} mice demonstrated that the MT₁ receptor is required for the melatonin-mediated phase shift of the onset of overt circadian rhythm of locomotor activity (Dubocovich *et al.*,

2005). An independent study demonstrated that C3H/HeN mice (melatonin-proficient) entrained faster to a phase advance of dark onset than the C57BL/6J mice (melatonin-deficient), suggesting a facilitating role of endogenous melatonin on circadian reentrainment (Pfeffer *et al.*, 2012). However, we should note that faster entrainment could also result from genetic differences between the two mouse strains rather than different endogenous melatonin levels (Adamah-Biassi *et al.*, 2013). In a mouse strain producing endogenous melatonin, the faster entrainment to an abrupt advance of dark onset persisted in MT₁^{-/-} C3H/HeN mice but was lost in MT₂^{-/-} and double KOs (MT₁^{-/-}/MT₂^{-/-}) suggesting again the involvement of MT₂ receptors. This apparent contradiction could be explained by the activation of MT₂ and MT₁ receptors by endogenous and exogenous melatonin, respectively, at different periods of sensitivity (subjective night vs. subjective day, respectively). Changes in efficacy could also result from desensitization and/or internalization of MT receptors in response to exposure to physiological and supraphysiological melatonin concentrations as demonstrated by the phase shift of the peak of neuronal firing in the SCN by physiological levels of melatonin, which involved the desensitization of MT₂ receptors (Gerdin *et al.*, 2004).

MT receptor KO mice have been also used to elucidate the role played by these receptors in the regulation of the sleep/wake cycle. In MT₂^{-/-} NREM, sleep is decreased during the light phase (i.e. during the time that mice normally sleep), whereas MT₁^{-/-} mice showed an increase in the amount of NREM sleep during the dark phase (i.e. during active phase) (Ochoa-Sanchez *et al.*, 2011). Further analysis of the data indicated that MT₁ receptor signalling is implicated in the modulation of the daily rhythm of REM sleep (Ochoa-Sanchez *et al.*, 2011). An additional study in which

Table 3Biologically important MT₂ receptor variants

Amino acid change	Type of variant	Description	Reference
A8S	Missense mutation	Very rare variant identified in control population without obvious functional defect	Bonnefond <i>et al.</i> , 2012
A13V	Missense mutation	Very rare variant identified in control population without obvious functional defect	Bonnefond <i>et al.</i> , 2012
G21S	Missense mutation	Very rare variant identified in control population without obvious functional defect	Bonnefond <i>et al.</i> , 2012
W22L	Missense mutation	Very rare variant identified in type 2 diabetes patients, associated with type 2 diabetes risk, impaired G _i protein activation	Bonnefond <i>et al.</i> , 2012
G24E	Missense mutation	Common variant, not associated with type 2 diabetes risk but associated with prevalence of obesity and increased BMI shown in one study but not in another	Andersson <i>et al.</i> , 2010; Bonnefond <i>et al.</i> , 2012; Chaste <i>et al.</i> , 2010; Ebisawa <i>et al.</i> , 1999
A25T	Missense mutation	Very rare variant identified in control population without obvious functional defect	Bonnefond <i>et al.</i> , 2012
P36S	Missense mutation	Very rare variant identified in type 2 diabetes patients, without obvious functional defect	Bonnefond <i>et al.</i> , 2012
A52T	Missense mutation	Very rare variant identified in type 2 diabetes patients, associated with type 2 diabetes risk, impaired G _i protein activation	Bonnefond <i>et al.</i> , 2012
L66F	Missense mutation	Very rare variant identified in control population without obvious functional defect	Ebisawa <i>et al.</i> , 1999
A74T	Missense mutation	Very rare variant identified in control population and type 2 diabetes patients, associated with type 2 diabetes risk, impaired G _i protein activation	Bonnefond <i>et al.</i> , 2012
G109A	Missense mutation	Very rare variant identified in control population without obvious functional defect	Bonnefond <i>et al.</i> , 2012
M120V	Missense mutation	Very rare variant identified in control population without obvious functional defect	Bonnefond <i>et al.</i> , 2012
M120I	Missense mutation	Very rare variant identified in population with impaired fasting glucose and control population without obvious functional defect	Bonnefond <i>et al.</i> , 2012
S123R	Missense mutation	Very rare variant identified in population with impaired fasting glucose and control population without obvious functional defect	Bonnefond <i>et al.</i> , 2012
V124I	Missense mutation	Very rare variant identified in several populations including type 2 diabetes and ASD without obvious functional defect in one study and impaired ERK1/2 activation in another	Andersson <i>et al.</i> , 2010; Bonnefond <i>et al.</i> , 2012; Chaste <i>et al.</i> , 2010
R138C	Missense mutation	Rare variant, not associated with type 2 diabetes risk, no G _i and ERK1/2 activation	Andersson <i>et al.</i> , 2010; Bonnefond <i>et al.</i> , 2012; Chaste <i>et al.</i> , 2010
R138L	Missense mutation	Very rare variant identified in control population, associated with type 2 diabetes risk, impaired G _i protein activation	Bonnefond <i>et al.</i> , 2012
R138H	Missense mutation	Very rare variant identified in control population, associated with type 2 diabetes risk, impaired G _i protein activation	Bonnefond <i>et al.</i> , 2012
Y141F	Missense mutation	Very rare variant identified in type 2 diabetes patients, without obvious functional defect	Bonnefond <i>et al.</i> , 2012
M146V	Missense mutation	Very rare variant identified in control population without obvious functional defect	Bonnefond <i>et al.</i> , 2012
R154H	Missense mutation	Very rare variant identified in control population and type 2 diabetes patients without obvious functional defect	Bonnefond <i>et al.</i> , 2012

