

Interaction between pathogenic proteins in neurodegenerative disorders

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- Introduction
- The proteopathic basis of AD
- Protein interactions in PD
- Induction and spread of protein aggregates in NDDs
- Conclusions

Abstract

The misfolding and progressive aggregation of specific proteins in selective regions of the nervous system is a seminal occurrence in many neurodegenerative disorders, and the interaction between pathological/toxic proteins to cause neurodegeneration is a hot topic of current neuroscience research. Despite clinical, genetic and experimental differences, increasing evidence indicates considerable overlap between synucleinopathies, tauopathies and other protein-misfolding diseases. Inclusions, often characteristic hallmarks of these disorders, suggest interactions of pathological proteins engaging common downstream pathways. Novel findings that have shifted our understanding in the role of pathologic proteins in the pathogenesis of Alzheimer, Parkinson, Huntington and prion diseases, have confirmed correlations/overlaps between these and other neurodegenerative disorders. Emerging evidence, in addition to synergistic effects of tau protein, amyloid- β , α -synuclein and other pathologic proteins, suggests that prion-like induction and spreading, involving secreted proteins, are major pathogenic mechanisms in various neurodegenerative diseases, depending on genetic backgrounds and environmental factors. The elucidation of the basic molecular mechanisms underlying the interaction and spreading of pathogenic proteins, suggesting a dualism or triad of neurodegeneration in protein-misfolding disorders, is a major challenge for modern neuroscience, to provide a deeper insight into their pathogenesis as a basis of effective diagnosis and treatment.

Keywords: neurodegeneration • protein misfolding • oligomers • interaction • aggregation • spreading • pathogenic factors

Introduction

Neurodegenerative disorders (NDDs) such as Alzheimer disease (AD), Parkinson disease (PD), frontotemporal lobar degeneration (FTLD), Huntington disease (HD), prion and motoneuron diseases are being realized to have common cellular and molecular mechanisms including protein aggregation and inclusion body formation in selected areas of the nervous system. Therefore, these disorders are summarized as 'proteinopathies' [1–5], and are also called 'neurodegenerative conformational diseases' [6], 'protein aggregation diseases' [281], 'protein misfolding disorders' [182], or 'neurodegenerative foldopathies' [282]. The size, shape, location, and protein composition of the aggregates are characteristic features of the diseases. Although the different localizations of hallmark protein aggregates [extracellular amyloid- β (A β) deposits and intracellular hyperphosphorylated tau

(p-tau) in AD, α -synuclein (α Syn) containing cytoplasmic Lewy bodies (LBs) and neurites (LNs) in PD, α Syn containing glial cytoplasmic inclusions (GCI) in multiple system atrophy (MSA), intranuclear huntingtin inclusions in HD, TDP-43 intracytoplasmic and intranuclear inclusions in AD and FTLD] may suggest that each protein strikes a single cellular domain, recent studies indicate the possibility of common pathogenesis with overlap between the different disorders [2, 4, 7–13]. The deposits consist of insoluble fibrillary aggregates containing misfolded protein with β -sheet formation. The most probable explanation is that these inclusions and aggregates represent an end stage of a molecular or 'molecular misreading' [283] multistep cascade of complicated events that might result from an imbalance between protein synthesis, aggregation and clearance possibly

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because of the decline of cellular protein quality processes [14, 15] or 'molecular misreading' [283]. It appears reasonable that an earlier stage may be more directly tied up to the—hitherto unknown—pathogenesis of the disorders than the inclusions themselves, which may or may not represent diagnostic hallmarks or signposts. It has been suggested that the translocation of proteins to the mitochondrial membrane may play an important role in triggering or perpetuating neurodegeneration (ND) causing mitochondrial destruction [16, 17]. In many of these disorders, ND is likely to initiate at the synaptic site, where discrete protein aggregates, known as oligomers, impair neuronal transmission and functioning [18, 19, 92, 284].

Oligomers are usually diffusible, non-fibrillary, small-order aggregates, whereas larger polymers, in the form of amyloid fibrils, comprise the inclusion bodies and extracellular deposits that characterize these disorders and are now believed to represent a pathway for sequestration of more toxic oligomers [20]. Different types of A β oligomers are associated with various degrees of toxicity; they may differ in their underlying structure and may follow different assembly pathways [21]. The high contents of lipid rafts of the neuronal plasma membrane renders these cells particularly vulnerable to the cytotoxic attack of amyloid proteins and represents one of the reasons for the high vulnerability of the CNS to misfolded proteins [285]. Recent studies indicate that the presence of A β seeds, and not the age of the host is critical for the initiation of A β aggregation in the brain [22]. Small intermediates along the pathway from oligomer to fibril have also been reported to form 'pore-like' structures that might themselves disrupt ionic homeostasis and influence synaptic dysfunction, while large insoluble deposits might function as reservoirs of the bioactive oligomers that can lead to synaptic and mitochondrial dysfunction, neuronal apoptosis and cell death [23–25]. This, among others, is probably because of iron-related oxidative damage mediated by α Syn oligomerization *via* oxidative stress during the development of PD pathology [26–28]. On the other hand, brain-permeable small-molecule inhibition of heat shock protein Hsp90 has been shown to prevent α Syn oligomer formation and protect against α Syn-induced toxicity [29]. α Syn has recently been shown to occur physiologically as helically folded tetramers that resist aggregation. It has been hypothesized that α Syn tetramers undergo destabilization before aggregate formation [286]. A β promotes α Syn aggregation *in vivo* [215] and both might directly interact [8] to form hybrid channel-like structures [25]. Misfolding and subsequent aggregation of α Syn play a central role in the pathogenesis of synucleinopathies [30, 31]. The levels of soluble α Syn oligomeric species are increased by phosphorylation at Ser129 [32]. Elevated levels of soluble α Syn oligomers have been detected in postmortem brain extracts from patients with dementia with Lewy bodies (DLB), which were significantly higher than in AD and controls [33]. Evidence further suggests that protein propagation might contribute not only to the spreading and progression of the disease, but also to ND. Recent studies suggest that such protein spreading might occur in AD, PD, FTLN and other NDDs [1, 23, 34, 35]. Seeding induced by α Syn oligomers, the toxicity of which has been demonstrated *in vivo* [36], can induce intracellular α Syn aggregation, providing evidence for spreading of α Syn pathology [37, 38] similar to that of prions [34] and seeding of normal tau by pathological tau conformers drives pathogenesis of Alzheimer-like tangles

[56], but the exact molecular pathways of transmissible proteins are not yet fully understood [39].

