

Proteinopathies: Deciphering Physiology and Mechanisms to Develop Effective Therapies for Neurodegenerative Diseases

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Abstract

Neurodegenerative diseases (NDs) are a cluster of diseases marked by progressive neuronal loss, axonal transport blockage, mitochondrial dysfunction, oxidative stress, neuroinflammation, and aggregation of misfolded proteins. NDs are more prevalent beyond the age of 50, and their symptoms often include motor and cognitive impairment. Even though various proteins are involved in different NDs, the mechanisms of protein misfolding and aggregation are very similar. Recently, several studies have discovered that, like prions, these misfolded proteins have the inherent capability of translocation from one neuron to another, thus having far-reaching implications for understanding the processes involved in the onset and progression of NDs, as well as the development of innovative therapy and diagnostic options. These misfolded proteins can also influence the transcription of other proteins and form aggregates, tangles, plaques, and inclusion bodies, which then accumulate in the CNS, leading to neuronal dysfunction and neurodegeneration. This review demonstrates protein misfolding and aggregation in NDs, and similarities and differences between different protein aggregates have been discussed. Furthermore, we have also reviewed the disposal of protein aggregates, the various molecular machinery involved in the process, their regulation, and how these molecular mechanisms are targeted to build innovative therapeutic and diagnostic procedures. In addition, the landscape of various therapeutic interventions for targeting protein aggregation for the effective prevention or treatment of NDs has also been discussed.

Keywords Aggregates · Chaperone · Heat shock proteins · Misfolded protein · Neurodegenerative diseases

Introduction

One of the biggest challenges in the field of neuroscience is the disease-modifying treatment which include several neuroprotective and neurorestorative interventions that focus on slowing the progression of NDs. NDs are a plethora of debilitating and degenerative diseases, including Alzheimer's disease (AD), Parkinson's disease (PD), amyotrophic lateral sclerosis (ALS), Huntington's disease (HD), frontotemporal dementia (FTD), traumatic encephalopathy, dementia with Lewy bodies, and prion diseases [1]. Despite having a difference in pathogenesis and clinical manifestation, these NDs share several common attributes, such as increased prevalence with age, progressive nature, selective neuronal loss, and synaptic dysfunction [2-6]. Importantly, the most prevalent and common feature of these NDs is the occurrence of misfolded proteins and their gradual accumulation, which is thought to be the main cause of these disorders [7–14]. Alpha-synuclein (α -Syn), amyloid-beta (A β), huntingtin (HTT), TAR DNA-binding protein 43 (TDP-43), Tau, and superoxide dismutase (SOD) are some of the proteins that are misfolded and accumulate in NDs [10–14]. In this review, we focused on A β , tau, α -Syn, HTT, and TDP-43, as they are the most common protein aggregates involved in the pathogenesis and progression of NDs. The distribution of the misfolded proteins involved in several diseases throughout the brain is depicted in Fig. 1, and Table 1 lists the different NDs caused by protein misfolding.

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Fig. 1 Distribution of unfolded protein in the brain in neurodegenerative diseases: Specific misfolded proteins are distributed through particular regions of the brain

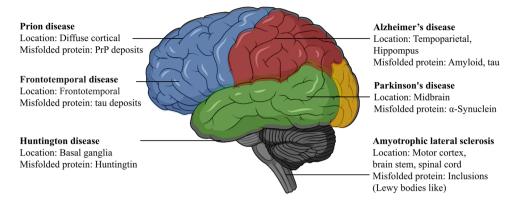


 Table 1
 Protein misfolding and aggregation associated with neurodegenerative diseases

S. No	Aggregated protein(s)	Diseases	Affected regions of the brain	Clinical hallmarks	Aggregate cellular locations	Transmission mode	Ref
1	α-synuclein	Parkinson disease, multiple system atrophy, dementia with Lewy body	Hypothalamus, substantia nigra	Movement disorder	Cytoplasmic	Rarely inherited, mostly sporadic	[31]
2	Tau	Alzheimer disease, Parkinson dis- ease, fronto-tem- poral dementia with parkinson- ism	Hippocampus, cerebral cortex	Progressive dementia	Extracellular, cytoplasmic	Inherited (6%) or sporadic (94%)	[32, 33]
3	Amyloid-β	Alzheimer disease	Cerebral cortex, hippocampus	Progressive dementia	Cytoplasmic, extracellular	Inherited (5%) or sporadic (95%)	[15]
4	Superoxide dis- mutase (SOD)	Amyloid lateral sclerosis	Brainstem, motor cortex	Movement disorder	Cytoplasmic	Inherited (9%) or sporadic (91%)	[34]
5	Huntingtin	Huntington, Tar DNA-binding protein 43 (TDP- 43)	Striatum, cerebral cortex	Dementia, psychi- atric and motor problems	Nuclear	Autosomal domi- nated (inherited)	[18, 35]
6	Prion	Cretzfeld–Jakob disease	Depending on the disease, differ- ent regions are involved	Ataxia, insomnia, dementia, or psy- chiatric problems	Extracellular	Infectious (3%), inherited (7%), or sporadic (89%)	[36]

One of the key components of these misfolded proteins is that during misfolding from their native states, they form intermolecular β -sheet-rich structures, ranging from small oligomers to large fibrillar aggregates, in NDs [7]. Protein misfolding results either in the loss of protein function or a gain of toxic function (via aggregation), resulting in cellular responses (for instance, synaptic dysfunction, inhibition of axonal transport, mitochondrial damage, and membrane disruption) that are toxic to cells leading to the progression of NDs [3, 15–18]. Alternatively, to deal with the accumulation of misfolded proteins, the cell adopts multiple mechanisms, including their synthesis, degradation, and clearance from the cell, to prevent their misfolding and aggregation [19, 20]. Multiple therapeutic strategies that can prevent or reverse the progression of NDs are currently being studied. The primary target of these studies is misfolded proteins and the aggregates formed by these proteins [21–27]. However, due to the dynamic nature of these proteins, targeting them remains a challenge [28]. This review discusses the common misfolded proteins, cellular mechanisms to deal with the generation of misfolded proteins, and degradation and clearance of these misfolded proteins as a therapeutic target for NDs.

Misfolded Protein Aggregates in NDs

Numerous clinical and experimental studies have provided comprehensive and compelling evidence that the key events that cause pathogenic abnormalities in the brain are protein misfolding, oligomerization, and accumulation during NDs [9–11, 29, 30]. The misfolded protein aggregates commonly implicated in NDs include A β (in AD); tau (in AD, frontotemporal dementia, chronic traumatic encephalopathy, etc.); α -Syn (in PD, multiple system atrophy, and dementia with Lewy bodies); TAR DNA-binding protein 43 (TDP-43) (in ALS and frontotemporal dementia); and HTT (in HD and prion proteins in Creutzfeldt–Jakob disease (CJD), bovine spongiform encephalopathy, chronic wasting disease, and scrapie) (Table 1). The commonly implicated protein aggregates are discussed below.

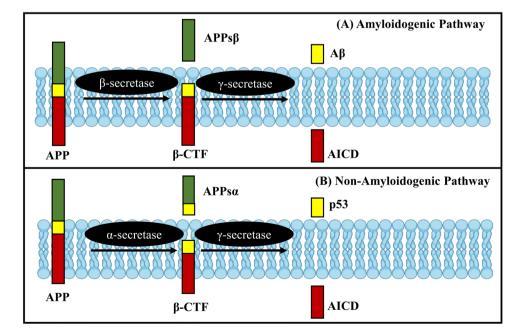
Amyloid-beta

AD is a progressive degenerative disease in elderly individuals characterized by the predominant neuropathological feature of the extracellular deposition of misfolded proteins in the brain [15, 21, 37]. There are two major types of aggregates found in AD: (1) intracellular aggregates formed of Tau protein (neurofibrillary tangles) and (2) extracellular aggregates of A β (senile plaques) [16, 38, 39]. Both neurofibrillary tangles and plaques formed by the aggregation of misfolded proteins increase the severity of dementia [2, 16, 38]. Increased production or downregulation of the clearing pathway (via ubiquitin proteosome pathway) of misfolded proteins leads to their deposition and accumulation within the organism. The accumulation of such proteins within the organism is toxic and affects many vital physiological pathways, such as lipid metabolism, mitochondrial dynamics, synaptic functions, and the release of neurotransmitters [40, 41]. Increasing clinical and experimental data suggest that oligomers, rather than fibers, are the main species causing 7515

toxicity and are involved in disease seeding and spread [42, 43]. Physiologically, the accumulation of A β induces oxidative stress and the generation of ROS resulting in dysfunctional mitochondria, the characteristic hallmark of AD [7, 44]. A β also induces the activation of the IkB a/NF-kB inflammatory pathway, resulting in a vicious cycle of neuroinflammation and oxidative stress culminating in mitochondrial dysfunction, neurodegeneration, and cognitive impairment [44–46].