(Continues)

Table 3 (Continued)

Amino acid change	Type of variant	Description	Reference
L166I	Missense mutation	Very rare variant identified in control population, associated with type 2 diabetes risk, impaired G _i protein activation	Bonnefond <i>et al.</i> , 2012
T201M	Missense mutation	Very rare variant identified in type 2 diabetes patients, without obvious functional defect	Bonnefond <i>et al.</i> , 2012
R222H	Missense mutation	Very rare variant identified in type 2 diabetes patients, associated with type 2 diabetes risk, impaired G _i protein activation	Bonnefond <i>et al.</i> , 2012
I223T	Missense mutation	Very rare variant identified in type 2 diabetes patients, without obvious functional defect	Bonnefond <i>et al.</i> , 2012
R231H	Missense mutation	Rare variant, not associated with type 2 diabetes risk	Andersson <i>et al.</i> , 2010; Bonnefond <i>et al.</i> , 2012; Chaste <i>et al.</i> , 2010
A234T	Missense mutation	Very rare variant identified in control population without obvious functional defect	Bonnefond <i>et al.</i> , 2012
E237K	Missense mutation	Very rare variant identified in control population without obvious functional defect	Bonnefond <i>et al.</i> , 2012
S238G	Missense mutation	Very rare variant identified in type 2 diabetes patients, without obvious functional defect	Bonnefond <i>et al.</i> , 2012
K243R	Missense mutation	Common variant, not associated with type 2 diabetes risk	Bonnefond <i>et al.</i> , 2012
D246N	Missense mutation	Very rare variant identified in type 2 diabetes patients, without obvious functional defect	Bonnefond <i>et al.</i> , 2012
F250V	Missense mutation	Very rare variant identified in type 2 diabetes patients with impaired ERK1/2 activation	Bonnefond <i>et al.</i> , 2012
R316H	Missense mutation	Very rare variant identified in control population without obvious functional defect	Bonnefond <i>et al.</i> , 2012
R330W	Missense mutation	Very rare variant identified in type 2 diabetes patients, associated with type 2 diabetes risk, impaired G _i protein activation	Bonnefond <i>et al.</i> , 2012
R330Q	Missense mutation	Very rare variant identified in control population without obvious functional defect	Chaste <i>et al.</i> , 2010
A342V	Missense mutation	Very rare variant identified in type 2 diabetes patients, without obvious functional defect	Bonnefond <i>et al.</i> , 2012
I353T	Missense mutation	Very rare variant identified in type 2 diabetes patients and control population, associated with type 2 diabetes risk, impaired G _i protein activation	Bonnefond <i>et al.</i> , 2012
A359E	Missense mutation	Very rare variant identified in control population without obvious functional defect	Bonnefond <i>et al.</i> , 2012

Common [minor allelic frequency (MAF) >1%], rare (MAF 0.1–1%) and very rare (MAF < 0.1%) variants.

double KOs (MT₁^{-/-}/MT₂^{-/-}) were used indicated that removal of both receptors induced an increase in wakefulness and a reduction in REM sleep (Comai *et al.*, 2013). Hence, these data seem to indicate that removal of MT receptors may affect wakefulness rather than sleep.