Amyloid- β causes downstream loss of dendrites and synapses, and functional disruption of neuronal networks [40, 41]. It induces the neurodegenerative triad of spine loss, dendritic changes and neuritic dystrophies through calcineurin activation [42], oxidative stress, mitochondrial dysfunction, impaired synaptic transmission, disruption of membrane integrity and impaired axonal transport [43], whereas soluble tau species rather than aggregated ones induce ND [44]. Cellular prion protein (PrP^c) is a high-affinity receptor for A β oligomers mediating their toxicity on synaptic plasticity [45–50], but it mediates neurotoxic signalling of β -sheet-rich conformers independent of prion replication [248]. Co-transfection of tau gene in cortical neurons with a proteasome activity reporter (GFP-CL1) resulted in down-regulation of the proteasome system, suggesting a possible mechanism that contributes to intracellular PrP^c accumulation, indicating a possible crosstalk between tau and prion proteins in the pathogenesis of tau-induced ND [287]. Likewise, tau-inhibiting tubulin oligomerization induced by prion protein points to a possible molecular link between NDDs and transmissible spongiform encephalopathies [288]. A case with a rare PRNP mutation (Q160X) resulting in the production of truncated PrP suggests that PRNP mutations that result in a truncation of PrP lead to a prolonged clinical course consistent with AD-like pathology [289].

Tau phosphorylation proceeds to tau aggregation that is favoured by kinases like glycogen synthase kinase-3 β (GSK-3 β) [51], while inhibition of GSK-3 β activity prevented not only tau phosphorylation but also tau aggregation in the hippocampus [52]. It is unclear whether tau accumulation or its conformational changes are related to tau-induced ND [53]. Recent studies showed that caspase activation, observed in a tg mouse model overexpressing GSK-3 β [54], precedes tangle formation [55]. Seeding of normal tau by pathological tau conformers further drives pathogenesis of neurofibrillary tangles (NFT) [56].

TDP-43 proteinopathies are distinct from most other NDDs because they are due to protein misfolding without amyloidosis, while TDP-43 inclusions show abnormal phosphorylation, ubiquitination and C-terminal fragments [57]. However, TDP-43 is present in AD, other NDDs and normal ageing, suggesting that TDP-43 proteinopathies can be considered in two classes—primary and secondary [58]. The presence of TDP-43 changes in AD and Down syndrome may be a secondary phenomenon, relating more to aging than to AD itself, but it may be integral to the pathology of AD and to some extent determine its clinical phenotype [290]. TDP-43 and fused in sarcoma, both DNA-/RNA-binding proteins, show genetic interaction in amyotrophic lateral sclerosis (ALS) and FTLN [59, 60]. The molecular mechanisms of TDP-43-mediated ND have been critically reviewed recently [291].

However, the mechanism by which oligomers trigger ND still remains elusive, and it is unclear, whether there is a common underlying pathogenic mechanism inducing both ND and fibrillary protein aggregates that are typical for different disease processes (double or triple amyloidosis) or if they represent a common final pathology leading to ND. The aim of this article is to review the molecular mecha-

nisms and interactions between the various pathological proteins in NDDs.

The proteopathic basis of AD

The brains in patients with AD, in addition to neuron and synapse loss, are characterized by two hallmark lesions—A β containing plaques and NFT, which are composed of hyperphosphorylated forms of microtubulus-associated tau protein [61, 62] (Fig. 1). Progression of NFT pathology throughout the brain strongly correlates with disease progression [63], while brain oligomeric A β but not total amyloid plaque burden correlates with neuronal loss and astrocytic inflammatory response in APP/tau tg mice [64] and in humans with the APP (E693 Δ) mutation [292, 293]. Loss of synapses is one of the earliest events that has been associated with functional impairment [65, 66]. Although both A β and tau have been extensively studied with regard to their separate modes of toxicity [67], suggesting that both proteins exhibit synergistic effects on mitochondrial function finally leading to ND [68], more recently new light has been shed on their possible interactions and synergistic effects in AD, linking A β and tau [69–71]. There is an interaction between tau and A β mediated by increased activity of GSK-3 β , a major kinase that hyperphosphorylates tau to produce pathological forms of tau [72–75], which may represent an interesting link between the two pathogenic hallmarks of these disorders [74, 76–78]. In addition, there may be a participation of the protein 14-3-3 in the oligomerization and aggregation of tau [294]. Hyperphosphorylation of tau may be a consequence of A β toxicity via the regulator of calcineurin gene RCAN1 and GSK-3 β , producing a sequential mechanism for A β and tau pathology [295].

The senile plaque, where A β deposits and tau-positive processes meet, is probably one important site of interactions: the cytoplasmic domain of amyloid precursor protein (APP), phosphorylated on threonine 668, could be the intermate as it appears to be associated

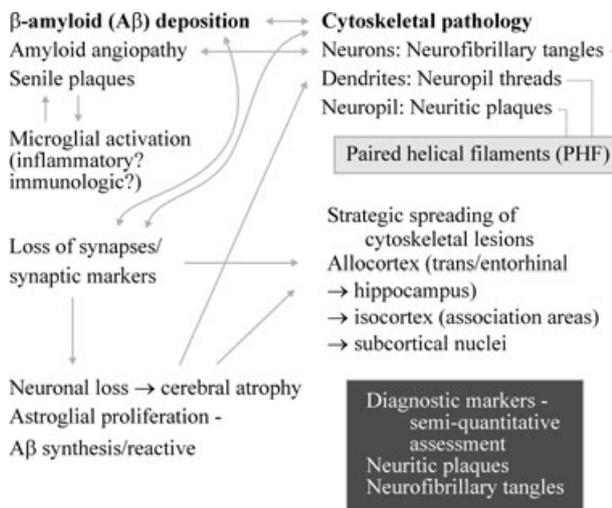


Fig. 1 Neuropathology of Alzheimer disease and morphological markers.

both with tau and A β [79]. There are also well-documented data indicating that A β and tau meet at the synapse, as in about 25% of synapses preserved from cryopreserved material, phospho (p)-tau and A β were co-localized [80]. Recent studies established a common, direct and synergistic toxicity of pathologic APP and tau products in synaptic mitochondria contributing to synaptic deterioration in AD [296], which is associated with reduction of the postsynaptic scaffold protein PSD-95 in both tg mice and AD [297].