A β commonly occurs in two variants, A β 40 and A β 42. A β is formed from amyloid precursor protein (APP), a membrane-bound protein, by the action of β - and γ -secretase, known as the amyloidogenic pathway (Fig. 2) [47, 48]. In amyloidogenesis, APP is cleaved by β -secretase, generating APPs β and β -C-terminal fragments followed by the action of γ -secretase, generating A β and amyloid precursor protein intracellular domain (AICD) by acting on the transmembrane domain [47, 48]. However, in the non-amyloidogenic pathway, α -secretase cleaves APP within the sequence of A β and thereby limits its production [49]. Briefly, α -secretase cleaves the ectodomain of APP, generating the APPsa fragment and α -CTF. α -CTF is then cleaved by γ -secretase into AICD and P3 peptides [38, 49]. Most of the A β in the human brain under normal conditions contains Aβ40, while in diseased conditions, excess AB42, the major constituent of amyloid plagues, is formed. The presence of 42-residue $A\beta$ (1-42) results in severe neurotoxicity and aggregates faster than the 40-residue peptide A β (1–40) [29]. Although the exact function of A β (1–42) is not clear, few studies report that these monomers are neuroprotective in nature [50]. Monomeric A β lacks toxicity, and thus, the prevention of monomer aggregation can prevent toxic species formation.

Fig. 2 Processing of APP: (i) In amyloidogenic pathway, the transmembrane protein secretase act on Amyloid Precursor Protein (APP) and cleave to release APPsß and β-CTF (C-terminal fragment). The latter is then cleaved by y-Secretase and produce P3 and AICD (amyloid precursor protein intracellular domain). (ii) In non-amyloidogenic pathway, the transmembrane protein α-Secretase act on Amyloid Precursor Protein (APP) and cleave to release APPsa and α-CTF (C-terminal fragment). The latter is then cleaved by γ-Secretase and produce P3 and AICD (amyloid precursor protein intracellular domain)



The primary structure of AB comprises an N-terminal hydrophilic region, a central region containing hydrophilic and hydrophobic residues, and a C-terminal hydrophobic end. The N-terminal region contains a β -sheet region [7, 51, 52]. The partially folded protein units combine by hydrophobic and hydrogen bonds, resulting in the formation of the perinucleus, which has the potential to associate with other Aß molecules to form a structure called the protofibril. Protofibrils can also self-assemble to form long fibrillar aggregates [51, 52]. The formation of long fibrillar aggregates depends on the concentration of monomeric units and oligomers. Aß monomers aggregate to form oligomers that act as intermediates that, upon further aggregation, lead to the formation of fibrils by primary nucleation. Once a particular concentration of the fibrils is attained, they catalyze the formation of oligomers on the surface (secondary nucleation) [53].

Tau Protein

Tau protein, a microtubule-associated protein, represents another misfolded protein found commonly in NDs such as AD, PD, HD, and frontotemporal dementia with parkinsonism (FTDP) [15, 39, 54]. Under physiological conditions, tau is located in the axon; however, disruption of either the structure or function of the tau results in the accumulation of tau in the soma or dendrites of neurons [55, 56]. The presence of hyperphosphorylated forms of tau within the neurons that aggregate to form NFTs is another hallmark of AD [13]. The accumulation of tau increases with age and is correlated with cognitive decline, forebrain atrophy, and neuronal loss in the hippocampus and neocortex region of the brain [57]. It is believed that the amount of tau present in the brain increases approximately 10–15 years before the onset of the symptom of the disease [58].

Humans express six different Tau isoforms between 50 and 70 kDa in size, the shortest of which is present within the fetal brain, while the adult brain contains all six isoforms [33]. The variable number of specific inserts at the N-terminal region and in the microtubule-binding region (MTBR) is responsible for the presence of 6 different tau isoforms. Although all 6 isoforms are present in diseased condition such as AD, they may be present in variable quantity [33]. These tau isoforms are encoded by the microtubule-associated protein tau (MAPT) gene, which is present on chromosome 17 [8]. Tau mRNA contains 16 exons comprising an N-terminal domain, 3 or 4 microtubule-binding domains (3R or 4R), a proline-rich domain, and the C-terminal region [59]. The tau inclusions are ultrastructurally made of paired helical filaments (PHFs) and straight filaments (SFs). The core of these filaments is made of identical subunits that comprise nearly 350 tau proteins. These are known to adopt a cross β/β helix structure [60]. Tau contains approximately

90 phosphorylation sites in the longest isoform that is known to be phosphorylated by 20 kinases [61, 62]. Tau binds to microtubules and aids in the anterograde and retrograde transport of biomolecules. Enhanced expression of tau obstructs kinesin-dependent trafficking in neuronal cells. It enhances dynein binding to the microtubule by binding to the dynein-activator complex. A low level of tau promotes kinesin binding to microtubules, which facilitates transport along the axon [63]. At the synaptic junction, increased concentrations promote kinesin release, thereby facilitating the binding of dynein to microtubules. Hyperphosphorylation results in loss of biological activity of tau, microtubule destabilization, and damage to protein transport, thus resulting in the aggregation of toxic molecules [62].

Tauopathy is also observed in HD patients. A study conducted by Nogales et al. (2014) found that the amount of the 3R binding domain isoforms in the cortex of normal and HD patients was similar; however, a marked increase in the 4R binding domain in HD patients was observed. Similarly, the 4R binding domain was found to be much more elevated than 3R isoforms in the striatum of HD patients [64]. An increase in 4R/3R is also observed in the postmortem patients who recently had undergone transplantation surgeries [65]. These experiments prove that an imbalance of 4R/3R tau binding domains results in HD.

Tau is secreted from damaged neurons in the extracellular medium (CSF; blood serum). Extracellular Tau is responsible for toxicity and can also result in damage to other neuronal cells. Extracellular tau expression increases phosphotidylserine signal on the neuronal cells that induce neuronal loss. Furthermore, extracellular Tau protein activates microglia's phagocytic activity and enhances its proliferation. Since, in cultures where microglia were depleted, neuronal loss was not observed, microglial cells are considered to be accountable for tau-induced neurotoxicity [39]. This finding indicates that neuronal loss caused by tau is due to the activation of microglia. It is also believed that microglia-mediated inflammation causes tau pathology [66]. Co-existence of microglia activation along with tau accumulation indicates that microglial cell activation that is considered as a part of the repertoire of immune response not only acts as an inflammatory epiphenomenon but also drives tau pathology [67].

Alpha-Synuclein Protein

Alpha-synuclein is a key component that is found in the aggregates of misfolded proteins in PD [31]. Three members of the synuclein family, alpha, beta, and gamma, are present. Alpha and beta are concentrated in the neuronal terminals, while gamma is present throughout the neuron [31]. Alpha and beta can inhibit phospholipase D224, which is involved

in cytoskeletal regulation and endocytosis. Thus, these forms are responsible for vesicular transport.

Alpha-synuclein is approximately 140 amino acids long and is known to play a vital role in vesicular transport. α -syn consists of 3 regions — the central hydrophobic terminal flanked by an acid carboxyl-terminal and the N-terminal that contains seven repeats of KTKEGV, which forms the membrane-binding domain [68-70]. The central region is responsible for fibrillization, and any deletion in this area explains fibrillization under stress conditions [71]. The circular dichroism (CD) spectra of mutant E46 monomers were found to be randomly coiled, while it exists in the β -pleated structure under assembly conditions indicating that in the oligomeric form, the structure of the protein changes to a β -pleated structure similar to A β [72]. The polymerization of α -syn is similar to that of A β and is nucleation dependent. Figure 3 depicts the polymerization of α -syn in the Lewy body. When misfolded, α -syn monomers form a β -pleat structure that shows a high affinity for the other monomers, thus resulting in the formation of oligomers. These oligomers act as intermediates and are later formed into protofibrils, fibrils, and finally Lewy bodies via nucleation. Lewy bodies are the insoluble fibrillar species containing intracellular globular cytoplasmic inclusions (consists of proteins, lipids, and membranous organelles). The process of polymerization can be divided into 3 phases. The first phase is slow that allows α -syn monomers to form partially folded oligomers ad ordered oligomers. During the second phase (elongation phase), the ordered proteins cause misfolding of other monomers resulting in formation of larger fibrils. The last phase is fast and fibrils attain their maximum size, beyond which they do not grow [73]. Postmortem brain reports show a similarity between α -syn and A β . Like amyloid fibrils, these are unbranched, contain an anti-parallel β-sheet structure, and are resistant to proteolysis, which is even seen in prion proteins. Alpha-synuclein also binds to thioflavin-T, which is a characteristic feature of Aß [72]. Under acidic conditions, the net charge is neutral, decreasing the intramolecular repulsions, which makes it prone to aggregation [70, 74]. Furthermore, postmortem reports of patients suffering from PD suggest that α-syn undergoes posttranslational modifications such as ubiquitination, phosphorylation, and nitration [75]. However, Bartels et al. (2011) demonstrated that α -syn purified from the brain could form aggregates and that posttranslational modification did not alter the process of aggregation [76]. This indicates that modifications of the protein do not affect the polymerization of the protein.