The effect of MT receptor removal has been also investigated in the mouse retina, where these receptors are widely distributed (Baba *et al.*, 2009; Baba *et al.*, 2013). Removal of either receptor has profound effects on photoreceptors function as it abolishes the daily rhythms in the scotopic and photopic electroretinogram (Baba *et al.*, 2009; Alcantara-Contreras *et al.*, 2011; Sengupta *et al.*, 2011). Such a result also indicates that MT₁ and MT₂ receptors form heterodimers in mouse photoreceptors (Baba *et al.*, 2013). Further studies have also demonstrated that removal of MT receptors in

addition affects the viability of the photoreceptors and retinal ganglion cells during aging (Baba *et al.*, 2009; Alcantara-Contreras *et al.*, 2011; Giancesini *et al.*, 2016) as well as corneal biology (Baba *et al.*, 2015).

As mentioned before, recent studies have also implicated MT receptors in the pathogenesis of T2D in humans (Bouatia-Naji *et al.*, 2009; Lyssenko *et al.*, 2009; Bonnefond *et al.*, 2012). Thus, a few studies used MT receptor KO mice to determine the mechanisms by which these receptors contribute to regulation of glucose homeostasis and insulin sensitivity (Stumpf *et al.*, 2008; Muhlbauer *et al.*, 2009; Contreras-Alcantara *et al.*, 2010). Mice lacking MT₁ receptors exhibit higher mean blood glucose levels than controls (Muhlbauer *et al.*, 2009) and tend to be more glucose intolerant and insulin resistant than WT and MT₂^{-/-} mice

Table 4Mutations in the *MTNR1B* gene associated with susceptibility to type 2 diabetes

Amino acid change	Type of variant	Description	Reference
A42P	Missense mutation	Very rare variant identified in type 2 diabetes patients, associated with type 2 diabetes risk, no melatonin binding and signalling	Bonnefond <i>et al.</i> , 2012
L60R	Missense mutation	Very rare variant identified in control population and type 2 diabetes patients, associated with type 2 diabetes risk, no melatonin binding and signalling	Andersson <i>et al.</i> , 2010; Bonnefond <i>et al.</i> , 2012
P95L	Missense mutation	Very rare variant identified in type 2 diabetes patients, associated with type 2 diabetes risk, no melatonin binding and signalling	Bonnefond <i>et al.</i> , 2012
Y308S	Missense mutation	Very rare variant identified in type 2 diabetes patients, associated with type 2 diabetes risk, no melatonin binding and signalling	Bonnefond <i>et al.</i> , 2012

Very rare (minor allelic frequency <0.1%) variants.

(Contreras-Alcantara *et al.*, 2010). Furthermore, removal of MT₁ or MT₂ receptors abolishes the daily rhythm in blood glucose levels (Owino *et al.*, 2016).

Finally, it is important to mention that although the reproductive system of mice is not sensitive to photoperiod, the development of MT receptor KO mice provided an important tool for dissecting the mechanisms by which melatonin regulates reproduction in photoperiodic species. For example, MT₁ receptor signalling controls the rhythmic expression of the clock gene *Period 1* in the pituitary gland (von Gall *et al.*, 2002), and further studies have shown that the rhythmic expression of several other clock genes (*Per1*, *Per 2*, *Bmal1* and *Cry 1*) in the mouse *Pars tuberalis* depends on MT₁ receptor signalling as well (Jilg *et al.*, 2005). MT₁ receptor signalling has been also reported to be crucial for the photoperiodic response of gene expression in the ependymal cell layer and thus for the photoperiodic regulation of gonadal activity (Sheynzon and Korf, 2006; Yasuo *et al.*, 2009). Finally, we should mention that a recent study reported that MT₁ receptor signalling plays a key role in photoperiodic programming of serotonergic neurons as well as depression- and anxiety-related behaviours in mice (Green *et al.*, 2015).

