

Protein folding stress in neurodegenerative diseases: a glimpse into the ER

Soledad Matus^{1,2}, Laurie H Glimcher^{3,4} and Claudio Hetz^{1,2,3}

Several neurodegenerative diseases share common neuropathology, primarily featuring the presence in the brain of abnormal protein inclusions containing specific misfolded proteins. Recent evidence indicates that alteration in organelle function is a common pathological feature of protein misfolding disorders, highlighting perturbations in the homeostasis of the endoplasmic reticulum (ER). Signs of ER stress have been detected in most experimental models of neurological disorders and more recently in brain samples from human patients with neurodegenerative disease. To cope with ER stress, cells activate an integrated signaling response termed the unfolded protein response (UPR), which aims to reestablish homeostasis in part through regulation of genes involved in protein folding, quality control and degradation pathways. Here we discuss the particular mechanisms currently proposed to be involved in the generation of protein folding stress in different neurodegenerative conditions and speculate about possible therapeutic interventions.

Addresses

¹ Center for Molecular Studies of the Cell, Institute of Biomedical Sciences, Faculty of Medicine, University of Chile, Santiago, Chile

² Biomedical Neuroscience Institute, Faculty of Medicine, University of Chile, Chile

³ Department of Immunology and Infectious Diseases, Harvard School of Public Health, USA

⁴ Department of Medicine, Harvard Medical School, Boston, MA, USA

Corresponding authors: Glimcher, Laurie H (lglimche@hsph.harvard.edu) and Hetz, Claudio (chetz@med.uchile.cl)

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Introduction

Most neurodegenerative disorders share a common neuropathology associated with the accumulation of abnormal protein aggregates or inclusions in the brain containing specific misfolded proteins. These diseases include Parkinson's disease (PD), amyotrophic lateral sclerosis (ALS), Alzheimer's disease (AD), Huntington's disease (HD), prion-related disorders (PrDs), and many others [1–4]. Abnormal protein aggregation in these diseases alters essential cellular functions, leading to neuro-

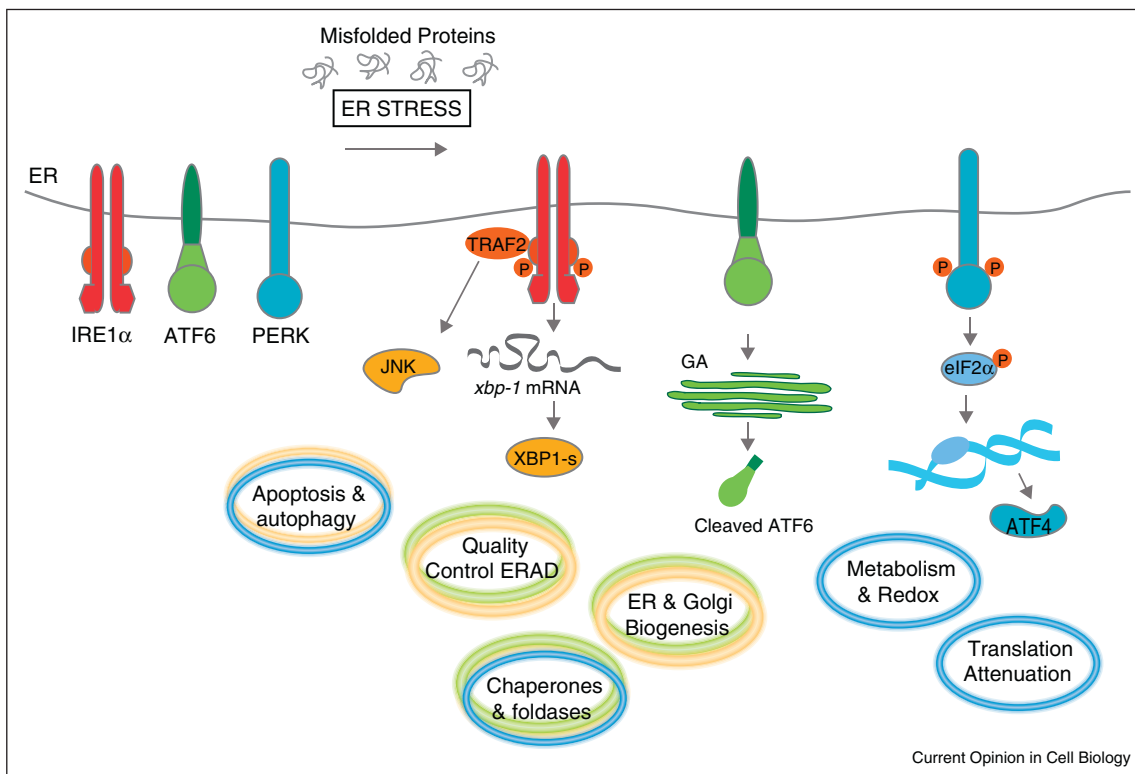
logical impairment and, in many cases neuronal loss. General perturbations to neuronal function could be related to synapse abnormalities, alteration in axonal transport, oxidative stress, proteasome inhibition, among other effects. Accumulating evidence in different neurodegenerative diseases indicates that subcellular organelle stress is a salient pathological event. Much attention has been given in the last ten years to the alterations of a particular subcellular organelle, the endoplasmic reticulum (ER), in the disease process. The ER is an essential compartment for the maturation and processing of proteins folded through the secretory pathway. In many neurodegenerative diseases the appearance of signs of ER stress is observed in the symptomatic and late disease stage. This article centers on recent findings illustrating the impact of protein folding stress at the ER in neurodegenerative conditions with distinct etiologies.