According to the amyloid cascade hypothesis, A β formation is the critical step in driving AD pathogenesis, implying the aggregation of A β as critical, early trigger in the chain of events that leads to tauopathy, neuronal dysfunction and dementia [81] (Fig. 2). Support for this concept stems from the identification of pathogenic mutations in

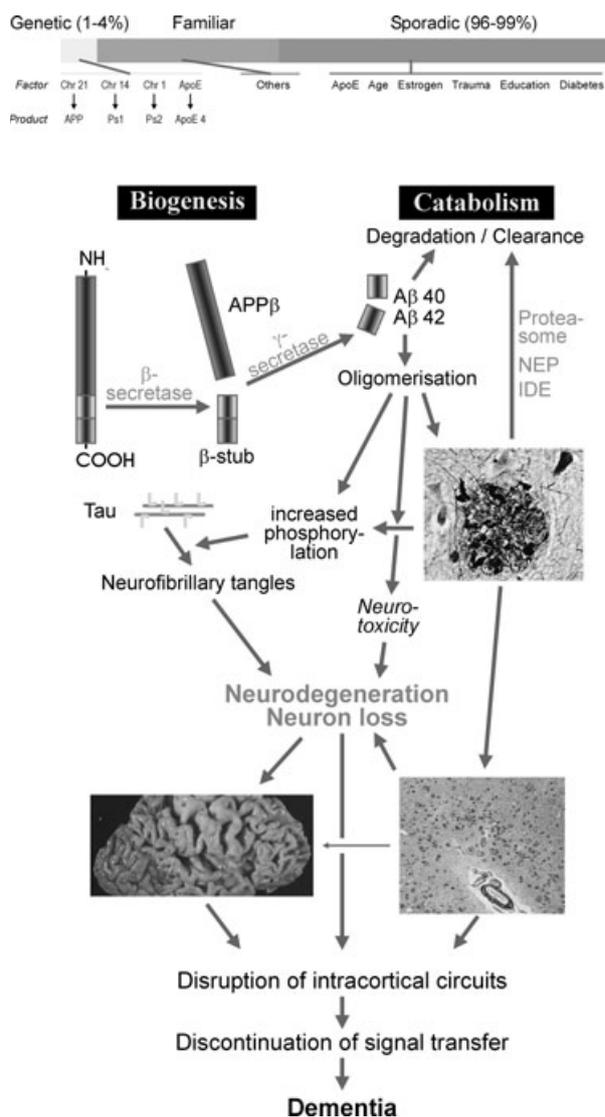


Fig. 2 Pathogenesis of Alzheimer disease (major factors).

patients with familial AD linked to A β formation and a higher frequency of AD in people with trisomy 21, who carry an additional APP allele [82]. All firmly established genetic risk factors for AD promote the buildup of A β , either by increasing its production, promoting its aggregation or impeding its elimination [83]. While oral, intravenous, intraocular and intranasal inoculation yielded no detectable introduction of cerebral β -amyloidosis in APP23 tg mice, intracerebral transmission through A β -contaminated steel wires [84] and intraperitoneal inoculation with A β -rich extracts after prolonged incubation times did [85]. Soluble A β seeds also mediated β -amyloidosis in the brain [86] and may be induced in β APP tg rats that are relatively refractory of spontaneous original A β deposits [87], whereas peripheral reduction of A β may reduce brain A β [88]. Previous studies of A β induction have used short incubation periods to dissociate seeded A β induction from endogenous A β deposition of the host, showing that A β deposition, actuated in one brain area, eventually spreads throughout the brain (for a review, see [22]). Recent longitudinal imaging studies indicate that cerebral A β deposition precedes clinical AD by a decade or more [89]. How A β aggregates impair neuronal function remains uncertain, but evidence is growing that oligomeric forms of the protein, which can range in size from dimers to dodecamers or larger [90–93], are more deleterious to brain function than are histologically obvious A β lesions such as senile plaques and cerebral amyloid angiopathy (CAA). On the other hand, according to recent data, at least some of the A β toxicity appears to be tau-dependent [70, 94].

Although A β and tau exert toxicity through separate mechanisms [95], evidence from both *in vitro* and *in vivo* models suggest that there are three possible models of interaction between the two: (1) A β drives tau pathology, supported by induction of tau hyperphosphorylation by A β formation in APP tg mice [96], induction of neuronal tau hyperphosphorylation by A β oligomers [97] or A β -derived diffusible ligands (ADDL) [97], and, together with neuritic degeneration, by soluble A β -protein dimers isolated from Alzheimer cortex [93] or by A β -rich brain extracts [98]. Tau hyperphosphorylation leads to tau dissociation from microtubules and increased accumulations in some dendritic compartments [99]. Together with NFT formation, it seems to be linked to abnormal mitochondrial distribution in neurons [298], whereas abnormal interactions between the GTPase dynamic-related protein 1 (Drp1), acting in the outer mitochondrial membrane, and A β have recently been identified in AD brains [299]. Furthermore, aggravation of NFT pathology is induced by intracranial injection of synthetic A β into mutant tau tg mice [100]. A β exacerbates neuronal dysfunction caused by human tau expression in a *Drosophila* model of AD [101], whereas inhibition of GSK-3 ameliorates A β pathology in this model [102]. The pathogenic effects of A β -42 were also significantly suppressed when A β -42 is expressed in a *Drosophila* tau null line, demonstrating an interaction between the two proteins [102]. Overall, the *Drosophila* models of tauopathy in which both tau and APP are co-expressed can provide valuable insights into the cellular pathways mediating the interaction between these two proteins [103]. Amyloid precursor protein tg mice develop abundant A β accumulation as well as tau pathology similar to that observed in AD [104], but none of the APP models fully recapitulate AD cellular and behavioral pathology [300, 301]. In an AD mouse model, A β accelerates the spa-

tiotemporal progress of tau pathology, particularly in the perforant pathway, whereas tau pathology did not have the same effect on A β pathology [105]. In APP/PS1K1 mice, transient intraneuronal A β rather than extracellular plaque pathology correlates with neuron loss in the frontal cortex [302]. Glucocorticoids increased A β and tau pathology in another mouse model of AD [106].