In conclusion, studies in the last 20 years using MT receptor KO mice have greatly helped to understand the role(s) played by these receptors in the regulation of many physiological functions, and they have provided important insights on the mechanisms by which melatonin signalling affects these functions.

Functional role of MT receptors in physiology and pathophysiology

MT receptors are involved in many physiological processes that will however not all be covered by this review but can be consulted in other reviews (Dubocovich *et al.*, 2010; Tosini *et al.*, 2012; Karamitri *et al.*, 2013; Tosini *et al.*, 2014; Johnston and Skene, 2015). Here, we have focused our attention on two major processes, the immune system and the CNS. Important progress has been made recently in both fields, and links to diseases have been established justifying a review of our

current knowledge on these aspects. Finally, we will make a critical assessment of reports of receptor-independent effects of melatonin, such as its binding to additional binding sites and the intrinsic antioxidant and free radical scavenger properties of this hormone.

MT receptors in the immune system

The role of melatonin as a player in immunity, first proposed by Berman in 1926, is now well accepted (Carrillo-Vico *et al.*, 2013). Several reports have demonstrated that melatonin produced by the either pineal gland or immune cells can regulate the activation of an immune response. Melatonin derived from activated human lymphocytes induces the synthesis of IL-2 and IL-2 receptors (Carrillo *et al.*, 2004; Carrillo-Vico *et al.*, 2013). Luzindole and targeted deletion of the *MNTR1A* gene (Lardone *et al.*, 2006; Lardone *et al.*, 2010) block the effect of lymphocyte-derived melatonin. Interestingly, daily rhythms of plasma melatonin and IL-2 are transiently lost in non-infectious human inflammatory conditions, and the recovery of the IL-2 rhythm follows the restoration of the daily melatonin rhythm (Pontes *et al.*, 2007). In addition, the daily and seasonal variation of melatonin production contributes to the seasonality of some diseases. In multiple sclerosis (MS), melatonin blocks the differentiation of Th17 cells and boosts the generation of protective type 1 regulatory T-cells by an MT₁ receptor-dependent mechanism, resulting in the seasonal variation of MS symptoms (Farez *et al.*, 2015). Seasonality of regular immunity is also related to changes in the melatonin system (Weil *et al.*, 2015). In the spleen of several species, extended light exposure decreases MT₁ receptor expression (Maestroni, 1993; Lahiri and Haldar, 2009; Yadav and Haldar, 2013). In healthy conditions, rolling and adhesion of neutrophils to the endothelial cell layer are inhibited by activation of MT₂ receptors and ligands binding to the putative MT₃ binding site, respectively (Lotufo *et al.*, 2001). In contrast, other effects of melatonin such as the inhibition of transcription factors that mediate acute inflammation induced by LPS (Tamura *et al.*, 2010) or *N*-formyl-l-methionyl-l-leucyl-l-phenylalanine (fMLP) (Cernysiov *et al.*, 2015) were not

blocked by luzindole suggesting a mode of action independent of MT receptors.

MT receptors also play an important role in promoting engulfing of bacteria, fungi and parasites. Melatonin facilitates the invasion of erythrocytes by *Plasmodium falciparum* (Hotta *et al.*, 2000), the invasion of macrophages by *Leishmania amazonensis* (Laranjeira-Silva *et al.*, 2015) and the phagocytosis of zymosan by colostrum polymorphonuclear and mononuclear cells (Pires-Lapa *et al.*, 2013) and the RAW 264.7 macrophage cell line (Muxel *et al.*, 2012). The entrance of different microorganisms in polymorphonuclear and mononuclear cells, including colostrum and lineage-established cell lineages, is blocked by luzindole. Indeed, parasites, bacteria and fungi activate the NF- κ B pathway in these two cell models resulting in the expression of arylalkyl-N-acetyltransferase and the synthesis of melatonin. Luzindole and 4P-PDOT blocked the expression of dectin-1, a protein that is important for phagocytosis, suggesting the participation of MT₂ receptors in this effect (Muxel *et al.*, 2012; Pires-Lapa *et al.*, 2013; Muxel *et al.*, 2016). Thus, the evaluation of binding parameters and functional states of MT receptors in immune-competent cells needs to consider the masking effect of on-demand synthesized melatonin.

