

Are amyloid diseases caused by protein aggregates that mimic bacterial pore-forming toxins?

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Abstract. Protein fibrillization is implicated in the pathogenesis of most, if not all, age-associated neurodegenerative diseases, but the mechanism(s) by which it triggers neuronal death is unknown. Reductionist *in vitro* studies suggest that the amyloid protofibril may be the toxic species and that it may amplify itself by inhibiting proteasome-dependent protein degradation. Although its pathogenic target has not been identified, the properties of the protofibril suggest that neurons could be killed by unregulated membrane permeabilization, possibly by a type of protofibril referred to here as the 'amyloid pore'. The purpose of this review is to summarize the existing supportive circumstantial evidence and to stimulate further studies designed to test the validity of this hypothesis.

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1. Introduction

A compelling circumstantial case can be made that amyloid fibril formation is a primary cause of neurodegeneration in Alzheimer’s disease (AD), Parkinson’s disease (PD), prion diseases, and related diseases (see Table 1) (Rochet & Lansbury, 2000; Stefani & Dobson, 2003). Supporting evidence for this case, is derived from (1) pathology: fibrillar protein aggregates often colocalize with neuronal loss, (2) genetics: the gene encoding the fibrillar protein is linked to disease (autosomal dominant mutations cause familial disease, polymorphisms can be susceptibility factors, and some haplotypes are linked to risk), (3) animal modeling: overexpression of the fibrillar protein reproduces many features of the human disease, and (4) biophysics: proteins containing disease-associated mutations aggregate more rapidly than wild-type proteins. However, the mechanism by which amyloid fibril formation causes neurodegeneration and the identity of the pathogenic species have not been determined. It is not possible to directly observe the pathogenic event. Therefore, one is left to extrapolate from simplified models in order to produce a working hypothesis, which can then be tested experimentally. The design of a successful therapeutic strategy based on a working hypothesis will be taken as a ‘proof’ of its veracity.

The pathogenic pathway is likely to be much more complicated than an evolutionarily optimized process like, say, ribosome assembly. Furthermore, there is no *a priori* reason to assume that cell death in neurodegenerative disease occurs by a single mechanism or that, if protein aggregates are responsible, a single species is capable of acting alone as the pathogenic trigger. Despite these caveats, this review will apply Occam’s razor and start with the working hypothesis that a single species of protein aggregate may be responsible for initiating a cascade of events that culminate in neurodegeneration. It is our hope that this review will stimulate others to design experiments to test the relevance, or lack of thereof, of this working hypothesis.

The majority of research in the field of neurodegeneration has focused on the cause of neuronal death, rather than on the identity of the neurotoxic species. This review will focus on *in vitro* studies aimed at the characterization of an intermediate on the amyloid pathway as one potential toxic species. This review is based on the premise that understanding the structures of the protein aggregates and the dynamics of their interconversion *in vitro*, can establish potential links between aggregation and toxicity. The key to such an approach is to allow genetic information, especially regarding autosomal dominant (gain of function) mutations, to guide these experiments. Before summarizing these studies, it is important to emphasize that any reductionist approach must ultimately explain essential features of the *in vivo* process that it is seeking to elucidate. In the case of neurodegeneration, these are:

- (1) Aging is one of the strongest susceptibility factor for all of the neurodegenerative diseases. Even those that are purely genetic, like Huntington's disease, are primarily adult-onset. This does not necessarily mean that the pathogenic process takes a long time, but only that neurons become more susceptible to occurrence of a pathogenic event as they age.
- (2) All of these diseases show selectivity to particular types of neurons (hence the diverse symptoms).
- (3) Mutations cause early-onset forms of these diseases that are transmitted in an autosomal dominant manner.

Points (2) and (3) are linked, since different mutations in the same protein can produce distinct clinical entities that affect different neuronal subpopulations (three examples are fatal insomnia, which results from a point mutation in the prion protein (Gambetti *et al.* 1995), hereditary cerebral haemorrhage with amyloidosis of the Dutch type, caused by a mutation in amyloid precursor protein (APP)/A β (Maat-Schieman *et al.* 1992), and dementia with Lewy bodies, caused by a mutation in α -synuclein (Zarranz *et al.* 2004)).

Several lines of evidence suggest that *in vitro* amyloid fibril formation mimics the *in vivo* process: (a) fibrils formed *in vitro* strongly resemble those in diseased tissues (Sunde *et al.* 1997), (b) protofibrillar intermediates, first detected *in vitro*, and later *in vivo* (see Table 1) exhibit strikingly similar structural and neurotoxic properties (Roher *et al.* 1996) and (c) the specificity of *in vitro* assembly is reflected *in vivo* (Wetzel, 1994; Helms & Wetzel, 1996; Rajan *et al.* 2001; Kheterpal *et al.* 2003). Taken together, these observations suggest that structural and mechanistic clues derived from *in vitro* studies are relevant to the role of protein fibrillogenesis in neurodegenerative diseases and may provide molecular targets for the design of desperately needed therapeutic agents.