Cellular adaptation to protein folding stress: the UPR, ERAD and autophagy

One of the main functions of the ER is to initiate protein folding in the secretory pathway. A complex and dynamic network of protein chaperones, foldases, and co-factors are expressed at the ER lumen that catalyzes the folding and maturation of proteins, preventing their abnormal aggregation or misfolding. The ER also operates as a major calcium intracellular store and plays a vital role in the synthesis of lipids. Different alterations in ER homeostasis trigger the accumulation of abnormally folded proteins in the ER lumen, leading to a condition referred to as ER stress. ER stress engages the unfolded protein response (UPR), an adaptive signaling reaction that augments the cell's capacity to produce properly folded proteins and decreases the unfolded protein load [5]. Activation of the UPR affects the expression of different proteins with functions in almost every aspect of the secretory pathway, including folding, quality control, protein entry into the ER, ER-associated degradation (ERAD), autophagy-mediated degradation, and many other effects (Figure 1). The ERAD pathway is constituted by different components including chaperones, protein transporters, and ubiquitin-related enzymes that sense, deliver, and retrotranslocate misfolded proteins to the cytoplasm for proteasome mediated degradation [6].

There are three main types of ER resident transmembrane signaling proteins that operate as stress sensors that activate UPR signaling responses. These sensors include double-stranded RNA-activated protein kinase-like endoplasmic reticulum kinase (PERK), activating transcription factor 6 (ATF6), and inositol requiring kinase 1

Figure 1



The unfolded protein response (UPR). Accumulation of misfolded proteins at the ER lumen triggers an adaptive stress response known as the UPR mediated by three types of ER stress sensors: IRE1 α , PERK, and ATF6. In cells undergoing ER stress, IRE1 α dimerizes and autophosphorylates, leading to the activation of its endoribonuclease activity at the cytosolic domain. Active IRE1 α processes the mRNA encoding XBP1, which is a transcription factor that upregulates many essential UPR genes involved in folding, ERAD, organelle biogenesis, and protein quality control. In addition, active IRE1 α activates alarm responses mediated by the JNK. Additionally, activation of PERK decreases the general protein synthesis rate through phosphorylation of the initiation factor eIF2 α . eIF2 α phosphorylation increases the translation of the ATF4 mRNA, which encodes a transcription factor that induces the expression of genes involved in amino acid metabolism, antioxidant responses, apoptosis, and autophagy. ATF6 is a type II ER transmembrane protein encoding a bZIP transcriptional factor on its cytosolic domain and localized at the ER in unstressed cells. Upon ER stress induction, ATF6 is processed at the golgi apparatus (GA) releasing its cytosolic domain, which then translocates to the nucleus where it increases the expression of some ER chaperones, ERAD-related genes, and proteins involved in ER and GA biogenesis.

(IRE1) (Figure 1). All these proteins transduce information about the protein folding status at the ER lumen to the nucleus and cytosol by controlling expression of specific transcription factors and other rapid effects on protein synthesis. IRE1 α is a Serine/Threonine protein kinase and endoribonuclease that directly regulates through its ribonuclease domain the unconventional splicing of the mRNA encoding the transcription factor X-Box Binding protein-1 (XBP1). This mRNA processing event leads to the translation of a more stable protein, XBP1s [7–9]. XBP1s translocates to the nucleus and controls the induction of a subset of UPR-related genes that function in protein quality control, folding, the ERAD system, and ER and GA biogenesis [5] (Figure 1). The intensity and kinetics of IRE1 α signaling are tightly regulated by the formation of a protein complex with many regulators, a scaffold termed the *UPRosome* [10,11] (reviewed in [12,13]). IRE1 α has other functions in cell signaling, initiating the activation of

alarm pathways mediated by Apoptosis Signal-regulating Kinase 1 (ASK1) and c-Jun-N terminal kinase (JNK) pathway [14–16], in addition to modulating macroautophagy levels, here referred to as autophagy [17]. Macroautophagy is a survival pathway classically linked to adaptation and survival against nutrient starvation. Conversely, in cells undergoing ER stress, autophagy may serve as a mechanism to eliminate abnormally aggregated proteins and damaged organelles [18].