On the other hand, a single-dose intraventricular injection of an A β antibody in 4-month-old mice cleared intraneuronal A β pathology and reduced early cognitive deficits [107], and inhibition of GSK-3 β attenuated A β -induced tau phosphorylation *in vitro* and can reduce tau pathology *in vivo* [52, 108]. Other data suggest induction of NFT formation by amyloidogenic peptides rather than specifically by A β [109]. While the 3xTg AD mouse model, based on early intraneuronal accumulation of A β played an important role in supporting the 'intraneuronal A β hypothesis' [107], recent evidence claims that these mice early and age-dependently accumulate APP instead of A β within neurons [110, 111], thus challenging this hypothesis. The intracellular domain of APP alters gene expression and induces neuron-specific apoptosis [112, 113]. It should be recognized, however, that the 3xTG-AD mouse model demonstrates AD-like pathology but with some key differences to human AD, suggesting divergent pathogenic mechanisms [114]. In the human brain APP rather than A β is detected intracellularly when using specific antibodies [303]. (2) Synergistic effects of A β and tau by impairment of mitochondrial respiration in triple tg mice that display both A β and tau pathologies [115]. This indicates the convergence of A β and tau on mitochondrial deterioration and establishes a molecular link in AD pathology *in vivo* [116, 117].

(3) Tau mediates A β toxicity, supported by the observation that tau^{-/-} neurons are protected from A β -induced cell death in cell culture [94, 99, 118]. Tau reduction also prevents A β -induced defects in axonal transport of mitochondria and other cargoes [119], which may link the 'tau hypothesis' to other ones, the axonal transport impairment hypothesis, according to which tau induces failure of axonal transport [120, 121], and the 'oxidative stress hypothesis', which suggests that mitochondria are functionally impaired, resulting in the production of reactive oxidative species [122]. Astrocytes have been shown to be important mediators of A β -induced neurotoxicity and tau hyperphosphorylation in primary cultures [54]. Soluble oligomeric forms of A β stimulate A β production *via* astroglialosis in the rat brain [123].

Although knowledge about the roles of tau and its interactions with A β is increasing (see [1, 124]), many questions about the scaffolding partners for tau in its interaction with A β are still unanswered. While this phenomenon may result from direct cross-seeding of tau by aggregated A β [125, 126], indirect pathways such as A β -induced tau phosphorylation, inflammation and/or disruption of proteostasis [70, 77, 127] have not been excluded.

While structural and functional changes in tau mutant mice neurons are not linked to the presence of NFTs, or co-occur independent of mature NFTs [128], the incidence of plaques and tangles correlates positively in human AD, but a consistent anatomical relationship between these lesions is not apparent [61]. Cross-sectional analysis of postmortem human brain reveals a characteristic progression of A β plaques and a highly stereotypical appearance of NFTs [129]. A β

plaques develop first in the neocortex, followed by the allocortex and then the subcortex, and the progression of their appearances often corresponds to functionally and anatomically coupled brain regions [130–133]. Neurofibrillary tau pathology first arises in the locus ceruleus (LC) and entorhinal brain regions [134–137]. The pattern that emerges from these studies implies neuronal transport and synaptic exchange mechanisms in the spread of AD lesions within the brain [120, 136]. Several studies indicating that tau pathology of AD begins in the brainstem [137–139], and the recent demonstration of tau-positive pretangle material or early NFT stages without the presence of A β plaques in the LC before the involvement of the entorhinal region of the cortex in young individuals [137, 140] may indicate that not only reclassification of currently existing neuropathological staging NFT categories for AD could be necessary but also a rethinking of the amyloid cascade hypothesis that might not be valid for sporadic AD cases [129]. According to these authors, sporadic AD could be the result of two separate factors: first, a tauopathy, possibly beginning in young age and, second, negative influences of A β after a given threshold is crossed. As shown in animal models, A β might be capable of exacerbating the underlying tauopathy so that it develops into clinical AD [100, 104], but, currently, too little is known about the pace with which the pathologic process in human brain develops. A novel antibody capture assay for paraffin-embedded tissue detected wide-ranging A β and paired helical filament tau in cognitively normal older adults [141], and other recent findings indicate that A β -associated brain volume loss occurs only in the presence of p-tau (in cerebrospinal fluid or CSF) in humans at risk for dementia [142].

As we gain a deeper understanding of the different cellular functions of tau, the focus shifts from the axon, where tau has a principal role as microtubule-associated protein, to the dendrite, where it mediates A β toxicity [70]. On the other hand, according to several data, tau aggregates may be a consequence rather than a cause of ND [55, 143]. Therefore, the effects promoted by A β and tau should be analyzed more specifically to identify the mechanisms that underly A β and tau toxicity and/or neuroprotection to find appropriate therapeutic targets [144].

Protein interactions in PD

Intracytoplasmic proteinaceous inclusions, primarily composed of tau and/or α Syn, are predominant pathological features of AD and PD, respectively [145]. However, the co-existence of these and other pathological proteinaceous aggregates like A β has been identified in many NDDs [146–148]. Proteomic analysis of cortical LBs revealed 296 proteins [149], while in brainstem LBs 90 proteins were identified, differing from Pick bodies and suggesting a complex formation process [150]. A recent proteomic study of the LC of PD brains revealed a total of 2495(!) proteins of which 87 were different from controls. The majority of these proteins are known to be involved in processes that have been implicated in the pathogenesis of PD previously, including mitochondrial dysfunction, oxidative stress, protein misfolding, cytoskeleton dysregulation, alterations in autophagy, and inflammation. Several individual proteins were identified that have hitherto not been associated with PD, such as regucalcin, which

plays a role in maintaining intracellular calcium homeostasis, and isoform 1 of kinectin, which is involved in transport of cellular components along microtubules. These findings indicate that the proteome of PD-LC and non-neurological controls provide data that are relevant to the pathogenesis of PD, reflecting both known and potentially novel pathogenetic pathways [151]. Mitochondrial dysfunction significantly contributes to PD pathology; however, to what extent it contributes to the pathogenesis of sporadic PD remains to be elucidated [304].

The co-occurrence of both α Syn and tau or other pathologic proteins highlights the interface between them [7, 11, 152, 153]. They may be co-aggregated in the same brain or even in the same region or in the same cell in human brains [147, 154–156] and tg mice [157]. Recent data suggest that α Syn secretion might be triggered by the toxic properties of overexpressed α Syn and that tau specifically enhances α Syn secretion. The synergistic effect between α Syn and tau may be relevant for many NDDs that show co-occurrence of both proteins, as an increase in p-tau is one of the key features in the brains of all tauopathies and has been shown to reduce binding of tau to microtubules [158].