Alpha-synuclein has been found to directly promote SNARE (Soluble NSF Attachment protein Receptor) complex assembly (plays an important role in vesicle fusion) that involves the binding of the N-terminal of α -syn to phospholipids and the C-terminal to synaptobrevin. The SNARE complex assembly formation

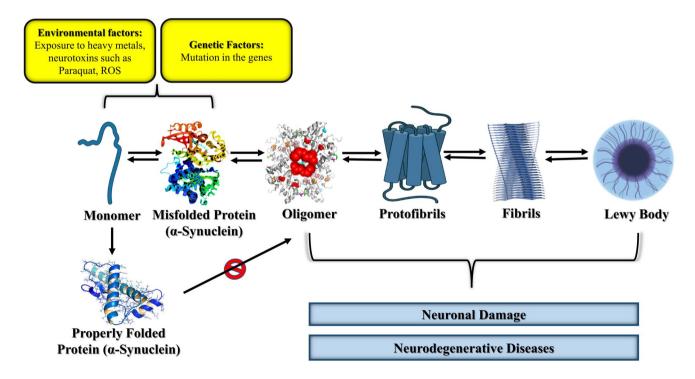


Fig. 3 Mechanism of formation of large sized aggregates in Parkinson disease: Under normal conditions, the protein (α -synuclein) is folded properly. However, environmental and genetic factors trigger misfolding of protein which leads to the formation of aggregates

which results in formation of Lewy body. Formation of Lewy body causes neuronal damage which results in neurodegenerative disease, Parkinson promotes the vesicle fusion. Loss of SNARE-mediated fusion leads to loss of neuronal function [77]. Thus, loss of function of α -syn is directly related to loss of neuronal function, and these functions of the protein are accomplished by interacting with the lipid bilayer. Pfefferkorn et al. (2010) studied the effect of tryptophan (Trp) mutation on the membrane-binding ability of α -syn. Trp contains an indole ring in its side chain, which is sensitive to the local environment; thus, Trp mutation is ideal to study the membrane-binding property of α -syn [78]. In the study, they substituted Trp and observed that although the membrane-binding affinity was not affected to a greater extent, Trp-4 and Trp-94 showed high membrane affinity. It was also observed that the membrane affinity increased under acidic conditions.

Huntingtin Protein

Guo and his colleague (2018) described the structure of HTT by cryo-electron microscopy. According to them, HTT is an α -helical protein weighing approximately 350 kDa. It consists of three domains: the N-terminal, central, and C-terminal regions. The N-terminal bears 2 membrane-binding regions and contains repeats arranged in a solenoid. The C-terminus is also believed to contain multiple HEAT repeats. The terminals are joined by the salt bridge domain. They also identified HAP-40 (huntingtinassociated protein 40) as the central regulator of proteins that stabilize HTT protein upon binding [9]. However, Guo believed that the heterogeneity in the conformation of HTT prevents a better understanding of its structure. Costanzo (2013) also demonstrated that transfer is cell-cell mediated [79]. The aggregation of these proteins is due to the expansion of polyglutamine residues in the N-terminal. The length of the repeat determines the tendency of aggregation [80]. It is believed that when mutant HTT contains more than 35 polyQ repeats, it forms oligomers, which are responsible for collapsing proteostasis, such as autophagy and the ubiquitin-proteasome system (UPS) [35]. A major mode of regulation of several cellular processes is through posttranslational modifications. These modifications include phosphorylation and acetylation, which affect the 3D structure of the protein and modulate the physiology of the protein. The cytoplasmic and nuclear localization of HTT is mediated by phosphorylation at serine and threonine residues, particularly Ser-13, Ser-16, and Thr-3 [81, 82]. Acetylation of lysine residues within the N-terminal modulates aggregation of the protein and affects membrane binding [83].

TAR DNA-Binding Protein 43

TDP-43 (TAR DNA-binding protein 43) is a versatile RNA/DNA-binding protein that is involved in RNA metabolism [84, 85]. In 2006, TDP-43 was identified as one of

the key components of insoluble inclusions isolated from ALS patients. The TDP-43 protein is an approximately 400 amino acid long peptide that encodes the TARDBP gene and is located on the 1st chromosome. TDP-43 has an N-terminal domain, two RNA recognition motifs, a nuclear export signal, and a C-terminal domain. The N-terminal domain has a nuclear localization signal that allows the protein to enter the nucleus. TDP-43 is primarily localized in the nucleus but can export to the cytoplasm under specific conditions [86]. The C-terminal region has a glutamine/asparagine-rich domain and a glycine-rich region [18, 87–89]. This protein has multiple functions and is involved in RNA metabolism (transcription, translation, mRNA stabilization, etc.) [4, 18]. TDP-43 proteinopathies are distinguished by cytoplasmic localization of the protein, the presence of hyperphosphorylated and ubiquitinated forms of the protein, the deposition of these forms, the formation of inclusion bodies, the formation of toxic C-terminal TDP-43 fragments, and protein aggregation.

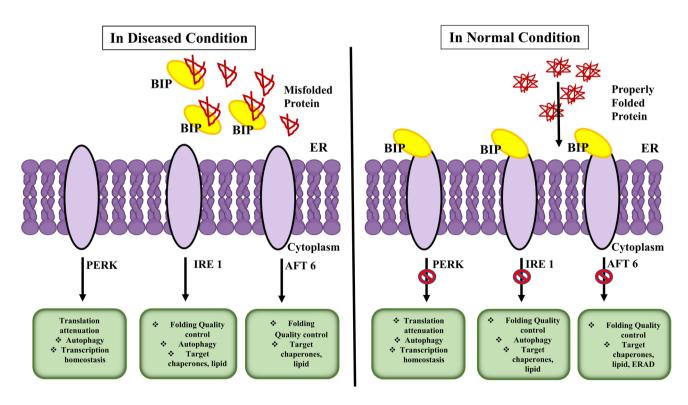
Prions Such as the Nature of Misfolded Proteins and NDs

The seeding property was first established for infectious prion particles [90]; however, recent studies have demonstrated that the seeding property is inherent to all misfolded protein aggregates involved in NDs [90-93]. Prion is composed of misfolded prion protein (PrPSc) aggregates that self-replicate and spread (seed) in the infected brain. The fact that seeding is a common attribute of the misfolded protein aggregates involved in NDs suggests that such protein aggregates have the potential to be infectious and result in conversion from the normal state to a misfolded state [90, 94]. Recently, scientists have also found prion-like proteins in other NDs that are not infectious [80, 91, 93]. These proteins are known to seed by the formation of tunneling nanotubes [92] or by the process of endocytosis [95]. The process of misfolded protein seeding during NDs is supported by the fact that inoculating brain tissue homogenates from ND patients or transgenic animals containing A β , tau, and α -Syn protein aggregates resulted in disease induction in the recipient in vitro cellular model system or in vivo in animal models [95–97]. Of note, the transmission of synthetic or recombinant misfolded protein aggregates prepared in vitro has also been established. However, more efficient seeding has been witnessed with tissue homogenates than with purified or recombinant proteins, signifying the role of other cellular mediators in the pathological transmission of NDs [97-99]. Last, the pathogenic spreading of ND has even been witnessed with the systemic administration of seeds. However, whether spreading or seeding of protein misfolding is restricted to the protein aggregate accumulation of tissue damage and disease progression is an active area of research.

Cellular Response to Misfolding of Proteins

Misfolded proteins can have three fates — they may be degraded, refolded, or delivered to the quality control center that can sequester harmful misfolded proteins [20, 100]. The misfolded proteins present in the cytosol and the endoplasmic reticulum (ER) are recognized by cellular sensors that generate a response that blocks translation, recruits' chaperones to refold the proteins, and if necessary, degrades the proteins or causes apoptosis [20, 101].

