

Review

Unfolded Protein Response and Macroautophagy in Alzheimer's, Parkinson's and Prion Diseases

Irina Milisav ^{1,2,†}, Dušan Šuput ^{1,†} and Samo Ribarič ^{1,*,†}

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¹ Institute of Pathophysiology, Faculty of Medicine, Zaloška 4, Ljubljana SI-1000, Slovenia; irina.milisav@mf.uni-lj.si (I.M.); dusan.suput@mf.uni-lj.si (D.S.)

² Faculty of Health Sciences, Zdravstvena pot 5, SI-1000 Ljubljana, Slovenija

* Correspondence: samo.ribaric@mf.uni-lj.si; Tel.: +386-1-543-7053; Fax: +386-1-543-7021

† These authors contributed equally to this work.

Abstract: Proteostasis are integrated biological pathways within cells that control synthesis, folding, trafficking and degradation of proteins. The absence of cell division makes brain proteostasis susceptible to age-related changes and neurodegeneration. Two key processes involved in sustaining normal brain proteostasis are the unfolded protein response and autophagy. Alzheimer's disease (AD), Parkinson's disease (PD) and prion diseases (PrDs) have different clinical manifestations of neurodegeneration, however, all share an accumulation of misfolded pathological proteins associated with perturbations in unfolded protein response and macroautophagy. While both the unfolded protein response and macroautophagy play an important role in the prevention and attenuation of AD and PD progression, only macroautophagy seems to play an important role in the development of PrDs. Macroautophagy and unfolded protein response can be modulated by pharmacological interventions. However, further research is necessary to better understand the regulatory pathways of both processes in health and neurodegeneration to be able to develop new therapeutic interventions.

Keywords: Alzheimer's disease; autophagy; neurodegeneration; Parkinson's disease; prion diseases; proteostasis; unfolded protein response

1. Proteostasis in Neurodegeneration

There are integrated biological pathways within cells that control the protein synthesis, folding, trafficking and degradation of proteins referred to as protein homeostasis or proteostasis. There are dynamic interconnections between the cytosolic and endoplasmic reticulum protein syntheses, quality control, folding and degradation mechanisms in neurons. Protein folding capacity may become saturated in the stages prior to neurodegeneration; e.g., due to large amounts of misfolded proteins, protein aggregation and mutant proteins (Figure 1). Oversaturation of both, cytoplasmic and endoplasmic reticulum (ER) protein synthesis and folding pathways, is rescued by proteasomal degradation and autophagy of unfolded, misfolded, mutant or damaged (e.g., oxidised) proteins. In addition to the ER associated protein degradation pathway (ERAD), the oversaturation of ER triggers also an unfolded protein response (UPR) to reduce the load of newly synthesized proteins temporarily. If these mechanisms do not manage to clear the aberrant proteins, if there is a proteasome overload, proteasome is defective or there are excess ROS in the cytoplasm, misfolded proteins may form aggregates and the UPR mechanism is extended. These aggregates are attempted to be cleared by macroautophagy. The further inefficient clearance of aggregates, formation of toxic aggregates and prolonged oxidative stress further inhibit the proteasome and ERAD, resulting in chronic stress and apoptosis that may be triggered by the UPR [1].

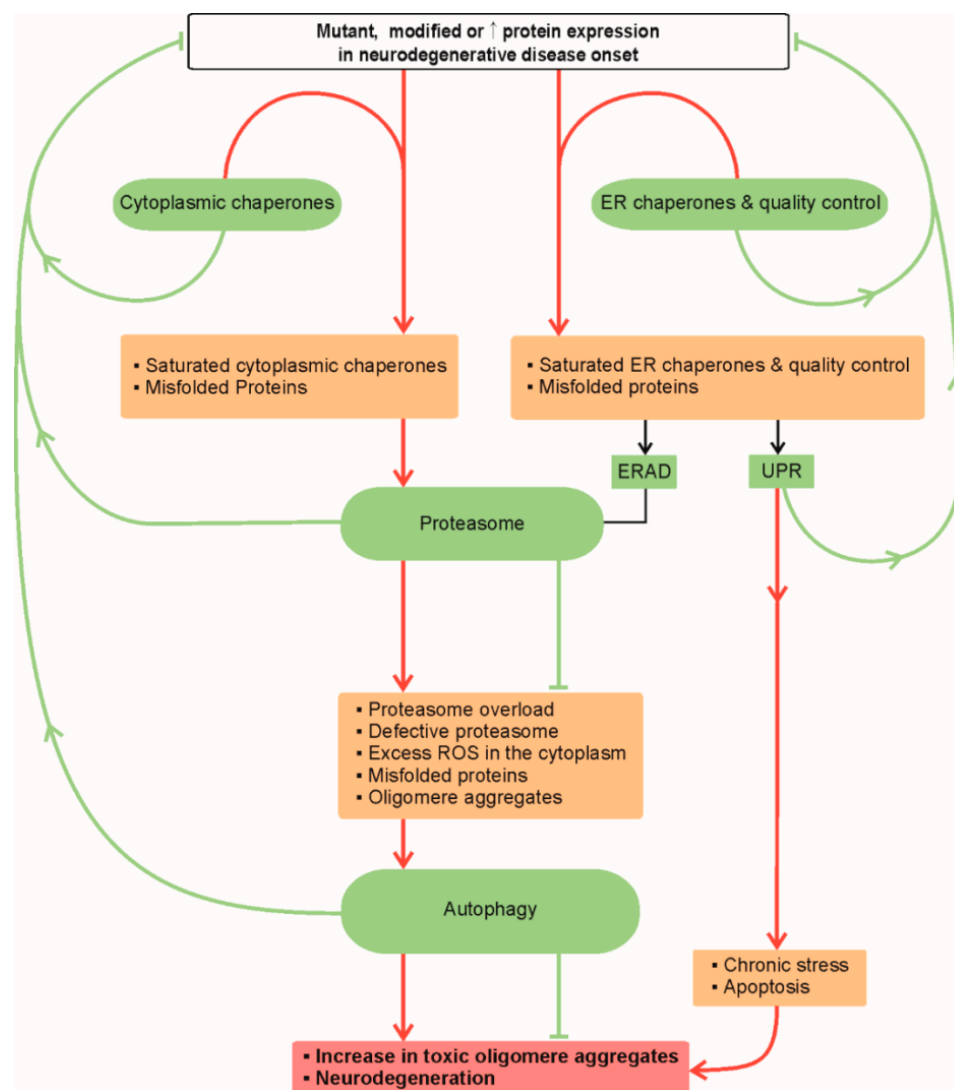


Figure 1. Proteostasis in neurodegeneration. Red lines and arrows indicate progressive failure of proteostasis ultimately leading to neurodegeneration. Green arrows and lines indicate appropriate response of proteostasis to altered proteins that prevents or slow-downs the progress of neurodegeneration. Abbreviations: ER (endoplasmic reticulum); ERAD (endoplasmic reticulum associated protein degradation); ROS (reactive oxygen species); UPR (unfolded protein response).

Proteostasis in the brain is more susceptible to perturbations than in other organs for the following reasons: (a) an increased susceptibility of neurons even to a brief episode of hypoxia/ischemia due to the dependence on a continuous supply of oxygen and glucose; (b) the absence of cell division that prevents replacement of damaged neurons after apoptosis or necrosis and leads to an increased exposure of nerve cells to age-related changes of proteostasis [2,3]; (c) effects of chronic disorders (e.g., protein glycation in diabetes); and (d) the high turnover of cell components involved in synaptic transmission coupled with the high metabolic rate at the synapses.

Alzheimer’s disease (AD), Parkinson’s disease (PD) and prion diseases (PrDs) have different clinical manifestations of neurodegeneration, however, all share an accumulation of misfolded pathological proteins associated with perturbations in unfolded protein response [1,4], and macroautophagy [5,6]. This paper will focus on the role of unfolded protein response and macroautophagy in AD, PD and PrDs as examples of perturbed proteostasis in neurodegenerative disorders.

1.1. Endoplasmic Reticulum

One of the key functions of the ER, composed of double membrane sheets adjacent and continuous with the outer layer of the nuclear envelope, is the synthesis, folding and quality control of cell membrane proteins. ER and Golgi (G) work in concert to target newly synthesized proteins to their final destination [1]. In contrast to the continuous connection between the nucleus and ER, the bi-directional transport between ER and G is enabled by membrane bound vesicles. The coating proteins for these vesicles are COPI and COPII. COPI targets vesicles to the G, and COPII enables retrograde transport [7]. The shuttle of these transport vesicles is enabled by molecular motors and the cytoskeleton, a flexible cytosolic network that rapidly responds to regional requirements by adjusting its assembly/disassembly ratio. A key component of human and animal cells' cytoskeleton are microtubules, made of polymerised tubulin. Some neurodegenerative disorders, e.g., PD and AD, are associated with changes in tubulin polymerisation [8,9].

Discrete sites of ER, the mitochondria-associated ER membranes or MAMS (Figure 2), are intimately associated with mitochondria, enabling for example, membrane lipids, lipid, Ca^{2+} and ROS transfer to the mitochondria, mitochondrial fission, inflammasome formation and preparation of mitochondrial membranes for autophagy; for a review see [10]. The PKR-like ER kinase (PERK) is important for the integrity of the MAMs contact points [11]. An increased presence of proteins, e.g., $\text{A}\beta$ and presenilin 2, increase the number of MAMs [12,13]. ER is the major Ca^{2+} storage site in the cell. The net flux of Ca^{2+} , from ER to mitochondria, increased by ER stress, is due to the interaction between inositol 1,4,5-trisphosphate receptor (IP3R) and cytochrome c. Cytochrome c blocks the Ca^{2+} dependent inhibition of IP3R, leading to an Ca^{2+} efflux from the ER and cell wide cytochrome c release result in apoptosis [12–16].