Activated PERK phosphorylates the eukaryotic translation initiation factor 2 α (eIF2 α), inhibiting translation into the ER [19,20]. eIF2 α phosphorylation augments the specific translation of the mRNA encoding activation of transcription-4 (ATF4), a transcription factor that controls the upregulation of a subset of UPR-target genes that function in redox homeostasis, amino acid metabolism, apoptosis, and autophagy [21–24,25*,26] (Figure 1). Finally, activation of ATF6 leads to its translocation from

the ER membrane to the Golgi apparatus where it is proteolytically processed, releasing the cytosolic domain which expresses a transcription factor that translocates to the nucleus and upregulates several ER chaperones, ERAD-related genes and XBP1 mRNA [27,28].

Prolonged ER stress leads to apoptosis where different regulators have been identified (reviewed in [5,29,30]), including members of the BCL-2 family of proteins [10,29,31–33]. Activation of ASK1 and JNK also regulates apoptosis under ER stress conditions [15,16]. Sustained PERK signaling is proposed as a pro-apoptotic effector [34] possibly through the induction of CHOP/GADD153 and the BCL-2 family member BIM and PUMA [19,35–37]. Many additional components of the ER stress apoptosis pathway have been identified (see specialized reviews in [31,33]).

A function of the UPR in the physiology of the nervous system?

ER stress is observed in many physiological processes in secretory cells such as plasma B lymphocytes, salivary glands and pancreatic beta cells. In all these tissues the UPR plays an essential role in maintaining survival and functionality of secretory cells (reviewed in [13,38,39]). The high demand for efficient protein folding and secretion in those cells constitutes an endogenous and physiological source of stress associated with the presence of large amounts of abnormally folded proteins that are generated during the normal protein synthesis and maturation process [6].

Although the impact of the UPR in maintaining the integrity of several secretory organs is known, its actual role to the physiology of the nervous system remains highly speculative. A possible role of XBP1 in the nervous system was proposed from genetic studies of human patients affected with bipolar disorders [40,41]. A polymorphism in the XBP1 promoter was identified as a risk factor for bipolar disorder and schizophrenia (see examples in [42–44]). Studies in *Xenopus* embryos demonstrated that XBP1 is a negative regulator of neuronal tissue differentiation during early brain morphogenesis [45]. Interestingly XBP1 expression is induced during neuronal development in *Caenorhabditis elegans* and its function regulates the assembly and transport of the glutamate receptor to the plasma membrane [46], an essential event for synaptic activity.

A role for XBP1 as a downstream signaling component of brain-derived neurotrophic factor (BDNF) was linked to neurite outgrowth [47]. Another report described activated UPR components in neurites [48]. Gene expression profile analysis from *xbp1* deficient primary neurons revealed that XBP1 controls the induction of GABAergic markers by BDNF signaling [49] perhaps explaining the neurite extension defects described in XBP1 knockout

neurons. Translational control is essential for synaptic plasticity and learning and memory [50]. Interestingly, genetic evidence suggests that targeting ATF4 or eIF2 α phosphorylation enhances memory acquisition, an effect mediated by GCN2 [51–53], an eIF2 α kinase regulated by nutrient fluctuations (but not ER stress). Finally, a recent report indicated that chronic ER stress augments spontaneous excitatory neurotransmission in hippocampus cultured neurons [54]. It remains to be determined whether or not the UPR participates in cognitive functions of the nervous system.

ER stress in neurodegenerative conditions

Although signs of ER stress are observed in a variety of neurodegenerative diseases, the *in vivo* contribution of the pathway to the disease process has been established only in a few cases, and existing data are either correlative or arise from *in vitro* evidence. The functional significance of ER stress to neurodegeneration is complex and lends itself to three distinct but paradoxical interpretations. Activation of the UPR could promote neuronal protection by increasing the efficiency of protein folding and quality control, or it may represent a degenerative signal triggered by chronic disturbance of ER homeostasis. UPR activation may also represent a late and downstream event associated with extensive neuronal damage and cellular collapse not essential for the disease process (epiphenomena). In the following sections we discuss specific evidence linking ER stress to major neurodegenerative diseases.

Amyotrophic lateral sclerosis

ALS is the most common motoneuron neurodegenerative disease affecting adults, characterized by atrophy, muscle weakness and paralysis. ALS is associated with the selective degeneration of brain and spinal cord motoneurons [55,56]. Most ALS cases are referred to as sporadic (sALS), lacking a clear genetic component, whereas ten percent of the cases are familial (fALS). The primary mechanisms contributing to motoneuron degeneration observed in ALS remain controversial, and multiple alterations have been uncovered (see examples in [57–59]).