The unfolded protein response (UPR) is a process that maintains homeostasis within a cell. The UPR is activated under stress conditions, as in AD [102]. The ER membrane contains three proteins that act as sensors: PERK (protein kinase R-like endoplasmic reticulum kinase), IRE1 inositol requiring kinase 1), and ATF6 (activating transcription factor 6). These proteins are bound to another protein known as BiP that inactivates the proteins [100]. When BiP dissociates under stress, these proteins are activated and cause modification of the transcription and translation process and prevent cellular damage, while BiP acts as a molecular chaperone and refolds proteins (Fig. 4) [103]. The protein level of BiP/GRP78 is increased in AD, where they assist in refolding of the proteins [104]. The transmembrane protein PERK dimerizes and phosphorylates the translation initiation factor eIF2a, which blocks translation. PERK is also responsible for the activation of ATF4 which increases the expression of chaperones [105]. The expression of ATF4 for a longer duration is linked with apoptosis [100]. IRE1 homodimerizes and undergoes a conformational change that activates the RNase domain in the cytosolic region of the protein and modulates the expression of XBP-1, a transcription factor that transactivates genes related to UPR proteins [106]. Duran et al. (2017) demonstrated that IRE1 deletion resulted in reduced expression of APP in a mouse model, indicating the role of IRE1 in the pathogenesis of NDs [107]. Under stressful conditions, ATF6 is transported to the Golgi body via vesicles where its cytoplasmic domain is cleaved in the cytosol. The domain is then transported to the nucleus, where it acts as a transcription factor. It is believed that ATF6 responds to stress caused by lipids and proteins via separate mechanisms [108]. The UPR is activated in AD [102, 104].



UNFOLDED PROTEIN RESPONSE

Fig. 4 Unfolded protein response (UPR) in diseased and normal conditions: Under normal conditions, BiP (chaperone) remains associated to the transmembrane proteins (PERK1, IRE1, ATF6). Under diseased conditions, the sensors get activated and cause transcription of genes that regulate transcription, translation, and chaperones. BiP also binds to misfolded proteins and cause refolding The proteins in the secretory pathway are thermodynamically more stable due to posttranslational modifications (such as glycosylation or disulfide linkage); however, the proteins in the cytosol are less stable due to fewer posttranslational modifications [109]. In the cytosol, misfolded proteins with exposed hydrophobic amino acids are recognized by molecular chaperones (HSP70, HSP90, HSP100, and sHSP) [20] and are subjected to three different fates as described below:

A Degradation of misfolded proteins

Misfolded intracellular proteins can be degraded by the ubiquitin-proteasome pathway (UPP), which involves the covalent binding of ubiquitin with the protein followed by the degradation of the protein. The ubiquitin molecule is released during the process and can be reused [20]. For example, Tau is ubiquitinated at the Lys254, Lys257, Lys311, Lys317, and Lys63 residues and degraded by E3 ubiquitin ligase [101, 110]. Misfolded proteins can also be transferred to acidic compartments, such as lysosomes, where the proteins are exposed to low pH, which ensures their unfolding and cleavage by proteolytic enzymes [75]. The importance of lysosomal enzymes can be predicted, as the inhibition of lysosomal enzymes in rat brains can induce the formation of tangles [111]. Recently, it has been discovered that α -syn can be degraded via selective autophagy [112], which is termed synucleinopathy. According to this mechanism, α -syn in neurons activates microglia, which engulf proteins in autophagosomes. These autophagosomes are then degraded via selective autophagy [112]. Misfolded proteins can also undergo chaperone-mediated autophagy in which HSP70 recognizes the proteins and then degrades them by lysosomes; however, this process is selective for proteins [75]. Notably, α -syn-mediated neurotoxicity was enhanced several folds when chaperone-mediated autophagy was suppressed in neurons [113].

B Refolding

Upon sensing the presence of misfolded proteins, the cell selects several molecular chaperones that cause the refolding of the protein. Chaperones such as BiP are activated as discussed above by dissociating from transmembrane proteins, binding to the target protein and promoting folding. Several other chaperones in the ER are activated by the UPR, which accelerates the folding of the proteins. Heat shock proteins (HSPs) play a major role under stressful conditions, as their transcription is upregulated which promotes protein folding [114]. In the cytoplasm, the unfolded proteins are recognized by Hsp70 and Hsp40 cochaperones. More mature folding intermediates are recognized by Hsp90 or TRiC/CCT (TCP1-ring complex or chaperonin containing TCP1).

Protein aggregation is also reduced by sHsps. These chaperones aim to refold misfolded proteins. The activity of each of these molecular chaperones is discussed in detail in a later section. In the ER, the roles of Hsp70, Hsp40, and Hsp90 in damage recognition are conserved, and there is no TRiC/CCT homolog. The role of sHsps is also restricted to the ER [115].

C Protein sequestration

When the concentration of misfolded proteins rises, the cell employs a strategy to avoid chaperone saturation. Other misfolded proteins are sequestered in quality control centers as part of this strategy [20, 28]. The concentrated proteins stored in the centers are later degraded or refolded depending on the cellular condition. Cytosolic proteins that are misfolded or cannot be refolded or degraded accumulate in the juxtanuclear quality control compartment (JUNQ). These proteins accumulate in the JUNQ under unfavorable conditions and can be recycled to the cytoplasm when the conditions are ambient where they can be refolded [20]. When the cell fails to refold, degrade, or sequester the misfolded proteins, the concentration of misfolded protein increases within the cell. Under such conditions, the proteins are likely to form aggregates and cause cytotoxicity.

Role of Molecular Chaperones in Protein Folding/Aggregation During NDs

Under adverse cellular conditions, cells produce proteins that can maintain homeostasis within the cell. Such proteins are termed heat shock proteins (HSPs) or molecular chaperones [15, 114]. They are intricately involved in the prevalence of protein misfolding diseases by (i) preventing aggregation of wrongly folded proteins, (ii) promoting the refolding of proteins, and (iii) facilitating degradation of the misfolded protein [15]. Chaperones interact transiently with protein [116]. However, a change in the interaction between the protein and the chaperone modulates the activity of the chaperone and vice versa [68]. This has been demonstrated in a study where it was observed that a change in the activity of the chaperone modulates the interaction with protein disturbing the balance and leading to PD [68]. Based on the structural and functional similarities of these proteins, they are categorized into different families. Members of these families may be constitutively expressed or may be expressed only when required and possess the ability to recognize misfolded proteins in the cytoplasm and the ER [117, 118]. Table 2 gives an overview of molecular chaperones found within the cell. These chaperones are commonly found in the cytoplasm, but they move to other compartments under stress. It has been recently discovered that HSPs can be secreted by non-neuronal cells into the micro-environment and can be subsequently utilized by

S. No	Chaperone	Cellular location	Co-chaperone	Structure	Mechanism of action	Functions	ATP dependent	Ref
-	HSP60 [Chaperonin (Cpn)]	Mitochondria + cyto- sol	0IdSH	Two stacked hepta- meric ring	Chaperonins undergo significant confor- mational changes during a folding reaction as a result of ATP enzymatic hydrolysis along with binding of substrate proteins and cochaperonins such as GroES	Protein folding and conformation main- tenance	Yes	[115, 121]
6	HSP70 [Constitutive (HSC70) Induced (HSP70)]	Cytosol + ER + mito- chondria + nucleus	HSP40 NEF (nucleotide exchange factor, for example, HSP110)	N-terminal ATPase domain and C-terminal peptide- binding domain	Hsp70 system com- municates with extended peptide segments of proteins along with partially folded proteins to cause protein aggregation in key pathways, resulting in activity down- regulation	Protein folding and preventing protein aggregation; dis- sociate protein complexes	Yes (hydrolysis of ATP promotes bind- ing to the substrate)	[101, 114, 115]
<i>c</i> 0	06dSH	Cytosol + ER + mito- chondria + nucleus	PP5; HSP82; Stil; SGTA; Tahl; AHA1; FKBP51 and/or FKBP52; CHIP; CYP40, p23; TTC4; Unc45	Has 3 domains: N-terminal, C-terminal domain that interacts with co-chaperone	The Hsp90 protein has three functional domains: ATP-bind- ing, protein-binding, and dimerizing, each of which is critical to the protein's function	Prevent aggregation stabilization of mon- omer, maturation of steroid receptors and protein kinases	Yes	[122, 123]
4	HSP100 (AAA+chaperones)	Cytoplasm + nucleus	HSP70 system, ClpP, ClpS	Form oligomeric ring structures	In the target aggre- gate, the Hsp100 hexamer forms multivalent contacts. When ATP is hydro- lyzed, the Hsp100 oligomer changes conformation, disrupting contacts between aggregated proteins	Unfolding, prote- olysis, thermotoler- ance, resolubiliza- tion of aggregates, remodeling	Yes	[124]

