



Exploring the Promise of Targeting Ubiquitin-Proteasome System to Combat Alzheimer's Disease

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Abstract

The ubiquitin (Ub)-proteasome system (UPS) is considered as a central protein degradation system in all eukaryotes. The UPS comprises of several factors such as Ub and Ub-like molecules, Ub hydrolases, E3 Ub ligases, and the proteasome itself. Numerous studies have demonstrated that the dysfunction of UPS plays an essential role in the pathogenesis and progression of Alzheimer's disease (AD). Furthermore, current evidence has suggested that the UPS components can be connected with the initial stage of AD that is characterized by synaptic dysfunction, and to the late phases of AD, marked by neurodegeneration. In AD patients, the accumulations of insoluble protein in the brain can be caused by overload or dysfunction of the UPS, or by conformational alterations in the protein substrates that prevent their degradation and recognition by the UPS. Synaptic dysfunction is also caused by defective proteolysis that has found in the initial stage in AD as the UPS is widely recognized to play a pivotal role in the regular activities of synapses. Conversely, its precise cause and pathogenesis are unclear. Presently accepted medicines for AD give symptomatic relief, though they are unable to stop the progression of the disease. Besides, the components of the cellular quality control system demonstrate a significant emphasis on the advancement of targeted and effective treatments for AD. In this review, we focus on the role of UPS in the pathogenesis of AD and highlight how the UPS-linked treatments influence in the management of AD.

Keywords Alzheimer's disease · Ubiquitin-proteasome system · Proteasome · Amyloid beta · Tau

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Introduction

Alzheimer's disease (AD) is a progressive neurodegenerative disorder of the central nervous system (CNS), which is featured by gradual loss of cognitive functions such as memory, attention, judgment, comprehension, language, and reasoning, ultimately resulting in severe dementia (Uddin et al. 2019a, 2019b; Kabir et al. 2019a, 2019b). Intracellular neurofibrillary tangles (NFTs) and extracellular beta-amyloid (A β) plaques are the main pathological hallmarks of AD (Price and Sisodia 1998; Uddin et al. 2019c, 2019d; Hossain et al. 2019; Mathew et al. 2019; Mamun et al. 2020). The A β plaques result from precise proteolytic processing of amyloid precursor protein (APP) that is positively controlled by the presenilins 1 (PS1) and presenilins 2 (PS2) (De Strooper et al. 1998; Al Mamun and Uddin 2020). Currently, *PS1* and *PS2* have been revealed to be substrates of the ubiquitin (Ub)-proteasome system (UPS) (Kim et al. 1997; Marambaud et al. 1998; Steiner et al. 1998; Johnston et al. 1998). Additionally, UPS is accountable for expressing various fundamental cellular functions.

Numerous neurodegenerative diseases such as AD, transmissible spongiform encephalopathies, Parkinson's disease, Huntington's disease, neurodegeneration following spinal cord injury, and amyotrophic lateral sclerosis are connected with the UPS dysfunction (LEIGH et al. 1991; Neumann et al. 2006; Uddin et al. 2018a, 2020b). In these neurodegenerative disorders, the influence of the UPS may be linked to deficits in the removal of misfolded proteins leading to the intracellular accumulation of protein, neuronal cell death, and cytotoxicity (Demuro et al. 2005; Schwartz and Ciechanover 2009; Sahab Uddin and Ashraf 2020).

The UPS also plays a central role in neuronal signaling pathways that control the release of neurotransmitter, synaptic plasticity, and synaptic membrane receptor turnover (Zhao et al. 2003; Patrick 2006). In this article, we discuss the role of UPS in the pathogenesis of AD and emphasize how the UPS-associated treatments to combat AD pathogenesis.

Molecular Biology of Ubiquitin-Proteasome System

The UPS is situated in the cytosol and the nucleus. Ub is a protein of 76-amino acid residues that are vastly evolutionarily conserved in all eukaryotes (Hershko and Ciechanover 1998; Nandi et al. 2006). Moreover, the ubiquitination process is involved in 3 successive stages concerning 3 enzymes known as activating (E1), conjugating (E2), and ligating (E3) enzymes (Fig. 1). Furthermore, the 26S proteasome is a large multi-subunit complex that plays a pivotal role in the degradation of the Ub-conjugated proteins. The Ub chain is prepared by E1 and E2 enzymes, which are subsequently attached to target proteins with the help of the E3 enzyme. The ubiquitination process starts when the Ub-activating enzyme E1 triggers an Ub molecule through an adenosine triphosphate (ATP)-dependent mode. Ub is then bound with an internal E1 Cys moiety through an intermediate thiolester bond producing E1-S~Ub. Subsequently, Ub is shifted to one of the various E2 forms. Afterward, the attachment of Ub to the protein substrate is catalyzed by several E3s—a large and different set of proteins with discrete motifs (Ciechanover 1994).