Whereas α Syn can spontaneously polymerize into amyloidogenic fibrils, *in vitro*, tau polymerization requires an inducing agent [159]. Dopamine facilitates α Syn oligomerization and promotes formation and secretion of non-fibrillary α Syn oligomers [305, 306], and the chaperone Hsc70 affects the cellular propagation of α Syn aggregates and their spread throughout the CNS in PD [307]. Cellular models, various transgenic and other experimental PD models provided novel insights into the role of α Syn in the hyperphosphorylation of tau protein observed in disease [159–167]. These data suggest that oxidatively modified α Syn is degraded by the proteasome and plays an pro-aggregatory role for tau [166], and that α Syn is an *in vivo* regulator of tau protein phosphorylation at Ser(262). Toxic interactions with α Syn may lead to hyperphosphorylation of tau and eventually to the deposition of both proteins in the disease [168]. Oxidatively modified α Syn degraded by the proteasome further promotes the recruitment of tau to protein inclusions in oligodendroglial cells in synucleinopathies [166]. E46K human α Syn tg mice develop Lewy-like and tau pathology associated with age-dependent motor impairments, and studies on the ability of E46K α Syn to induce tau inclusions in cellular models suggest both direct and indirect mechanisms of protein aggregation being possibly involved in the formation of tau inclusions observed in PD, supporting the notion that α Syn is involved in the pathogenesis of human diseases [169]. On the other hand, tau enhances α Syn aggregation and toxicity and disrupts α Syn inclusion formation in cellular models [156].

Recent postmortem studies showed increased accumulation of tau protein phosphorylated at Ser 262 and 396/404 in the striata of PD patients and in the A53T α Syn mutant mouse model of PD [162, 170]. This is related to increased activity of GSK-3 β [75, 161, 164], a major kinase that hyperphosphorylates tau to produce pathologic forms of tau [50, 74]. This is stimulated by α Syn that associates with the actin cytoskeleton [171] and by GSK-3 β [172]. On the other hand, α Syn is a substrate for GSK-3 and GSK-3 inhibition protects against 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) and other Parkinsonian toxins [308]. Dopamine D1 receptor activation induces tau

phosphorylation *via* cyclin-dependent kinase 5 (cdk5) and GSK-3 β signalling pathways [173]. Expression of both GSK-3 β and microtubule-associated protein/microtubule affinity-regulating kinase 2 inhibited the formation of α Syn-induced tau aggregation [159]. Reduced 19S and 20S proteasomal subunit activities in PD striata suggest that they account for the abnormal disposal of α Syn and p-tau. The small decrease in proteasomal activity in PD striata is consistent with other studies that showed no significant changes of these proteins in PD striata but lower activity in substantia nigra (SN) [174]. In an MPTP model and in MPP⁺ cellular models, α Syn has been shown to induce GSK-3 β -catalysed tau phosphorylation [175–177]. Parkinson disease-associated risk factors such as environmental toxins and α Syn mutations promote tau phosphorylation at Ser 262, causing microtubule instability, which leads to neuronal degeneration [165]. Rotenon exposure may also induce α Syn and A β aggregation, as well as increased hyperphosphorylation of tau, while high concentrations of the pesticide lead to cell death before protein aggregation [167].

Hyperphosphorylation of tau by α Syn in the MPTP model of parkinsonism has been observed [175]. Tau in MPTP models and in human postmortem PD striata is hyperphosphorylated at the same sites (Ser 202, 262 and 396/404) as in AD [170], whereas phosphorylation of soluble tau differs in AD and Pick disease brains [178]. Tauopathy in PD striata is restricted to dopaminergic neurons, whereas degeneration in the inferior frontal cortex, associated with increased tau deposition because of diminished proteasomal activity in the absence of oxidative stress and pGSK-3 β activity is not associated with tauopathy [170]. In the α Syn overexpressing mouse model of PD tauopathy, along with microtubule destabilization, exists primarily in the brainstem and striatum, the two brain regions known to express high levels of α Syn and undergo the highest levels of degeneration in human PD. Thus, tauopathy in PD may have a restricted pattern of distribution [163], which differs from its generalized affection in AD. Whether there are differences in the three- and four-repeat tau pathology between these disorders is not yet fully understood and needs further investigation, as has recently been performed for both AD and four-repeat tauopathies using new methods [179].

There is strong interaction between α Syn, tau and A β , particularly in their oligomeric forms, which might synergistically promote their mutual aggregation and *vice versa* [30, 168, 180]. Cross-seeding between dissimilar proteins that share β -sheet structures has been described, for example, of A β and α Syn [25], tau and α Syn [181] and prion protein and A β [182]. *In vivo* interactions between α Syn and tau are supported by genetic studies that link the *MAPT* gene, which encodes tau, with increased risk of sporadic PD [183–186], and in familial PD [155], fibrillation of α Syn and tau is caused by the A53T mutation [181]. A family with early onset dementia showed widespread appearance of LBs and NFTs, but no amyloid deposits [187]. There is recent evidence that prions trigger hyperphosphorylation of tau in genetic, sporadic and transmitted forms of prion diseases in the absence of amyloid plaques [11].

Neurofibrillary tau pathology is modulated by genetic variations of α Syn [188]. Tau phosphorylation is found in synapse-enriched fractions of frontal cortex in PD and AD [189] and in brainstems of α Syn mice [190]. Direct links between α Syn and tau are supported by the

accumulation of both proteins within synaptic terminals in AD brains and APP Swedish mutant mice [19, 189], the co-localization of both proteins in both NFTs and LBs, especially in neuronal populations vulnerable for both aggregates [154, 191–193], in the olfactory bulb in AD with amygdaloid LBs [191] and in neuronal and glial cytoplasmic inclusions in MSA [194, 195]. Between 15% and 60% of AD brains show numerous α Syn lesions in the amygdala, even in the absence of subcortical LBs [196, 197]. Alzheimer disease with amygdala LBs is considered to be a distinct form of α -synucleinopathy [198] in which tau and α Syn pathology are co-localized [191]. In AD patients with clinical extrapyramidal symptoms, between 50% and 88% of the patients showed extensive α Syn pathology co-localized with p-tau in SN, tau and less α Syn pathology in brainstem significantly increasing with higher neuritic Braak stages [199–201]. Co-occurrence of abnormal deposition of tau, α Syn and TDP-43 in AD, DLB and other NDDs [146, 202, 203], highlight the interface between these and other misfolded proteins.