 Table 2
 Overview of molecular chaperones in the cell

S. No Chaperone	Cellular location	Co-chaperone	Structure	Mechanism of action Functions	Functions	ATP dependent	Ref
5 sHSP	Cytosol + ER + mito- chondria + nucleus		Conserved C-termi- nal, alpha-crystallin and n-terminal	Conserved C-termi- Prokaryotic sHSPs Destabilizes the nal, alpha-crystallin appear to have aggregates and n-terminal numerous multi-type Facilitate refolding substrate-binding residues that can be hierarchically activated in a temperature-depend- ent manner, acting as temperature-regu- lated chaperones	Destabilizes the aggregates Facilitate refolding	Ŷ	[125-127]

neurons. The most studied extracellular chaperone is HSP70 which is known to confer neuroprotective role (by masking toxic extracellular proteins, driving adaptive immune signaling, and stalling expression of proteins playing role in synaptic pruning). Several studies are now being conducted to treat NDs by targeting the extracellular HSPs; however, the complete knowledge of extracellular HSPs and the role played by them is imperative for developing a therapy [119, 120].

One of the largest molecular chaperone families is HSP70. HSP70 in eukaryotes occurs in two different forms: HSC70 (heat shock cognate protein 70), which is constitutively expressed and HSP70 which is expressed under stressful conditions [128]. HSP70 is known to play a major role in diseases involving misfolded proteins such as Alzheimer's and tauopathies wherein it is responsible for facilitating refolding and disaggregation [129]. HSP70 binds to the hydrophobic region of proteins via its C-terminus in an ATP-dependent manner [114, 130]. HSP70 bound to ATP has a low affinity for the substrate. Hydrolysis of ATP increases the affinity toward the substrate. Thus, ATP hydrolysis regulates the affinity between the chaperone and the target protein. This process necessarily requires the presence of HSP40, which acts as a cochaperone and aids the process. The importance of HSP70 in proteinopathies is demonstrated by the fact that its knockdown makes neurons more vulnerable to cytotoxicity and neurodegeneration [19]. Alternatively, overexpression of HSP70 by pharmacological and genetic approaches promotes neuroprotection in misfolded NDs, such as PD [131, 132], AD [133], and HD [134]. HSP70 binds to the hydrophobic region of these proteins and promotes the recovery of the native conformation, preventing the formation of aggregates.

HSP90 is another important HSP that requires ATP hydrolysis for activation and proper functioning [135]. Several cochaperones influence the ATP cycling process and facilitate bonding with the substrate [136]. HSP90 is a dimeric protein found in the cytosol and ER. It is involved in maintaining protein homeostasis by ensuring the proper folding of proteins and degrading misfolded proteins. The two major HSP90 isoforms HSP90ß are expressed constitutively, and HSP90 α , whose expression is induced under stress, exists in the cytosol [122]. Selective Hsp90 α/β inhibitors have been found to promote clearance of inclusion bodies formed by mutant HTT in rodents [137]. Furthermore, HSP90 binds to HTT via the N-terminus and recruits the deubiquitinating enzyme USP-19 (ubiquitin specific protease 19) to modulate the protein and aggregate of HTT [117]. Hsp90 has several cochaperones that aid in the proper functioning of HSP90 [123]. The most common cochaperones are cdc37 (cell division control protein 37), HSP82, Sti1 (stress-inducible protein 1), and PP5 (protein phosphatase 5) [123, 138]. P23 is another cochaperone of HSP90 that is

also a therapeutic target, as gedunin, a p23 inhibitor, prevents neurotoxicity induced by 1-methyl-4-phenyl pyridine (MPP+) [138].

Small heat shock proteins (sHSP) are a group of proteins that weigh less than 40 kDa and are upregulated during stress [126, 139, 140]. These proteins work in an ATPindependent manner and are expressed under unfavorable conditions [139]. Small HSPs play a vital role in refolding proteins, destabilizing, and facilitating the solubilization of aggregates [125, 127, 141]. These proteins carry a conserved sequence called the α -crystallin domain between the N and C terminals. HSP27, a low-molecular weight protein, is known to mitigate cellular damage and neuronal cell death during NDs [75], whereas HSPB5 reduces cellular toxicity and prevents fibril formation by α -syn [127]. It acts as an anti-apoptotic protein and molecular chaperone when it exists in large oligomers [125]; however, it regulates the microfilament dynamics when it exists in small oligomers [141]. Reduction in the level of HSP27 with methylglyoxal results in the aggregation of α -syn, impaired clearance, and neurotoxicity, an effect that was reversed by overexpression of Hsp27 [140]. Studies have demonstrated that the terminal regions of Hsp are important for stable fibril binding and that these regions can play a cytoprotective role in vivo [126].

The Landscape of Therapeutics Targeting Protein Misfolding or Aggregation in NDs

Regardless of the extensive information and advancements in the field of NDs, no effective cure or treatments are available for preventing NDs. This is a consequence of lack of understanding of the tertiary structures of the misfolded proteins, inability of the drug to cross the BBB, recognition of few epitopes by the antibodies, etc. Despite facing these challenges, misfolded protein aggregates remain the primary target for effective therapeutic intervention for NDs. Of note, molecules/drugs are now being formulated that have the potential to diffuse or dilute the aggregates formed in the various brain regions.

Antibodies Targeting Misfolded Proteins

Recently, antibodies have been developed against misfolded proteins that can stimulate both humoral and cell-mediated immunity in the patients [142]. These antibodies are specific to the target proteins and can offer long-term clearance of these proteins. They can dissolve soluble and insoluble aggregates. Both active and passive immunizations have been explored and have shown remarkable potential for the treatment of NDs [143]. However, the major disadvantage of using antibodies is their ability to cross the blood–brain barrier and recognize only a limited number of epitopes. Table 3 shows a list of antibodies that have been generated against α -syn, A β , HTT, and tau. The antibodies target different regions of these proteins and aim to reduce oligomerization and prevent cell-to-cell transfer. Several of these antibodies may be supplemented with other drugs to reduce symptoms in patients suffering from NDs.

Monoclonal antibodies are considered a therapeutic strategy for AD. One such monoclonal antibody is bapineuzumab which is currently discontinued due to its lack of efficacy [168]. Crenezumab is another monoclonal IgG4 antibody that binds to monomeric and aggregates of A β . It is known to block the aggregation of monomers and has the potential to induce disaggregation. Crenezumab lowers the Aß concentration in the cerebrospinal fluid in AD patients [161]. Amyloid-beta fibril formation is also inhibited by chronic intranasal treatment of single-chain fragments derived from IgG that can inhibit neurotoxicity and neutralize neurotoxicity related to A β in transgenic mice [184]. Another antibody studied is aducanumab which when administered to patients intravenously suffering from AD for a year, caused regression of A β plaques in a dose-dependent manner. However, intravenous infusion of the monoclonal antibody has several side effects on patients, including upper respiratory tract infection, urinary tract infection, and headache [162]. Due to a high number of side effects observed, aducanumab is now discontinued. Bosch (2014) showed that immunized dogs show smaller amyloid plaques than nonimmunized dogs [21]. Purified anti-A β 40 IgGs were given to dogs, and these exhibited stronger immunoreactivities to disperse plaques. A parallel study carried out with commercial anti-Aß 40 IgGs demonstrated an increase in the immunoreactivity toward neuritic plaques [21]. Xing et al. (2017) developed a monoclonal antibody (3F5) against 11 amino acid residues of the N-terminal region of A_β. Treatment with 3F5 has certain disadvantages, as it may result in microhemorrhage lesions and cerebrovascular edema; however, 3F5 also decreased the death rate of neuronal cells in mice and the amount of A β deposits [22]. Several other antibodies, such as solaneuzumab, gantenerumab, and ponezumab, offer passive immunity, while AN-1792, ACI-24, CAD-106, ACC-001, and ABvac40 offer active immunity and target AB and its aggregates [27, 158, 164, 166, 167, 169, 170, 172].