Although complex, the role of melatonin on the immune system is now beginning to be understood. MT₁ and MT₂ receptor types appear to play different roles, with MT₁ receptors as the main target in acquired immune response and MT₂ receptors as the target for innate immune responses.

MT receptors in the CNS

MT receptors are widely expressed throughout the CNS and are particularly well characterized in the SCN of the hypothalamus, where they are known to inhibit neuronal firing and mediate the phase shifting effect of melatonin on circadian rhythms (see above). In addition to its chronobiotic effect, melatonin participates in the modulation of neuronal functions, neurodevelopment at early and late stages (Kong *et al.*, 2008; Chen *et al.*, 2014) and affects brain structures underlying sleep regulation (Ochoa-Sanchez *et al.*, 2011), drug-related learning (Wang *et al.*, 2005; Savaskan *et al.*, 2006) and reward (Hutchinson *et al.*, 2012; Clough *et al.*, 2014). MT receptors mediate the melatonin-induced increase in dendrite length, thickness and complexity of hippocampal neurons, as these effects were partially blocked by luzindole (Dominguez-Alonso *et al.*, 2015). Similarly, melatonin-induced differentiation and maturation of adult neural stem cells were almost abolished in the presence of luzindole (de la Fuente Revenga *et al.*, 2015). A recent study using MT₂^{-/-} mice showed that MT₂ receptors were essential for axogenesis and for the formation of functional synapses (Liu *et al.*, 2015). MT₂ receptors were also involved in melatonin-induced protection against oxidative stress and memory impairment in a mouse model of ageing (Shin *et al.*, 2015). Recent advances in the understanding of presynaptic MT receptors and their role in neurodegenerative diseases are discussed in the following sections.

Presynaptic MT receptors. The role of melatonin on the regulation of calcium-dependent dopamine release from axon terminals in brain and amacrine cells in the retina was shown in the early 1980s (Zisapel and Laudon, 1982;

Dubocovich, 1983). However, more direct and global proof for the presence of presynaptic melatonin heteroreceptors (i.e. receptor for a transmitter or hormone other than the neuron's own neurotransmitter) capable of regulating neurotransmitter release was still insufficient. A recent protein interaction network analysis has established that MT₁, but not MT₂ receptors, are expressed on presynaptic axon terminal membranes in the hypothalamus, striatum, cortex and hippocampus, where they are part of the presynaptic protein network (Benleulmi-Chaachoua *et al.*, 2016). Notably, this study shows a strong physical association between MT₁ receptors and presynaptic proteins such as synapsin, SNAP25, Munc-18 and voltage-gated Ca_v2.2 channels. Interaction with the latter was responsible for constitutive inhibition of calcium entry by MT₁ receptors in a G β γ -dependent manner (Benleulmi-Chaachoua *et al.*, 2016).

These recent findings provide strong support for the involvement of MT receptors in synaptic functions, particularly in neurotransmitter release as indicated by previous studies. Indeed, activation of MT receptors has been implicated in the inhibition of ³H-dopamine release from the ventral hippocampus, medulla pons, preoptic area and hypothalamus (median and posterior) (Zisapel and Laudon, 1982; Dubocovich, 1983). This effect followed a diurnal rhythm in the hypothalamus with a maximum and a minimum observed at ZT 5 and ZT 13–15, respectively (Zisapel *et al.*, 1985). 6-Chloromelatonin-mediated modulation of noradrenaline turnover via activation of presynaptic melatonin heteroreceptors was demonstrated in hypothalamus (Fang and Dubocovich, 1990). In this model, luzindole, applied during the night when melatonin levels are high, accelerated noradrenaline turnover suggesting the involvement of MT receptors stimulated by endogenous melatonin (Fang and Dubocovich, 1990). The presence of presynaptic MT heteroreceptors on retino-hypothalamic fibres innervating superficial retinorecipient layers of the avian optic tectum has been inferred by the presence of 2-[¹²⁵I]-MLT binding sites and its decrease following transection of the retinotectal pathway (Krause *et al.*, 1992; Krause *et al.*, 1994). The function of these presynaptic MT receptors is currently unknown, but a modulatory role of these receptors on the light input pathway to visual and circadian target responses is likely. Recent electrophysiological evidence suggests that melatonin acting through presynaptic MT receptors increases glutamatergic neurotransmission in the habenula, an effect blocked by luzindole (Evely *et al.*, 2016). Finally, it is worth mentioning in this context that MT receptors were first shown to be involved in the inhibition of depolarization-evoked calcium-dependent neurotransmitter (dopamine) release from amacrine cells in the chick and rabbit retina (Dubocovich, 1983; Dubocovich, 1985). These mammalian functional presynaptic heteroreceptors were used to establish the first structure–activity relationship for MT receptor ligands, which correlated with the pharmacological profile of MT₂ receptors (Dubocovich *et al.*, 1997), and to identify and pharmacologically characterize the first competitive MT receptor ligands, luzindole and 4P-PDOT (Dubocovich, 1988).