In conclusion, genetic, pathologic and biochemical evidence support a role for tau in the pathogenesis of PD [168], and concurrence of tau, α Syn and TDP-43 pathology in brains of AD and LB diseases provide a better understanding of the pathogenic pathways in these disorders [146]. It has been suggested that the process of LB formation is triggered, at least in part, by Alzheimer pathology [147, 204], while the interaction between α Syn and tau in MSA awaits further elucidation [195, 205]. Recent data suggest that PD and AD could be linked by progressive accumulation of p-tau, activated GSK-3 β and α Syn [162, 170, 206], while activation of caspase and caspase-cleaved Δ tau may represent a common way of abnormal intracellular accumulation of both tau and α Syn, promoted by A β deposition, and unifying the pathology of AD and LB diseases [8, 207, 208] (Fig. 3). Emerging evidence suggests that secreted proteins such as A β and cytosolic proteins such as tau and α Syn, are spreading by cell-to-cell transmission, thus unifying the pathogenesis of many NDDs [34, 209], but is not fully understood whether they are the result of similar protein aggregation and misfolding mechanisms.

Combined determination of α Syn, tau and A β concentrations in CSF show differential patterns in these disorders [210]; in particular, tau/ α Syn ratios can contribute to the discrimination of PD [211], while different soluble isoforms of APP and other CSF biomarkers

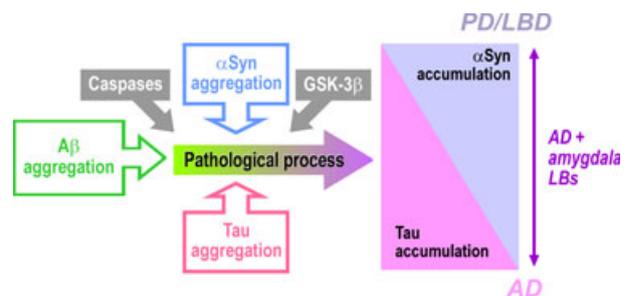


Fig. 3 Hypothetic diagram unifying pathologic processes in Alzheimer and Lewy body diseases. PD: Parkinson disease; LBD: Lewy body disease; LBs: Lewy bodies; AD: Alzheimer disease.

may differentiate between AD and LB diseases [212]. Other studies have suggested that A β is more likely to promote the deposition of α Syn than tau [213], and A β is known to initiate hyperphosphorylation of tau [71]. Cortical α Syn load is associated with A β plaque burden in a subset of PD patients [214]. A β peptides enhance α Syn accumulation and neuronal deficits in a tg mouse model [215], and α Syn-induced synapse damage is enhanced by A β -42 [216]. Both can be linked by separate mechanisms driven by a common upstream component [217]. Recent studies showed that A β -42 tightly binds to tubulin polymerization-promoting protein (TPPP/p25) and causes aberrant protein aggregations inhibiting the physiologically relevant TPPP/p25-derived microtubule assembly.

TPPP/p25 expression enhances cellular sensitivity to dopamine toxicity [218], and the interaction of TPPP/p25 and A β can produce pathologic aggregates in AD and LB diseases [219], although other proteins, for example, α Syn and tau, have also been shown to interact with p25 [219]. p25 α was found in LBs in PD and DLB, but does not co-localize with the inclusions in tauopathies [220]. Expression of p25 α and α Syn in a rat oligodendroglial cell line resulted in disruption of the microtubule cytoskeleton, formation of α Syn oligomers and apoptosis [221]. p25 α promotes the oligomerization of α Syn and accelerates inclusion formation leading to oligodendroglial death [222], p25 α probably being an early event for the formation of GCLs in MSA.

Interactions between A β , α Syn and tau may be a molecular mechanism in the overlapping pathology of AD and PD/DLB [8, 208], probably generated by the same stimulus with the outcome possibly having an inverse relationship depending on genetic background or environmental factors. These lesions represent a collision of two or more processes, but it is unclear whether there is a common underlying final pathology leading to neuronal degeneration (see [9]) (Fig. 4).

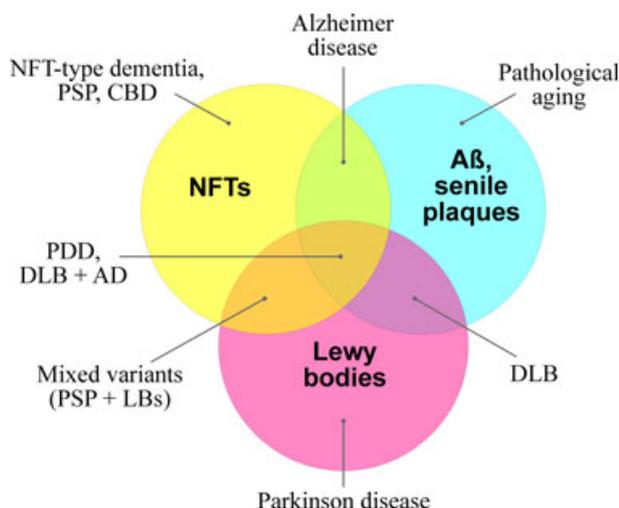


Fig. 4 Morphologic interrelations of synucleinopathies, tauopathies and amyloidopathies. NFTs: neurofibrillary tangles; PSP: progressive supranuclear palsy; CBD: corticobasal degeneration; PDD: Parkinson disease dementia; DLB: dementia with Lewy bodies; AD: Alzheimer disease; LBs: Lewy bodies.

Induction and spread of protein aggregates in NDDs

Mounting evidence implicates that templated corruption of disease-specific proteins and the propagation of proteins may be a unifying mechanism of disease progression and, thus, has important implications for understanding the onset and progression of various NDDs (Table 1). In PD, α Syn-rich lesions that characterize LB pathology, first arise in the lower brainstem and in the anterior olfactory nucleus and olfactory bulb; they subsequently appear in a predictable sequence in mesencephalic and neocortical regions [230–232], although the reliability of Lewy pathology staging in sporadic PD has been a matter of discussion [233–236]. The concept that α Syn lesions ramify within the CNS by a seeding-like process is supported by the observation that foetal dopaminergic transplants in the striatum of a subset of PD patients surviving more than 5 years may develop α Syn-positive LBs in some cells [237–239]. These data imply for a host-to-graft propagation of α Syn, and a neuron-to-neuron (interneuron) transmission or transsynaptic spread of α Syn appears a likely interpretation for the propagation of the disease. Similar accumulation of α Syn occurs in stem cells transplanted into transgenic mice [34]. It has been suggested that LBs develop in transplanted dopaminergic neurons in a fashion similar to that in the host SN [240], but it could not be determined whether the LB-like inclusions were formed by the spread of α Syn fibrils, or whether some other toxic effect of the neighbouring diseased neurons introduced these inclusions [35]. Moreover, the effects of LBs in the grafted neurons are unclear, as LB pathology in neurons does not necessarily mean their functional impairment. Secreted α Syn can recruit endogenous α Syn in the recipient cells, act as a permissive template and promote misfolding in small aggregates [241]. Some of the uptake of α Syn from the extracellular space appears to occur *via* endocytosis, although additional mechanisms might also contribute [241, 242]. It is probable to trigger the formation of large LB-like aggregates in cultured cells, when artificial methods, bypassing physiologic uptake mechanisms, are used to promote the entry of misfolded α Syn [34, 239]. These suggestions are supported by the observation that neural grafts placed into tg mice expressing human α Syn take up the human protein and form Syn-positive aggregates [227, 241, 243].

