

REVIEW ARTICLE

Epigenetic regulation of melatonin receptors in neuropsychiatric disorders

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Melatonin, the primary indoleamine hormone of the mammalian pineal gland, is known to have a plethora of neuroregulatory, neuroprotective and other properties. Melatonergic signalling is mediated by its two GPCRs, MT₁ and MT₂, which are widely expressed in the mammalian CNS. Melatonin levels and receptor expression often show a decrease during normal ageing, and this reduction may be accelerated in some disease states. Depleted melatonergic signalling has been associated with neuropsychiatric dysfunction and impairments in cognition, memory, neurogenesis and neurorestorative processes. The anticonvulsant and mood stabilizer, valproic acid (VPA), up-regulates melatonin MT₁ and/or MT₂ receptor expression in cultured cells and in the rat brain. VPA is known to affect gene expression through several mechanisms, including the modulation of intracellular kinase pathways and transcription factors, as well as the inhibition of histone deacetylase (HDAC) activity. Interestingly, other HDAC inhibitors, such as trichostatin A, which are structurally distinct from VPA, can also up-regulate melatonin receptor expression, unlike a VPA analogue, valpromide, which lacks HDAC inhibitory activity. Moreover, VPA increases histone H3 acetylation along the length of the MT₁ gene promoter in rat C6 cells. These findings indicate that an epigenetic mechanism, linked to histone hyperacetylation/chromatin remodelling and associated changes in gene transcription, is involved in the up-regulation of melatonin receptors by VPA. Epigenetic induction of MT₁ and/or MT₂ receptor expression, in areas where these receptors are lost because of ageing, injury or disease, may be a promising therapeutic avenue for the management of CNS dysfunction and other disorders.

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Abbreviations

ALS, amyotrophic lateral sclerosis; BDNF, brain-derived neurotrophic factor; CpG, 5'-C-phosphate-G-3'; CREB, cAMP response element binding protein; DNMT, DNA methyltransferase; GDNF, glial cell line-derived neurotrophic factor; GSK3 β , glycogen synthase kinase 3 β ; HAT, histone acetyltransferase; HDAC, histone deacetylase; HP1, heterochromatin protein 1; Nrf2-ARE, NF-E2-related factor 2-antioxidant responsive element; SCN, suprachiasmatic nucleus; SMC, structural maintenance of chromosomes; VPA, valproic acid

Introduction

Melatonin receptors

The mammalian **melatonin** receptor subtypes, **MT₁** and **MT₂**, are localized on neuronal dendrites and somata in areas that include the cerebral cortex, basal forebrain, hippocampus, basal ganglia, diencephalon and mesencephalon (Lacoste *et al.*, 2015). The anatomical distribution patterns of MT₁ and MT₂ receptors in the adult rat brain, which are detailed in recent reports (Lacoste *et al.*, 2015; Ng *et al.*, 2017), occur in a complementary fashion, in which relative increases in MT₁ receptor expression correspond with relative decreases in MT₂ receptors, or *vice versa*. For example, in the hypothalamus, the expression of MT₁ receptors is relatively high in the suprachiasmatic nucleus (SCN), whereas that of MT₂ receptors is relatively high in the supraoptic nucleus. This property may be indicative of their unique functional specializations (Lacoste *et al.*, 2015).

Functional studies have revealed that both melatonin receptor subtypes are coupled to various pertussis-sensitive and insensitive G proteins. A cornerstone of melatonergic signalling involves the inhibition of adenylate cyclase activity and attenuation of cAMP accumulation, PKA activity and cAMP response element binding protein (CREB) phosphorylation (Brydon *et al.*, 1999); however, the involvement of several other signal transduction pathways has been reported (Dubocovich *et al.*, 2010). Studies of melatonin receptor regulation in the ovine pars tuberalis demonstrated that stimulation of cAMP production, by forskolin or cholera toxin, increases MT₁ receptor expression (Barrett *et al.*, 1996). Since cAMP levels regulate the transcription of many genes through the cAMP/PKA/CREB pathway, the transcription factor CREB has been implicated in the regulation of melatonin receptors (Barrett *et al.*, 1996). Cloning of the proximal 1.5 kb region of the rat MT₁ promoter (GenBank AY228510) allowed for a more precise analysis of the regulation of MT₁ receptor transcription. MT₁ promoter activity assays have identified paired-like homeodomain transcription factor 1, a transcription factor widely distributed throughout the rodent and ovine pituitary, as an important regulator of MT₁ receptor transcription (Johnston *et al.*, 2003).