Protein folding is enabled by several ER chaperone proteins (e.g., 78 kDa glucose-regulated protein, GRP78/BiP; protein disulphate isomerase, PDI) and is essential for the transport of newly synthesized proteins from ER to G. Misfolded proteins or proteins that can't be folded are targeted for degradation by the ER-associated protein degradation (ERAD) pathway and returned to the cytosol; they are ubiquitinated by the ER-associated ubiquitin ligases for degradation by the proteasome. The ER responds to different stressors, for example to oxidative stress, overexpression of proteins (e.g., α -synuclein, α SYN; amyloid beta, $\text{A}\beta$), hypoxia/ischemia and insulin resistance, by (a) slowing the rate of protein folding and transiently increasing the content of unfolded proteins; and (b) by an overall translational block and activation of ER stress responsive genes that will increase the protein folding capacity and decrease the protein folding load in the ER [1,4,17].

1.2. Unfolded Protein Response

Oxidative stress, increased protein synthesis, decreased ER-associated protein degradation, disturbed calcium signalling and disturbed lipid homeostasis can result in ER stress and activate the unfolded protein response [18]. In mammals there are three classes of ER stress sensors that respond to the levels of unfolded/misfolded proteins in the ER. All of them are ER membrane-associated proteins: (a) activating transcription factor 6, (ATF6); (b) pancreatic ER eIF2 α kinase (PERK, also, PKR-like ER kinase, double-stranded RNA-activated protein kinase-like ER kinase); and (c) inositol-requiring kinase 1 (IRE1) (Figure 2) [19]. The luminal domain of each stress sensor is bound to the chaperone GRP78/BiP in the resting state. GRP78/BiP dissociate upon the ER stress to bind unfolded proteins in mammals [19,20]. There are two mammalian IRE1 homologues IRE1 α and IRE1 β . IRE1 α is expressed ubiquitously, while IRE1 β is mostly in intestinal epithelium [19,21]. Like Ire1p from yeast, the mammalian IRE1 β may bind unfolded proteins directly [22]. Similarly, there are two ATF6 isoforms in mammals; their N-terminal cytosolic fragments (ATF6f) are transcription factors. The relative levels of the two ATF6 isoforms may contribute to the regulation of strength and duration of ATF6f dependent ER stress response gene induction [23]. The induced genes have ER stress response elements (ERSE) within their promoter encoding proteins that collectively may reduce ER stress, produce a transcript for pro-survival transcription factor and a target of IRE1, X-box

binding protein-1 (XBP1, see below) and of the pro-apoptotic transcription factor C/EBP homologous protein (CHOP) during the sustained ER stress [20,24].

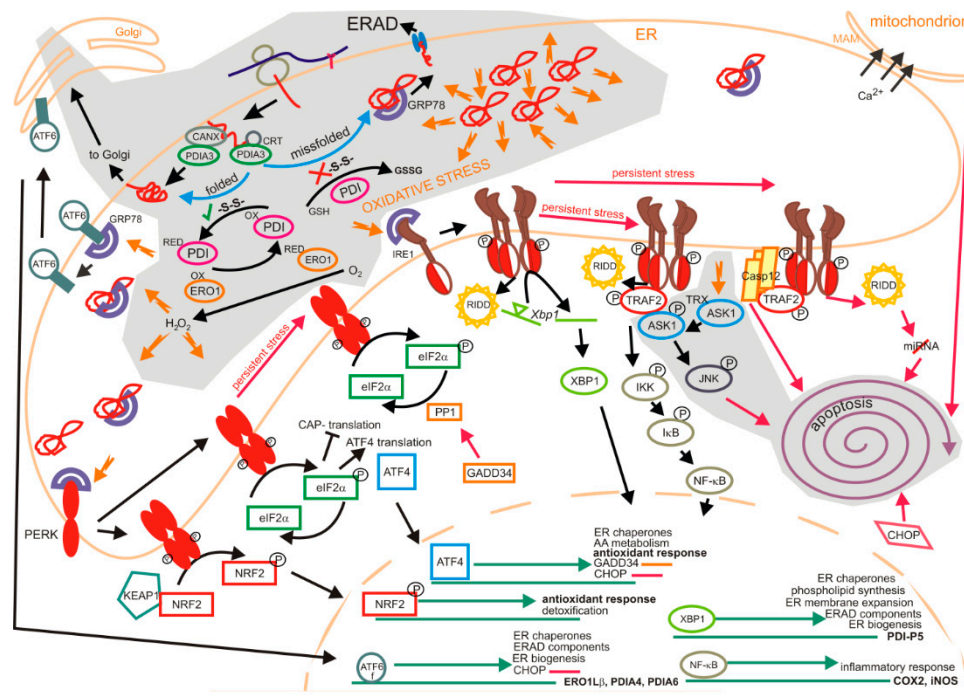


Figure 2. Basic mechanisms of unfolded protein response. There are three phases of UPR. The adaptive, transition (black arrows) and the late phase (red arrows); the last two phases occur if the stress is not resolved and there is prolonged stress. Protein load in the ER is decreased during the early adaptive phase. ATF6, PERK and IRE1 are the three classes of main ER stress sensors that respond to the levels of unfolded/misfolded proteins in the ER. They are activated by the dissociation of GRP78/BiP upon increased amounts of misfolded proteins or direct binding of unfolded proteins in the case of yeast Ire1p and possibly IRE1 β . Then the cell survival or cell death pathways are conveyed through complex parallel and convergent signal transduction pathways. Impact of oxidative stress on protein folding and unfolded protein response is depicted on the grey background. Protein disulphate isomerases (PDIs) assist in folding of nascent chains by catalization of disulphide bond formation (top left). For example, PDIA3 or Erp57 is expressed in many tissues, including liver, pancreas, kidney, placenta and lungs and to lower extent in heart, skeletal muscle and brain.. Its activity is enhanced when it is in complex with calnexin (CANX) and calreticulin (CRT). The proper formation of disulphide bonds between two cysteine residues in nascent proteins is necessary for correct protein folding. Two cysteines in the active site of PDI accept two electrons from the cysteines of the folding polypeptide. PDI is then oxidized by oxidoreduction 1 (ERO1) proteins that subsequently transfer the electrons to oxygen to produce H₂O₂. Improperly paired disulphide bonds are reduced by PDI, while producing the oxidized glutathione. Misfolded proteins are exported to the cytosol to be degraded by the proteasome in the process ER-associated degradation (ERAD). ROS produced during protein folding and the decrease of GSH upon the reduction of improperly paired disulphide bonds of misfolded proteins may shift the redox balance towards the oxidative stress. Likewise, oxidative stress is the consequence of excess of misfolded proteins. Upon oxidative stress, all three ER stress sensors, ATF6, PERK and IRE1 α are activated. Apoptosis signal-regulating kinase (ASK1) is activated by oxidative stress, ER stress and inflammation (e.g., TNF α). It dissociates from (oxidized) thioredoxin (Trx) and binds TRAF2 to convey the apoptosis signal through JNK activation.

PERK and IRE1 are protein kinases that sense ER stress by its luminal domains, detect alterations in the lipid composition of the ER membrane through their transmembrane regions and propagate

downstream events through cytosolic regions [25,26]. Most of the PERK signalling is mediated through phosphorylation of the alpha subunit of eukaryotic initiation translation factor 2 (eIF2 α) which result in inhibition of delivery of the initiator methionyl-tRNA to the ribosome, resulting in general inhibition of protein translation (cap-dependent translation) to decrease protein influx into ER [27,28]. eIF2 α phosphorylation also promotes the translation of selective mRNAs with internal entry ribosomal site (IRES), leading to the translation of genes associated with UPR, namely the transcription factor gene 4 (ATF4) [28,29]. This results in an up-regulation of genes associated with redox homeostasis, energy metabolism and protein folding [30,31]. PERK also phosphorylates other proteins, like NRF2 and NF- κ B; this may result in adjustments of redox metabolism and inflammatory processes [25]. Apart from pro-survival signalling pathways, there are also pro-apoptotic ones initiated downstream of PERK and ATF4 that are important during the persistent ER stress and may contribute to neurodegeneration. Growth arrest and DNA damage - inducible 34 (GADD34) regulates the activity of protein phosphatase 1 (PP1) that inactivates eIF2 thus resumes the cap-dependent translation [32] and increases protein load in the ER, while CHOP is the transcription factor, for example needed for transcription of pro-apoptotic BCL2 genes. CHOP expression is induced by ATF4 in combination with other transcription factors [33].

Activated IRE1 is a kinase participating in cell fate determination through mitogen protein kinase (JNK, also c-Jun N-terminal kinase) and an endonuclease splicing mRNA for the transcription factor XBP-1 to trigger its translation [21]. XBP-1 modulates expression of UPR target genes, including ER chaperons, glycosylation enzymes, ERAD components and those involved in the synthesis of phospholipids [25]. Other RNAs are targeted through a process called regulated IRE1-dependent decay (RIDD) that reduces the amount of proteins targeted to the ER. In the case of persistent ER stress, IRE1 ceases to splice *Xbp-1* mRNA to repress adaptive responses and activate apoptosis through RIDD [21]. RIDD can increase ER stress intensity through degradation of selective UPR target genes like GRP78 [21]. As the ER stress intensity reaches its threshold, IRE1 degrades some microRNAs linked to regulation of apoptosis, among them pre-miRNA for Caspase-2 [21]. Modulation of IRE1 activity depends on its interacting proteins. IRE1 also controls cell fate determination through its kinase activity. The cytosolic domain of IRE1 binds the adaptor protein TNF-receptor-associated factor 2 (TRAF2) that promotes the activation of apoptosis-signal regulating kinase 1 (ASK1) and JNK (c-Jun N-terminal kinase), [25]. IRE1 can also modulate other MAP kinases (ERK, p38) [34,35] and NF- κ B pathway through interacting with inhibitor κ B kinase (IKK) through TRAF2 [36]. CHOP upregulation may be a point of convergence for all 3 arms of UPR, as there are binding sites for ATF6, ATF4 and XBP1 in its promoter [24]. PERK and IRE1 are active throughout the duration of ER stress [21]; there is also a view that ATF6 and PERK may be activated before IRE1 α , as they promote adaptational responses. IRE1 has a dual role transmitting both survival and apoptotic signals [24]. Two novel mechanisms that can reduce the protein burden within minutes of ER stress were published in 2014. "Rapid ER stress-induced export" (RESET) removes misfolded GPI-anchored proteins through the secretory pathway for lysosomal degradation [37,38]. The second mechanism is selective release of mRNAs for ER-targeted proteins from the ER membrane upon the ER stress, [39]. The molecular mechanisms of UPR triggering and propagation are depicted in Figure 2.