The variety of diverse Ub protein ligase E3s could distinguish a precise substrate due to its high specificity as well as the selectivity to the UPS (Ciechanover 1998). Furthermore, the most significant recognition pattern is the destabilizing N-terminus amino acids including lysine and arginine. This distinctive N-terminus destabilizing residues could assess the half-life of an intracellular protein which is known as the N-end rule. Subsequently, multiple cycles of ubiquitylation take place to form a polyubiquitin chain on the substrate. Then, polyubiquitinated proteins are recognized and degraded by the 26S proteasome. Then, the polyubiquitin chain is

disassembled by deubiquitinating enzymes (DUBs), and the free ubiquitin monomers can be reused to tag other substrates.

Ubiquitin-Proteasome System in the Pathogenesis of Alzheimer's Disease

Degradation of protein is mainly carried out by proteasomes in the cytosol and the nucleus of all cells (Lecker et al. 2006; Uddin et al. 2018b). In the nervous system, these processes are regulated by the Ub-proteasome pathway (UPP). The damage of the UPP-dependent protein degradation system leads to the development of several neurodegenerative diseases such as AD. In recent times, many researchers have observed that UPS has an impact on the AD pathogenesis, and ubiquitinated proteins are greatly present in AD patients (Gentier and van Leeuwen 2015; Tramutola et al. 2016). UPS controls not only the metabolism of A β but also the degradation of tau through the 26S proteasome. Conversely, the malfunction of these proteins in the neurons can cause both the aggregation of ubiquitinated proteins and the modifications in the combination of proteasome subunits, which reduces the function of proteasome and α -secretase, triggering the generation of A β . Nonetheless, the precise fundamental mechanism of this progression remains unclear. The activity of proteasome is reduced in the diverse parts of the AD brain including, the inferior parietal lobe, the superior and middle temporal gyri, and the parahippocampal gyrus, which specifies the functional failure of UPP throughout the AD pathogenesis (Necchi et al. 2011).

Furthermore, the relationship between the impairment of synaptic plasticity and the UPP is more widely investigated in AD (Vriend et al. 2015; Cheng et al. 2016). There are some cellular events such as the oxidation of DUBs, the aggregation of mutated Ub, the changes of proteasome subunits, and the downregulation of E1 and E2 enzymes are found both in transgenic mice with A β and in AD patients (Choi et al. 2015). The accumulations of A β and the hyperphosphorylation of tau, as well as neurodegeneration in AD, are closely connected with the dysfunction of UPS (Fig. 2). The impairment of UPS leads to the generation of A β by inducing the activity of α -secretase in AD neurons (Gentier and van Leeuwen 2015). Normally toxic A β is generated by inducing β -secretase targeted APP cleavage and produces a C-terminus portion (Uddin and Kabir 2019). Then the γ -secretase plays an essential role in the cleavage of this portion and generates toxic A β 40 and A β 42 portions (Uddin et al. 2020a). The inhibitors of the proteasome can reduce the activity of β -secretase by the upregulation of APP-C99 (Renziehausen et al. 2015). The primary sign for the pathological connection between UPS and tau is resulting from the recurrent colocalization and the aggregation of Ub in paired helical filaments (PHFs) and NFTs. Research detected