In summary, proteomic studies of the MT₁ receptor interactome has revived interest in the function of presynaptic MT receptors and reinforced previous functional studies

indicating the role of presynaptic MT receptors in neurotransmitter release. Use of MT receptor KO mouse models will be particularly instrumental in this context, as they will clarify the respective roles of MT₁ and MT₂ receptors. Based on current data, a predominant role of MT₁ receptors in presynaptic functions, such as neurotransmitter release, and a potential role of MT₂ receptors in axogenesis and synapse formation can be postulated.

MT receptors in neurodegenerative diseases. Altered expression of MT receptors has been frequently reported in neurodegenerative diseases and psychiatric disorders, including Alzheimer's disease (AD), Parkinson's disease (PD), Huntington's disease (HD) and ASD. In AD patients, MT₁ receptor expression in the SCN and MT₂ receptor expression in the hippocampus are reduced compared to control subjects in *post-mortem* brains (Wu *et al.*, 2007). Intriguingly, higher expression of MT₁ receptors was detected in hippocampal arteries of AD brains (Savaskan *et al.*, 2002), which might be due to a compensatory response to the low levels of circulating melatonin in these patients (Zhou *et al.*, 2003). These observations suggest that the expression of MT receptors under pathological conditions can be differentially regulated depending on the brain area. In PD patients, down-regulation of MT₁ and MT₂ receptor expression was observed in the substantia nigra and amygdala, the two most relevant areas in PD pathogenesis (Adi *et al.*, 2010). Small case-control studies accessing MT₁ and MT₂ receptor expression in HD patients showed no changes in the SCN (van Wamelen *et al.*, 2013), while decreased expression of MT₁, but not of MT₂ receptors, was detected in the striatum (Wang *et al.*, 2011). Interestingly, the progressive loss of MT₁ receptors correlates with HD severity, also confirmed in a mouse model of HD (Wang *et al.*, 2011). In ASD patients, no information on MT₁ and MT₂ receptor expression is available, but several MT₁ and MT₂ receptor mutants with strongly reduced function have been identified (Chaste *et al.*, 2010).

Additional evidence supports the emerging concept of MT receptor dysfunction as a permissive condition favouring the development and/or progression of neurodegenerative diseases. The neuroprotective effect of endogenous and exogenous melatonin has been demonstrated in different systems (see Escribano *et al.*, 2014). In a neuroinflammatory model induced by LPS administration, cerebellar neuronal death was observed only in animals pretreated with luzindole (Pinato *et al.*, 2015). Similarly, depletion of endogenous melatonin by pinealectomy caused spontaneous neuronal loss in the hippocampal CA1 area, which was prevented by treatment with agomelatine (Tchekalarova *et al.*, 2016). The requirement of MT receptors for the neuroprotective action of melatonin has also been elegantly demonstrated in a series of *in vitro* studies in which luzindole treatment or siRNA-mediated knockdown of MT₁ receptors enhanced neuronal vulnerability to cell death (Wang *et al.*, 2011). Different cell stressor conditions such as temperature shift or treatments with hydrogen peroxide, TNF or with the HD-related protein huntingtin, resulted in reduced levels of MT₁ receptors. Accordingly, the AD-related neurotoxic amyloid β peptide (A β) impairs the function of MT receptors (Cecon *et al.*, 2015), implying that these receptors and melatonin

signalling are among the primary molecular targets affected in the course of AD.