Accumulating evidence suggests that ER stress contributes to both sALS pathogenesis and fALS pathogenesis [60]. Increased levels of a variety of ER stress markers have been reported in spinal cord tissue of sALS patients [61,62^{••},63–65]. Approximately 20% of fALS cases are linked to more than 110 dominant mutations in the gene encoding superoxide dismutase-1 (SOD1). These mutations induce the misfolding and abnormal intracellular aggregation of SOD1, which is thought to contribute to the occurrence of neuronal dysfunction and death. Recent studies also suggest that Wild-type SOD1 aggregates and accumulates in sALS spinal cord [66]. Activation of the three major UPR signaling branches is observed in different mutant SOD1 transgenic mice [64,67–70,71[•],72^{••},73,74]. A recent study

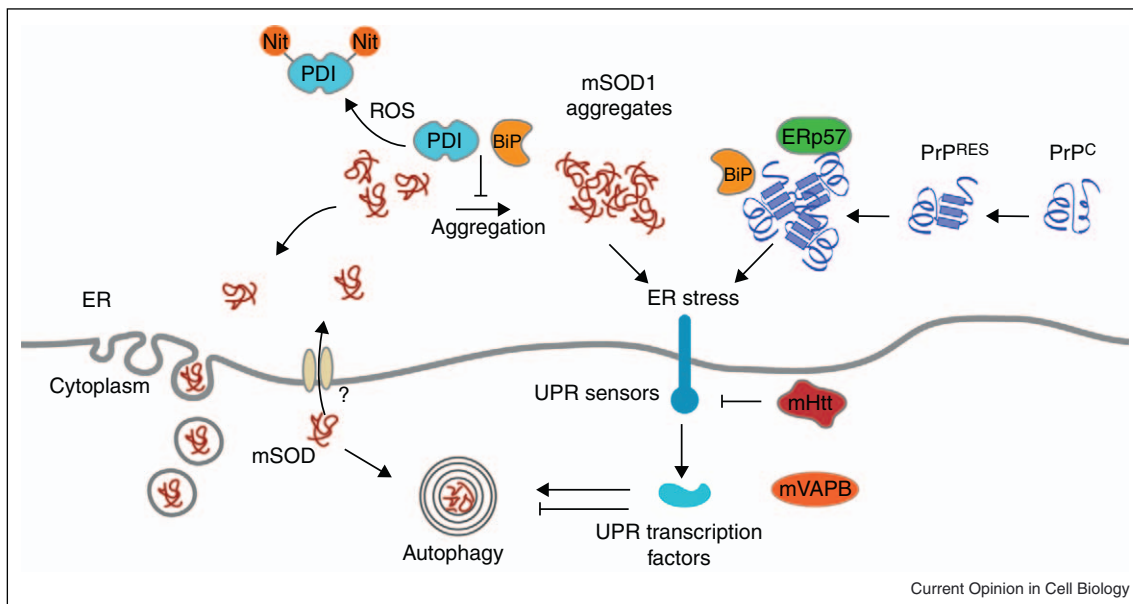
showed that only affected motoneurons of fALS mouse models are selectively prone to undergo ER stress, a pathological process observed from birth with activation before the detection of the earliest denervation [72^{**}]. A proteomic analysis of spinal cord tissue from symptomatic SOD1^{G93A} transgenic mice identified ERp57 and PDI as the most highly induced proteins present. These two studies point to the occurrence of ER stress as a major cellular response activated in ALS models [67,72^{**}].

A fraction of insoluble-high molecular weight species of mutant SOD1 accumulates inside the ER *in vivo* as demonstrated by many studies [67,69,75,76]. SOD1 possibly interacts with PDI or with BiP/GRP78 in ER enriched lysates [67,69] (Figure 2). The therapeutic effects of targeting the UPR were demonstrated after treatment of mutant SOD1 transgenic mice with salubrinal, a small molecule that induces eIF2 α phosphorylation [77]. Salubrinal led to significant protection against disease progression, improved motoneuron survival, and extended life span [72^{**}]. Similarly, another molecule that decreases ER stress levels, termed SUN N8075, also protects against experimental ALS [78]. We also recently investigated the possible contribution of ER stress to ALS using a genetic strategy [62^{**}]. We knocked down components of the three UPR branches in a cellular model of fALS. As predicted reduced levels of ATF4 and ATF6

increased the rate of mutant SOD1 aggregation [62^{**}]. In contrast, knocking down XBP1 unexpectedly reduced the generation of mutant SOD1 aggregates in cultured motoneurons. We also generated mutant SOD1 mice with a specific deficiency of *xbp1* in the nervous system [62^{**}]. These mice exhibited delayed ALS disease onset and increased life span, uncovering an unexpected beneficial effect of targeting the IRE1 α branch of the UPR [62^{**}]. Both cellular and *in vivo* approaches in the context of XBP1 deficiency revealed an enhancement of mutant SOD1 degradation due to autophagy in motoneurons (Figure 2).

