Chapter 28 At the Crossing of ER Stress and MAMs: A Key Role of Sigma-1 Receptor?



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Abstract Calcium exchanges and homeostasis are finely regulated between cellular organelles and in response to physiological signals. Besides ionophores, including voltage-gated Ca²⁺ channels, ionotropic neurotransmitter receptors, or Store-operated Ca²⁺ entry, activity of regulatory intracellular proteins finely tune Calcium homeostasis. One of the most intriguing, by its unique nature but also most promising by the therapeutic opportunities it bears, is the sigma-1 receptor (Sig-1R). The Sig-1R is a chaperone protein residing at mitochondria-associated endoplasmic reticulum (ER) membranes (MAMs), where it interacts with several partners involved in ER stress response, or in Ca^{2+} exchange between the ER and mitochondria. Small molecules have been identified that specifically and selectively activate Sig-1R (Sig-1R agonists or positive modulators) at the cellular level and that also allow effective pharmacological actions in several pre-clinical models of pathologies. The present review will summarize the recent data on the mechanism of action of Sig-1R in regulating Ca^{2+} exchanges and protein interactions at MAMs and the ER. As MAMs alterations and ER stress now appear as a common track in most neurodegenerative diseases, the intracellular action of Sig-1R will be discussed in the context of the recently reported efficacy of Sig-1R drugs in pathologies like Alzheimer's disease, Parkinson's disease, Huntington's disease, or amyotrophic lateral sclerosis.

Keywords Sigma-1 receptor \cdot Calcium \cdot Mitochondria \cdot ER stress \cdot UPR \cdot MAMs \cdot Neurodegenerative disease \cdot Alzheimer's disease \cdot Amyotrophic lateral sclerosis \cdot Addiction \cdot Pain

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28.1 Introduction: Physiopathology of Sigma-1 Receptor (Sig-1R)

The Sigma-1 receptor (Sig-1R), discovered in the mid 1970s [1] was identified as a 223-amino acid protein only in the mid-1990s [2, 3]. Although its involvement in physiopathology started to be documented earlier, its cellular role was precised only 10 years ago [4] and cellular biology studies continue to precise its intracellular partners and functions. It shares no homology with any other known protein, except some steroid related/emopamyl-binding enzymes [2, 5, 6]. The protein was initially viewed as a receptor since, very early, specific and selective small molecules have been identified binding to Sig-1Rs and triggering (for so-called agonists) or preventing (for so-called antagonists) biological responses. However, its activation by physiological triggers, including ER stress or oxidative stress [4, 7, 8], and its mode of action, relying on modifications of protein-protein interactions rather than coupling to second messenger systems, suggested more a chaperone-like identity than a classical receptor nature [4]. Indeed, the present review will detail the effects of Sig-1R at intracellular organelles and show that it offers a unique opportunity to finely tune its activity, thereby impacting numerous physiopathological pathways, through a very classical pharmacological approach involving agonists, positive modulators or antagonists.

The Sig-1Rs are expressed in numerous organs, including liver, heart, lung, gonads and the nervous system, and numerous cell types, including, in the latter, neurons and glial cells (astrocytes, microglia, oligodendrocytes, Schwann cells) and vascular cells [9–11]. The particular density of Sig-1R in the nervous system is coherent with its importance in numerous psychiatric and neurological conditions. Sig1-Rs have indeed been involved in epilepsy [12, 13], stroke [14–16], drug abuse [17–19], pain [20, 21], and neurodegenerative pathologies. Interestingly, the last field of research is currently very active and recent evidence show both that Sig-1Rs play a role in the physiopathology of several neurodegenerative disease and that Sig-1R agonists have effective neuroprotective effects in preclinical models that deserve translation in clinical trials and better understanding of the mechanism of action of Sig-1R drugs against neurodegeneration. In parallel to the accumulating evidences that small molecules acting as Sig-1R agonist have pharmacological action in preclinical models of neurodegenerative diseases, and thus therapeutic potential, arguments are also brought confirming that Sig-1R exerts its cell homeostatic and cytoprotective activities mainly by directly targeting ER/mitochondria communication. We will here detail these arguments.