Protective effects of melatonin

Antioxidant effects. The CNS is highly vulnerable to damage from oxidative stress because of its large composition of lipids, high demands for oxidative metabolism and, relatedly, production of toxic metabolites (Wang and Michaelis, 2010). Melatonin exerts many protective effects in the mammalian CNS. The NF-E2-related factor 2-antioxidant responsive element (Nrf2-ARE) signalling cascade is one of the intracellular pathways that mediates the regulation of antioxidant gene expression by melatonin. Melatonin induces Nrf2 expression, as well as the downstream targets of Nrf2-ARE signalling in multiple models of peripheral (Tripathi and Jena, 2010) and central oxidative stress (Wang *et al.*, 2012). Recent studies in Klotho mutant mice show that the Nrf2-related antioxidant actions of melatonin involve MT₂ receptor-mediated activation of the ERK pathway (Shin *et al.*, 2015).

In addition to regulating intracellular antioxidant pathways, melatonin, as well as its metabolites, has direct free radical scavenging capabilities. As such, a single melatonin molecule can forage and neutralize multiple highly toxic reactive oxygen, nitrogen and hydroxyl radicals at any one time (Rosen *et al.*, 2006). Although free radical scavenging and avoidance are widely beneficial properties, they are especially protective of mitochondrial integrity because of the increased susceptibility of this organelle to oxidative damage. Melatonin readily enters the mitochondrial matrix, where it limits electron leakage from the electron transport chain and free radical production (Reiter *et al.*, 2003). While the direct free radical scavenging effects of melatonin do not involve its receptors, other antioxidant effects, such as maintaining glutathione levels and stimulating the activities of catalase and superoxide dismutase, are mediated by melatonin receptors (Rezzani *et al.*, 2006).

Neurotrophic factor modulation. Melatonin is thought to promote neuronal development, differentiation and survival in the nervous system by modulating neurotrophic factor expression. Melatonin, as well as its analogues, has been shown to up-regulate neurotrophic factors such as glial cell line-derived neurotrophic factor (GDNF; Armstrong and Niles, 2002; Kong *et al.*, 2008b), nerve growth factor (Pongsa-Asawapaiboon *et al.*, 1998) and brain-derived neurotrophic factor (BDNF; Molteni *et al.*, 2010; Boulle *et al.*, 2014). Reduced expression of these targets has been implicated in the pathogenic mechanisms driving several brain disorders. Therefore, controlling the expression of these and other neurotrophic factors is thought to have therapeutic potential for both neurodegenerative (Allen *et al.*, 2013) and psychiatric disorders (Castrén, 2014).

There is limited information about the mechanisms involved in the modulation of neurotrophic factors by melatonin. The melatonin-induced increase in GDNF mRNA expression in C6 cells, which express both MT₁ and MT₂ receptors (Armstrong and Niles, 2002), may be mediated by the MT₁ subtype, as this effect is not blocked by the MT₂ antagonist, **4P-PDOT (4-phenyl-2-propionamidotetraline)** (Niles and Armstrong, 2002). The increase in GDNF protein levels induced by melatonin in primary astrocytes is blocked by the PI3K/Akt antagonist, wortmannin and the non-selective melatonin receptor antagonist, **luzindole**, indicating the involvement of this pathway and melatonin receptors in this effect (Kong *et al.*, 2008a). Recently, melatonin treatment in the presence of the pro-inflammatory cytokine, IL-18, was found to increase the mRNA and protein expression of GDNF and BDNF in neural stem cells, whereas luzindole blocked these effects, indicating that this effect is mediated by stimulation of melatonin receptors (Li *et al.*, 2017). As discussed later, epigenetic regulation of gene transcription, including chromatin remodelling *via* histone modifications, has been linked to synaptic plasticity, neurotrophic factor induction, neuroprotection and related effects (Schmidt *et al.*, 2013; Harrison *et al.*, 2015). Evidence that melatonin can acetylate histone proteins in cultured cells and *in vivo* (Sharma *et al.*, 2008; Niles *et al.*, 2013) suggests that epigenetic induction of gene expression may underlie its effects on neurotrophic factors and other neuroprotective targets.

Moreover, blockade of melatonin-induced histone acetylation by luzindole, in human SH-SY5Y neuroblastoma cells, indicates the involvement of melatonin receptors in these effects (Pan and Niles, 2015).

Melatonergic signalling in psychiatric and neurodegenerative disease

Several *in vitro* and *in vivo* studies have revealed aberrations in the expression patterns of MT₁ and/or MT₂ receptors in various models of CNS disorders. *Post-mortem* analyses of human brain tissue from related disorders have also revealed changes in melatonin receptor expression patterns, but these findings are complicated by the fact that the affected patients may have received prolonged treatment with therapeutic drugs, which may induce changes in receptor expression independent of the disease (Hirsch-Rodriguez *et al.*, 2007).