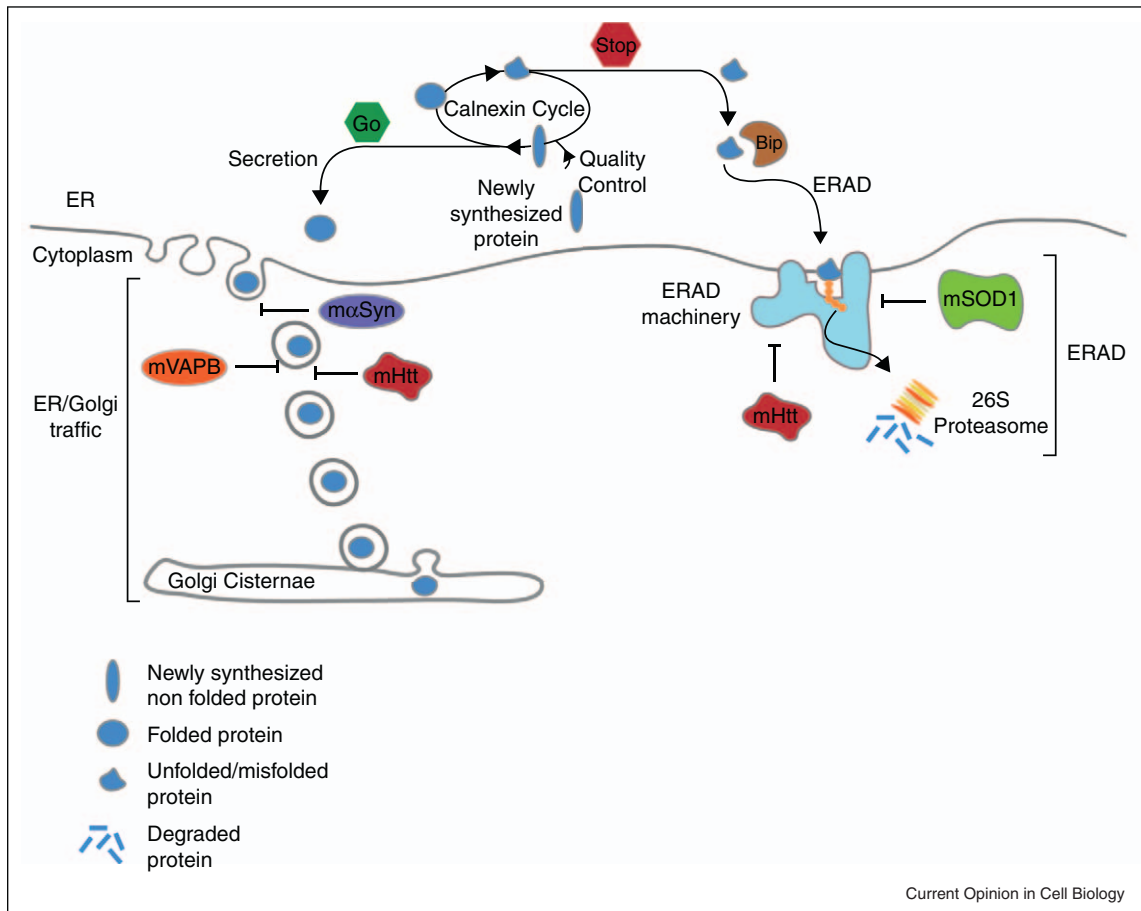
Several reports have uncovered possible causes of ER stress in ALS. For example, the cytosolic subpopulation of mutant SOD1 inhibits ERAD activity via decreased retro-translocation of ERAD substrates to the cytosol, inducing ER stress [71^{*}] (Figure 3). Mutant VAPB causes fALS [79], through interacting with and inhibiting ATF6 and XBP1 [80–82] (Figure 3), increasing the vulnerability of motoneuron cells to ER stress-induced death [83]. Oxidative modifications of PDI, a key ER foldase, are also observed in sALS spinal cord tissue and in fALS mouse models [73]. PDI inactivation likely triggers a general perturbation of ER folding networks, possibly leading to chronic ER stress (Figure 2). Other factors may also contribute to the occurrence of ER stress in ALS,

Figure 2



Alterations in the function of ER chaperones and UPR-related components in neurodegenerative diseases. In many neurological diseases such as AD, PD and ALS, the oxidative modification of the active site of PDIs by nitrosylation leads to their enzymatic inactivation. This event may perturb the folding process at the ER, triggering ER stress. In addition, mutant SOD1 and PrP^{RES} accumulate and aggregate at the ER, which correlate with their stable interaction with ER chaperones such as BiP, PDI and ERp57/Grp58. This interaction may trap ER chaperones, altering protein folding networks with concomitant ER stress. In addition, expression of VAPB mutants (mVAPB) linked to fALS or mutant Htt (mHtt) alters the activity of UPR stress sensors and transcription factors. Accumulation of disease-related protein aggregates at the ER may directly or indirectly activate UPR stress sensors. UPR transcription factors control several cellular responses (Figure 1), including the positive and negative modulation of autophagy-mediated degradation of protein aggregates.