Most recent studies demonstrated that preformed fibrils generated from full-length and truncated recombinant α Syn enter primary hippocampal neurons, probably by adsorptive-mediated endocytosis, and promote recruitment of soluble endogenous α Syn into insoluble PD-like LBs and LNs. Remarkably, endogenous α Syn was sufficient for formation of these aggregates, and overexpression of wild-type or mutant α Syn was not required. Accumulation of pathologic α Syn led to selective decrease in synaptic proteins, impairment of neuronal excitability and connectivity and, eventually, neuron death [35].

In vivo approaches in cell culture could not discriminate between a ‘prion-like’ corruptive templating mechanism—host-derived—translocated α Syn inducing misfolding of α Syn generated in the graft, *versus* a simple translocation of aggregated synuclein from the host to the graft, as in cell culture all the mechanisms needed for prion-like behaviour of misfolded α Syn appear to be possible [227, 241, 243].

Table 1 Evidence for spreading of non-prion protein aggregates in the central nervous system (modified from [34])

Inoculum	Host	Propagation effect
Amyloid-β		
Brain homogenates from Alzheimer disease or APP transgenic mice	APP transgenic mice (intracerebral injection)	Amyloid- β deposition at injection site and in adjacent brain structures [84, 223, 224]
Tau		
Tau fibrils	Cultured neuronal cells	Endocytic uptake of exogenous tau fibrils and induction of cytoplasmic endogenous tau proteins. Cell-to-cell transmission of tau taken up by cultured cells [225, 226]
Brain extracts from tau transgenic mice	Transgenic mice expressing human wild-type tau (intracerebral injection)	Spreading of tau from site of injection to other brain structures [194]
α-Synuclein (αSyn)		
Aggregate-producing neuronal cell cultures	Neuronal cells	Endocytic uptake of α Syn aggregates [227]
Introduction of α Syn aggregates by preformed fibrils generated from truncated recombinant human wild-type α Syn	Primary hippocampal neurons	Adsorptive-mediated endocytosis promoting soluble α Syn into insoluble PD-like LBs and LNs [35]
Transgenic mice overexpressing human α Syn	Mouse neuronal progenitor cells grafted into mouse brains	Interneuronal transmission of human α Syn [227]
Brains of patients with Parkinson disease	Foetal stem cells grafted into the brains of patients with Parkinson disease	Interneuronal transmission of Lewy inclusions [223, 228, 229]
PolyQ proteins		
<i>In vitro</i> -generated polyQ peptide fibres	Mammalian cells in culture	Internalization of fibres with subsequent recruitment of soluble endogenous polyQ proteins and aggregate formation [228]

APP: amyloid precursor protein; PD: Parkinson disease; polyQ: polyglutamine; LBs: Lewy bodies; LNs: Lewy neurites.

These and other data suggest that α Syn pathology could be induced in cells and may spread by a 'prion-like' mechanism involving the transmission of conformationally altered α Syn [244–247]. Recent studies indicated that cellular prion (PrP^C) mediates neurotoxic signalling of β -sheet-rich conformers independent of prion replication [248]. Although the mechanism of spread remains uncertain, there is evidence that prions can be conveyed between neurons by transsynaptic transport [244]. Prion toxicity may be exerted by neither PrP^C nor PrP^{Sc} but *via* a toxic intermediate, the generation of which requires conversation to take place and is therefore dependent on local availability of PrP^C [249]. Transmissible prion disease can be induced by PrP structures different from that of authentic PrP^{Sc} suggesting a new mechanism designated as "deformed templating" postulates that a change in the PrP folding pattern from the one present in rPrP fibrils to an alternative specific for PrP(Sc) can occur [309]. The propagation of α Syn lesions by cell-to-cell passage has been demonstrated, as has the induction of proteinaceous lesions associated with other NDDs [262], such as aggregates of superoxide dismutase 1 (SOD1) in ALS [250, 251], aggregates of polyamine [228], which typify HD and spinocerebellar ataxias, or cytosolic aggregates of TDP-43 [252], which are present in ALS and FTLD with

TDP-43-positive inclusions (FTLD-TDP) [253]. The capability of passing between living cells is not limited to prions and those cited before; it was also shown for aggregates of truncated tau, consisting of the microtubule-binding region and a fluorescent protein tag that can leave and enter cells in culture and promote the aggregates and fibrilization of normal tau within them [1, 34, 124, 226, 254–256]. It should be emphasized, however, that with the recognition that tau, α Syn, A β , TDP-43 and other pathological conformers are transmissible, there is no evidence that they are infectious. Hence, it appears important to distinguish between cell-to-cell transmission from brain-to-brain transmission (α Syn, tau, A β , TDP-43). Therefore, it seems important to make a clear distinction between transmissible, non-infectious disease proteins (active in NDDs) and prions, which, by definition, are proteinaceous infectious particles, as the evidence that AD, PD, DLB, FTLD, HD and ALS are infectious is not supported by many studies that clearly demonstrated this for iatrogenic Creutzfeldt-Jakob disease [257, 258]; see also reference [1]. Amyloid transformers can spread from cell to cell in the brains of affected individuals, thereby spreading the specific neurodegenerative phenotypes distinctive to the protein being converted to amyloid. This transmissibility mandates re-evaluation of emerging neuronal graft and stem cell

therapies [310]. Accumulation of cellular proteins within dystrophic neurites in amyloid plaques in AD brain could support the hypothesis that PrPc accumulation in dystrophic neurites reflects a response to impairments in cellular degradation, endocytosis, or transport mechanisms associated with AD rather than a non-specific cross-reactivity between PrPc and aggregated A β or tau [311]. On the other hand, the identification of molecules able to mimic or recapitulate anti-amyloidogenic and antioxidative functions of PrPc may provide a new avenue for the battle against the devastating ND in AD [259]. A profound molecular cross talk between misfolded proteins in animal models of AD and prion disease may have important implications for understanding the origin and progression of these disorders [312]. Although the exact involvement in the pathophysiology of prion disorders and NDDs and a possible overlap between both disease categories have to be further investigated, the interaction between prion protein and toxic A β assemblies can be therapeutically targeted at multiple sites [260].