Aberrant melatonergic function has been implicated in various neuropsychiatric conditions. The potential therapeutic use of melatonin in neuropsychiatric disorders has been reviewed recently with a note on the need for selective targeting of receptor subtypes (Mahmood *et al.*, 2016), which exhibit distinct functional specialization. For example, a study of sleep regulation, using receptor knockout mice, revealed that MT₁ and MT₂ receptor signalling regulate rapid eye movement sleep and non-rapid eye movement sleep respectively (Comai *et al.*, 2013). The sleep-promoting role of MT₂ receptors is further supported by the observation that MT₂ receptor ligands produce a hypnotic effect, which is eliminated in mice lacking MT₂ receptors (Ochoa-Sanchez *et al.*, 2011). MT₂ ligands have also been observed to have an antinociceptive effect in rodents, which can be blocked by MT₂ receptor antagonists, implying a role for this receptor in pain regulation (Lopez-Canul *et al.*, 2015). Increased MT₁ receptor expression, but not MT₂, has been observed in the hypothalamic tissue of depressed patients *post-mortem* (Wu *et al.*, 2013). Mice lacking the expression of MT₁ receptors exhibit neurobiological variations characteristic of depression, including hyperstress responses, psychomotor disturbances and increased anhedonic and depressive-like behaviours in comparison to their wild-type counterparts (Comai *et al.*, 2015), suggesting a role for the MT₁ subtype in the aetiology of depression.

Abnormal melatonin receptor expression profiles have also been noted in various neurodegenerative conditions. For example, rodent models revealed that MT₁ receptor expression was reduced in the spinal cords of transgenic amyotrophic lateral sclerosis (ALS) mice (Zhang *et al.*, 2013). Analysis of *post-mortem* brain tissue revealed increased MT₁ (Savaskan *et al.*, 2002) and decreased MT₂ receptor expression (Savaskan *et al.*, 2005) in the hippocampus of Alzheimer's disease patients. The reason for the different expression of these receptor subtypes in Alzheimer's disease awaits clarification but could involve discrete differences in their localization or other neurodegenerative changes associated with this disorder. Other studies have reported regional decreases in melatonin receptor expression in Alzheimer's disease, including reduced hypothalamic, pineal and cortical MT₁ expression (Brunner *et al.*, 2006; Wu *et al.*, 2007), as well as pineal, cortical and retinal MT₂ expression (Brunner *et al.*, 2006;

Savaskan *et al.*, 2007), relative to healthy controls. Similarly, *post-mortem* analysis of brains from patients with Parkinson's disease revealed decreases in both MT₁ and MT₂ receptor expression in the substantia nigra as well as the amygdala in comparison to healthy controls (Adi *et al.*, 2010). Consequently, impairments in melatonergic signalling related to aberrant MT₁ and/or MT₂ expression profiles could contribute to the overall deterioration of the nervous system in these disorders. Evidence that the neuroprotective effect of melatonin in a transgenic mouse model of ALS involves inhibition of receptor interacting protein-2-induced activation of the caspase-1 pathway *via* the MT₁ receptor (Zhang *et al.*, 2013) supports the importance of melatonin receptors in brain preservation. Drug-induced up-regulation of melatonin receptors, as proposed in this review, is a potential strategy for restoring depleted melatonin receptor expression in areas where it is lost as a result of normal ageing, injury or disease.

Valproic acid and melatonin receptors

Valproic acid (VPA) or 2-propylpentanoic acid is a branched short-chain fatty acid with well-known anticonvulsive and mood-stabilizing effects. A recent study has shown that VPA may be an effective adjunct to antidepressant therapies in treatment-resistant depression (Ghabrash *et al.*, 2016). In addition to the multiple targets and pathways influenced by VPA (Monti *et al.*, 2009), increasing evidence indicates an interaction between this psychotropic agent and the melatonergic system. Treatment with VPA enhances the expression of tryptophan hydroxylase, which contributes to melatonin biosynthesis (Qiu *et al.*, 2015) and reduces the sensitivity of melatonin to light (Hallam *et al.*, 2005). Initial studies on the effects of VPA on melatonin receptor expression were completed in rat C6 glioma cells (Castro *et al.*, 2005; Kim *et al.*, 2008) and in human MCF-7 breast cancer cells (Jawed *et al.*, 2007). This work revealed a dose-dependent relationship in which VPA caused a robust increase in MT₁ receptor mRNA and/or protein (Castro *et al.*, 2005; Jawed *et al.*, 2007; Kim *et al.*, 2008). These findings set the groundwork for *in vivo* studies, which showed that chronic VPA administration causes a robust increase in MT₁ and MT₂ receptor mRNA levels in the rat hippocampus (Niles *et al.*, 2012). Moreover, an *in situ* hybridization study revealed significant increases in MT₂ receptor expression in the CA1-3 and dentate gyrus regions of the rat hippocampus, following a similar treatment with VPA (Bahna *et al.*, 2014). As discussed below, this up-regulation of melatonin receptors, especially the MT₁ subtype, is thought to involve an epigenetic mechanism.