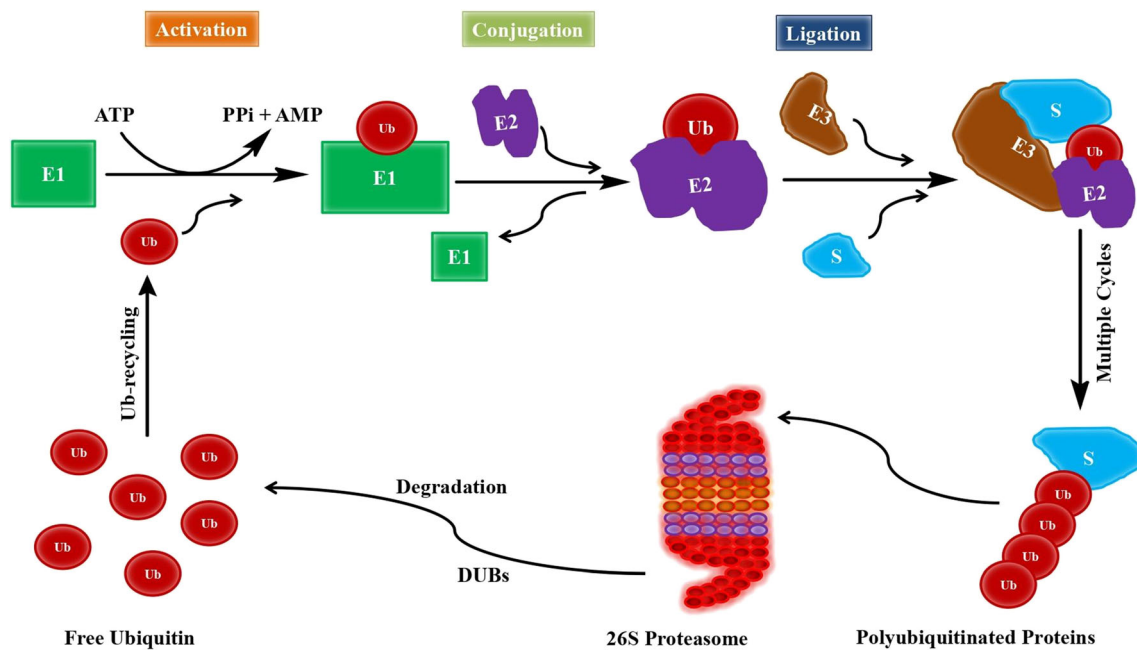


Fig. 1 General overview of the ubiquitin (Ub)-proteasome system. The ubiquitination process starts when the Ub-activating enzyme E1 triggers a Ub molecule through adenosine triphosphate (ATP)-dependent mode. Ub is then bound with an internal E1 Cys moiety through an intermediate thioester producing E1-S~Ub. Subsequently, Ub is shifted to one of the various E2 forms. Then, the E2 interacts with a substrate-bound E3 Ub ligase, which catalyzes the transfer of Ub to a lysine residue in the

substrate to generate a stable isopeptide bond. Multiple cycles of ubiquitylation can take place to form a polyubiquitin chain on the substrate. Polyubiquitinated proteins are recognized and degraded by the 26S proteasome. The polyubiquitin chain is disassembled by the 26S proteasome. The free ubiquitin monomers can be reused to tag other substrates. Abbreviations used are Ub, ubiquitin; DUBs, deubiquitinating enzymes

that polyubiquitinated tau within PHF is primarily in the Lys48-related poly-Ub form, which is the most recognized degradation signal. Moreover, this powerfully advocates the role of UPS-targeted tau removal in defense against the pathogenesis of AD (Cripps et al. 2006).

However, the direct connection between the UPS and the AD pathogenesis was acknowledged with the detection of a frameshift mutation in the Ub transcript that leads to the elongation of the molecule with 20 amino acids moiety UBB + 1 (Fig. 2), which had been selectively found in AD patients who were affecting with late-onset AD (van Leeuwen et al. 1998). UBB + 1 is an effective acceptor for polyubiquitination, although it could not be activated by E1 (because of the absence of vital G76 moiety) and be shifted to a substrate or to another Ub portion. The resultant chain of poly-Ub is difficult to disassemble by DUBs, especially isopeptidase T (Lam et al. 2000) which needs for its function in a manifested G76 moiety at the proximal Ub portion. Moreover, the aggregated poly-Ub chains block the degradation of the proteasome (Lindsten et al. 2002) that leads to the apoptosis of neurons (Bardag-Gorce et al. 2002). Hence, UBB + 1 expression rises noticeably with aging in the brain, which can possibly result in dominant suppression of the UPS, leading to the aggregation of toxic proteins with the neuropathologic outcome including AD.