ER and mitochondria are interconnected physically and functionally by mitochondria-associated ER membranes (MAMs, top right). A sustained ER stress of more than 24 h or the induction of apoptosis results in the release of ER calcium at the MAM that triggers loss of mitochondrial membrane potential to promote apoptosis [40].

In conclusion, UPR signalling is at first aimed at cell survival and it is an adaptive response during the early phases of ER stress [21]. The goals are reduction in the ER protein folding load and increased ER folding capacity [35]. Protein folding capacity is enhanced by expansion in ER volume and by increased synthesis of ER chaperones. Depending on the duration of stress, the UPR signalling changes to repress the adaptive response and trigger apoptosis [21]. Pathophysiological conditions, like elevated levels of fatty acids and cholesterol, high or low glucose levels, inflammatory cytokines

and hypoxia can chronically activate the UPR [18]. As UPR signalling is interconnected with oxidative stress and inflammatory response pathways, its persistent signalling in prolonged stress has a role in many diseases, including metabolic and inflammatory diseases, cancer and neurodegeneration [18].

1.2.1. Impact of Oxidation on the Unfolded Protein Response

Oxidative environment in the ER favours formation of disulfide bonds. The proper formation of disulfide bonds between two cysteine residues is necessary for correct protein folding. These reactions are catalyzed by protein disulfide isomerases (PDIs) that are ubiquitously expressed in the ER [41,42]. The members of PDI family also cleave disulphide bonds of misfolded proteins and catalyze isomerization of incorrect disulfides [41], while aberrant proteins are cleared through ER-associated degradation (ERAD) [43]. Most of about 20 members of the PDI family [44–46] contain ER retention signal (KDEL) and at least one thioredoxin (Trx)—like catalytic domain. PDI family include PDIA3/ERp57, see Figure 2), ERp44 [47], ERdj5, etc. ERdj5 is required for ER export of terminally misfolded proteins in the ERAD; it reduces the disulphide bonds in ERAD substrates [48,49].

Oxidoreductin proteins 1 oxidize PDIs and regenerate themselves by transferring electrons to oxygen to produce H_2O_2 [41,42]. Peroxiredoxin IV was reported to metabolize H_2O_2 into H_2O [50]. There are two members of oxidoreductin 1 in mammals, Ero1 α and Ero1 β , which differ in transcriptional and post-translational regulation, tissue distribution and catalytic turnover [51]. Besides from assisting in disulfide bond generation, Ero1 α also regulates calcium release from the ER and secretion of disulfide-linked oligomers through its reversible association with the chaperone ERp44 [51].

Redox status in ER is maintained also by glutathione concentrations. Like elsewhere in the cell, the balance between the reduced and oxidized glutathiones (GSH and GSSG, respectively) is important. The ratio of GSH to GSSG in the ER is 1:1 to 1:3, compared to the 30:1 to 100:1 in the cytosol [52]. The reduction of improperly paired disulfide bonds by PDIs is accompanied by glutathione oxidation (Figure 2). Disruption of redox balance in the ER due to environmental or intrinsic factors can result in loss of ER homeostasis and triggers the UPR due to accumulation of misfolded proteins. Increased incorrect disulfide bond formation during protein folding and their reduction in misfolded proteins result in redox imbalance and oxidative stress. Therefore, there is a close relationship between the oxidative and ER stresses and control of UPR is also through the regulation of ER redox capacity [53].

The role of transitional metal ions in the development of human disease has been recently reviewed by Valko *et al.* [54]. Copper, iron, and zinc ions, have an important role in various biological processes. Dysregulation of their homeostasis, *i.e.*, oxidative stress, can lead to an increased, uncontrolled formation of reactive oxygen species (ROS) and reactive nitrogen species (RNS) that overwhelms their elimination by antioxidant defence systems and leads to an increased frequency of damage to DNA, protein and lipid molecules. An increase, or a decrease, in the concentration of metal ions can lead to dysregulation of their homeostasis. For example, increased concentrations of redox-active iron or copper ions promote the formation of ROS, while increased ROS formation is associated with depletion of redox-inert zinc ions. Zinc is not only an essential component of proteins involved in defence mechanisms against oxidative stress but is also the most abundant metal in the brain.

1.2.2. Degradation of Oxyproteins by the Unfolded Protein Response

An important mechanism to restore ER proteostasis is the removal of misfolded proteins. Misfolded proteins are exported from the ER before degradation. There are two protein degradation pathways: autophagy and ERAD; the latter delivers the proteins to proteasome. Activation of UPR triggers both pathways [55–57]. Autophagy was reported to be the main degradation pathway in neural cells [58]; however, ERAD seems closely linked to the UPR, which has a role in protection

and progression of neurodegenerative diseases. Interestingly, impairment of ERAD resulted in decreased UPR activation and protection against the ER stress toxicity in SK-N-SH and HeLa cells [59]. The authors reported that there was a modulation of UPR upon the inhibition of ERAD; the response involved also re-localization of lysosomes. Large parts of ER can be sequestered into autophagosomes [56] and particular proteins can be removed by autophagy. The examples of the latter are the removal of ubiquitinated-protein aggregates that develop during diabetes mellitus-induced oxidative stress in pancreatic beta cells [60] and of misfolded GPI-anchored proteins that were recently shown to be removed from the ER through the secretory pathway for lysosomal degradation described in Section 1.2 [32].

ERAD targets the misfolded proteins to the cytosol for the proteasome degradation; such proteins are either in the ER lumen or are ER membrane proteins [43]. Removal of ER proteins involves substrate recognition [43,48,61–64], dislocation [62,64–69], ubiquitination [43,63] and degradation. Although many components that are necessary for ERAD were identified, the knowledge on its core components, the precise molecular mechanism of dislocation as well as the energy source still need some improvement. Even now there are hints of connections between the UPR and ERAD, e.g., the UPR activation increases the levels of ERAD genes, like EDEM1 [70].

1.2.3. Unfolded Protein Response in Neurodegenerative Disorders

UPR is a complex signalling network that may result either in alleviation of ER stress or in cell death. Although many papers have described its key role in normal neuronal function and there are more and more papers implying its role in neurodegeneration, the reports often contradict each other, as the UPR activation seems to have specific and even opposing effects on neurodegeneration. The contributing factors to such dichotomous response seem to depend on the disease stage and include several stress sensors with complex signalling at protein and nucleic acid levels as well as the cross-talk with other cellular stress responses, for review see [1,4]. The role of UPR in Alzheimer's, Parkinson's and prion diseases is described in Sections 2.2, 2.3, 3.2, 3.3, 4.2 and 4.3 respectively.

1.3. Macroautophagy

Autophagy is essential for maintaining cellular homeostasis and is divided into macroautophagy (MA), microautophagy (MI), and chaperone-mediated autophagy (CMA). Among the three types of autophagy, MA is the best understood process and is often referred to as autophagy. MA is the only known mechanism that eukaryotic cells possess to degrade protein aggregates and superfluous or damaged organelles that cannot be processed by the proteasome [71]. During MA, portions of the cytoplasm are enveloped by a double-membrane sac (*i.e.*, phagophore) that expands into a cytosolic vesicle called an autophagosome. The outer membrane of the completed autophagosome is fused in mammalian cells with lysosomal membrane forming an autolysosome that shares the contents of both and enables lysosomal acid hydrolases access to the inner autophagosome membrane and its cargo, which is digested and recycled by the cell [72]. Autophagosome formation is often monitored by analysing the level of LC3-II which is associated with autophagosome membranes and is degraded after formation of the autolysosome [73].

The uptake of cytoplasmic materials by MI is a two-step process, first by invagination of the lysosome membrane and then by pinch off of the vesicles containing the cytosolic substrates into the lysosomal lumen, where they are rapidly degraded [74]. Proteins targeted for degradation by CMA, for example α SYN or LRRK2, are identified one-by-one by the cytosolic chaperone Hsc70 that delivers them to the surface of the lysosomes [75]. The substrate proteins bind, unfold and enter the lysosome through a receptor-channel on the lysosomal membrane, enabling direct translocation of unfolded proteins across the lysosome membrane [76,77].

In contrast to the ubiquitin-26S proteasome system, MA often mediates non-selective and bulk degradation of cytoplasmic contents, including entire organelles, for example mitochondria (mitophagy) endoplasmic reticulum (reticulophagy) or ribosomes (ribophagy) [78–80]. Mitophagy

removes dysfunctional mitochondria, thus reducing mitochondria derived ROS that could generate mitochondrial DNA mutations during aging [81]. However, in some cases, MA has substrate specificity, for example in the cytoplasm-to-vacuole-targeting (CVT) pathway where autophagy has a biosynthetic role [82–84].

MA is regulated by protein kinases; mTOR inhibits MA, while AMPK and ULK1 promote MA. Downstream regulators of MA are proteins RAB1a, Beclin1 and ATG protein family that promote the initiation of MA [6]. Under normal conditions, the basal MA of brain cells is low compared to other organ systems. However MA, together with ER, significantly contributes to intracellular quality control, especially in post mitotic nerve cells, that are susceptible to accumulation of misfolded or degraded proteins over decades of human life [5,85,86].