28.2 Sig-1R at the MAM

The ER of a cell spread almost all over a cell either in close proximity or in direct contacts with other subcellular components including the Golgi, mitochondria, nucleus, and plasma membrane. Through those close encounters, the ER plays many critical functions in the cell. One such important contact site for the ER is the mitochondria-associated ER membrane, termed the MAM [22], which harbors not only the lipid exchange [22], mitochondrial DNA exchange, Ca²⁺ signaling between the ER and mitochondria [4, 23–27] but also plays a role in the ER-nucleus signaling for cellular survival [28]. Recent evidences also indicate that the MAM is the origin of the isolated membrane for autophagy [29]. In addition, the MAM is critical in the formation of inflammasome [30, 31].

The MAM contains a plethora of functional proteins [24, 32]. Among those is the Sig-1R which is an ER molecular chaperone with two transmembrane regions from cellular biology studies [4, 33] but only one from the X-ray crystallographic study [34]. At the MAM, the Sig-1R chaperones the inositol-1,4,5 trisphosphate receptor type 3 (IP_3R_3) which would otherwise degrade after the stimulation of IP_3 , ensuring thus proper Ca^{2+} signaling from the ER into mitochondria [4, 35]. At the MAM, the Sig-1R also chaperones inositol-requiring enzyme 1 (IRE-1), one of the ER stress sensors, to facilitate the signaling of the unfolded protein response from the ER into nucleus to call for the transcriptional activation of antioxidant proteins and chaperones [28]. The Sig-1R was also found to attenuate free radical formation around the MAM area to reduce the activation of caspase that would have degraded the guanine nucleotide exchange factor to inactivate Rac GTPase that is essential for dendritic spine formation [36]. The Sig-1R also plays a role, likely at the MAM, in binding and transferring myristic acid to p35 to facilitate the p35 degradation by proteasome at the plasma membrane, thereby diverting p35 from forming p25 that would otherwise stun the axon elongation [37]. However, it remains to be totally clarified how those molecular actions of the Sig-1R at the MAM may contribute to the overall cellular and physiological functions of the MAM in general in a cell.

Upon the stimulation of Sig-1R agonists, Sig-1Rs dissociate from innate cochaperone binding immunoglobulin protein (BiP) and translocate to other parts of cell to interact with and regulate the function of receptors, ion channels, and other functional proteins at the plasma membrane, mitochondria, ER reticular network, and nucleus [38, 39]. Thus, due to the nature and dynamics of Sig-1Rs, the receptor plays multiple physiological roles in living systems.

One of the important physiological roles of the Sig-1R is to regulate Ca^{2+} signaling not only at the MAM but also at the ER reticular network and plasma membrane. Sig-1Rs at the MAM facilitate Ca^{2+} influx from the ER into mitochondria by chaperoning IP₃R3 at the MAM [4]. At the ER reticular network, the supranormal release of Ca^{2+} from the ER in medium spiny neurons of the YAC128 transgenic Huntington's disease mice was attenuated by a Sig-1R agonist [40]. The release of Ca^{2+} from the ER reticular network is mainly controlled by the IP₃R type 1 and the ryanodine receptor. Thus, this report suggests an inhibitory effect of Sig-1Rs on the IP₃R1 or the ryanodine receptor, which is in contrast to the facilitative effect of Sig-1Rs on IP₃R3. More experiments are needed as such.

The following three studies showed inconsistent effects of Sig-1Rs on the $[Ca^{2+}]_i$ in nevertheless different systems. Also, the site of action of Sig-1Rs were not identified. By using cultured cortical neurons, Sig-1R agonists were found to attenuate the ischemia-induced increase of $[Ca^{2+}]_i$ [41]. A recent study showed an

increased $[Ca^{2+}]_i$ when Sig-1Rs were activated by agonists in cultured embryonic mouse spinal neurons from ALS-causing mutants [42]. As well, methamphetamineinduced increase of $[Ca^{2+}]_i$ was shown to be attenuated by Sig-1R agonists in dopaminergic neurons [43]. Again, sites of action of Sig-1Rs in those three studies were not identified. It remains to be seen if those actions of Sig-1Rs were at the MAM, the ER reticular network, or the plasma membrane. Possibility exists that results were manifestation of concerted actions at all of those sites.