Prospective Targets of Ubiquitin-Proteasome System for Alzheimer's Disease

Numerous ubiquitination enzymes are prospective targets for AD therapies that control not only the A β metabolism but also the UPS in AD brains. E2-25K is one of the distinctive Ub-conjugating enzymes that is upregulated and leads to the toxicity of A β (Song et al. 2008). A β raises the E2-25K/Hip-2 expression that subsequently stabilizes the caspase-12 and apoptotic protein by suppressing the activity of proteasome (Song et al. 2003, 2008). The expression of E2-25K/Hip-2 knockdown inhibits neuronal cell death in AD mice model and in cultured neurons. In a study, Lonskaya et al. revealed that the intracellular aggregation of A β and damaged proteasome activity could be restored by the Ub E3 ligase parkin (Lonskaya et al. 2012, 2014). Furthermore, parkin has the capability to defend neurons against diverse insults, which leads to the prevention of AD (Fig. 3). The expression of parkin can decrease the level of A β , and it also reverses damaged long-term potentiation and behavioral aberrations of the AD model mouse by reversing the deleterious effects of A β on the proteasome.

Moreover, parkin increases beclin-dependent autophagy by which it helps the removal of A β (Khandelwal et al. 2011). Conversely, Ub carboxyl-terminal hydrolase