Epigenetic mechanisms

The term epigenetics refers to heritable changes in gene expression, which do not involve an alteration in DNA sequence. Three major mechanisms including DNA methylation, regulation of transcription by non-coding RNAs and histone modification are involved in the epigenetic-regulation of gene expression. Dysfunction of any of these interacting mechanisms can result in the abnormal expression or silencing of genes and the possible onset of 'epigenetic diseases' (Egger *et al.*, 2004; Hwang *et al.*, 2017).

DNA methylation. The methylation of 5-cytosine residues to 5-methylcytosine, in cytosine-guanine (CpG) dinucleotides, is an established epigenetic mechanism for gene silencing. The methylation of CpG sites within the mammalian genome is maintained by a number of DNA methyltransferases (DNMTs). DNMT3A and DNMT3B are involved in the *de novo* methylation of DNA, while DNMT1 performs a maintenance function by methylating the complementary strand in hemimethylated DNA before its replication (Bayraktar and Kreutz, 2017). It is now apparent that DNA demethylation can occur *via* deaminases, which catalyse the conversion of 5-methylcytosine to thymidine. A second mechanism involves ten-eleven translocation enzymes that reverse the methylation status of DNA by the successive oxidation of 5-methylcytosine to 5-carboxylcytosine, which is subjected to a base-excision-repair process to regenerate cytosine (Nabel and Kohli, 2011).

Regulation of transcription by non-coding RNAs. Another category of epigenetic regulators includes non-coding RNAs such as microRNAs (miRNAs), small interfering RNAs and long non-coding RNAs. To date, the most studied are miRNAs, which are thought to target more than 60% of human genes (Friedman *et al.*, 2009) and to regulate gene transcription primarily by suppression of target translation or induction of mRNA decay (Huntzinger and Izaurralde, 2011). Their ability to regulate gene expression in pathways linked to major physiological processes, including neurodevelopment, neurogenesis and neuroprotection, has implicated miRNAs in various central pathological states such as neurodegeneration and psychiatric dysfunction (Kim *et al.*, 2016; Boone *et al.*, 2017).

Histone modification. Chromatin consists of nucleosomes, each composed of about 146 base pairs of genomic DNA, which is wrapped around an octamer of core histone proteins consisting of two copies each of H2A, H2B, H3 and H4. Histone proteins have long N-terminal tails that are key targets in multiple post-translational modifications including acetylation, methylation, phosphorylation, sumoylation, ubiquitination and ADP-ribosylation. Acetylation and methylation are the most widely studied of these covalent modifications, which cause conformational changes in chromatin structure and influence the access of transcription factors and other regulatory proteins to their

DNA targets (Bannister and Kouzarides, 2011). Enzymes that alter the electrostatic interactions between the negatively charged DNA and the positively charged histone core, *via* histone acetylation or deacetylation, are involved in the epigenetic regulation of gene transcription, as illustrated in Figure 1. Histone acetylation, which is catalysed by histone acetyltransferase (**HAT**) enzymes from various families (Roth *et al.*, 2001), neutralizes the positive charge on histone proteins, causing a reduced affinity between the histone protein and the DNA strand. The associated chromatin assumes a more loosened structure, known as euchromatin, which exposes regulatory genetic sequences and permits the binding of transcription factors to activate transcription (Morse, 2007). The reverse process, deacetylation, is catalysed by histone deacetylase (**HDAC**) enzymes, which cause chromatin condensation leading to the termination of transcriptional activity (Bannister and Kouzarides, 2011).

Based on gene sequence, subcellular localization or functional differences, 11 zinc-dependent HDACs have been assigned to different classes as follows: Class I (HDAC 1, 2, 3, 8), Class IIa (HDAC 4, 5, 7, 9), Class IIb (HDAC 6, 10) and Class IV (HDAC 11). Class III HDACs are a distinct family of nicotinamide adenine dinucleotide-dependent enzymes, termed sirtuins. Several HDAC inhibitors have been examined in studies aimed at identifying clinically relevant epigenetic regulators. Of particular relevance to this review, VPA inhibits the activity of multiple Class I and Class II HDACs (Gurvich *et al.*, 2004), which are involved in critical aspects of CNS physiology, including neurodevelopment and cognition (Morris and Monteggia, 2013).