At the plasma membrane, Sig-1Rs showed a presynaptic action in inhibiting N-type Ca^{2+} channels in cholinergic interneurons in rat striatum, resulting in a decrease in presynaptic $[Ca^{2+}]_i$ [44]. The Sig-1R co-immunoprecipitated and co-localized with the N-type Ca^{2+} channel [24]. In rat brain microvascular endothelial cells, the store-operated calcium entry (SOCE) was attenuated by a Sig-1R agonist cocaine [45]. The mechanism of this interesting action of Sig-1R was reported in an elegant study in the same year. The Sig-1R was shown to bind stromal interaction molecule 1 (STIM1) at the ER when extracellular Ca^{2+} was depleted, and, as a result slowed down the recruitment of STIM1 to the ER-plasma membrane junction where STIM1 binds Orai1 [46]. The resultant inhibition of SOCE was seen when Sig-1Rs were overexpressed or when cells were treated with Sig-1R agonists. The Sig-1R antagonists or shSig-1R treatment enhanced the SOCE [46].

The calcium channels on the plasma membrane were examined in autonomous neurons taken from neonatal rat intracardiac and superior cervical ganglia (SCG). It was found that Sig-1Rs depressed high-voltage activated calcium currents from all calcium channel subtypes found on the cell body of these neurons, which includes N-, L-, P/Q-, and R-type calcium channels [47]. This study suggests that the activation of sigma receptors on sympathetic and parasympathetic neurons may modulate cell-to-cell signaling in autonomic ganglia and thus the regulation of cardiac function by the peripheral nervous system [47]. No direct interaction between Sig-1Rs and those calcium channels were demonstrated in this study however. The effect of Sig-1Rs on the potassium chloride-induced Ca²⁺ influx was examined by using retinal ganglion cell line (RGC)-5 and rat primary RGCs by the whole-cell patch clamp technique [48]. Sig-1R agonists inhibited the calcium influx and the Sig-1R antagonist reversed the inhibitory effect of Sig-1R agonist [48]. The Sig-1R was found to co-immunoprecipitate with the L-type calcium channels in this study.

Calcium homeostasis is critical to cellular physiology and plays an important role in many central nervous system (CNS) diseases, in particular the neurodegenerative diseases [49–54]. Since Sig-1Rs play critical role in calcium signaling at several loci of a cell, Sig-1Rs may be related to neurodegenerative diseases which show dysfunctional calcium homeostasis. However, a direct link between Sig-1R-regulated calcium signaling and a neurodegenerative disease has only been recently demonstrated in Huntington's disease as mentioned above [40].

Nevertheless, because Sig-1Rs reside mainly at the MAM which is increasingly recognized as an important loci related to many neurodegenerative diseases [25, 49, 52, 53, 55, 56], it is possible that the Sig-1R at the MAM may participate in those diseases in a manner either directly related to calcium signaling or *via* other yet-to-be-revealed mechanisms at the MAM.

A study has specifically examined the role of Sig-1Rs at the MAM on ALS. Using primary motor neuron cultures, the study found that the pharmacological or genetic inactivation of Sig-1Rs led to motor neuron axonal degeneration [57]. They also found that the disruption of Sig-1R function in motor neurons disturbed ER-mitochondria contacts and affected intracellular calcium signaling, and was accompanied by activation of ER stress and defects in mitochondrial dynamics and transport (direct quotes) [57]. It is interesting to note that several other studies have implicated Sig-1Rs in ALS although they did not directly examine if the action of Sig-1Rs was at the MAM [58–61].

Sig-1Rs have been related to Alzheimer's disease (AD). Several Sig-1R agonists, including PRE-084, MR-22, afobasole, ANAVEX1-41, ANAVEX2-73 or dehydroepiandrosterone, prevented amyloid- $\beta_{25,35}$ (A $\beta_{25,35}$)-induced toxicity in rat neuronal cultures [62, 63] and/or A $\beta_{25,35}$ -induced toxicity and learning impairments in mice in vivo [64-69]. Among the biochemical markers of toxicity in both in vitro and in vivo models, the Sig-1R drugs appear particularly effective in alleviating oxidative stress. Similar data were obtained in transgenic animal models of AD by Fisher et al. [70] who reported that AF710B, a mixed M1 mAChR/Sig-1R agonist, administered for 2 months in female 3xTg-AD mice, attenuated memory impairments and neurotoxicity. The drug also diminished soluble and insoluble $A\beta$ species accumulation, the number of plaques and Tau hyperphosphorylation [70], thus confirming the neuroprotection and potentially disease-modifying effects of the drug. Moreover, invalidation of the Sig-1R expression, using Sig-1R knockout mice or a repeated treatment with the Sig-1R antagonist NE-100, increased learning deficits and neurotoxicity in Ag25-35-injected mice or after cross-breeding with APP_{Swe,Ldn} mice [71]. Therefore, it appeared that the absence of Sig-1R could worsen A_β toxicity and behavioral deficits while it activation by therapeutic drugs showed neuroprotection.