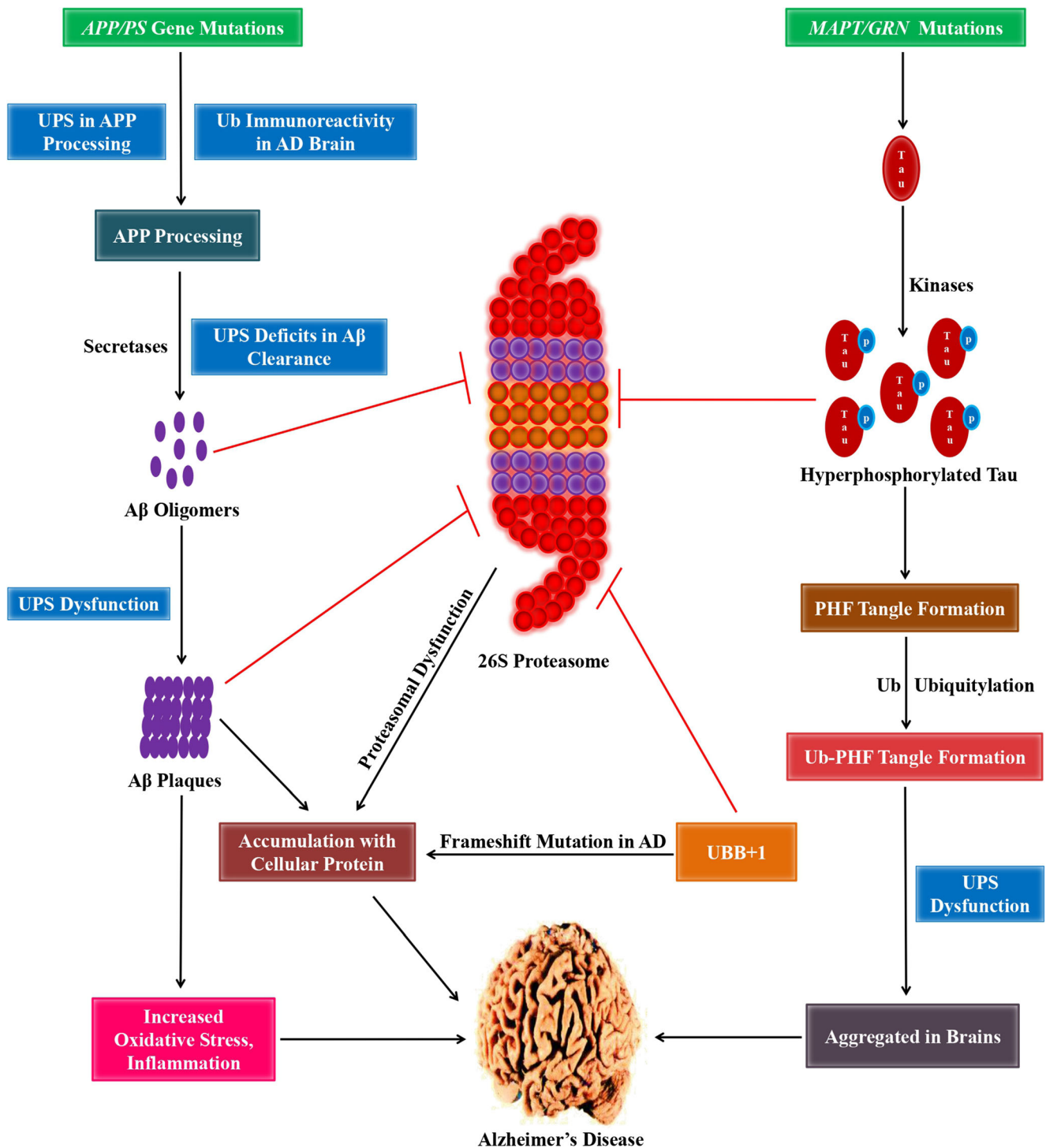


Fig. 2 The ubiquitin-proteasome system in the pathogenesis of Alzheimer's disease. Intracellular neurofibrillary tangles (NFTs) and extracellular beta-amyloid (Aβ) plaques are the main pathological hallmarks of AD. The figure shows only increased generation of Aβ42 (a splice variant of Aβ) due to the mutations of *APP* and *PS* gene, whereas the formation of tau takes place owing to the mutations of *MAPT* and *GRN* gene. The roles of the UPS in the steps leading to AD pathogenesis are

shown in blue boxes. Furthermore, the ubiquitin mutant UBB + 1 is also connected with AD, although it is vague that how the mutation contributes to discrete pathologies in many patients remains mysterious. Abbreviations used are: Aβ, amyloid beta; AD, Alzheimer's disease; APP, amyloid precursor protein; GRN, progranulin, *MAPT*, microtubule-associated protein tau; PHFs, paired helical filaments; PS, presenilin; Ub, ubiquitin; UPS, ubiquitin-proteasome system

1 (UCHL1) has been found in Ub-enriched inclusion bodies in AD brains. According to the study by Zhang et al.,

the overexpression of UCHL1 enhances contextual memory and recovers synaptic activities in APP/PS1 model