Dysregulation of MA contributes to the development and progression of Alzheimer's, Parkinson's and prion diseases [5,6,71,87]. In neurodegenerative disorders, there is a significant increase in autophagosomes [88]. When interpreting the presence of an increased number of autophagosomes it is important to distinguish between measurements that evaluate the numbers of autophagosomes and those that measure flux through the MA pathway. Blockage of MA flux, for example due to disturbance in lysosomal function, leads to autophagosome accumulation and has to be distinguished from fully functional MA that includes fusion of autophagosome with lysosomes, autolysosome formation, cargo degradation and recycling [5]. Most studies support the role of MA in preventing or at least attenuating the progression of neurodegenerative disorders. For example, impaired autophagic flux enables accumulation of toxic A β [89]. Clearance of aggregate prone forms of α SYN is mediated by MA [90]; pharmacological activation of MA by lithium or trehalose accelerates clearance of aggregate prone A30P and A53T mutants of α SYN [91]. In contrast to PD and AD, where an enhanced MA seems to protect or at least slow down the progression of neurodegenerative disorders, MA seems to have opposing effects in prion diseases. Fibroblasts from *Atg5*^{-/-} autophagy deficient mice were significantly less infectable with murine prions than the wild-type fibroblasts and re-introduction of *Atg5* via lentiviral transduction improved the infection rate in *Atg5*^{-/-} mice [5]. In a prion infected cell model, MA reduced the cellular content of the normal form of prion protein (PrP^C) and the infectious prion protein isoform (PrP^{Sc}), MA inhibitors increased cellular PrP^{Sc}, and lithium, trehalose and rapamycin reduced the level of cellular PrP^{Sc} presumably by activating MA [5,92,93].

2. Alzheimer's Disease

Alzheimer's disease (AD) is the most common cause of dementia with significant pathological and clinical diversity among clinically diagnosed AD patients. Most elderly patients have several pathological changes in the brain, as observed in autopsy studies that in addition to the senile plaques also include Lewy bodies, white matter changes, TDP-43 inclusions or angiopathy [94–101]. Biomarker tools for AD are being developed that have enabled detection of AD related pathological brain changes years before emergence of the first clinical symptoms. For example, cerebrospinal levels of tau are positively correlated to neurodegeneration and neurofibrillary tangle pathology, however, cerebrospinal fluid (CSF) levels of the aggregation prone 42 amino acid A β (A β 42) are negatively correlated to plaque pathology. Amyloid plaques and tau can be detected with positron emission tomography [102,103]; the appearance of the A β 42 marker precedes tau by 5–10 years [104,105]. There is a need for further development of diagnostic markers for AD. A recent Cochrane review concluded that measuring CSF amyloid beta (A β 40 or A β 42), as a single test, lacks the accuracy to identify patients with mild cognitive impairment who would develop Alzheimer's disease dementia or other forms of dementia [106]. AD is associated with systemic manifestations that are present in early as well as in the late stages of this neurodegenerative disorder [107]. Some systemic disorders are associated with an increased risk of developing AD like for example type 2 diabetes [108–110] and inflammation [111]. The role of oxidative stress biochemical pathways in the overlapping of some of the AD and type 2 diabetes clinical signs has been recently reviewed by Rosales-Corral *et al.* [112].

2.1. Amyloid β ($A\beta$) and Tau

The key pathological change in Alzheimer's disease is the modification of soluble amyloid β -peptides ($A\beta$ s), for example $A\beta_{42}$, that accumulate in the intracellular and extracellular space, into toxic, soluble $A\beta$ oligomers leading to cell death [113]. $A\beta_{42}$ monomer *per se* is not toxic, but has a neuroprotective role mediated by activation of the phosphatidylinositol-3-kinase pathway, and the stimulation of receptors of the insulin superfamily [114]. $A\beta$ s are derived by proteolytic cleavage of the type 1 membrane glycoprotein, amyloid precursor protein (APP). The APP is processed by two pathways: (a) the amyloidogenic pathway, where the APP is sequentially cleaved by β - and γ -secretase; and (b) the non-amyloidogenic pathway where the APP is cleaved by α - and then γ -secretase. The non-amyloidogenic pathway produces the soluble sAPP α that have neuroprotective and memory-enhancing effects [115,116]. In physiological conditions, $A\beta$ could present a negative feedback loop in the regulation of synaptic plasticity and neuronal survival since low concentrations of $A\beta$ are present in the central nervous system of non-demented individuals [117].

Amyloid processing of APP is concentrated in lipid rafts, and non-amyloid processing is located mainly in the non-raft regions of the cell membrane [118–122]. In physiological conditions, the majority of APP is processed by the non-amyloidogenic pathway, therefore increased $A\beta$ production correlates with decreased sAPP α levels [123–126]. Both APP processing pathways are modulated by various factors; some metalloproteases have α secretase activity and could contribute to the production of soluble sAPP α [127]. The amyloidogenic pathway activity, and by extension $A\beta$ production, is attenuated by cholesterol lowering drugs, metal chelators, steroid hormones or non-steroidal anti-inflammatory drugs [128]. Decreased cellular cholesterol levels disrupt the lipid raft's structure and function, leading to a concomitant decrease in $A\beta$ and an increase in sAPP α formation [129,130].

The products of β , and γ secretase cleavage are peptides with 39 to 42 amino acids; $A\beta_{40}$ is the most common and $A\beta_{42}$ is the most susceptible form to conformational changes leading to amyloid fibrillogenesis. Lower levels of $A\beta_{42}$ are present in healthy individuals and higher levels in patients with AD (e.g., in familial AD). An increased $A\beta_{42}$ to $A\beta_{40}$ ratio has been observed in AD associated mutations in the APP gene [131] and in the PSEN1 gene for presenilin1, the catalytic subunit of the γ -secretase complex [132–135]. Modified $A\beta_{42}$ peptides enter the cells via endocytosis and lead to lysosomal fusion dysfunction [136]. The overall effect is an enhanced transport of vesicles by the exosomal pathway with increased shedding of modified $A\beta$ peptides into the extracellular space and a reduced $A\beta$ digestion rate by macroautophagy [136]. In AD, $A\beta_{42}$ oligomers promote neuronal death by:

- (a) Reducing Ca^{2+} /Calmodulin-dependent protein kinase II synaptic distribution and thus decreasing the density of AMPA synaptic receptors [137];
- (b) Uncoupling metabotropic glutamate receptors' (mGluR5) dependent activation of PKC [138];
- (c) Binding with PrP^c to the mGluR5 and stimulating mGluR5 clustering at synapses; mGluR5 seems to act as a scaffold for the $A\beta$ oligomer—PrP^c signalling complexes [139–147];
- (d) Binding with PrP^c to *N*-methyl-D-aspartate receptors (NMDAR) and
- (e) Reducing glutamate reuptake thus promoting an increased NMDAR and mGluR5 mediated entry of Ca^{2+} [148].

PrP^c binding to NMDAR enhances its desensitisation and $A\beta_{42}$ binding attenuates its desensitisation, thus increasing the probability of intracellular Ca^{2+} overload [149,150]. The overall effect of $A\beta_{42}$ oligomers on the nerve cells is loss of synapses and ultimately cell death due to intracellular Ca^{2+} overload, promoted by increased Ca^{2+} release from intracellular stores and persistent Ca^{2+} entry through NMDARs with attenuated desensitisation.

The modification of $A\beta$ into toxic misfolded $A\beta$ monomers, oligomers and intermediate products [151,152] is accelerated by $A\beta$ oxidation [153]. The oxidation of $A\beta_{42}$ at the methionine residue 35, $A\beta_{42}$ -MET35-OX, promoted by H_2O_2 or copper ions, seems to accelerate the production of

toxic A β 42 products. Also, A β 42-MET35-OX leads to further protein oxidation and lipid peroxidation and increased oxidative stress [153]. This A β 42 associated oxidative stress depends on the formation of a sulphur-centred, transient free radical at the methionine residue [153]. In a neuroblastoma cell model, ROS (*i.e.*, H₂O₂) catalysed by copper ions promote stabilization of A β oligomers by dityrosine cross-links in A β 42, thus promoting internatilsation of toxic A β into lysosomes [154]. *In vitro*, the dityrosine crosslinked A β oligomers had the capability to assemble further to form amyloid fibrils. The authors also demonstrated the presence of dityrosine cross-links within plaques in brain samples of patients with AD [154].

Tau is a microtubule-associated protein, located mainly in axons, that stabilises neuronal microtubules during intracellular transport [155]. Tau is necessary for the outgrowth of neuritis-axons or dendrites [156]. In AD, tau is phosphorylated at Ser262 or at Ser214 leading to its detachment from microtubules [157]. AD associated tau is hyperphosphorylated at many sites [158–160], often at Ser-Pro or Thr-Pro motifs, and abnormal tau phosphorylation occurs before tau aggregation [161]. The main consequences of tau hyperphosphorylation are the disappearance of microtubules, the breakdown of intracellular traffic and the “dying back” of axons. During AD, tau is redistributed from an axonal to a somato-dendritic pattern which could be the result of an increased tau synthesis as a response to increased tau hyperphosphorylation [161]. Although tau is a very soluble protein it can still form tau aggregates that combine into neurofibrillary tangles (NFT), composed of twisted filaments of hyperphosphorylated tau protein [162]. Oxidation, glycation and proteolytic fragments of tau promote tau aggregation [163–166]. According to post-mortem reports, NFTs are highly associated with neuronal loss and the severity of cognitive decline [167,168], while A β plaques appear at the presymptomatic stage and their levels stabilize relatively early in the disease process [169]. A recent study on five patients with AD and five age-matched healthy controls demonstrated longitudinal changes in tau pathology in patients with AD that was consistent with post-mortem observation of tau pathology in the different stages of AD and correlated with the rate of cognitive decline in patients with AD [170].