Insights in the effects of MT receptors on cognitive functions are also obtained from MT receptor KO mice. MT₂^{-/-} mice show impaired long-term potentiation and performance in memory tests (Larson *et al.*, 2006). However, the double KO MT₁^{-/-}/MT₂^{-/-} mice show no clear differences from WT mice in memory test performances and show increased long-term potentiation responses, even though the deletion of MT receptors negatively affected the expression of important proteins for synaptic activity, such as phospho-synapsin and spinophilin (O'Neal-Moffitt *et al.*, 2014). The relevance of MT receptors for cognitive performance was clearly shown with an AD mouse model lacking MT₁ and MT₂ receptors, in which melatonin treatment failed to improve performance on hippocampal-dependent spatial learning tasks, as observed in the AD mouse model in the presence of MT₁ and MT₂ receptors. Impressively, the lack of MT receptors *per se* markedly increased the mortality in young AD mice (O'Neal-Moffitt *et al.*, 2015). Finally, the therapeutic use of melatonin has been proposed and tested in a number of murine models and clinical trials in several neurodegenerative conditions, including AD (Olcese *et al.*, 2009; Cardinali *et al.*, 2010; Peng *et al.*, 2013; Wade *et al.*, 2014; Zhang *et al.*, 2016), amyotrophic lateral sclerosis (Weishaupt *et al.*, 2006; Zhang *et al.*, 2013), PD (Medeiros *et al.*, 2007; Naskar *et al.*, 2015; Zhang *et al.*, 2016) and HD (van Wamelen *et al.*, 2015). The therapeutic use of melatonin is usually associated with sleep improvement and better alignment of circadian parameters, and its beneficial effect on neuroprotection and cognitive performance is starting to be recognized (Joshi *et al.*, 2015; Wade *et al.*, 2014). Dysfunction or down-regulation of MT receptors is likely to be part of the primary pathophysiological mechanisms rather than a consequence of advanced neurodegeneration and, thus, prophylactic hormonal replacement and/or early stage intervention strategies to restore MT receptor expression and function might provide the most efficient result.

Taken together, the subcellular localization and role of MT receptors in neuronal functions and their participation in neurodegenerative diseases are now starting to be understood and suggest a broad modulatory role of melatonin in neuronal function, development and plasticity.

Melatonin as antioxidant and free radical scavenger

The IUPHAR classifies only clearly identified pharmacological targets in mammals. However, some effects of melatonin persist even in the absence of MT₁ and MT₂ receptors or upon complete pharmacological blockade of MT receptors, indicating the existence of MT receptor-independent mechanisms, which are still not fully understood. In addition, MT receptor-dependent and -independent mechanisms can participate simultaneously, as demonstrated by O'Neal-Moffitt *et al.* (2015) regarding the antioxidant and pro-cognitive effects of melatonin on AD mice models, for example. Two main mechanisms have been put forward to explain the antioxidant and free radical properties of melatonin: these are melatonin binding to the MT₃ binding site (Nosjean *et al.*, 2000; Dubocovich *et al.*, 2003) and to the

cytosolic enzyme quinone reductase 2 (QR2) (Nosjean *et al.*, 2000; Dubocovich *et al.*, 2003), and melatonin scavenging of free radicals, as this hormone has been suggested to be an electron donor (see Tan *et al.*, 2015). Binding of melatonin to intracellular targets is readily achieved, due to the hydrophilic nature of this indolamine. Melatonin binds with nanomolar affinity to *MT3*/*QR2* binding sites but shows a pharmacological profile distinct from *MT1* and *MT2* receptors. The order of affinities for the *MT3* binding site is 2-iodomelatonin > *N*-acetyl-serotonin > melatonin (Dubocovich, 1995; Nosjean *et al.*, 2000), the order for *MT1* and *MT2* receptors is 2-iodomelatonin > melatonin >>>>*N*-acetyl-serotonin. MCA-NAT (5-methoxycarbonylamino-*N*-acetyltryptamine), prazosin and *N*-acetyltryptamine are selective ligands for the membrane *MT3* binding site (Dubocovich, 1995; Molinari *et al.*, 1996; Nosjean *et al.*, 2000). Nosjean *et al.* (2000) showed that a cytosolic binding site identified as QR2 has the pharmacological characteristics of the membrane *MT3* binding site. QR2 is a cytosolic flavin adenine dinucleotide (FAD)-dependent flavoprotein that reduces menadione and other quinones by using *N*-ribosyl- and *N*-alkyldihydronicotinamides as the co-substrates (Liao and Williams-Ashman, 1961), thus acting as a detoxifying enzyme to increase the antioxidant defence (Jockers *et al.*, 2008). There are still open questions as to whether the melatonin binding site on QR2 corresponds to the *MT3* binding site, in particular regarding those sites that are membrane-associated.