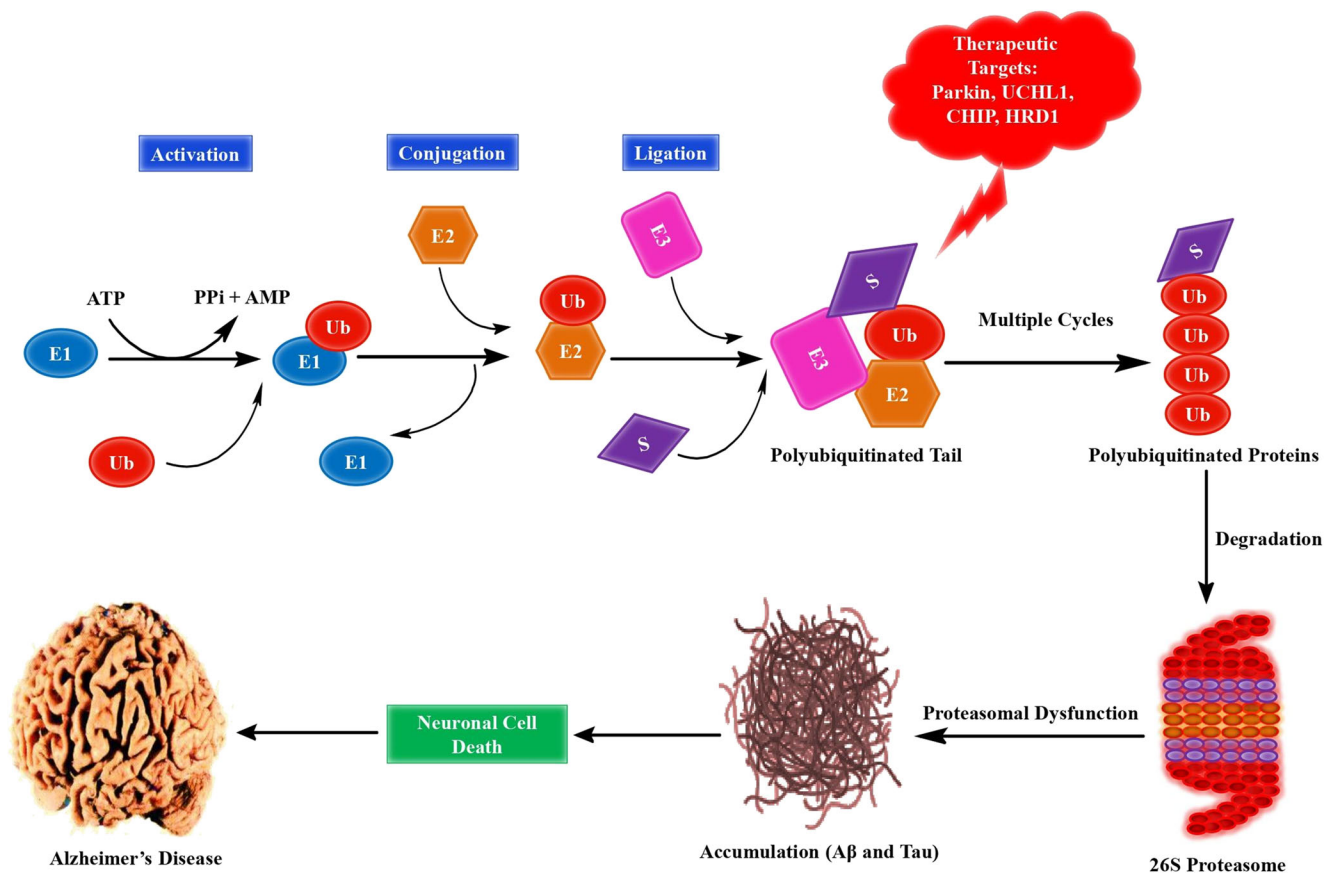


Fig. 3 Potential therapeutic targets of ubiquitin-proteasome system for AD. Ubiquitin proteasomal dysfunction causes the accumulation of A β and tau, which leads to neuronal cell death and ultimately resulting in Alzheimer's disease. The polyubiquitinated tail is the best potential therapeutic targets for parkin, UCHL1, CHIP, HRD1 because it

predominantly regulates substrate specificity and selectivity and plays an important in the management of AD. Abbreviations used are AD, Alzheimer's disease; A β , amyloid beta; UCHL1, ubiquitin carboxy-terminal hydrolase L1; CHIP, C-terminus of HSC70-interacting protein; HRD1, The HMG-CoA reductase degradation protein 1

mouse (Zhang et al. 2015) by decreasing the β -secretase enzyme 1 (BACE1) levels and subsequently reduces the cleavage products of BACE1 (APPC-end portion C99 and A β) (Zhang et al. 2012; Guglielmo et al. 2012). BACE1 is a novel substrate of E3 ligase C-terminus of Hsc70-interacting protein (CHIP) that advocates the destabilization of BACE1 by attaching through the U-box domain of CHIP (Singh and Pati 2015). Additionally, CHIP decreases the level of BACE1 by enhancing its ubiquitination and proteasomal degradation that subsequently reduces the processing of APP and A β generation in neurons. Moreover, the level of HMG-CoA reductase degradation protein 1 (HRD1) is considerably reduced in the cerebral cortex of AD human model, which is inversely connected with the generation of A β (Saito et al. 2010; Gerakis et al. 2016). The increased expression of HRD1 also enhances the ubiquitination and degradation of APP that results in reduced A β generation (Kaneko et al. 2010).

Crosstalk of Alzheimer's Targets and Ligands—Ubiquitin-Proteasome System Components

Advancement of drugs and treatment strategies that target UPS components would need a well comprehending of the role of proteolysis in the progression of AD. The proteasome, Ub-conjugating enzymes, and DUBs are potential drug targets in the UPS. Furthermore, E3s are excellent prospective therapeutic targets amid other enzymes since they predominantly regulate substrate specificity (Fig. 3). As the substrate-binding area possesses specificity to E3s and allosteric modification of this area using small molecules can cause specificity to E3s either increase or decrease affinity to specific substrates, which is one of the ways of regulating aggregation of the ubiquitylated substrate (Upadhy and Hegde 2005). Moreover, selective engineering of the UPS components allows modification of their transfer to a precise affected area and consequent degradation of particular aggregated

ubiquitylated proteins or protein accumulates could offer a substitute strategy to small allosteric molecules (Upadhy and Hegde 2005). Conversely, no robust E3 agent has been applied in AD until now.