2.2. Unfolded Protein Response in Alzheimer’s Disease

Despite being one of the most common neurodegenerative disorders, few studies evaluated the impact of the UPR on AD *in vivo*; most of the studies are correlative associations or cell culture experiments [1]. Several studies imply that A β interferes with ER functioning. Analyses of AD post-mortem brain revealed altered levels of ER stress markers, like GRP78/BiP, IRE1 α , PERK, eIF2 α phosphorylation and PDI [4,171–174]. However, there may be contradictory results when following a single marker. For example, there are reports of no change [175], an increase [176,177] or a decrease [178] in the expression of GRP78/BiP in AD brains. It has been suggested to follow the changes of several factors, for example GRP78/BiP and PDI to assess the UPR activation [4]. A β interferes with ER functioning, leading to ER stress in the early stages of AD [177,179,180]. For example, exogenous A β induces ER stress in primary neuronal cultures and activates mitochondrial and ER mediated cell death pathways [181–183]. In PC12 cells and knock-in mice expressing mutant PS1 it was shown that the up-regulation of protein levels of CHOP/GADD153 was followed by the down-regulation of the anti-apoptotic protein Bcl-2. Concomitantly, the authors observed that mutant PS1 sensitizes cells to the deleterious effects of ER stress culminating in cell death, this effect being attenuated by anti-sense mediated suppression of CHOP/GADD153 production [184]. In the hippocampus of the triple transgenic mouse model of AD (3xTg-AD) increased levels of CHOP/GADD153 precede the increase in BACE and A β levels [185]. *Post mortem* immunohistochemical studies of brain tissue samples reveal that markers specific for UPR activation are increased in AD brain tissue compared to non-demented control brain tissue [17,186,187]. Metabolic stress induces phosphorylation of endogenous tau via activation of the UPR. In a cell model, this increase in phosphorylated tau was reversed upon restoration of metabolic homeostasis and was concomitant with the reversal of the levels of UPR markers PERK, IRE1 α and Grp78/BiP.

The increase in stress induced levels of phosphorylated tau was abolished by the UPR inhibitor TUDCA or by GSK2606414, an inhibitor of the PERK signalling pathway [188]. Tau increased the levels of ubiquitinated proteins in the brain thus leading to activation of the UPR; depletion of soluble tau levels reversed UPR activation [189]. *In vitro* and *in vivo* models of tau over-expression and AD brains imply that soluble tau impairs ERAD and the result of this impairment is the activation of UPR in the ER [189].

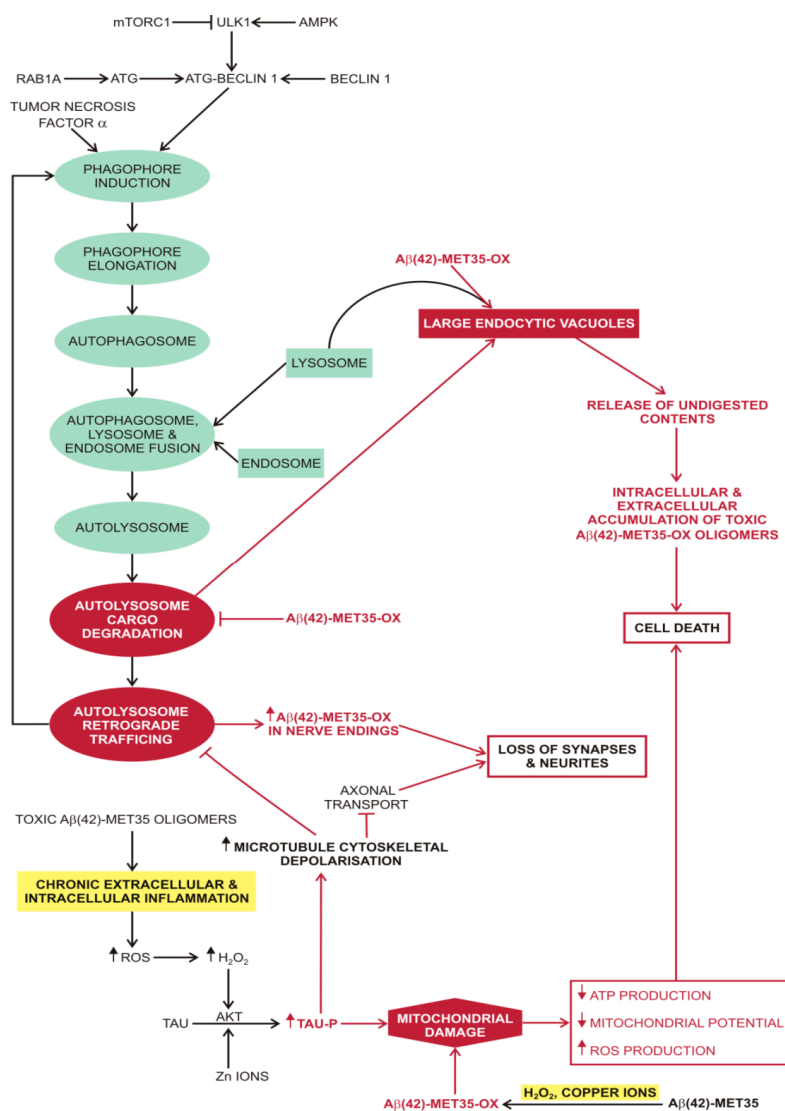


Figure 3. Macroautophagy and oxidated Aβ. Oxidised Aβ peptides attenuate macroautophagy and mitochondrial function. This toxic effect is further exacerbated by the formation of soluble Aβ oligomers that stimulate chronic inflammation with increased production of ROS. A positive feedback loop develops between chronic inflammation and the production of oxidised Aβ peptides, leading to loss of synapses and neurites and ultimately cell death. Abbreviations: ⊥ (attenuation); ↓ (decreased); ↑ (increased); Aβ42-MET35 (soluble amyloid β-peptide with a single methionine residue at position 35); Aβ42-MET35-OX (soluble amyloid β-peptide with a single oxidised methionine residue at position 35); AKT (protein kinase B); AMPK (5' AMP-activated protein kinase); ATG (autophagy-related protein); ATP (adenosine triphosphate); Copper ions (copper ions in different oxidative states from +1 to +4); mTORC1 (mammalian target of rapamycin complex 1); RAB1A (Ras-related protein Rab-1A); ROS (reactive oxygen species); TAU (tau protein); TAU-P (phosphorylated tau protein); TNFα (tumour necrosis factor alfa/cachexin); ULK1 (serine/threonine-protein kinase).

2.3. Macroautophagy in Alzheimer's disease

Compared to A β 42, oxidised A β 42 is more resistant to degradation by autophagy and endosome-lysosome fusion (Figure 3) which further contributes its accumulation and toxic effects due to release of undigested contents into the cytosol [190–193]. The toxicity of amyloid β -peptide derivatives decreases with protofibril and fibril formation and terminates in the formation of stable and inert amyloid plaques [151,152]. Increased ROS formation, inside or outside the cell, favours the transition of A β monomers into toxic forms and also stimulates the breakdown of microtubule cytoskeleton by promoting zinc or H₂O₂ induced tau phosphorylation [152,194]. Impaired mitochondrial transport, due to the breakdown of microtubule cytoskeleton, impairs Ca²⁺ homeostasis in synapses and contributes to the loss of synaptic connections in the brain [195]. A β 42 toxic forms and tau contribute to mitochondrial dysfunction; modified A β 42 attenuates complex IV (*i.e.*, cytochrome c oxidase) activity and tau attenuates complex I (*i.e.*, NADH-CoQ reductase) activity [195]. In summary, hyperphosphorylated tau, together with toxic forms of A β 42 lead to an increased production of ROS, a reduced mitochondrial concentration at the synapses, progressive mitochondrial damage with subsequent reduction in ATP production and reduced intracellular Ca²⁺ homeostasis, increased apoptosis signalling, and finally to apoptosis or cell necrosis [195,196]. Not only do toxic β -Amyloid fragments target mitochondria and cause mitochondrial dysfunction [197], but there is some evidence that mitochondrial cytochrome oxidase is defective in AD [198]. AD patients have a significantly decreased cytochrome c oxidase activity in the temporal cortex and hippocampus. These brain regions are involved in processing sensory input, memory and spatial memory [198].

3. Parkinson's Disease

Parkinson's disease (PD) is the second most common degenerative disorder of the central nervous system, affecting about 1% of people over the age of 60, with diffuse motor and non-motor clinical signs [199]. Animal studies on knock-out mice have linked α SYN with spatial learning and working memory [200]. The primary symptoms of PD are caused by death of dopamine-secreting cells in the *pars compacta* region of the *substantia nigra*. The characteristic pathological changes in the brain are cytosolic inclusions that displace other cell components, *i.e.*, the Lewy bodies (LBs); their number increases with cognitive decline [201]. α SYN is a key component of LBs, other associated proteins are ubiquitin, neurofilament protein, α B crystallin and tau proteins [202–206]. Point mutations in the α SYN gene lead to early onset familial forms of PD with typical PD pathogenesis [207–210].

3.1. α -Synuclein (α SYN)

α SYN is predominantly localised to presynaptic terminals of the central nervous system; it is in a membrane bound and in a predominantly cytosolic form, and modulates vesicular release of dopamine [211–213] by attenuating dopamine release under circumstances of repeated firing [214]. α SYN is also localised to the nucleus of mammalian brain neurons [215] and to the inner membrane of neural mitochondria, where it inhibits the complex I activity of the respiratory chain [216]. In addition to modulation of synaptic transmission, α SYN also binds with cytoskeleton associated proteins, for example with tubulin and microtubule associated proteins like tau [217,218]. Therefore, α SYN also modulates the functioning of the neuronal Golgi and vesicle trafficking [219].

In vivo, α SYN can be present as a soluble unfolded protein that aggregates into progressively less soluble oligomers, protofibrils and insoluble amyloid fibril form and ultimately LBs [220]. α SYN overexpression is associated with a disruption of the microtubule network [217,221–226]. As a general rule, the interaction of α SYN with cytoskeleton associated proteins is stronger for α SYN multimers than for the monomers. For example, in a human neuronal cell line model, a mixture of oligomers and protofibrils of wild type α SYN multimers reduced tau promoted microtubule assembly. In contrast

microtubule movement was significantly reduced by α SYN oligomers, but not by fibrils, nor by the mixture of oligomers and protofibrils of the wild type α SYN multimers [8].