The recent demonstration of tau-positive pretangle material in the LC before involvement of the transentorhinal region of the cerebral cortex in young individuals [137, 140] suggests a progression of tau pathology *via* neuron-to-neuron transmission and transsynaptic transport of tau protein aggregates [136], and seeding of neuronal tau by pathological tau conformers drives pathogenesis of Alzheimer-like tangles [56]. The induction and spread of both A β and tau aggregates in experimental animals is well documented (see mutant P201S tau), as found in frontotemporal dementia with parkinsonism (FTDP-17); it is capable of spreading through the cortex of an Alz17 tg mouse expressing the human wild-type protein and induce an NFT-like pathology that consists of human tau in brain areas distant from the injection site [255]. These and other data raise the possibility that neurodegenerative pathologies could spread within the brain *via* a mechanism analogous to prion-like self-propagation *via* dissemination by cells, although alternative mechanisms, such as disruption of basic cellular proteostasis by exogenous aggregates, cannot be excluded [261]. However, the means by which templated conversion occurs, remain poorly understood [34, 244, 246, 262]. *In vitro*, aggregates of pathogenic proteins can all be taken up by endocytosis and induce the misfolding of the corresponding intracellular proteins, while cytoplasmic protein aggregates can translocate from one cell to another [7, 100, 117, 170, 175, 231, 245]. It appears well documented that α Syn and SOD1 are secreted into the cell medium [34, 244, 263]. Furthermore, tau and α Syn are present in blood and CSF in both monomeric and oligomeric forms, suggesting release of these normally intracellular proteins *in vivo* [211, 263–265]. The intercellular transfer of cytosolic protein aggregates may also occur through nanotubes, exosomes or microvesicles [244]. Like other pathogenic proteins, A β can be taken up, modified and secreted by cells *in vitro* [118, 266], and—together with tau—it is also present in the CSF [267–269]. At the current state of knowledge, the exact involvement in the pathophysiology of prion disease and the NDDs is not fully understood and deserves further investigation to elucidate the possible overlaps between these disorders. Most recent cell culture studies showed that embryonic stem cell neurons can modulate the activity of a network of host neurons [270].

Conclusions

Synergies between A β , tau and α Syn have been recently described, suggesting that they accelerate ND and cognitive decline [272]. Interaction between these proteins may be a molecular mechanism in the overlapping pathology of LB disease and AD, possibly representing a complex continuum, characterized by variable amounts of pathologic proteins, and A β is suggested to promote accumulation of both α Syn and tau. The procession from A β to neurite pathology in the cerebral cortex of AD and DLB may be unifiable [8, 208]. DLB-3xtg-AD mice exhibit accelerated formation of α Syn and LB-like inclusions in the cortex, and enhanced increase of p-tau deposits immunoreactive for antibody AT8 in the hippocampus and neocortex provide further evidence that tau, α Syn and A β interact *in vivo* to promote accumulation of each other and accelerate cognitive dysfunction, although accumulation of α Syn alone can significantly disrupt cognition [271, 272]. Polymorphic tau and A β -tau aggregates may be due to sequences which are prone to variable turn locations along the tau repeats, suggesting that synergistic interactions between repeats in tau protein and A β may be responsible for accelerated aggregation *via* polymorphic states [126]. These changes and common inflammatory mechanisms in these disorders [273] could be generated by the same stimulus, with the outcome possibly having an inverse relationship depending on genetic backgrounds and environmental factors. Although recent data documented co-localization of α Syn and tau in LBs [191], of A β and p-tau in synaptosomes [80], synaptic terminals [19] and in triple transgenic mice [115], why tau, A β and α Syn pathologies are so intimately associated remains one of the major questions of the pathogenesis of ND in selected/vulnerable brain regions that are typical for different disease processes (double or triple amyloidoses). It has been suggested that these pathologies represent a common final pathway leading to or preventing neuronal damage [9, 157, 206].

The induction and proliferation of proteinaceous aggregates by corruptive templating appears to be a common feature of multiple, clinically diverse disorders, although many questions remain to be answered [274]. The basic molecular mechanisms (presumed regional differences in proteasomal, caspase and GSK-3 β activities, oxidative stress in the presence of α Syn deposition, etc.) need further elucidation, and the molecular basis of the synergistic effects of α Syn, p-tau, A β and other pathologic proteins, suggesting a dualism or triad of ND, are a major challenge for modern neuroscience [275]. In humans, A β deposition begins decades prior to the onset of cognitive decline and, therefore, has been considered an early and predictive indicator of AD [89]. *In vivo*, the appearance of soluble A β seeds may precede the appreciable A β deposition in plaques and blood vessels. As potent A β seeds, like prions [276], appear to be relatively small [86], soluble A β forms could serve as biomarkers in body fluids, and an effective disease-modifying therapy should be initiated prophylactically, before the disease has inflicted irreversible damage to the brain. The early appearance of pathological aggregates in the peripheral nervous system and their relatively systematic spread within the brain [277, 278] in synucleinopathies, and other neurodegenerative proteinopathies [5] suggests that seeds travelling

between cells from one region to another might be profitable objectives for therapeutic interference [246]. Inhibition of early α Syn aggregation events would consequently prevent α Syn oligomer-related toxicity [279], which would fit also for other proteinopathies [1]. Furthermore, the cell-to-cell transfer and the induction of pathogenic protein aggregates in cellular grafts [224, 243, 246] emphasize the needs to protect grafted cells from host-induced protein templating [1]. The hypothetical risk of transmission of non-prion proteinopathies—like that of prion diseases [84, 280, 313]—suggests a need for more research into the epidemiology of such disorders as well as analysis of tissue and organ donations to minimize the risk for transmission of such diseases. An extended multidisciplinary research of the molecular and cell biology of protein aggregation is needed to improve our insight into the molecular pathogenesis of proteinopa-

thies and related NDDs thereby improving diagnostic and therapeutic possibilities.

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Conflict of interest statement

The author confirms that there are no conflicts of interest.

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