The role of the MAM in the pathogenesis of AD remains an important area of research. Interestingly, a study has related the toxicity of A β to the increase of $[Ca^{2+}]_i$ and the overload of mitochondrial calcium [72]. Nanomolar concentrations of A β was shown to increase MAM-associated proteins and caused an increase of the MAM [55]. Importantly, knockdown of Sig-1Rs resulted in neurodegeneration [55, 71]. Moreover, a direct examination of the effects of Sig-1R drugs in isolated mitochondria exposed to β -amyloid peptide showed that agonists decreased A β_{1-42} -induced increase in reactive oxygen species (ROS) and attenuated A β_{1-42} -induced alterations in mitochondrial respiration related to decreases in complex I and IV activity [73]. The Sig-1R agonists increased complex I activity, in a Ca²⁺-dependent and Sig-1R antagonist-sensitive manner in physiological conditions. These observations identified direct consequences on mitochondria of Sig-1R activity. However, further research on the involvement of the MAM in Alzheimer's disease is certainly warranted.

Moreover, Sig-1R agonists, and particularly PRE-084, have been shown to be neuroprotective in mouse models of Parkinson's disease [74], Huntington's disease [75], amyotrophic lateral sclerosis (ALS) [76, 77], multiple sclerosis [78] or retinal neurodegeneration [79, 80], notably. Several recent reviews addressed the different progresses made so far [17, 51, 81–86]. For instance, a study examined the role of Sig-1Rs in Parkinsonism in a mouse model of intrastriatal lesion by 6-hydroxydopamine and found that the Sig-1R agonist significantly improved the fore-limb use [74]. At the molecular level, the study found that the agonist increased the density of dopaminergic fibers at the most denervated striatal regions and also caused an increase of neurotrophic factor brain-derived neurotrophic factor (BDNF) [74]. Interestingly, the agonist treatment induced a wider intracellular distribution of Sig-1Rs [74]. Because Sig-1Rs can translocate to other parts of neuron upon the stimulation by an agonist, it is tempting to speculate that the action of Sig-1Rs in the improvement of Parkinsonism may occur at the MAM as well other parts of neuron.

The Sig-1R has been shown to relate to Huntington's disease. Most of the evidence cam from studies using a drug called pridopidine which was effective against Huntington's disease in preclinical models and in phase two clinical trial at the secondary end-point level [87]. Originally thought to be a dopamine D2 ligand, pridopidine was nevertheless found to have a 100-fold higher affinity at the Sig-1R than at the dopamine D2 receptor [88]. In an in vivo radioligand binding assay, behaviorally relevant doses of pridopidine blocked about 57–85% of radiotracer binding to Sig-1Rs while blocked only negligible fraction of D2 receptor [89]. Recently, pridopidine was found to attenuate the phencyclidine-induced memory impairment through the Sig-1R antagonist NE-100 [90].

The exact mechanism and therefore the cellular site of action of Sig-1Rs underlying the action of pridopidine against Huntington's disease are however not fully clarified. However, couple of studies provide some interesting results. In Q175 knock-in (Q175 KI) vs Q25 WT mouse models, the effect of pridopidine versus sham treatment on genome-wide expression profiling in the rat striatum was analyzed and compared to the pathological expression profile. Then a broad, unbiased pathway analysis was conducted, followed by testing the enrichment of relevant pathways [87]. Results showed that pridopidine upregulated the BDNF pathway (P = 1.73E-10), and its effect on BDNF secretion was Sig-1R-dependent [87]. It remains to be investigated how Sig-1Rs may upregulate BDNF at the molecular level. As mentioned before, the action of pridopidine was examined in a mouse model of Huntington's disease with a specific focus on intracellular calcium signaling [40]. Results showed that pridopidine attenuates spine loss of medium spiny neurons and the effect was absent with the neuronal deletion of Sig-1Rs [40]. Pridopidine suppressed supranormal ER Ca²⁺ release, restored ER calcium levels and reduced excessive SOCE entry into spines. Interestingly, normalization of ER Ca^{2+} levels by pridopidine was prevented by Sig-1R deletion [40]. Whether those effects of Sig-1Rs originate at the MAM or beyond are not clear at present.