Long term imaging *in vivo* demonstrated that the inclusion of preformed α SYN fibrils can seed the progressive conversion of endogenous α SYN into neuronal inclusions that resemble the human LBs and lead to selective neuronal degeneration [227]. This finding supports the suggestion that PD is a neurodegenerative disorder that involves spreading aggregation of specific proteins through the brain by a prion-like mechanism [228–230]. Therefore, just an increased level of α SYN is sufficient to promote aggregation and development of PD with LBs [231,232].

3.2. Unfolded Protein Response in Parkinson's Disease

PD is a protein misfolding disorder and chronic ER stress contributes to degeneration of dopaminergic neurons of the *substantia nigra* [1]. ER stress was also identified in neuronal cultures generated from induced pluripotent stem cells from PD patients [233]. Overexpression of ER chaperone GRP78/BiP was neuroprotective in mice [234], in contrast to the removal of ATF6, which enhanced the susceptibility to PD-inducing neurotoxins [235,236]. Salubrinal, an inducer of eIF2 α phosphorylation [237] was neuroprotective in α SYN transgenic mice [238]. Combining cellular PD models with biochemical reconstitution assays revealed that α SYN inhibited ATF6 signalling directly through physical interactions and indirectly through restricted incorporation of ATF6 into COPII vesicles. Impaired ATF6 signalling was associated with decreased ERAD function and increased pro-apoptotic signalling [239]. There are very few data on UPR activation from *post-mortem* studies on PD patients. However, the immunohistochemical localisation of phosphorylated PERK and eIF2 α was characterised in *post-mortem* samples of the *substantia nigra* (SN). Immunoreactivity for phosphorylated PERK and eIF2 α was observed in PD samples in neuromelanin containing neurons of the SN, while these markers were absent in samples from control subjects [240]. Intracellular accumulation of α SYN is also present in the sporadic neurodegenerative disorder multiple system atrophy (MSA). Double immunohistochemistry using fluorescent antibodies revealed increased phosphorylation of PERK, eIF2 α , and IRE1 activity that were closely associated with glial cytoplasmic inclusions containing α SYN [241].

3.3. Macroautophagy in Parkinson's Disease

The soluble, unfolded α SYN monomer is degraded by CMA [220]. Attenuation of this autophagy pathway could precipitate the development of PD. The most common cause of familial PD are mutations in leucine-rich repeat kinase 2 (LRRK2). LRRK2 is also degraded by the CMA pathway. The most common mutant form of LRRK2, G2019S, is poorly degraded by this pathway and also interferes with organization of the CMA translocation complex. This interference leads to defective CMA degradation of α SYN, and formation of α SYN oligomers at the lysosomal membrane that further block CMA and precipitate the formation of LBs in PD patients with mutant LRRK2 [75]. Attenuation of CMA leads to a compensatory increase in autophagy, an accumulation of autophagosomes, and ultimately to cell death due to the release of undigested contents into the cytosol [242]. α SYN oligomers, protofibrils and amyloid fibrils cannot be digested by autophagy. Posttranslational modifications of α SYN, for example by phosphorylation, ubiquitination, nitration or oxidation, also reduce autophagosome degradation and promote α SYN oligomerisation. The toxic effect of these posttranslational modifications can be compounded by the propensity of α SYN to bind to various molecules in neuronal cells [243]. For example, iron ions, dopamine or H₂O₂ oxidise methionine residues in the α SYN monomer, that is the predominant form of oxidised α SYN, and also promote the formation of stable oligomers with a resistance to fibrillization that is proportional to the number of oxidised methionine residues [244]. The oxidised α SYN monomer can interact with lipids, as well as with proteins, changing their redox state and function thus sharing similarities with the A β 42-MET35-OX [245]. For example, the oxidised α SYN monomer disrupts autophagy (Figure 4) at several stages (inhibits RAB1A activity, attenuates chaperone-mediated autophagy, autophagosome

cargo degradation and endolysosome content digestion) and also disrupts mitochondrial function by damage to complex I of the electron transport chain [71,246,247] thus promoting apoptosis or cell necrosis.

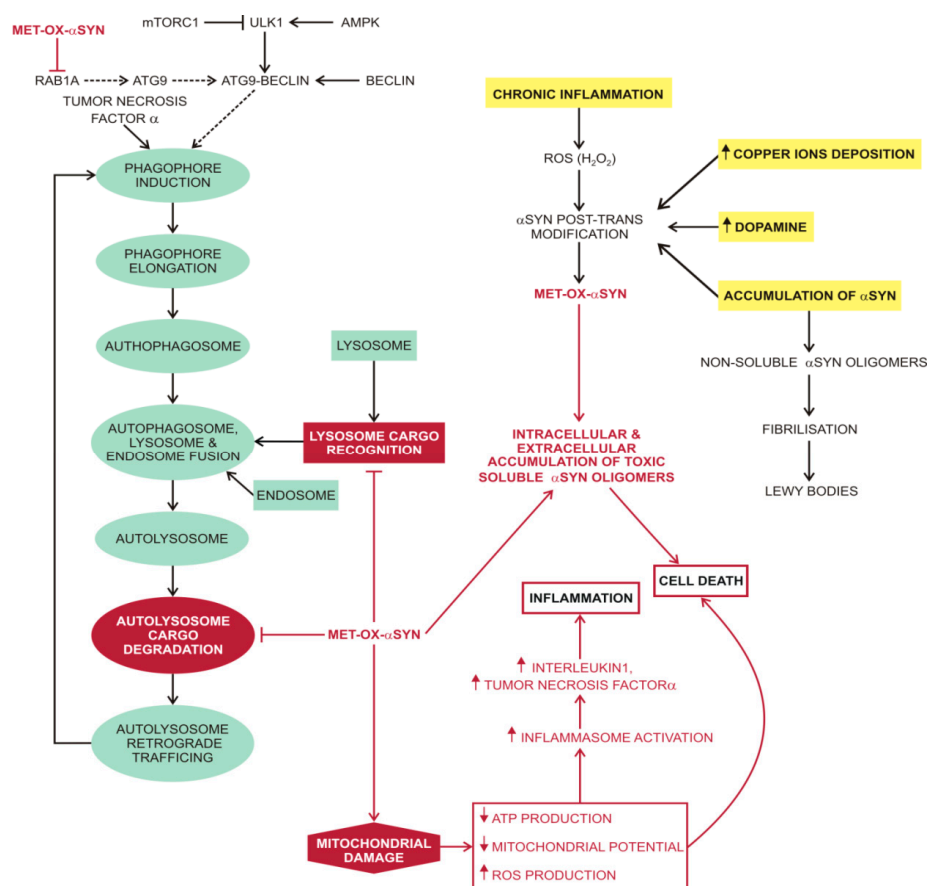


Figure 4. Macroautophagy and oxidised α SYN. Several processes, e.g., chronic inflammation, copper ion deposition, accumulation of dopamine or even just intracellular accumulation of α SYN promote oxidation of α SYN. Oxidised α SYN attenuates macroautophagy and mitochondrial function. This toxic effect is further exacerbated by the formation of soluble and autophagy resistant α SYN oligomers that stimulate chronic inflammation with increased production of ROS. A positive feedback loop develops between chronic inflammation and the production of soluble α SYN oligomers, leading to cell death. Abbreviations: \perp (attenuation); \downarrow (decreased); \uparrow (increased); α SYN (alpha-synuclein); ATG (autophagy-related protein); ATP (adenosine triphosphate production); Copper ions (copper ions in different oxidative states); MET-OX- α SYN (alpha-synuclein oxidised on methionine residues); mTORC1 (mammalian target of rapamycin complex 1); POST-TRANS (post-translational) RAB1A (Ras-related protein Rab-1A); ROS (reactive oxygen species); TNF α (tumour necrosis factor alfa/cachexin); ULK1 (serine/threonine-protein kinase).

Mitochondrial dysfunction, associated with oxidative stress, can trigger α SYN accumulation and aggregation [248]. Recessive forms of familial PD are associated with mutations in proteins pink1 and parkin, that regulate mitophagy, mitochondrial function and biogenesis [249–254]. *PINK1* gene encodes a serine/threonine kinase with a mitochondrial targeting sequence and *PARKIN* gene encodes an E3 ubiquitin ligase which forms part of the ubiquitin-proteasome system [255]. It is assumed that both function in the same pathway whereas pink1 is upstream of parkin [255]. Loss of mitochondrial membrane potential due to oxidative stress, mitochondrial DNA mutations or herbicides, e.g., paraquat [256,257], leads to translocation of parkin from cytosol to depolarized mitochondria where it ubiquitinates many outer mitochondrial membrane proteins (e.g., mitofusins

and Miros), thus promoting colocalization of mitochondria with autophagy marker LC3 and initiating mitophagy [256]. Binding of pink1 to the translocase of the outer mitochondrial membrane precedes parkin binding and both proteins seem to interact with each other [258,259]. During prolonged mitochondrial depolarization parkin also interacts with autophagy/beclin-1 regulator 1 protein (AMBRA1), initiating AMBRA1 promoted autophagy of depolarised mitochondria by activation of class III phosphatidylinositol 3-kinase complex [260,261]. Mutated pink1 and parkin proteins can lead to accumulation of oxidized lipids, proteins and DNA from damaged mitochondria thus increasing the risk of cell death [262]. However, excessive mitophagy, not balanced with sufficient mitochondrial biogenesis, may over-stress the remaining mitochondria, inducing mitochondrial damage and triggering cell death [263–266].