Epigenetic regulation of melatonin receptors by VPA

VPA can directly inhibit HDAC activity, which results in the conversion of chromatin to an acetylated and transcriptionally active conformation (Phiel *et al.*, 2001). Several factors are involved in the maintenance of chromatin structure in the normal state, such as the structural maintenance of chromosomes (SMC) family of proteins, which are required for the general stabilization of chromosome conformation (Yokomori, 2003), and heterochromatin protein 1 (HP1), which maintains DNA in the heterochromatin state (Maison and Almouzni, 2004). VPA treatments stimulate a conformational change in chromatin structure, from a highly

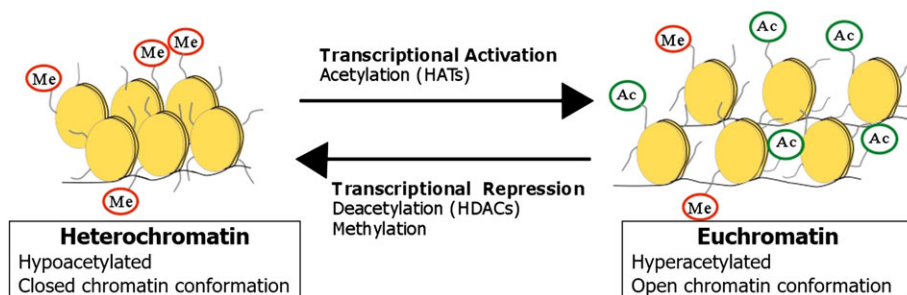


Figure 1

Regulation of chromatin conformation by histone acetylation and methylation. Histone acetylation, methylation or other covalent modifications of lysine residues on the N-terminal tail of the histone core can alter gene transcription *via* changes in the accessibility of DNA to regulatory factors.

condensed state to a more loosened structure, which corresponds with a decreased expression of the proteins which promote heterochromatin stability (Marchion *et al.*, 2005; Felisbino *et al.*, 2014).

As noted earlier, VPA treatment up-regulates melatonin receptors in cultured mammalian cells and the rat brain (Castro *et al.*, 2005; Niles *et al.*, 2012), but the mechanism(s) involved awaits clarification. Recent studies indicate that an epigenetic mechanism, specifically that of MT₁ promoter histone acetylation due to HDAC inhibition, underlies the transcriptional activation of the MT₁ receptor gene by VPA (Bahna and Niles, 2017). This is supported by the observation that structurally diverse drugs, such as the potent HDAC inhibitor, trichostatin A, also increase the expression of MT₁ receptors (Kim *et al.*, 2008), whereas valpromide, a VPA analogue without HDAC inhibitory properties, does not (Bahna and Niles, 2017).

VPA and other HDAC inhibitors can alter the demethylation of DNA, either globally or gene-specifically, by enhancing DNA demethylase activity *via* histone acetylation or other mechanisms (Detich *et al.*, 2003). This is important as several CpG islands are located within the promoter regions of many genes, which, when methylated, suppress transcription (Cedar and Bergman, 2009). As noted earlier, diverse epigenetic mechanisms interact in the regulation, amplification and fine-tuning of gene expression (Egger *et al.*, 2004). For example, the inhibition of HDAC activity and the attenuation of DNA methylation induced by VPA are not mutually exclusive events but rather are thought to be in a dynamic correlation and can impose compounded effects on gene transcription (Milutinovic *et al.*, 2007). In view of the foregoing, it is possible that DNA demethylation contributes to the regulation of melatonin receptors by VPA.

Chromatin decondensation surrounding the MT₁ promoter region allows transcription factors to access regulatory sequences along the MT₁ promoter to initiate transcription of the gene. The ability of VPA to prevent heterochromatin formation following histone acetylation (Marchion *et al.*, 2005), suggests that it can influence the transcriptional kinetics of MT₁ receptors. It is interesting to note that histone acetylation is thought to precede the modulation of HP1 and SMC protein expression by VPA (Marchion *et al.*, 2005), suggesting that the conformational changes in chromatin structure induced by VPA can cause prolonged induction of the melatonin receptor (Figure 2).