Several physiological effects of melatonin such as inhibition of leukocyte adhesion to rat endothelial cell layers were mimicked by *MT3* agonists (Lotufo *et al.*, 2001). Similar observations were made for the expression of adhesion molecules by granulocytes (Cernysiov *et al.*, 2015), the increase in dopamine levels in chick retina (Sampaio Lde *et al.*, 2014) and the reduction of intraocular pressure (IOP) in rabbits (Alarma-Estrany *et al.*, 2009). However, it has been questioned whether the functional effects of MCA-NAT are indeed mediated by QR2, as the lack of QR2 did not prevent the MCA-NAT-induced reduction on IOP, and overexpression of QR2 did not promote receptor-like responses (Vincent *et al.*, 2010). In addition, MCA-NAT turned out to be a partial agonist for *MT1* and *MT2* receptors at submicromolar concentrations suggesting the possibility that some of the effects of MCA-NAT might be mediated by *MT1* and/or *MT2* receptors (Vincent *et al.*, 2010).

Melatonin and its metabolites, with or without open ring structures, have been described as potent electron donors. Cyclic-3-hydroxymelatonin, *N1*-acetyl-5-methoxykynuramine (secondary metabolite) (AMK, tertiary metabolite) and *N*-acetyl-*N*-formyl-5-methoxykynuramine (AFMK, quaternary metabolite) scavenge free radicals neutralizing reactive oxygen and nitrogen species (Ressmeyer *et al.*, 2003; Tan *et al.*, 2007; Zavala-Oseguera *et al.*, 2014). Hence, one melatonin molecule and its associated metabolites could scavenge a large number of reactive species, and thus, the overall antioxidant capacity of melatonin is believed to be greater than that of other well-known antioxidants, such as vitamin C and vitamin E, under *in vitro* or *in vivo* conditions (Gitto *et al.*, 2001; Sharma and Haldar, 2006; Ortiz *et al.*, 2013). However, the ability of melatonin in reducing oxidative stress does not only rely on donating electrons. Indeed, by acting on *MT1* and *MT2* receptors, low pM and low nM concentrations of melatonin increased the expression or activity of enzymes such as superoxide dismutase, catalase and glutathione peroxidase, which are involved in oxygen

detoxification (Rosen *et al.*, 2009). Thus, depending on the dose of exogenous or endogenous melatonin, receptor-dependent or -independent mechanisms may be involved. A further complexity in the interplay between receptor-dependent and -independent processes could arise from the fact that melatonin, by changing the redox state of the cell, might influence receptor-mediated functions. Indeed, the function of several GPCRs has been shown to be sensitive to the cellular redox state. Whether this is also the case for MT receptors has to be addressed in future studies. Although endogenous melatonin levels are typically considered to range from low pM to low nM concentrations, much higher concentrations may be reached locally in the brain (Legros *et al.*, 2014) and in activated immune cells (Conti *et al.*, 2000). In addition, melatonin can be actively taken up through the GLUT1 glucose transporter (Hevia *et al.*, 2015). In conclusion, the role of the *MT3* binding site is still not fully understood and warrants further attention. Concerning the free radical scavenging properties of melatonin, it is surprising that opposing opinions are still in the literature. Overall, the antioxidant effects of melatonin appear to be complex, relying on a mixture of MT receptor-dependent and -independent processes.

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Conflict of interests

The authors declare no conflicts of interest.

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