Several antibodies show the potential to target α -syn protein and cause the reduction of extracellular protein. BIIB054 and prasinezumab are the most advanced projects to date. Administration of BIIB054 has been seen to have several mild side effects, such as headaches. However, no symptoms of cardiovascular disease or stroke were visualized [149]. MEDI1341 is an antibody that targets the C-terminal of α -syn and attenuates cell-to-cell transmission of preformed fibrils in mammalian models such as mice [153]. Administration of α -syn oligomer selective antibodies (mAb47,

 Table 3
 Antibodies targeting misfolded proteins in NDs

S. No	Antibody	Target	Type of immunization	Trial	Comments	Ref
1	mAb47	Protofibril structure of α-Syn	Passive immunization	Preclinical	 Reduce oligomerization Reduce protofibrils 	[144, 145]
2	Naturally occurring autoantibody NAb-Syn	α-Syn oligomer	Passive immunization	Preclinical	• Reduction of soluble form, phosphoryl- ated and oligomers of α-Syn	[146]
3	Prasenizumab (PRX002)	α-Syn aggregates	Passive immunization	Clinical (phase II)	• Reduce free α-Syn in serum but not in CSF	[23, 147]
4	BIIB054	N-terminal of α -Syn	Passive immunization	Clinical	 Antibody forms complex with α-Syn of the serum 	[148, 149]
5	Recombinant α-Syn	C-terminus of α -Syn	Active immunization	Preclinical	 Reduced accumula- tion 	[150]
6	AFFITOPE	α -Syn aggregates	Active immunization	Clinical (phase I)	 Generates anti-α-Syn antibodies Reduce neuronal loss 	[151, 152]
7	MEDI1341	C-terminal of α -Syn	Passive immunization	Preclinical	• Attenuates cell to cell of fibril	[153]
8	Anti-Aβ 31–35	Αβ42	Passive immunization	Preclinical	 Prevent apoptosis Restore synaptic plasticity 	[154]
9	Bapineuzumab	N -terminal of Aβ and Aβ plaques	Passive immunization	Clinical (discontinued)	• Several adverse effects noticed	[155, 156]
10	Solaneuzumab	Mid domain of $A\beta$	Passive immunization	Clinical (phase III) (discontinued)	• Could not improve cognitive decline	[27, 157]
11	Gantenerumab	Aβ aggregates and N-terminal of Aβ	Passive immunization	Clinical (phase III)	Dose-dependent reduction of plaquesReduce cognitive decline	[158, 159]
12	Crenezumab	Mid-domain of Aβ	Passive immunization	Clinical (phase III) (discontinued)	 Reduce aggregation IgG4 antibody Reduced inflammatory Low efficacy 	[160, 161]
13	Aducanumab	N-terminal of Aβ (soluble and insoluble)	Passive immunization	Clinical (phase III) (discontinued)	• Reduce plaques formation	[162, 163]
14	Ponezumab	C-terminal of Aβ	Passive immunization	Clinical (discontinued)	 Reduce Aβ in CNS and blood No effect on cogni- tive decline 	[164, 165]
15	AN-1792	Αβ	Active immunization	Clinical (discontinued)	 Cleared Aβ40, Aβ42, and Aβ43 plaques Severe side effects 	[166]
16	ACI-24	Aβ aggregates	Active immunization	Clinical (phase II)	• Trigger immune response in patients	[1 <mark>67</mark>]
17	CAD-106	Αβ	Active immunization	Clinical (phase II)	 No severe effects Increased anti-Aβ antibodies 	[168, 169]
18	ACC-001	N-terminal of Aβ	Active immunization	Clinical (phase II)	 No severe side effects Increased anti-Aβ antibodies 	[170, 171]
19	ABvac40	C-terminal of A _β	Active immunization	Clinical (phase II)	 Increased anti-Aβ antibodies 	[172]

 Table 3 (continued)

S. No	Antibody	Target	Type of immunization	Trial	Comments	Ref
20	Tau379-408	Tau	Active immunization	Preclinical	 Triggered anti-tau antibody Reduce aggregates Clearance of tau species 	[173]
21	AADvac1	Tau oligomer	Active immunization	Clinical (phase II)	• Reduction in cogni- tive decline	[174]
22	ACI-35		Active immunization	Clinical (phase II)	 Reduce aggregation 	[175]
23	CBTAU-22.1	Tau	Passive immunization	Preclinical	 Reduce aggregation, seeding, and spread Reduce tau helical filaments 	[176]
24	43D, 77E9	N-terminal of tau	Passive immunization	Preclinical	 Reduced total and phosphorylated tau Reduced memory impairment 	[177]
25	TOMA	Tau oligomer	Passive immunization	Preclinical	 Reduce oligomers Reduced memory loss	[178]
26	C2N, 8E12, gos- anemab, zagoten- emab, semorinemab	Tau	Passive immunization	Clinical (phase II)	• Reduce aggregates	[179]
27	C10.2	Tau	Passive immunization	Preclinical	• Reduced tau seeding	[180]
28	ABBV-8E12	Tau	Passive immunization	Clinical (phase II)	• Stop or slow the progression of tau pathology	[181]
29	INT41	Htt	Passive immunization	Preclinical	 Reduced nuclear translocation Reductions in aggre- gates 	[182]
30	sc-Fv-C4	Htt	Passive immunization	Preclinical	Increases solubilityInhibits aggregation	[183]

mAb49G, mAb38E2) can increase the clearance of α -syn added exogenously. Administration of the antibody rescued the astrocyte from mitochondrial damage and decreased the aggregates. Of all the antibodies, mAb47 showed the most promising effect [144]. In addition, AFFITOPE generates anti- α -syn antibodies and reduces neuronal loss. This drug is currently under phase I clinical trial.

Administration of antibodies targeting tau protein has also been shown to reduce the polymerization of tau. Administration of the C10.2 antibody targets tau aggregates and reduces tau seeding [180]. Administration of a single chain variable fragment of MC1 reduced tau pathology in rodents. The delivery of the antibody was achieved by adeno-associated virus (AAV). Administration of the antibody decreased the insoluble and soluble tau forms in the cortex and hippocampus [185]. BIIB092 is a monoclonal antibody that recognizes full-length tau and N-terminal tau fragments. The N-terminal tau fragments are found extracellularly in the cerebrospinal fluid (CSF). Administration of this monoclonal antibody reduced the induction of tau aggregation. Antibodies targeting HTT have also been discovered; however, few antibodies targeting HTT are known. A monoclonal antibody (C6-17) is known to target the exposed region of HTT and inhibit cellular uptake of the protein in vitro [185]. Other antibodies include INT41, sc-Fv-MW1, sc-Fv-MW2, and sc-Fv-C4 target mutant forms of HTT and aggregates [182, 183, 186]. These antibodies reduced the aggregates of the protein and increased cell survival.

Targeting Chaperones

A promising treatment for NDs is the development of neuroprotective therapies that target protein misfolding and aggregation. Chaperones are critical targets in protein folding and degradation. Chaperones are divided into three types: molecular chaperones, chemical chaperones, and pharmacological chaperones. Within the cell, there are molecular chaperones [129]. Targeting the expression of these molecules appears to protect the cell from toxicity caused by protein misfolding. Several natural molecules influence molecular chaperone activity [187]. They may increase or decrease the expression of chaperones that protect the cell from proteinopathies. Furthermore, several synthetic drugs that target molecular chaperones or act as chaperones themselves are being developed to improve the stability of folded proteins [188]. Table 4 gives an overview of several natural and synthetic molecules that cause protein folding, protein degradation, activation of chaperones, and inhibition of chaperones that are responsible for protecting the cell from a toxic gain of function of misfolded proteins.

Geldanamycin and radicicol act as HSP90 inhibitors and impair the interaction of HSP90 and the protein. The interaction between HSP90 and protein was lost after 24 h of treatment with the drug. It was also observed that