Molecular regulation of melatonin receptors by VPA

VPA influences the expression and binding affinities of various transcription factors in cultured cells, as well as in the brain (Monti *et al.*, 2009). These effects may involve its influence on the post-translational modifications of various intracellular kinases, which regulate the activation and subsequent gene expression of transcription factors. VPA is a positive regulator of the AMP-activated protein kinase (Avery and Bumpus, 2014), MAPK, PI3K and Akt (PKB) and PKC signalling pathways, and a negative regulator of glycogen synthase kinase 3 β (GSK3 β) signalling (Monti *et al.*, 2009). We have reported that pharmacological inhibition of MAPK (Castro *et al.*, 2005), PI3K/Akt, PKC or GSK3 β

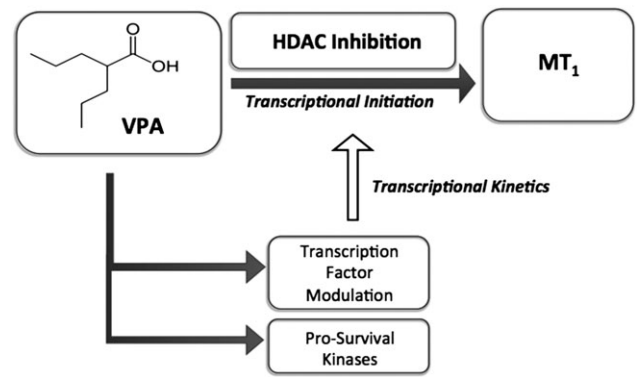


Figure 2

Proposed mechanism for the induction of MT₁ receptors by VPA. VPA activates the transcription of MT₁ receptors by causing chromatin remodelling, mediated by HDAC inhibition and MT₁ promoter hyperacetylation. VPA also acts *via* intracellular kinases to regulate the expression of transcription factors that control the activity of the MT₁ promoter, suggesting a role for this drug in the transcriptional kinetics of MT₁ receptor expression.

does not affect melatonin MT₁ receptor up-regulation (Bahna and Niles, 2017), further supporting our epigenetic hypothesis.

Although the above findings suggest that these kinase pathways are not involved in the up-regulation of MT₁ receptors by VPA, caution should be exercised when interpreting the effects of kinase inhibitors, which exhibit limited selectivity (Bain *et al.*, 2007). Moreover, given the multiple cellular and molecular effects of VPA, its administration could affect not just melatonin receptors but also other targets or pathways, which may in turn influence melatonergic function. One such target is tetrahydrobiopterin (BH₄), an essential cofactor in the biosynthesis of neurotransmitters including 5-HT and catecholamines, and the enzyme, nitric oxide synthase, which produces nitric oxide (Werner *et al.*, 2011), a modulator of glutamate release (Neitz *et al.*, 2011). Given the functional interaction between melatonin and neurotransmitters such as 5-HT (Matheus *et al.*, 2010), it is possible that melatonergic activity following VPA treatment could also be modulated by other pathways or *in vivo* systems activated by this pleiotropic drug.

Recently, VPA was reported to inhibit internalization of the MT₁ receptor and its cAMP signalling by interfering with the association between the receptor and β -arrestin-2 (Hong *et al.*, 2016). If this effect, which was observed in an *in vitro* expression system, translates to the *in vivo* mammalian CNS, it is possible that it could negatively affect the anticipated benefits of melatonin receptor up-regulation. Nonetheless, the novel idea of using epigenetic drugs to restore deficient melatonin receptor expression is worth exploring in various *in vivo* models of neurological or psychiatric disorders, where potential benefits would depend on the net effect of VPA or other HDAC inhibitors on melatonin receptor expression and function. Given the neuroprotective, anti-manic and other effects of VPA treatment, the up-regulation of melatonin receptors by this drug in conjunction with the administration of agonists

(e.g. melatonin, **agomelatine** and **ramelteon**), which are similarly beneficial, could produce enhanced therapeutic outcomes.

Clinical relevance of epigenetic up-regulation of melatonin receptor expression

The protective effects of increasing melatonin receptor expression have been demonstrated using several *in vitro* models of glutamate toxicity. Melatonin treatments in cultured embryonic rat VSC4.1 motor neurons transfected with MT₁ and/or MT₂ receptors were found to have a large increase in cell survival markers and a concurrent suppression in apoptotic and inflammatory markers (Das *et al.*, 2013). Melatonin treatments in untransfected cells did not have the same effect, emphasizing the importance of receptor density in the neuroprotective effects of this hormone (Das *et al.*, 2013). The beneficial effects of melatonin receptor overexpression have also been explored in the periphery. In human MCF-7 breast cancer cells, melatonin was found to have a greater antiproliferative effect in MT₁-transfected cells than in untransfected cells (Yuan *et al.*, 2002).