28.3 Sig-1R and ER Stress

The ER is an essential organelle of the cell that plays important role in protein folding and quality control [91, 92], lipid synthesis [93] and Ca²⁺ homeostasis [94]. During the life of the cell, different factors may perturb these functions, leading to a cellular state referred to as 'ER stress'. These stressors may be intrinsic, *i.e.*, cancer [95–98], neurodegenerative disease [99, 100], or diabetes [101, 102], or extrinsic, *i.e.*, micro-environmental stress [103], exposure to ER stressors [104], temperature [105] or reactive oxygen species production [106, 107]. Nevertheless, every time the ER is stressed, it triggers an adaptive response. This adaptive response is called the unfolded protein response (UPR). This UPR will help the cells to counter the stress by attenuating protein synthesis, clearing the unfolded proteins and enhancing the ability of the ER to fold proteins.

The UPR is an intracellular signal transduction mechanism that protects cells from ER stress. Three ER-resident transmembrane proteins function as stress sensors: RNA-activated protein kinase (PKR)-like endoplasmic reticular kinase (PERK); activating transcription factor 6 (ATF6); and IRE1. In basal state, these three transmembrane proteins are bound to BiP, an ER resident chaperone and are inactive [108, 109]. Upon a stress, the folding capacity of the ER is surpassed, leading to the dissociation of BiP from PERK, ATF6 and IRE1. This dissociation allows the activation of the three sensors [110]. Their activations transduce the unfolded protein stress signal across ER membrane and lead to UPR activation [111]. PERK is transmembrane ER resident protein of 1116 amino acids with two functional domains, a luminal and a cytosolic Ser/Thr kinase domain [112]. The dissociation of BiP from the luminal domain leads to oligomerization [108] and trans-autophosphorylation [113]. Activation of the PERK pathway leads to attenuation of general protein translation by phosphorylation of the α subunit of eukaryotic translation initiation factor 2 (eIF2 α) [114]. Phosphorylated eIF2 α inhibits eukaryotic translation initiation 2B activity, thus leading to a decrease of protein synthesis [115]. The blockage of the translation during ER stress diminishes the protein load on the ER folding machinery and is a prerequisite to a reestablishment of the ER homeostasis. In contrast to its attenuation of translation, $eIF2\alpha$ phosphorylation can selectively enhance the translation of mRNAs containing inhibitory upstream open reading frames in their 5' untranslated region, such as activating transcription factor 4 (ATF4) [116]. The production of ATF4 induces the expression of a plethora of adaptive genes involved in amino acid transport, metabolism, protection from oxidative stress, protein homeostasis and autophagy [117]. Finally, ATF4 favors the expression of CAAT/enhancer-binding protein (C/EBP) homologous protein (CHOP), which will result in the expression of genes that are involved in protein synthesis and the UPR. If the expression of CHOP is sustained, the increased protein synthesis will lead to oxidative stress and cell death [118].

The second ER stress sensor is ATF6. ATF6 is also an ER resident transmembrane protein of 670 amino acids and two functional domains, an N-terminal cytosolic containing basic leucine zipper and a C-terminal luminal domain. When BiP dissociates from ATF6, this one is exported to the Golgi where it will be cleaved by site-1 and site-2 proteases [119]. This cleavage releases a fragment of 400 amino acids corresponding to ATF6 cytosolic N-terminal domain. This released fragment of ATF6 will then translocate to the nucleus in order to act as a transcription factor. ATF6 will bind to the promoter of UPR-inducible genes, resulting in an upregulations of proteins, which role is to adjust ER protein folding, including ER chaperones and X-box-binding protein-1 (XBP-1) [120, 121].