 Table 4
 Chaperones as a therapeutic target

S. No.	Name	Molecular formula	Origin/ Type	Fu	nctions	Disease	Chemical structure	Ref
1.	Geldanamycin (Hsp90 Inhibitor)	C ₂₉ H ₄₀ N ₂ O ₉	Natural (Antibiotic)	AA	Inhibits Hsp90 interactions Increases Hsp70 expression and activity	PD(α-Syn) AD (tau, Aβ) HD(HTT)		[189 191]
2.	17-AAG (Tanespimycin) (Hsp90 Inhibitor)	C ₃₁ H ₄₃ N ₃ O ₈	Semi-synthetic derivative of geldanamycin	AA	Inhibits Hsp90 interactions Increases Hsp70 expression and activity	PD(α-Syn) AD(Aβ)	H ₂ C H ₂ C H ₃ C	[192]
3.	SNX Compounds (Hsp90 Inhibitor)	C ₂₅ H ₃₀ F ₃ N ₅ O 4	Synthetic	A A	Inhibits Hsp90 interactions Increases Hsp70 expression and activity	PD(α-Syn) AD(Aβ)		[188]
4.	Carbenoxolone (HSF-1 modulator)	C ₃₄ H ₅₀ O ₇	Glycyrrhetinic acid synthetic derivative	A A	Activates HSF-1 activation Induces downstream Hsp70 expression	PD(α-Syn); HD(HTT); AD(Aβ)		_{он} [193]
5.	Celastrol (HSF-1 modulator)	C ₂₉ H ₃₈ O ₄	Natural	A A	Activates HSF-1 activation Induces downstream Hsp70 expression	PD(α-Syn) HD(HTT); AD(Aβ)	о о о о	[194 - 196]
6.	Trehalose	C ₁₂ H ₂₂ O ₁₁	Osmolyte	A A	Create environment that promote protein stabilization and folding Prevent protein aggregation	HD(HTT), PD(α-Syn)		1
7.	Mannitol	$C_{6}H_{14}O_{6}$	Osmolyte	^ ^	Create environment that promote protein stabilization and folding Prevent protein aggregation	PD(α-Syn)		[198] H
8.	MSP-M Based Chaperone	NaH ₂ PO ₄	Synthetic	>	Promote Clearance of aggregates	AD(Aβ)	o-ÖH ÖH	[199]
9.	Curcumin	$C_{21}H_{20}O_6$	Natural (Polyphenol)	A	Monomer Stabilization Firbril Disassembly	PD(α-Syn) AD(Aβ) HD(HTT)	HO CH ₃ H ₃ CO	[200]

10.	EGCG	C ₂₂ H ₁₈ O ₁₁	Natural	>	Monomer Stabilization	PD(α-Syn)	OH [187
			(Polyphenol)	>	Firbril Disassembly	AD(Aβ)	
11.	Baicalecin	$C_{21}H_{18}O_{11}$	Natural	~	Fibril Disassembly	PD(a-Syn)	
12.	Fasudil	$C_{14}H_{17}N_3O_2S$	Synthetic	~	Monomer Stabilization	PD	
13.	Squalamine	C ₃₄ H ₆₅ N ₃ O ₅ S	Natural (Sterol)	~	Lipid-dependent nucleation	PD	(1000000000000000000000000000000000000
14.	Trodusquemine	C ₃₇ H ₇₂ N ₄ O ₅ S	Natural (Sterol)	À À À	Lipid-dependent nucleation Seeding prevention	PD	
15.	Leucomethylthi oninium (LMTM)	$C_{16}H_{21}N_3S^{+2}$	Natural	>	Unknown	PD	Н [205]]
16.	Molecular tweezer (CLR01)	C ₄₂ H ₃₀ Na ₂ O ₈ P ₂	Synthetic	A A	Off-pathway aggregation Fibril disassembly	PD	$ \begin{array}{c} & & & & \\ & & & & \\ & $
17.	Anle 138b	C ₁₆ H ₁₁ BrN ₂ O 2	Synthetic	>	Anti-oligomeric	PD	
18.	Synu Clean-D	C ₁₃ H ₅ F ₃ N ₄ O ₅	Synthetic	>	Fibril Disassembly	PD	
19.	Tauroursodeoxy cholic acid (TUDCA)	C ₂₆ H ₄₅ NO ₆ S	Chemical Chaperone	A A	Reduce accumulation Apoptotic Inhibitor	AD(Aβ)	о о с [209 ,210 но н н он

inhibition of HSP90 β leads to the relocalization of α -syn to the mitochondria [68]. Wang et al. (2017) proved that the use of an HSP90 inhibitor (OS47720) can reach the brain and elicit a heat shock-like response by activating

heat shock factor (HSF1), which can translocate to the nucleus and activate numerous genes [226]. The HSP90 inhibitor was found to be nontoxic and capable of increasing Synapsin I, which can protect the synapse

20.	Ursodeoxycholi c acid (UDCA)	C ₂₄ H ₄₀ O ₄	Chemical Chaperone	AA	Reduce accumulation Apoptotic Inhibitor	AD(Aβ)	
21.	Oleocanthal	C ₁₇ H ₂₀ O ₅	Natural phenolic compound	AA	Prevent Aggregation Enhance clearance	AD (Aβ, tau)	
22.	Ambroxol	C ₁₃ H ₁₉ Br ₂ Cl N ₂ O	Pharmacological Chaperone	A A	Bind to target protein Promotes chaperone mediated proteostasis	PD	$HO \xrightarrow{H}_{H} \xrightarrow{H}_{H} \xrightarrow{H}_{H_2} \xrightarrow{Br} \begin{bmatrix} 24, \\ 213 \end{bmatrix}$
23.	Isofagomine	C ₁₀ H ₁₉ NO ₉	Pharmacological Chaperone	A A	Bind to target protein Promotes chaperone mediated proteostasis	AD(Aβ)	HO NH [214 HO'' OH
24.	Resveratrol	C ₁₄ H ₁₂ O ₃	Polyphenol	A A	Reduce Fibril formation Reduce phosphorylation of tau (prevents aggregation)	PD (α-Syn) AD (Aβ) HD (HTT)	HO OH [215 J
25.	Ginseng	C ₄₂ H ₆₆ O ₁₇	Natural	A	Reduce aggregation	AD PD	
26.	Chalcone derivatives	C ₁₅ H ₁₂ O	Chemical Chaperone	~	Prevent fibril formation	AD	<u>о́н</u> [217
27.	Tetra-hydro phenanthridine	C ₁₉ H ₁₆ N ₄ O ₇	Chemical Chaperone	~	Act as chaperone	PD	
28.	Isoindoline-1,3- dione derivatives	C ₈ H ₉ N	Chemical Chaperone	A A	Aggregation inhibition Induce proteostasis network	AD	
29.	Rutaecarpine (Ru)	C ₁₈ H ₁₃ N ₃ O	Chemical Chaperone	A A	High anti-oxidative Metal-chelating activity	AD	

from damage caused by A β . It also improved several cognitive functions of the brain.

It has also been observed that chaperones can indirectly affect the aggregation of misfolded proteins. Silveira (Ambroxof) can raise the clearance can be said that Ambro

et al. (2019) found that a chaperone of glucocerebrosidase (Ambroxol) can raise the level of glucocerebrosidase and increase the clearance rate of aggregate α -syn [24]. Thus, it can be said that Ambroxol acts as a potential treatment for PD.

Table 4 (continued)

30.	7,8- Dehydrorutaecar pine derivative (DHRu)	C ₁₈ H ₁₁ N ₃ O	Chemical Chaperone	High anti-oxMetal-chelar		
31.	Isoliquiritigenin (trihydroxychalc one)	C ₁₅ H ₁₂ O ₄	Chemical Chaperone	 Inhibition aggregation, Regulation activity, 	of protein AD of proteostasis	HO OH [214]
32.	Maritimetin	C ₂₁ H ₂₀ O ₁₁	Chemical Chaperone		ein aggregation AD gomerc species	[214] но с с с с с с с с с с с с с с с с с с с
33.	Luteolin	C ₁₅ H ₁₀ O ₆	Chemical Chaperone			HO, OH, OH, 221
34.	Chloro-oxime derivative (HSF-1 modulator)	C ₈ H ₈ CINO	Chemical Chaperone	➢ Hsfl activat	ion activity $AD(A\beta)$	
35.	Riluzole (HSF-1 modulator)	$C_8H_5F_3N_2OS$	Chemical Chaperone	Inhibits prot	ein aggregation ALS AD HD	$\begin{array}{c} F \\ F \\ F \\ \end{array} \\ \begin{array}{c} & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ & \\ \\ \\ & \\ \\ \\ & \\$
36.	Deacetoxy-7- oxogedunin (CYT1–3) (HSF-1 modulator)	C ₂₆ H ₃₀ O ₆	Chemical Chaperone	 Hsfl/Hsp70 Inhibits prot 		H ₃ C CH ₃ CH ₃ [225

Antisense Therapy Targets the Expression of Proteins

Recently, the use of antisense oligonucleotide (ASO) has been increased and has shown promising effects to treat NDs [5, 151, 227–229]. The ASO is a single-stranded nucleotide that can bind to the target protein and alter its expression. The mechanisms by which oligonucleotides alter the expression of the target protein include (i) mRNA degradation by RNase H recruitment, (ii) inclusion or exclusion of exons by alternate splicing, and (iii) inhibition of the binding of miRNA to the target protein [5]. ASO is resistant to exonuclease and therefore is not targeted by endogenous enzymes that promote the long-lasting effects of ASO. Direct delivery of leucine-rich repeat kinase 2 (LRRK2) ASO prevents α -syn pathology by suppressing of LRRK2 protein expression [229]. Likewise, delivery of amidobridged nucleic acid ASO (AmNA-ASO) enhanced the targeting potency and decreased the mRNA of α -syn in vivo and in vitro [228]. AmNA-ASO was also reported to decrease motor defects in a mouse model. An advantage of using AmNA-ASO is that no off-target effects were seen in the mouse model. ASO is also a potential target for HTT in HD patients. A study showed that targeting HTT by the ASO technique resulted in the suppression of the protein in the CNS [227]. DeVos et al. (2017) designed an ASO that is specific for tau and inhibited neuronal loss. It also reduced the expression of tau mRNA and protein expression, therefore reversing tau spreading and accumulating activity in a mouse model [5].