Figure 3



Alterations in ER-associated degradation (ERAD) and ER/Golgi trafficking triggers ER stress in some neurodegenerative diseases. Under normal conditions, newly synthesized proteins at the ER enter into the calnexin cycle for proper folding and quality control. If a protein becomes misfolded, it is targeted to the ERAD machinery for translocation to the cytosol and then degraded by the proteasome. Mutant Htt (mHtt) or mutant SOD1 (mSOD1) associated with fALS interacts with ERAD components, precluding the translocation of ERAD substrates from the ER to the cytosol, leading to the accumulation of abnormally folded proteins at the ER, generating ER stress. Properly folded proteins traffic from the ER to the Golgi for further maturation steps. Expression of mutant VAPB (mVAPB) associated with fALS and mHtt alter the trafficking between ER and Golgi. Similarly, mutant α Synuclein (α Syn) blocks the exit of vesicles from the ER. Inhibition of vesicle transport between the ER-Golgi leads to the accumulation of cargo vesicles, triggering the accumulation of immature proteins at the ER, causing ER stress.

including alterations to axonal and dendritic trafficking of vesicles. For a detailed review see [60].

Accumulating evidence indicates that alterations in two proteins related to mRNA metabolism have an important role in ALS pathogenesis, including altered expression of TAR DNA-binding protein 43 (TDP-43) and Fused in sarcoma protein (FUS) (see review in [84]). For example, abnormal subcellular distribution and cytoplasmic aggregation of TDP-43 are widely reported in sALS and fALS cases, in addition to frontotemporal lobar degeneration [85]. Mice transgenic for a disease-linked mutant form of human TDP-43 develop progressive neurodegeneration associated with motoneuron loss, motor impairment, and accumulation of ubiquitin-positive aggregates [86]. Mutations in FUS are also genetically linked to fALS

[87] and accumulation of FUS into protein inclusions is also observed in sALS cases [88]. Although protein misfolding and aggregation is associated with FUS and TDP-43-related neurodegeneration, it remains to be determined if ER stress is a relevant factor in their pathological effects.

Parkinson's disease

PD is the second most common neurodegenerative disease, and affects around 2% of individuals over 65 years of age [89]. PD is a slowly progressing neurodegenerative disorder affecting dopaminergic neuron viability in the *Substantia Nigra pars compacta* (SNpc). Most PD cases are sporadic but familial PD accounts for 2–3% of PD cases. One of the most studied PD-related genes is α -synuclein (α Syn) [90], which is observed in intracellular inclusions termed Lewy bodies.

Increasing evidence suggests that ER stress is a common pathological feature associated with several PD-linked genes and sporadic PD models. ER stress markers were reported in the *SNpc* of post-mortem tissue from sporadic PD human cases [91–93], and in another synucleinopathy (Multiple system atrophy) [94]. PDI inactivation occurs in PD brain through oxidative modification [95] (Figure 2). Cellular studies indicate that overexpression of mutant [96] and wild type [78] α Syn triggers chronic ER stress, inducing cell death. Reports in complementary model organisms demonstrated that the earliest defect following α Syn expression is a block in ER to Golgi vesicular trafficking [97,98]. Remarkably, the inhibition of ER-Golgi trafficking by α Syn expression triggers ER stress [97,98] possibly due to the accumulation of cargo vesicles, triggering the accumulation of immature proteins at the ER [12,99] (Figure 3). α Syn phosphorylation activates the UPR even before any detectable mitochondrial dysfunction is observed [100]. In addition, Parkin/PARK2 expression has a pro-survival activity against ER stress due to modulation of ERAD/proteasome pathway [101–103]. Expression of the Parkin substrate Pael-R triggers ER stress *in vivo* and *in vitro* [104–106], and manipulation of ER chaperone expression reverts the pathological effects of Pael-R [106]. Furthermore, loss of DJ-1/PARK7 triggers ER stress and proteasome inhibition [107]. Mutation in ATP13A2/PARK9 leads to its ER retention where it may exert neurotoxicity [108]. Finally, LRRK2/PARK8 deficiency in *C. elegans* triggers hypersensitivity to ER stress [109].

Remarkably, two gene expression profile analyses indicated that ER stress is a major cellular response in toxicological models resembling sporadic PD [110,111], and *chop* deficiency [112] or XBP1s overexpression [113] attenuated neurotoxin-mediated PD. Similarly, ATF6 deficient mice are more susceptible to neurotoxin-induced neurodegeneration at the *SNpc* [114]. At the mechanistic level, it was proposed that the generation of radical oxygen species by PD-triggering neurotoxins leads to the oxidation of proteins at the ER, possibly inducing protein misfolding and ER stress [115]. Taken together, these findings suggest that a common feature in sporadic and different genetic forms of PD is the occurrence of chronic ER stress.