4. Prion Diseases

Prion diseases (PrDs) are fatal, infectious neurodegenerative disorders that affect humans and other mammals. In humans, prion diseases are acquired, familial, or sporadic. Humans can be infected by contaminated food products or iatrogenic blood transfusion [267–280]. 10%–15% of patients with PrD have a genetic form of the disease, with more than forty different mutations of the human PrP gene, associated with the three heritable forms of prion disease [281]. Creutzfeldt-Jakob disease (CJD) is the most common form of PrD in humans and is characterised by a spongiform degeneration of the brain accompanied by the accumulation of a misfolded and protease-resistant form of the normal form of prion protein (PrP^c), the infectious prion protein isoform (PrP^{Sc}) [282]. PrP^c is essential for development of PrDs; replication and release of PrP^{Sc} by implants of prion-infected brain tissue failed to elicit PrD pathology in host PrP knockout brains [283] and transgenic mice with PrP^c neuronal depletion during prion infection showed continued extra-neuronal PrP^{Sc} accumulation but without neuronal loss or clinical disease [284]. PrP^c-dependent neurotoxicity induced by PrP^{Sc} occurs independently of prion replication [146]. Binding of A β to membrane-associated PrP^c triggers signalling via fyn, and causes hyperphosphorylation of tau, accompanied by synaptic and cognitive impairments [285]. PrDs are caused by the conversion of the host PrP^c to the misfolded form of PrP^{Sc} with a β -sheet-rich conformation; the PrP^{Sc} has the ability to convert more PrP^c into PrP^{Sc}, by propagating its misfolding, resulting in the accumulation of misfolded and aggregated PrP^{Sc} in the brain [282,286]. Prion conversion occurs after PrP maturation [287,288] either at the plasma membrane [289], and/or following endocytosis [287–294]. Whether the conversion of PrP^c to PrP^{Sc} requires the presence of a third essential factor, for example the putative protein X, has yet to be proved [295].

Protein aggregates can be seen in other neurodegenerative disorders, for example A β and microtubule-associated protein tau in Alzheimer's disease or α SYN in Parkinson's disease. Self-propagation of protein aggregates has also been demonstrated in an *in vivo* animal model of PD; the inclusion of preformed α SYN fibrils seeded progressive conversion of endogenous α SYN into neuronal inclusions that resembled the human LBs [227]. Also PrP^c and A β co-regulate some key cognitive processes, e.g., learning and memory, at the level of synaptic plasticity and neuronal survival [117]. For example, PrP^c accentuates NMDA receptor desensitization on nerve cells while A β 42 attenuates receptor desensitization; PrP^c contributes to A β 42 oligomers mediated nerve cell toxicity [138,139,141–147].

4.1. Normal Form of Prion Protein (PrP^c)

PrP^c is an extracellular protein enriched in α -helix domains, expressed in neurons of the brain and spinal cord, and secured *via* a glycosylphosphatidylinositol (GPI) anchor to the outer surface of the plasma membrane in cholesterol and sphingolipid-rich microdomains [296–298]. GPI-anchored PrP^c is not a transmembrane protein and cannot transduce signals into the cytosol, but can form signalling complexes with many molecules, for example with stress inducible protein 1 [299,300], neural cell adhesion molecule [301,302] and copper ions [303,304]. Expression levels of PrP^c correlate

with Cu/Zn superoxide dismutase, glutathione reductase and cytochrome c oxidase activities, copper-concentration and severity of hypoxia suggesting that PrP^c has a protective role against reactive oxygen species (ROS), for review see [305]. Failure of PrP^c to buffer increased intracellular copper ion concentrations leads to mitochondrial dysfunction, due to a reduced cytochrome c oxidase activity, and to activation of mitochondria mediated apoptosis [306]. It has been suggested that copper ion imbalance is an early change in prion disease [307]. PrP^c signalling complexes activate the cAMP-dependent protein kinase A and ERK1/2 pathways, thus influencing neural survival, neuritogenesis, and memory formation [308,309].

Lateral movement to detergent-soluble plasma membrane domains enables PrP^c internalisation via endosomes and contact with the autophagy degradation machinery [310]. In physiological conditions, most of the internalised PrP^c is recycled back to the plasma membrane [311]. Additional sources of cytosolic PrP^c are due to (a) retro-translocation from the ER [312,313]; (b) avoidance of translocation into the ER due to inefficiencies of the signal sequence [314–316]; or (c) ER pre-emptive quality control preventing translocation of newly formed PrP^c molecules during ER stress [317]. Cytosolic PrP^c is normally present in low concentrations due to rapid degradation; inefficient degradation leads to pathologic cytosol accumulation and formation of PrD promoting aggregates [281]. Cytosolic PrP^c protects human primary neurons from Bax-mediated apoptosis [318–320]. Co-expressed with PrP^c, but with a completely different amino acid sequence and unknown function, is the alternative prion protein form that localizes to mitochondria and is up-regulated by ER stress [321].

Although the physiological role of mammalian prion protein (PrP^c) is not fully understood, there is some evidence suggesting that it could play an important role as an antioxidant, an endogenous scavenger, protecting other structural and signalling proteins, since it has a high number of methionine residues [322–324]. Oxidation of these residues, usually during copper redox cycling, transforms the hydrophobic thioether side chain of methionine into a hydrophilic sulfoxide and can also affect the structural integrity of proteins [325]. PrP^c could also play an active role since methionine sulfoxidation is involved in cell signalling [326]. In healthy tissue the posttranslational modification of methionine is reversed by cellular methionine sulfoxide reductases [327]. The postulated age related degradation of this reversible oxidation could lead to progressive accumulation of oxidised methionine residues on the PrP^c and contribute to protein misfolding by initiating first the transition to a monomeric molten globule form with a conserved helical content, second promoting extended β -strand structures that lack a cooperative field and finally the appearance of the infective, self-propagating, autocatalytic, misfolded isoform PrP^{Sc} [328,329]. The transition of PrP^c N-terminal region from a random coil to a β -sheet structure, predominant over the α -helices content, transforms the soluble and protease-sensitive PrP^c into the oxidised, insoluble and relatively more protease-resistant PrP^{Sc} [330,331].

PrP^{Sc} monomers, small oligomers and oligomers induce nerve cell death after internalization and accumulation in the endolysosomal compartment where they cause lysosomal damage with subsequent proteolytic enzyme leakage and activation of caspase-dependent apoptosis [332,333]. Autophagy efficiency is also attenuated (Figure 5), due to PrP^{Sc} protease-resistance; aggregation of misfolded PrP^{Sc} also leads to mitochondrial failure [334–336]. The prion fibrils seem to be a stable and inert form of the prion protein [337]. In contrast to Parkinson's and Alzheimer's disease, inflammation is less pronounced in prion disease, suggesting that apoptosis predominates over cell necrosis [338]. Assuming that the primary role of PrP^c is to act as a global cell antioxidant, regulating the oxidative state of structural and signalling proteins, the conversion of the soluble PrP^c proteins to less soluble and aggregation prone oxidised PrP^{Sc} proteins could lead to a major depletion of PrP^c molecules and a catastrophic disruption in the cell's global oxidative-redox balance, thus leading to apoptosis.