The last ER stress sensor is IRE1. IRE1 is, like the two other sensors, an ER resident transmembrane proteins of 977 amino acids with three functional domains, an N-terminal luminal domain, a C-terminal Ser/Thr kinase domain and a C-terminal RNase L domain. The dissociation with BiP triggers oligomerization and activation of its cytosolic kinase domain. This activation facilitates the unconventional splicing of XBP-1 mRNA and subsequent translation of an active transcription factor, XBP1s [111, 121]. XBP1s is a basic leucine zipper transcription factor [122]. XBP1s controls the expression of several targets including chaperones, foldases and components of the ER-associated degradation (ERAD) pathway, in order to stop the ER stress and restore homeostasis [123]. The ERAD system destroys unfolded proteins through degradation in the cytosol [124]. Indeed, unfolded ER proteins are retro-translocated across the ER membrane into the cytosol in order to be degraded by the proteasome, following ubiquitination by ubiquitin-conjugating enzymes [125, 126]. Finally, the RNase activity of IRE1 may also target other genes via a mechanism named regulated IRE1-dependent decay (RIDD) [127]. RIDD is a conserved mechanism in eukaryotes by which IRE1 cleaves its target substrates [128]. The cleaved transcripts are degraded by exoribonucleases [129]. Therefore, RIDD seems to be required for the maintenance of ER homeostasis by diminishing ER protein load via mRNA degradation. Notably, it has been recently suggested that the physiological activity of RIDD may increase with the severity of the ER stress [130].

Interestingly, a substantial number of proteins involved in UPR are localized in MAMs [23]. Indeed, two of the three major proteins involved in UPR, PERK [131] and IRE1 [28], are enriched in MAMs. Intriguingly, some ER chaperones involved in UPR are also enriched in MAMs. For example, Calnexin, a type I integral membrane protein which helps in folding newly synthetize proteins which is essential in mitigating ER stress, is expressed in MAMs [132]. Another chaperone expressed in MAMs is the Sig-1R. The first evidence of the role of Sig-1R in ER stress came from the observation that under Ca^{2+} depletion or when stimulated by its ligand, Sig-1R dissociates from BiP, thus allowing a sustained Ca²⁺ efflux from the ER via IP₃R [4]. In addition, under ER stress following treatment with tunicamycin or thapsigargin, Sig-1R is upregulated, suggesting that it is protective against ER stress. Interestingly, overexpression on Sig-1R suppressed ER stress-induced activation of PERK and ATF6. IRE1 is expressed in MAMs and Sig-1R regulates the stability of IRE1 [28]. This enhanced stability favors the phosphorylation level of IRE1 under ER stress. Notably, the Sig-1R knock down potentiates the apoptosis of cells under ER stress. They showed that increased apoptosis was due to a diminution of the Xbp1 splicing [28]. In addition, activation of Sig-1R increases Bcl-2 expression, allowing Bcl-2/IP3R interaction, leading to increased mitochondrial Ca^{2+} uptake and ATP production [133] (see Penke et al. for review [134]).

It is well known that Sig-1R plays an important protective role in retinal disease [85]. Using *in situ* hybridization, Ola et al. [135] detected the Sig-1R mRNA in retinal ganglion cells, cells of the inner nuclear layer, photoreceptor and retinal pigment epithelium. The mRNA expression was confirmed by immunohistochemistry. Ha et al. [136] described that in Müller cells of the retina from Sig-1R KO mice, the expression of PERK, IRE1 and ATF4 was decreased, whereas the expression of BiP, CHOP and ATF6 was increased. Intriguingly, no difference was detected in whole brain or whole retina. Similar to what was described by Yang et al. [133], Ha et al. saw a decrease expression of Bcl-2 associated with decrease in NFkB and pERK1/2 [136]. Moreover, Wang et al. [137] demonstrated that loss of Sig-1R in a model of retinitis pigmentosa (rd10), aggravates the degeneration of the photoreceptors. They revealed that at P28, the expression level of Xbp1 and CHOP is increased in the rd10 mice without Sig-1R expression.