Huntington's disease

Huntington's disease (HD) is a late-onset autosomal dominant neurodegenerative disease associated with progressive cognitive defects and motor abnormalities [116,117]. The disease results in a widespread neuronal dysfunction and selective neurodegeneration in the central nervous system, mostly affecting the striatum [116]. The expansion of a glutamine stretch within the N-terminal region of *huntingtin* (Htt) gene over ~40 repeats generates severe dominant neurotoxic properties [116–120].

UPR activation was noted in post-mortem HD brain samples [121]. Similarly, several studies in cellular models of HD suggest that ER stress may contribute to neurodegeneration [15,16,24,122*,123] (reviewed in [124]). Expression of SCAMP5 is markedly increased in human HD striatum and SCAMP5 down-regulation alleviates ER stress-induced by mutant Htt expression in cell culture [125]. At this time, only three studies are available describing the occurrence of ER stress *in vivo* in HD animal models [121,125,126]. The 18 amino-acid amino-terminus region of Htt generates an amphipathic alpha helical that can reversibly target to the ER and autophagosomes [127]. In addition, the association of Htt and membranes is dynamic because this interaction is modulated by ER stress [127], which may be a relevant factor for Htt aggregation [127].

Expression of mutant Htt leads to a pronounced defect in ERAD in yeast cells and mammalian models of HD, associated with an recruitment of essential ERAD proteins, triggering ER stress [122*,128] (Figure 3). Further, a recent report suggested that ATF6 α processing is altered in animal models of HD and in patient HD samples [129]. However, most of these studies are correlative and no data on the function of ER stress/UPR signaling in the disease process *in vivo* are available. Genetic or pharmacological manipulation of the pathway is required to resolve this issue.

Prion-related disorders

PrDs are lethal neurodegenerative disorders whose hallmark is spongiform degeneration and accumulation in the brain of a protease-resistant and misfolded form of the cellular prion protein termed PrP^{RES} [130]. PrDs can be classified as sporadic, infectious, or autosomal dominant inherited forms, observed in both humans and other mammals. The most common PrD in humans is Creutzfeldt–Jacob disease (CJD) [130]. Upon synthesis, the normal cellular prion protein (PrP^C) is subjected to several post-translational processing events in the ER and Golgi before localizing to the plasma membrane in cholesterol-rich lipid rafts [131]. Most familial mutant PrP variants are retained and aggregated at the ER and Golgi [132]. In contrast, the generation of infectious PrP^{RES} is proposed to occur at the plasma membrane and during its cycling through the endocytic and lysosomal pathway [132]. The 'protein-only' hypothesis postulates that the pathogenesis of infectious PrD forms results from a conformational change of PrP^C to generate PrP^{RES}, possibly set off by a direct interaction between the two PrP forms [133].

Several groups have shown activated ER stress responses in PrD mouse models [134–139]. Similarly, cows affected with Bovine Spongiform Encephalopathy develop signs of ER stress in the brain [78]. Upregulation of Grp78/BiP, Grp94, and Grp58/ERp57 is observed in CJD brain

samples [136,140] and proteomic analysis of such brain samples demonstrated high expression of Grp58/ERp57 in cerebellum of human patients with sporadic CJD [140]. Grp58/ERp57 interacts with PrP and has neuroprotective effects *in vitro* against prion neurotoxicity [137] (Figure 2). In addition, scrapie infected neuroblastoma cells are more susceptible to cell death induced by the pharmacological activation of ER stress [136]. Further, expression of a familial PrP mutant triggers ER stress *in vitro* [141].

ER stress can trigger PrP^C misfolding and aggregation [142–144], and facilitates the conversion of PrP^C into PrP^{RES} in a cell free system [143]. Similarly, proteasome inhibition leads to the accumulation of a protease resistant form of PrP^C derived from the ERAD [145,146]. These observations may be relevant for understanding the occurrence of sporadic forms of CJD, the most common PrD in humans, where alteration in the folding/quality control process or the ER environment may be a key event in initiating PrP misfolding. To evaluate the possible involvement of the UPR in PrDs we tested the susceptibility of a brain specific XBP1 conditional knock-out mice to scrapie prion pathogenesis [135]. To our surprise, no effects were observed on the activation of ER stress responses, PrP^{RES} levels, neuronal loss or animal survival. Since the UPR in mammals is not limited to the IRE1/XBP1 pathway, activation of these alternative UPR pathways may well compensate for XBP1 deficiency in the prion model employed.

Alzheimer's disease

AD is the most common form of dementia of the elderly. AD is characterized by extracellular accumulation of fibrillar deposits of the amyloid- β peptide (A β) in senile plaques, intraneuronal neurofibrillary tangles consisting of abnormally hyperphosphorylated tau protein, in addition to oxidative stress, synaptic loss and neuronal degeneration [147]. A 4.5 kDa A β peptide is generated by successive proteolysis of the amyloid precursor protein (APP) by two proteases, beta-secretases and gamma-secretases. Mutations in the genes encoding APP or presenilin are associated with hereditary cases of AD and increased A β generation. Soluble oligomers of A β are highly neurotoxic, causing important deleterious effects on synaptic function and memory [148].