Another way of altering the expression of the gene is by synthesizing splice-switching antisense oligonucleotides (SSOs) which are short single-stranded ASOs that can bind to a specific RNA target. The binding of SSO to the target RNA results in the skipping of an exon (alternate splicing), regulating the expression of the protein. The mature RNA formed as a result of alternate splicing lacks the targeted exon. Chang et al. (2018) synthesized an SSO that induced the skipping of exon 17 in APP. The produced mRNA lacked exon 17, which is known to code for γ -secretase. As a result, APP could not produce A β , thereby decreasing the concentration of A β 42. The SSO they synthesized contained a 2-methoxyethyl-ribose and phosphorothioate modified backbone that was resistant to the action of the exonuclease [230]. The effect of SSO was also visualized in a mouse model that had similar results. This proves that SSO can be used to target the expression of the protein in NDs.

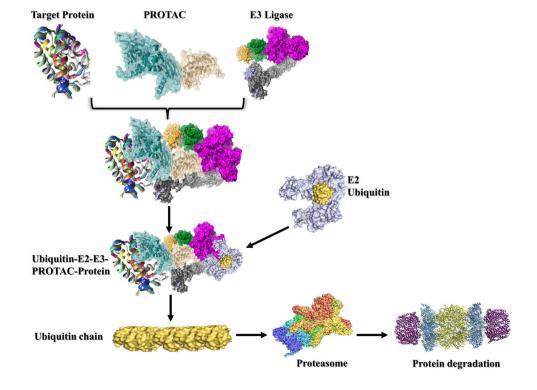
Proteolysis-Targeting Chimaera (PROTAC) Targets the Degradation of Undruggable Proteins

An emerging strategy to regulate protein concentration is PROTAC. PROTAC are small molecules that target "undruggable" proteins. These molecules bind to the target protein and E3 ubiquitin ligase and enhance the degradation of the protein (Fig. 5). PROTACs have been shown to have a more promising effect than other therapeutic strategies. Lu et al. (2018) have developed a peptide that can colocalize with Keap1 (substrate for ubiquitin E3 ligase) and downregulate intracellular tau dependent on the concentration [231]. Administration of the proteasome inhibitor MG132 proved that the developed peptide can cause proteasomedependent degradation of Tau. Similar results were obtained when Chu et al. (2016) synthesized TH006, which has tau and E3 ubiquitin ligase binding moieties [232]. TH006 has the potential to interact with Tau and cause its degradation by ubiquitination. QC-01-175 is a heterobifunctional molecule that can bind to Tau and carbon, which forms a part of the E3 ubiquitin ligase and triggers proteasomal degradation of Tau [233]. The direct introduction of a PROTAC targeting α -syn into the cell lines demonstrates its ability to regulate the expression of the protein. The designed peptide-induced degradation of α -syn in a proteasome-dependent pathway attenuates neurotoxicity [25].

Other Therapies

Neuronal survival can also be achieved by brain-derived neurotrophic factor (BDNF), which is present naturally throughout the CNS. Increased or decreased production of BDNF plays a vital role in the pathogenesis of NDs [58]. Overexpression of BDNF results in cognitive decline, while underexpression is linked to the progression of AD. Arancibia (2008) demonstrated its protective function against the amyloid-beta protein in rodents suffering from Alzheimer's disease [234]. Rats given BDNF therapy were shown to have improved learning skills and reversed loss caused by APP mutation [58, 235]. BDNF can also act on tau protein and interfere with its toxicity. Scientists have also been working on antibodies that can pass through the barrier, bind to misfolded proteins, and enhance their clearance; however, none of the antibodies produced to date is highly efficient in the process. Inhibitors of the enzyme acetylcholinesterase have been shown to improve performance in PDD (Parkinson's disease dementia) patients [236]. CRISPR/Cas9-mediated inactivation of the target protein is also a therapeutic strategy to treat NDs. CRISPR/Cas9mediated strategy results in the elimination of the pathogenic protein and is highly selective toward the target protein. Using this strategy, HTT aggregates have been attenuated in a mouse model of HD [237]. This technique has also been studied in AD [238]. However, this technique also results in off-target effects that make this strategy difficult to adopt.

Fig. 5 Mechanism of PROTAC: Proteolysis-targeting chimaeras (PROTAC) have protein binding and E3 ubiquitin ligase binding domain. On binding of the target protein and E3 ligase, E2 bound ubiquitin is recruited that adds ubiquitin to the target protein. Thus, the protein is directed toward the proteasome where it is degraded



Conclusion

Proteins are the structural unit of a cell. The secretory proteins are translated into the cytoplasm and then modified in the endoplasmic reticulum and Golgi body. These modifications fold the primary structure of proteins into tertiary or quaternary structures by the formation of chemical bonds. Proteins translated in the cytoplasm are modified and folded in the cytosol itself and can be folded into their native states with the help of chaperones in the cytosol. In a normal healthy cell, if the protein formed is not modified properly, the cell is likely to degrade the protein or activate proteins that in turn can remodify the protein [28, 75, 100]. In NDs, these proteins are not destroyed and thus form aggregates. A lack of understanding of the tertiary structure of these proteins is a major disadvantage. Under abnormal conditions, proteins can occur in multiple conformations; thus, targeting them is a challenge. The transcription of molecular chaperones under stress conditions is therefore increased in an attempt to restore the cellular condition [138, 140, 239]. Several different proteins form aggregates, such as A β , tau, α -Syn, SOD, and prion-like proteins [10, 15, 31, 40, 80]. It is believed that the polymerization of HTT is responsible for the aggregates formed in Huntington patients. These misfolded proteins are known to cause misfolding of other proteins, which results in a neuronal cell that contains a very high number of misfolded proteins. These proteins form aggregates that can be transported from one neuron to another via synaptic junctions and nanotube formation. Several drugs have been synthesized that target chaperones, the degradation of proteins, and the extracellular clearance of aggregates. However, these drugs lack efficacy, and none of them can remove or clear all the aggregates formed. Efforts are being made to produce a compound that has high penetration through the BBB and that can specifically bind to the target protein and dissolve the neuronal aggregates formed.

Future Perspective

With an advanced understanding of the underlying mechanisms of NDs, targeting these diseases is now possible. Since the salient feature of these diseases is the aggregation of misfolded proteins, scientists are synthesizing drugs that can target these proteins and cause their clearance. However, the dynamic nature of these misfolded proteins poses a challenge. These proteins occupy multiple conformations, making the understanding of the tertiary structure of these proteins difficult [28]. Several molecular chaperones are known to cause refolding, thus preventing aggregation. HSP70 is the most effective chaperone, which can start its process within 2 h following the minutest assault via the environment, as shown by our previous work [200, 240, 241]. Thus, targeting the genes of chaperones, causing their overexpression or supplying inhibitors of chaperones that promote cytotoxicity, such as HSP90, can be used as a therapy. Treatment by targeting chaperones, however, lacks effectiveness. Thus, focusing on developing a chaperone-targeted drug may be achieved by the application of the mathematical model. Additionally, working on increasing the short life of these drugs might be effective [226]. Another major challenge in the treatment of NDs is delivering the molecules across the BBB. Many of the antibodies that are under trial have low penetrability. However, intranasal delivery of drugs offers the shortest path to reaching the CNS and is considered safe. Thus, targeted delivery to the brain via the nasal pathway should be studied more [184]. Additionally, these proteins can be delivered in liposomes. Since liposomes are hydrophobic, they can cross the BBB and can carry such proteins inside them. Targeting the brain through liposomes has shown successful transfers in various experimental procedures, and thus, the aggregates present in the body can be cleared, deformed, or refolded into proper conformations. The use of ASO therapy has also shown promising effects and can be used to modulate the expression of misfolded proteins [230]. Thus, more research should be conducted targeting the expression of misfolded proteins. Furthermore, treating patients with a combination of multiple therapeutic strategies might prove to be an effective plan of action since use of single strategy fails to cure NDs.

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