Since Sig-1R is a receptor that can be activated or inhibited, different groups determined the effect of its activation or inhibition in following ER stress. Ha et al. [138] treated RGC-5 cells with (+)-pentazocine, a potent Sig-1R agonist. RGC-5 cells are a rat retinal ganglion cell line [139]. They showed that whereas the protein level of PERK, ATF4, ATF6 IRE1 and CHOP was upregulated during oxidative stress, in the presence of (+)-pentazocine, their expression level decreased, suggesting that Sig-1R plays a pivotal role in the UPR response. These results confirmed the initial observation of Wang et al. [140] that stimulation of Sig-1R protects against oxidative stress. Indeed, in human cell line FHL124, H₂O₂ treatment induces apoptosis, associated to an increase level of BiP, ATF6 and p-eIF2a. Application of (+)-pentazocine suppressed the induction of BiP and p-eIF2 α . Another agonist, fluvoxamine, alleviates induction of CHOP, cleaved caspase 3 and 4 in cancer neuronal cell SK-N-SH [141]. In another experiment, Omi et al. [142] showed that treatment of neuronal cell line Neuro2a induces overexpression of Sig-1R. This expression is mediated by ATF4, a downstream element of PERK activation. Interestingly, this overexpression is achieved without activating UPR. Intriguingly, the increased translation of ATF4 is dependent of the presence/function of Sig-1R since if the concomitant treatment of Neuro2a cells with Fluvoxamine and NE-100, a Sig-1R antagonist, abolished the ATF4 translation. This result was confirmed by the use of mouse embryonic fibroblasts (MEF) from Sig-1R KO mice. Indeed, fluvoxamine treatment of these MEF did not increase ATF4 expression. Morihara et al. [143] treated mice with Sig-1R agonist aniline derivative compound (Comp-AD) following ischemic stroke, since it is well known that Sig-1R protects against ischemic stroke but the role of ER stress was unknown. So, treatment of mice after 90 min of transient middle cerebral artery, diminished the expression level of p-PERK and p-IRE1, suggesting that activation of Sig-1R protects against ischemic stroke via the attenuation of ER stress.

If Sig-1R activation suppresses effectively ER stress, it should be expected that inhibition of Sig-1R should do the contrary. This was demonstrated by Ono et al. [144] using Sig-1R antagonist, by Hong et al. [145] using Sig-1R KO, and Alam et al. [146] using siRNA to knock down Sig-1R. Ono et al. [144] showed that NE-100 protects ER stress induced cell death in hippocampal HT22 cells after tunicamycin treatment. Indeed, NE-100 application attenuated the upregulation of CHOP. Interestingly, NE-100 treatment alone was capable of upregulate the expression of both ATF6 and BiP. Total ablation of Sig-1R in dopaminergic neurons of substantia nigra in mice led to an elevation of the expression level of p-eIF2 α and CHOP [145]. In cardiomyocytes treated with tunicamycin, the downregulation of Sig-1R by siRNA led to an increase of CHOP expression. They also showed that Sig-1R downregulation diminished IRE1 phosphorylation and Xbp1 splicing [146].

Mutations of Sig-1R in human may lead to Juvenile [58] and classic ALS [147] or distal hereditary neuropathy (dHMN) [148–151]. Interestingly, E102Q mutation, which induces juvenile ALS, leads to ER stress [59, 152]. Indeed, over-expression of Sig-1R mutant in MCF7 cells induced an aggregation of the mutant protein into the ER in contrast to the overexpression of the wild-type Sig-1R, which is localized in the ER, the nuclear envelope end ER-Golgi intermediate compartment. Using ER stress response element (ERSE) reporter assay, they detected an increase in ER stress in MCF7 cells. There was an increase expression level of p-eIF2a, BiP, HSP70, GADD. Moreover, they showed a co-localization of ubiquitin-positive Sig-1R mutant aggregates with 20S proteasome subunit, suggesting possible interference with the ubiquitin proteasome system machinery [59]. In parallel, they demonstrated that the proteasome activity was greatly reduced. In order to confirm the results observed in transfected cells, they generated immortalized primary lymphoblastoid cells (PLCs) from blood samples of ALS patients. In PLCs, they also showed an aggregation of mutant Sig-1R in the ER associated with an increase level of BiP and p-eIF2a together with an increase of HSP70, GADD and ubiquitin conjugates [59].