In addition, DUBs can be prospective drug targets when a specific role for these enzymes in AD is recognized. The regulation of specific DUBs by small molecules improves the deubiquitylation of poly-Ub chains of mutant UBB + 1 that can be an additional probability since these chains suppress proteasomes in the AD brains (Lam et al. 2000). Activation of the proteasome is another uninvestigated arena for novel drug discovery. Even though numerous proteasome inhibitors are available, however, there are no potent drugs that can improve the proteasome activity. As the aberrant accumulation of protein and the inhibition of proteasome are the usual hallmarks of AD and other neurodegenerative disorders, improvement of proteasome function with the aid of small molecules can be an effective method to eliminate the accumulations that aggregate in the AD brain (Upadhy and Hegde 2005). Resveratrol is a naturally occurring polyphenol found abundantly in grapes, grape juice, and red wine, which is suspected to possess antioxidant and neuroprotective activities (Savaskan et al. 2003; Jang and Surh 2003; Han et al. 2004). Numerous researches demonstrated that resveratrol has a strong anti-amyloidogenic activity by decreasing the levels of A β -produced and delays A β -induced toxicity in different experimental models (Savaskan et al. 2003; Jang and Surh 2003; Han et al. 2004; Marambaud et al. 2005). It has also been reported that resveratrol works by enhancing the intracellular degradation of A β using a mechanism that connects the proteasome (Marambaud et al. 2005). Ultimately, these investigations recommend a potential application for this compound in the management of AD.

Targeting the Ubiquitin-Mediated Protein Degradation in Alzheimer's Disease

The aggregation of toxic A β is controlled by the quality control systems of the cell (autophagy, molecular chaperones, and the components of UPS) (Morawe et al. 2012). Ub-mediated protein degradation takes place through two chief catabolic systems, for instance, the autophagy (endosomal/lysosomal system) and the ATP-dependent, non-lysosomal proteolysis system termed UPS.

Autophagy

Lysosomes damage normal and accumulated proteins through autophagy, which are generally observed under injury or stress conditions. Autonomous changes in the endocytic pathway trigger the lysosomal system and raise the quantity and density

of lysosomes as well as the expression of the gene (Cai and Yan 2013). Furthermore, the latter effect plays a central role in the synthesis of all types of lysosomal hydrolases, such as cathepsin (Nixon et al. 2001). Lysosomal cathepsin B is up-regulated both by the modulator 2-Phe-Ala-diazomethyl ketone (PADK) and by the accumulation of protein. Moreover, systemic administration of PADK enhances the activity of cathepsin B that raises the removal of intracellular A β and reduces its extracellular aggregation. Therefore, regulators of lysosomal activity exhibit great potential for treating neurodegenerative disorders including AD.

Autophagy decreases the aggregation and expedites the removal of regular/mutant A β (Cai and Yan 2013). The A β , which is produced in endosomes and autophagic vacuoles, is transferred to lysosomes wherein it is removed through lysosomal proteolysis under standard conditions (Yang et al. 2011). In a study by Yang et al., reported that in TgCRND8 transgenic mice (Yang et al. 2011), increasing lysosomal proteolysis enhanced the removal of autophagy substrates that decreased extracellular and intracellular levels of A β and recovered many cognitive dysfunctions. Furthermore, Cecarini et al. (Cecarini et al. 2012) exposed in human SH-SY5Y neuroblastoma cells stably transfected either 717 valine-to-glycine *APP*-mutated gene or with wild-type *APP* gene (Cecarini et al. 2012), and increased expression of the *APP* mutant isoform associated with a rise in oxidative stress as well as a remodeled pattern of protein degradation, with both significant suppression of proteasome activities as well as impairment in the autophagic flux.

In addition, rapamycin suppresses motor activity and increases autophagy; thereby it could be beneficial in stopping or recovering AD pathology. Rapamycin also suppresses the formation of NFT and the phosphorylation of tau, as well as decreases cognitive dysfunctions (Cai and Yan 2013). Therefore, agents that trigger autophagy can decrease or remove protein accumulations (Lane et al. 2012). The two proteolytic systems including UPS and autophagy-lysosomal pathway (ALP) are primarily accountable for the quality control of cellular protein in neurons and their significant roles in the pathogenesis of AD. Both the UPS and ALP pathways control proteostasis, forming a single network to maintain the homeostasis of protein (Balch et al. 2008). Even though the UPS and ALP are deliberated for a long time as independent mechanisms, numerous studies show close crosstalk as well as coordination between both pathways (Korolchuk et al. 2010). Likewise, A β and C-terminal membrane fragment β are the two main detrimental proteins for neuronal function, and these two proteins are removed by the UPS and ALP pathways (Bustamante et al. 2013; Xiao et al. 2015; Wang et al. 2017; González et al. 2017; Yang et al. 2017). Moreover, the growing number of evidence stated that some specific enzymes of the ubiquitylation machinery play a pivotal role in both degradation pathways. Any interferences in

normal molecular features of the UPS and ALP pathways are predominantly related to pathophysiological conditions that instigate the aggregation of abnormal proteins, for example in various neurodegenerative disorders, like AD.