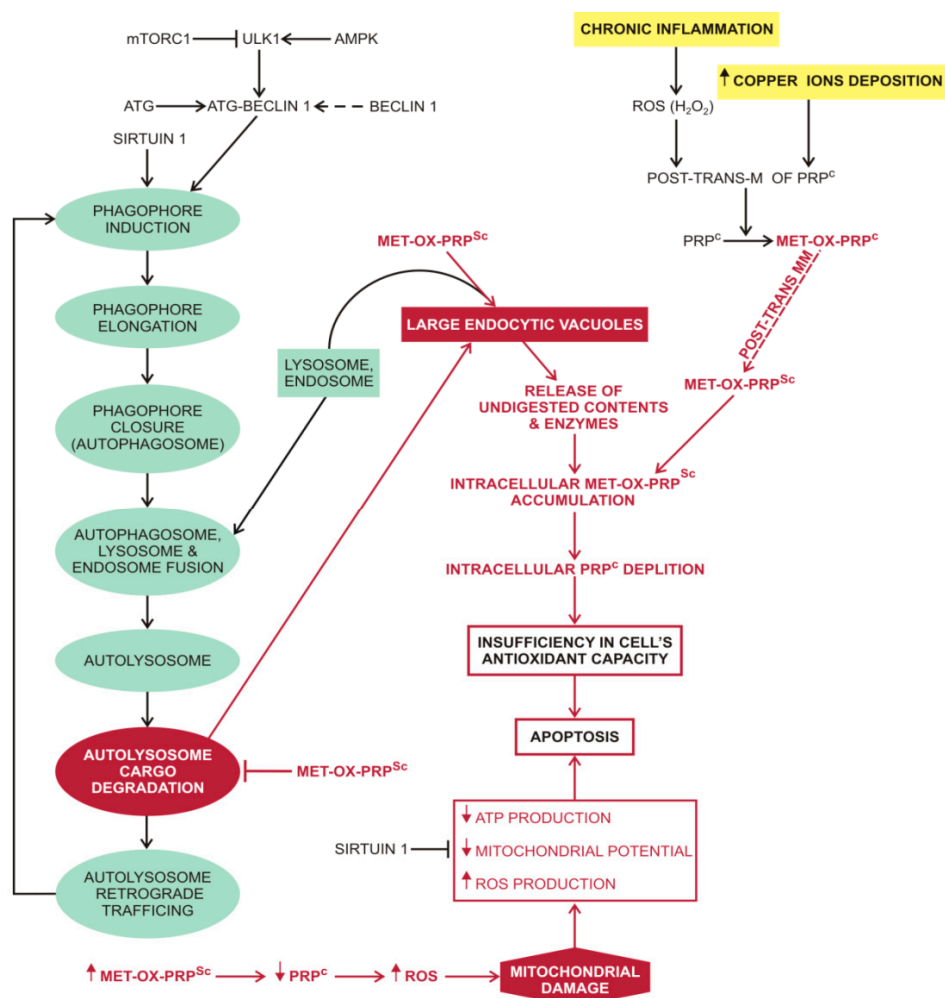


Figure 5. Macroautophagy of oxidated PrP^{Sc}. The predisposing factors for the transformation of the native prion protein (PrP^c) into the infectious, self-propagating prion protein form (PrP^{Sc}) are chronic brain inflammation and copper ion deposition. They promote many post translational modifications of PrP^c, including oxidation of its numerous methionine residues, to the prion protein in molten globule form (met-ox-PrP^c). Further post translational modifications of met-ox-PrP^c can also include a transformation into an oxidised and self-propagating infectious isoform of prion protein (met-ox-PrP^{Sc}). The met-ox-PrP^{Sc} is resistant to autophagy; attenuates autolysosome cargo degradation and also promotes the formation of large endocytic vacuoles that tend to release their undigested contents, including enzymes, into the cytosol. An intracellular increase in met-ox-PrP^{Sc}, due to its resistance to removal by autophagy and propensity for self-propagation, leads to an intracellular reduction of PrP^c. The intracellular reduction of PrP^c changes the cell's global oxidative-redox balance which is reflected in mitochondrial damage, a contributing factor to the met-ox-PrP^{Sc} induced apoptosis. Although chronic brain inflammation seems to be important for initiating the process of PrP^{Sc} production, it is not necessary to sustain it, since the PrP^{Sc} only needs the PrP^c molecules for its propagation. Abbreviations: ⊥ (attenuation); ↓ (decreased); ↑ (increased); AMPK (5' AMP-activated protein kinase); ATG (autophagy-related protein); ATP (adenosine triphosphate); Copper ions (copper ions in different oxidative states from +1 to +4); MET-OX-PRP^c (oxidised prion protein in molten globule form); MET-OX-PRP^{Sc} (oxidised and self-propagating prion protein); mTORC1 (mammalian target of rapamycin complex 1); POST-TRANS-M (post-translational modification); POST-TRANS-MM (post-translational modifications); PrP^c (normal form of prion protein); PrP^{Sc} (infectious isoform of prion protein); ROS (reactive oxygen species); SIRT1 (NAD-dependent deacetylase sirtuin-1); ULK1 (serine/threonine-protein kinase).

4.2. Unfolded Protein Response in Prion Diseases

ER stress has been described in models of infectious forms of PrDs [339,340]. However its contribution to pathogenesis is not clear, as disease progression does not seem to be affected by deficiency of *Xbp1* or caspase 12 [341,342]. When interpreting the role of caspase-12 in PrDs one should consider that caspase-12 is also involved in regulating inflammatory cytokines in mice [343] and that in the great majority of the human population caspase-12 is expressed as a truncated, inactive protein [344].

It was also observed that prion replication led to sustained eIF2 α phosphorylation responsible for the neurological and behavioural impairment of the prion-diseased infected mouse model through repression of synaptic proteins that are synthesized through the ER-Golgi secretory pathway [27]. The detrimental effects of sustained eIF2 α phosphorylation could be reversed by over-expression of GADD34 or by lentivirally-mediated anti-PrP RNAi; salubrinal accentuates these effects by inhibiting eIF2 α -P dephosphorylation [27]. Oral administration of a PERK inhibitor also protected animals from PrD related neurodegeneration [345]. However, pharmacological induction of ER stress with DTT or thapsigargin, in neuronal cell lines that expressed mutant PrP, decreased PrP^c aggregation and PrP^{Sc} accumulation [346]. One explanation that could reconcile the divergent results of prion research is that UPR activation is beneficial in prevention of and in the early stages of PrDs, however with progressive accumulation of misfolded PrP^c and PrP^{Sc}, derangements of UPR develop that contribute to progression of the disease. ER stress markers in the brain are upregulated in prion infected mice and in *post-mortem* samples of patients with CJD but to a considerably lesser degree than in the brain samples of AD patients [181]. An immunohistochemical study looking at the localization of phosphorylated PERK and eIF2 α -P in 25 human patients could not confirm the involvement of UPR in human prion diseases [181]. Only human prion disease cases that showed concomitant AD pathology had increased presence of pPERK and p-eIF2 α , suggesting that these markers were not related to the prion pathology [17]. Therefore comorbidity of neuropathological processes is an important factor in the study of UPR activation in human neuropathology and the precise role of PrDs in modulating the UPR needs further examination [17].

4.3. Macroautophagy in Prion Diseases

Autophagy vacuoles were described in neurons in animal experimental models of PrD [347,348] and also in prion-infected neuronal cell cultures [349]. The location of autophagy vacuoles was in neuronal perikarya, neurites and synapses in experimentally induced scrapie, Creutzfeldt-Jakob disease (CJD) and in Gerstmann-Sträussler-Scheinker (GSS) syndrome [350,351]. The presence of autophagy vacuoles was associated with an up-regulation of *scrapie responsive gene 1* in animal models of PrDs and in brains of patients with sporadic CJD [352–356]. PrP^c modulation of autophagy was demonstrated by an increased expression of LC3-II in neurons of Zürich I *Prnp*^{−/−} mice; this was attenuated by the reintroduction of an octapeptide region rich PrP^c into these cells [357]. It has been suggested that PrD modulated autophagy precipitates apoptosis, thus contributing to the formation of spongiform changes in the brain [350,358,359]. It is also possible that, before PrD related changes of PrP^c and during the early stages of PrD, autophagy contributes to degradation of PrP^c and PrP^{Sc}. Thus the failure of autophagy leads to activation of apoptosis and progression to PrD. The latter explanation is consistent with the observation of reduced levels of lysosomal activation marker LAMP-2 in the brain tissue of prion-infected galactin-3^{−/−} mice, prion-infected wild-type and in galactin-3^{−/−} mice where lower mRNA levels of autophagy markers Beclin-1 and Atg5 were detected, compared to mock infected control brains. This finding supports the hypothesis that endosomal/lysosomal dysfunction and reduced autophagy may contribute to the development of PrD [360]. Also the drug imatinib enhances lysosomal degradation of PrP^{Sc} [361], stimulates autophagy and/or autophagosome formation [362] and even delays, but does not prevent, neuroinvasion of PrP^{Sc} and the onset of clinical disease in prion-infected mice [363]. In summary, reduction of cellular of PrP^c and PrP^{Sc} can be achieved by pharmacological stimulation of autophagy

in an mTOR-independent manner (e.g., with lithium, trehalose, imatinib) or by inhibition of mTOR (e.g., with rapamycin). Compared to mock-treated control mice, rapamycin and lithium prolonged prion incubation times in contrast to trehalose and imatinid that delayed peripheral accumulation of PrP^{Sc} [5,92,93,364–367]. Inhibition of autophagy by pharmacological interference and siRNA gene silencing attenuated autophagy-mediated reduction of cellular PrP^{Sc} [5]. It seems that the further development of autophagy inducing compounds could lead to effective treatment of PrDs.

PrP^{Sc} is found in many different cell locations: on the plasma membrane, in the endolysosomal system, in the endosomal recycling compartment, in the trans Golgi network and Golgi, in the autophagic pathway and in the cytosol [290,291,293,294,368–370]. Autophagy is the major route of PrP^{Sc} degradation [371], alternative degradation pathways for newly endocytosed PrP^{Sc} are through the endolysosomal pathway [294] and the Golgi QC pathway [372,373]. Proteasome inhibition increased PrP^{Sc} levels in chronically-infected cultured cells and this increase was not accompanied by increased PrP^c expression [373]. In contrast, PrP^{Sc} is not ubiquitinated for degradation by the proteasome to a significant degree, suggesting proteasomal PrP^{Sc} degradation by a non-ubiquitin pathway, for review see [374]. Formation of insoluble PrP^{Sc} forms (*i.e.*, aggresomes) could be facilitated under conditions of increased cell stress that leads to proteasome inhibition or in the later stages of prion disease [375,376]. Recently, a comprehensive synthesis of prion formation, trafficking and degradation pathways has been presented [374]. PrP^{Sc} is assumed to form at the plasma membrane, in endosomes, in recycling vesicles or in lysosomes. PrP^{Sc} recycling to the plasma membrane stimulates prion propagation. The intracellular transport of PrP^{Sc} follows three pathways. One pathway enables PrP^{Sc} recycling to the plasma membrane, the other two target PrP^{Sc} for degradation. Newly formed and mature forms of PrP^{Sc} are degraded by different pathways. Newly formed PrP^{Sc} is moved by retrograde transport to the trans Golgi network (TGN) and Golgi, subjected to Golgi quality control and sent to lysosomes for degradation. Mature PrP^{Sc} forms, representing the majority of total cellular PrP^{Sc}, are moved to lysosomes via the endolysosomal, autophagy and proteasome degradation pathways [5,93,371,373]. To summarise, the increased cytosolic presence of PrP^{Sc} is due to (a) the lysosomal rupture caused by aggregated PrP^{Sc} that de-stabilise the lysosomal membrane [377]; (b) the low rate of ERAD ubiquitination of PrP^{Sc} for proteasomal degradation in the cytosol [378,379]; and (c) the low degradation rate or failure of the PrP^{Sc} ubiquitin-independent degradation by the proteasome. Thus, PrP^{Sc} accumulates and forms smaller and larger insoluble forms (*i.e.*, aggresomes) that are degraded by macroautophagy.

5. Conclusions

Alzheimer's disease, Parkinson's disease and prion diseases have different clinical manifestations of neurodegeneration, however, all three share the process of accumulating misfolded, pathological proteins. Proteostasis in these neurodegenerative disorders is further perturbed by age-related brain changes and associated chronic diseases, like for example diabetes mellitus. While both the unfolded protein response and autophagy have an important role in the prevention and attenuation of Alzheimer's and Parkinson's diseases progression, only macroautophagy seems to play an important role in the development of prion diseases. Autophagy and unfolded protein response can be modulated by pharmacological interventions. Further research is necessary to better understand the regulatory pathways of both processes, in health and neurodegeneration, to be able to develop new therapeutic interventions.

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