28.4 Sig-1R in the Nucleus

Although Sig-1R is known to be particularly enriched in MAMs, observation of Sig-1Rs at the nuclear envelope (NE) and within nucleoplasms have also been reported. First, after stimulation by agonists such as cocaine, Sig-1Rs were found to translocate from ER to the NE, where they bind NE protein emerin and recruit chromatin-remodeling molecules [37]. These partners include lamin A/C, barrier-to-autointegration factor, and histone deacetylase (HDAC), to form a complex with the gene repressor specific protein 3 (Sp3). The dynamics of the interaction was

confirmed when knockdown of Sig-1Rs attenuated the complex formation [37]. These observations were confirmed and developed by Mavlyutov et al. [153] who expressed APEX2 peroxidase fused to Sig1R-GFP in a Sig1R-null NSC34 neuronal cell line generated with CRISPR-Cas9. They observed that Sig1R actually resides in the nucleoplasmic reticulum, a specialized nuclear compartment formed via NE invagination into the nucleoplasm. A major consequence for this localization appears to be related to neurodegenerative pathologies since accumulation of Sig-1R may be common to neuronal nuclear inclusions in various proteinopathies [154]. Sig-1R immunoreactivity was shown to be co-localized with neuronal nuclear inclusions in TDP-43 proteinopathy, five polyglutamine diseases and intranuclear inclusion body disease, as well as in intranuclear Marinesco bodies in aged normal controls [154]. These authors interestingly proposed that Sig-1Rs might shuttle between the nucleus and the cytoplasm and likely play an important role in neurodegenerative diseases, characterized by neuronal nuclear inclusions, and known to particularly rely on ER-related degradation machinery as a common pathway for the degradation of aberrant proteins [154].

28.5 Conclusion

The Sig-1R protein is not specifically a MAM or ER protein, and direct interactions have been described at or close to the plasma membrane with potassium or sodium ion channels, ether-a-gogo-related gene (ERG) ionophores and metabotropic neurotransmitter receptors [39]. One of the complexity seen with Sig-1R is the multiplicity of its intracellular partners and consequent target pathways affected by its activation, as summarized in Fig. 28.1. This multiplicity of actions within different types of cells, in the brain as well as in other tissues, explain its involvement in numerous physiopathological processes and its value as a potential therapeutic target. Moreover, the well-known observation that bearing a relatively simple pharmacophore, Sig-1R binds small molecules, and even steroids or peptides, of diverse nature with high affinity, contributed to poorly considered it as a pertinent pharmacological target for therapeutic intervention. The data we discussed in this review allow to realize that we are now accumulating evidence on the mechanisms of action of Sig-1R, on its major role at MAMs and the ER, on its efficacy to maintain, and putatively restore cellular integrity and Ca^{2+} homeostasis (Fig. 28.1). The recent progression of several molecules in clinical phases in Alzheimer's disease or Huntington's disease strengthened the validity of Sig-1R as a pharmacological target. Moreover, their efficacies in preclinical models of different pathologies outlined the importance of MAM and ER alterations in neurodegenerative processes.

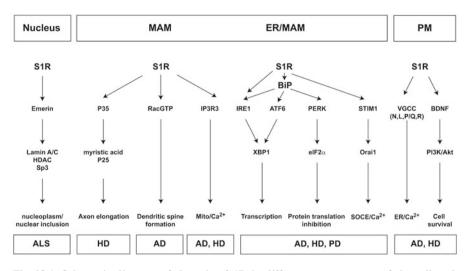


Fig. 28.1 Schematic diagram of the role of 1R in different compartment of the cell and putative major impacts in neurodegenerative diseases (AD, PD, HD, ALS)

In the nucleus, S1R interacts with Emerin [37]. This interaction leads to the recruitment of chromatin-remodeling molecules such as Lamin A/C and HDAC. This interaction is necessary for the creation of a supercomplex with Sp3. In the MAM, S1R interacts with P35 [37]. This will leads to the myristoylation of P25 and axon elongation. S1R interacts with RacGTP in order to foster dendritic spine formation [155]. S1R interacts with IP₃R3 in order to allow the proper Ca²⁺ efflux from the ER to the mitochondria [4]. In the ER, S1R interacts with BiP [4]. Upon stimulation, the dissociation of S1R with BiP induces activation of IRE1 [28] and ATF6 [136, 138, 144]. This will induce the splicing of XBP1 and the transcription of chaperones. The activation of PERK [144, 156] will induce the phosphorylation of eIF2 α , to stop protein translation. Finally, S1R interacts with STIM1 and this interaction will regulate Ca²⁺ fluxes into the ER thought the STIM1/Orai1 axe [46]. In the plasma membrane, S1R interacts with voltage-gated calcium channels (for review, [157]) in order to modulate Ca²⁺ homeostasis. S1R favors BDNF secretion [74, 87]. BDNF will activate the PI3K/Akt pathway in order to improve cell survival

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