The exact mechanism involved in neuronal dysfunction in AD remains speculative. Recent studies from different laboratories implicate the participation of ER stress in the disease process. ER stress is observed in post-mortem brain samples from AD patients [149–155], in addition to PDI inactivation by oxidative inactivation [95]. Signs of ER stress have been observed in many cellular models of AD by independent groups [156–165]. Some AD-related proteins also alter ER stress signaling, including IRE1 α and calcium homeostasis [148,166,167]. Some but not all

in vivo studies have detected signs of ER stress in animal models of AD [166,168–170].

Other pathologies

Although little data are available about the impact of the UPR in other pathologies, emerging evidence indicates that ER stress may have a broader impact on disease conditions affecting the nervous system.

Lysosomal storage diseases

Lysosomal storage diseases are fatal neurodegenerative disorders that belong to a family of inborn metabolism errors. ER stress is observed in several models of lysosomal storage diseases including GM1-gangliosidosis [171,172] and Infantile Neuronal Ceroid Lipofuscinoses [173,174]. In contrast, no evidence of UPR activation was reported in models of other lysosomal storage disorders including Gaucher disease [175] and Niemann Pick type C [176].

Spinal cord injury

Spinal cord injury (SCI), a major cause of partial or complete loss of mobility can occur from mechanical trauma, ischemia, tumor invasion or developmental abnormalities. ER stress markers are observed in several models of SCI due to trauma (contusion and hemisection) and ischemia as an early event [177–180]. Treatment with a chemical chaperone decreases tissue damage in a SCI mouse model, associated with a reduction in the levels of ER stress [181]. However, all of the studies performed to date are correlative and the contribution of ER stress to SCI has never been addressed directly.

Myelin-related disorders

Myelinating cells including oligodendrocytes in the central nervous system and Schwann cells in the peripheral nervous system produce large amounts of plasma membrane and proteins during the myelination process, that may render them particularly susceptible to secretory pathway function disruption (reviewed in [182]). ER stress markers are observed in models of various myelin-related disorders, including multiple sclerosis [183–188], Charcot-Marie-Tooth disease [189], Pelizaeus-Merzbacher's disease [190], and Vanishing White Matter Disease [191,192].

Retinitis pigmentosa

Mutations within the rhodopsin gene lead to retinitis pigmentosa, an inherited form of retinal degeneration. Several rhodopsin mutants trigger ER stress *in vitro* and in animal models [193,194,195,196]. Targeting *xbp1* in a *Drosophila melanogaster* model accelerates retinal degeneration [197]. Remarkably, subretinal delivery of a BiP expressing viral vector in a mutant rhodopsin transgenic rat led to reduction in ER stress levels, and improved neuronal survival and eye function [193]. Similarly, mutations in carbonic anhydrase IV, which is also linked

to retinitis pigmentosa, trigger chronic ER stress and apoptosis [198–200].

Concluding remarks

The exact role of the UPR in the central nervous system is not well defined. In this review we have summarized and discussed the available evidence supporting a strong association between accumulation of misfolded proteins and ER stress induction in several key neurodegenerative diseases. Although strong correlations exist between the misfolding and aggregation of an underlying protein and the presence of ER stress in neurodegenerative conditions, direct evidence to causally link the UPR and ER stress to neurological disorders *in vivo* is mostly lacking. Predicting whether and how ER stress affects is difficult because activation of the UPR may decrease neurodegeneration by increasing folding, protein quality control and autophagy, or extensive or chronic ER stress may result in irreversible neuronal damage and apoptosis. The mechanisms underlying modifications of ER homeostasis may differ in different disease contexts and include inhibition of ERAD function, perturbed vesicular trafficking, oxidative modifications of crucial ER foldases, and abnormal physical interactions with ER chaperones or UPR components (Figures 2 and 3). In addition, alterations in lipid, cholesterol or calcium metabolism may also affect ER function in many neurological disorders, contributing to the occurrence of ER stress.

Promising results have been obtained with pharmacological strategies to target ER stress in a disease context. Genetic manipulation of UPR components *in vivo* has been employed only in a few diseases to test the actual contribution of the pathway to neurodegeneration, and further efforts are needed to validate the role of ER stress in important diseases such as AD, PD and HD *in vivo*. Further we know little about the cell types in the brain that are primarily affected by ER stress nor have the endogenous stimuli that evoke the UPR been firmly identified. Neuronal populations with higher secretory requirements might display increased sensitivity to factors, genetic and environmental, that disrupt ER function. In this context, understanding the possible role of ER stress in cells such as oligodendrocytes, Schwann cells, or neuropeptide-secretory neurons is of particular relevance for future therapeutic intervention.

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