A limitation of these studies is how melatonin receptor overexpression is achieved. Gene therapy is a challenging approach and may not be a clinically suitable treatment option for a large number of patients (Gonin *et al.*, 2005). There is increasing evidence that dysregulated epigenetic processes underlie several neurological dysfunctions, including Parkinson's and Alzheimer's disease (Urduingio *et al.*, 2009; Masliah *et al.*, 2013) and especially psychiatric disorders such as depression and schizophrenia (Houtepen *et al.*, 2016; Pishva *et al.*, 2017). Diverse psychopharmacological agents including antidepressants, antipsychotics and mood stabilizers can influence epigenomic profiles, as reflected by histone protein modifications and DNA methylation (Boks *et al.*, 2012). While the mechanisms driving melatonin

receptor depletion are not yet known, accruing evidence proposes a role for dysregulated epigenetic processes in the pathogenesis of many neurological and neurodegenerative diseases (Saha and Pahan, 2006; Coppedè, 2014). This implies that the reduction in melatonin receptor expression in the diseased state may be a maladaptive response caused by an imbalance in epigenetic activities associated with disease progression. Given the central role of GPCRs in mediating the effects of diverse therapeutics, evidence that GPCR expression can be regulated by epigenetic mechanisms suggests that this approach of receptor regulation may be beneficial for a wide range of CNS disorders (Dogra *et al.*, 2016). As illustrated in Figure 3, epigenetic reprogramming of gene expression by VPA (or other HDAC inhibitors) to regain transcriptional control of the melatonin receptor gene can be a therapeutic strategy used to offset imbalances in receptor expression and, relatedly, melatonergic signalling. Some examples of neuropsychiatric disorders, which may benefit from the epigenetic manipulation of melatonin receptor expression, are discussed below.

Psychiatric disorders

It is well known that disruptions in the circadian rhythms of biological processes such as sleep and the secretion of hormones including melatonin are linked to mood disorders (Germain and Kupfer, 2008; Srinivasan *et al.*, 2009). Melatonin has shown efficacy in alleviating insomnia and sleep abnormalities in depressed patients (Ferracioli-Oda *et al.*, 2013). These beneficial effects are thought to involve the modulation of circadian function *via* melatonin receptors in the SCN, where the MT₁ subtype can inhibit neuronal activity while the MT₂ receptor plays a role in phase-shifting rhythms (Liu *et al.*, 1997). Adjunctive administration of slow-release melatonin decreased insomnia in patients with treatment-resistant depression, but it did not augment the effect of antidepressant treatment (Dalton *et al.*, 2000).

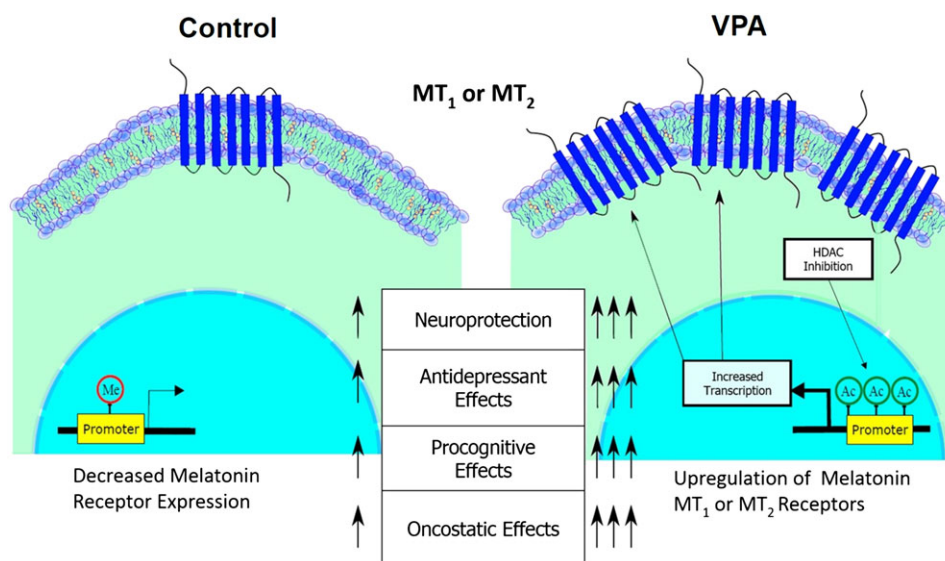


Figure 3

An overview of the potential therapeutic benefits of epigenetic up-regulation of melatonin receptors. While VPA is shown in this illustration, a similar epigenetic up-regulation of melatonin receptors can be induced by other HDAC inhibitors.