Molecular Chaperones—Heat Shock Proteins

Molecular chaperones and the UPS are considered as the first and the second lines of defense against misfolded protein and accumulation. Chaperones control the folding of freshly synthesized proteins as well as the refolding or transport of misfolded proteins to protein degradation systems (Morawe et al. 2012). Higher molecular weight heat shock proteins (Hsps) (> 43 kD) is ATP-dependent, while lower molecular weight Hsps (12–43 kD) is ATP-independent. Numerous investigations (Wilhelmus et al. 2007; Salminen et al. 2011; Takalo et al. 2013; Ou et al. 2014; Blair et al. 2014) have revealed that the chaperone system can be targeted to advance treatment approaches for controlling AD (Jinwal et al. 2010). Generally, chaperones attach to tau and A β toxic protein and control their degradation. In addition, not only Hsp90 but also Hsp70 takes part in the metabolism of APP (Gao and Hu 2008).

Hsp70 is ATP-dependent and the main target for treating AD. Elevated levels of Hsp70 suppress its ATPase activity and maybe a successful treatment approach for AD (Jinwal et al. 2010). Bobkova et al. showed that the recombinant human Hsp70 decreased the formation of A β plaque in 5XFAD transgenic mice (Bobkova et al. 2013). Furthermore, methylene blue suppresses Hsp70 and raises the removal of tau at very high concentrations (O’Leary et al. 2010). Many studies demonstrated that curcumin was able to enhance the activity of Hsp70 and Hsp90 that could suppress or linger the formation of amyloid and decrease neuronal cell death (Mishra and Palanivelu 2008; Maiti et al. 2014). Moreover, Bcl2-linked athanogene proteins are a family of co-chaperones that forms a complex with tau and Hsp70 and can suppress the degradation of tau in cell cultures, raising the levels of both APP and tau (Elliott et al. 2007, 2009).

In addition, Hsp90 controls the stabilization and the misfolding of neurotoxic proteins and expedites tau pathology in AD (Sarah Kishinevsky et al. 2013). Suppressing Hsp90 decreases the levels of Ser/Thr-mutated tau, hyperphosphorylated tau, and the kinases, which are involved in continuous hyperphosphorylation (Jinwal et al. 2011). Furthermore, the inhibition of Hsp90 triggers small Hsps, Hsp70, and heat shock factors. This suppression also expedites the binding of Hsp70 with aberrant proteins to produce a complex that is ubiquitinated by CHIP and damaged via proteolysis. Therefore, the suppression of Hsp90 raises the degradation of tau and maybe a prospective therapeutic approach for tau-based neurodegeneration in AD (Sarah Kishinevsky et al. 2013).

Conclusions

The components of UPS are the key factors for the treatment of AD. The UPS also influences in the AD pathology through several mechanisms. Comprehensive knowledge of the mechanisms of proteasomal function is crucial for the advancement of novel therapeutic as well as diagnostic approaches for the management of AD. Additionally, for the advancement of effective medicines also needs in-depth knowledge of the role of proteasome inhibition and how neuronal cell death takes place in AD brains. Although, A β inhibits proteasomes in vitro, however, it remains unclear whether AD patients exhibit the same pattern. Moreover, future treatments of AD may decrease the accumulation of protein (both A β and tau) by targeting specific UPS components such as the Ub, polyubiquitinated tail, DUBs, and 26S proteasome. Finally, for the development of novel treatments of AD, we need to entirely comprehend in what way the UPS components interact in the degradation of the protein.

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Author Contributions AAM and MSU conceived the original idea and designed the outlines of the study. AAM, MSU, and MTK prepared the draft of the manuscript. AAM prepared the figures for the manuscript. SK, MSS, BM, and MA participated in the literature review of the manuscript. AAM, MSU, AR, and GMA participated in revision and improved the manuscript.

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Compliance with Ethical Standards

Conflict of Interest The authors declare that they have no conflict of interest.

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