Other studies suggest that melatonin may be beneficial in reversing symptoms associated with anxiety and depression (Hansen *et al.*, 2014), among other psychiatric conditions (Mahmood *et al.*, 2016). The melatonin analogue, agomelatine, which couples agonistic activity at MT₁ and MT₂ receptors with antagonistic action at the 5-HT_{2c} receptor, is the first melatonergic agent approved for psychiatric treatment. Agomelatine has shown promise in the management of depression and other psychiatric conditions (Bourin and Prica, 2009; Spadoni *et al.*, 2011; Laudon and Frydman-Marom, 2014). Another melatonin MT₁/MT₂ agonist, ramelteon, improves sleep quality and duration across age groups including older insomniacs (Pandi-Perumal *et al.*, 2007; Schroeck *et al.*, 2016). These findings suggest that the melatonergic system is a worthwhile target for future psychiatric treatment strategies (Catena-Dell'Osso *et al.*, 2012).

Increasing evidence indicates that epigenetic dysfunction may contribute to psychiatric conditions, such as major depressive disorder and schizophrenia (Dogra *et al.*, 2016; Hoffmann *et al.*, 2017). As noted earlier, melatonin itself can induce histone acetylation in cultured brain-derived cells or in the mammalian brain by a mechanism that appears to involve MT₁ receptors and HAT (Pan and Niles, 2015). This raises the interesting possibility that combination therapy with VPA (or other HDAC inhibitors) and melatonin agonists could normalize epigenetic function with associated stabilization of brain physiology and related therapeutic effects.

Ageing and neurodegenerative disease

It is well-known that melatonin acts *via* its receptors to confer an assortment of neuroprotective and neurorestorative effects in the aged and neurodegenerative brain. Melatonin receptors are depleted during physiological ageing (Sánchez-Hidalgo *et al.*, 2009), as well as in various neurodegenerative states, as mentioned previously. This reduction may contribute to the overall deterioration of the CNS in neurodegenerative disorders. Melatonin treatments have been associated with delayed disease onset and progression, as well as decreased mortality. For example, melatonin attenuates dopaminergic cell loss in the nigrostriatal pathway in the Parkinson's disease brain of animal models and restores the associated motor function deficits (Capitelli *et al.*, 2008; Ma *et al.*, 2009; Carriere *et al.*, 2015). Other studies show that melatonin administration reverses impairments in cognition by augmenting adult hippocampal neurogenesis (Chern *et al.*, 2012; Liu *et al.*, 2013). Additional support for this notion comes from the observation that chronic melatonin treatment causes enhanced dendritic maturation and arborization in the mouse hippocampus (Ramirez-Rodriguez *et al.*, 2011). This is important because increasing adult hippocampal neurogenesis has been found to be capable of improving cognition (Sahay *et al.*, 2011).

In keeping with the above, low melatonin levels and disrupted circadian rhythmicity have been found in patients with Alzheimer's disease (Wu *et al.*, 2003). Melatonin has been reported to protect against memory impairment, synaptic dysfunction and neurodegeneration, by activating the PI3K/Akt/GSK3 β pathway, in a mouse model of Alzheimer's disease (Ali and Kim, 2015). The protective effects of melatonin on the aged and neurodegenerative brain further include

the modulation of energy metabolism, circadian function (Jenwitheesuk *et al.*, 2014) and suppression of the accumulation of toxic-free radicals and other metabolic by-products in the CNS (Reiter *et al.*, 2003). The ability to optimize melatonergic function by restoring depleted melatonin receptor populations in the CNS holds clear therapeutic promise in ageing and neurodegeneration.

Conclusions

GPCRs act as molecular sensors that convert extracellular stimuli into intracellular responses. The expression of melatonin receptors, as well as other GPCRs, is often depleted in the aged and/or diseased state. Although the mechanisms driving these receptor abnormalities are not yet characterized, increasing evidence suggests that epigenetic processes influence the development of several CNS diseases, which may also involve aberrant GPCR expression. VPA, as well as other HDAC inhibitors, up-regulates the expression of melatonin receptors *via* a mechanism that involves histone acetylation/chromatin remodelling with associated gene transcription. The epigenetic control of melatonin receptor expression provides a novel therapeutic strategy for offsetting the negative trajectory of melatonergic impairment associated with ageing and/or disease. However, the successful utilization of this strategy will require clarification of important issues, including which of the multiple HDAC isoforms inhibited by VPA or other HDAC inhibitors are specifically linked to the regulation of the MT₁ or MT₂ receptors, in order to permit selective targeting of melatonin receptor subtypes in future therapeutic approaches.

Nomenclature of targets and ligands

Key protein targets and ligands in this article 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 (Alexander *et al.*, 2015a,b).

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Conflict of interest

The authors declare no conflicts of interest.

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