2. What is the significance of the shared structural properties of disease-associated protein fibrils?

Approximately 24 human proteins form amyloid fibrils *in vivo* (Stefani & Dobson, 2003). These proteins are unrelated at the level of primary structure, consistent with the finding that many proteins with no connection to disease can form amyloid fibrils with a common core structure *in vitro*, suggesting that the amyloid fibril is an intrinsically stable structure (Dobson, 2001). Amyloid fibrils are not crystalline, so their structural similarity is based on lower-resolution approaches: X-ray fibril diffraction, electron and atomic force microscopy, and their ability to bind histopathological dyes like Congo Red and Thioflavin T (Sunde *et al.* 1997). The structural convergence among various amyloid fibrils is also corroborated by the findings that antibodies

Table 1. A summary of studies examining the structure and formation of protofibrils, including amyloid pores by several amyloid-forming proteins in vitro, cell cultures and in vivo grouped according to the amyloid disease to which they are relevant. Due to space limitations only the most relevant references are cited

Disease	Amyloid-forming proteins and peptides	Evidence for protofibrils <i>in vitro</i>	Evidence for protofibrils In cell culture and in vivo	Evidence for annular structures/amyloid pores	Evidence for channel/pore activity
Alzheimer's disease	A β 1-40 (WT)	Goldsbury <i>et al.</i> 2005; Harper <i>et al.</i> 1997a, b, 1999; Huang <i>et al.</i> 2000; Kaye <i>et al.</i> 2004; Lambert <i>et al.</i> 1998; Stine <i>et al.</i> 2003; Walsh <i>et al.</i> 1997, 1999; Yong <i>et al.</i> 2002)	Funato <i>et al.</i> 1999; Gong <i>et al.</i> 2003; Kuo <i>et al.</i> 1996; Lambert <i>et al.</i> 2001; Pitschke <i>et al.</i> 1998; Roher <i>et al.</i> 1996	Hafner <i>et al.</i> 2001; Kaye & Glabe, 2004; Klug <i>et al.</i> 2003; Lashuel <i>et al.</i> 2002b, 2003	Alarcon <i>et al.</i> 2006; Arispe <i>et al.</i> 1993a, b, 1994, 1996; Kagan <i>et al.</i> 2002; Kawahara & Kuroda, 2000, 2001; Kawahara <i>et al.</i> 2000; Kourie <i>et al.</i> 2001b; Lin <i>et al.</i> 1999; Singer & Dewji, 2006
	A β 1-40 (E22G)	Dahlgren <i>et al.</i> 2002; Lashuel <i>et al.</i> 2002b, 2003; Nilsberth <i>et al.</i> 2001	Morishima-Kawashima & Ihara, 1998; Podlisny <i>et al.</i> 1995; Walsh <i>et al.</i> 2000, 2002	Lashuel <i>et al.</i> 2002b, 2003	
	A β 1-42 (WT & E22G)	Dahlgren <i>et al.</i> 2002; El-Agnaf <i>et al.</i> 2000; Parbhu <i>et al.</i> 2002; Roher <i>et al.</i> 1996; Stine <i>et al.</i> 2003; Wang <i>et al.</i> 2002a		Chromy <i>et al.</i> 2003; Kaye <i>et al.</i> 2004; Lashuel <i>et al.</i> 2003; Lin <i>et al.</i> 2001	Bahadi <i>et al.</i> 2003a; Bhatia <i>et al.</i> 2000; Hirakura <i>et al.</i> 1999; Lin <i>et al.</i> 2001; Rhee <i>et al.</i> 1998
Parkinson's disease	α -Synuclein (WT, A53T & A30P)	Cappai <i>et al.</i> 2005; Conway <i>et al.</i> 2000, 2001; Ding <i>et al.</i> 2002; Kaylor <i>et al.</i> 2005; Lashuel <i>et al.</i> 2002a; Rochet <i>et al.</i> 2000; Shtilerman <i>et al.</i> 2002; Volles & Lansbury, 2003; Zhu & Fink, 2003	El-Agnaf <i>et al.</i> 2006; Feany & Bender, 2000; Gosavi <i>et al.</i> 2002; Lee & Lee, 2002; Lee <i>et al.</i> 2002; Lo Bianco <i>et al.</i> 2002; Masliah <i>et al.</i> 2000; Sharon <i>et al.</i> 2001, 2003a, b.	Lashuel <i>et al.</i> 2002a, b; Ding <i>et al.</i> 2002; Shtilerman <i>et al.</i> 2002; Rochet <i>et al.</i> 2000; Zhu & Fink, 2003; Crystal <i>et al.</i> 2003; Pountney <i>et al.</i> 2004; Zhu <i>et al.</i> 2004; Lowe <i>et al.</i> 2004; Quist <i>et al.</i> 2005	Volles & Lansbury, 2002; Volles <i>et al.</i> 2001

Familial British dementia	ABri	El-Agnaf <i>et al.</i> 2001a, b; Srinivasan <i>et al.</i> 2003	Holton <i>et al.</i> 2001	Srinivasan <i>et al.</i> 2003	Quist <i>et al.</i> 2005
Dialysis-associated amyloidosis	β_2 -Microglobulin	Kad <i>et al.</i> 2003		Kayed & Glabe, 2004	Hirakura & Kagan, 2001
Secondary systemic amyloidoses	Serum amyloid A	Wang <i>et al.</i> 2002b		Wang <i>et al.</i> 2002b	Hirakura <i>et al.</i> 2002
Prion-related diseases	MHM2 PrP 106 (Δ 23-88 and Δ 141-176)	Baskakov <i>et al.</i> 2000	Riesner <i>et al.</i> 1996; Supattapone <i>et al.</i> 1999		Kawahara <i>et al.</i> 2000; Kourie, 2002; Kourie & Culverson, 2000; Kourie <i>et al.</i> 2001a, 2003; Lin <i>et al.</i> 1997
	Prion, PrP 106-126 84-146	Kayed & Glabe, 2004 Sokolowski <i>et al.</i> 2003		Kayed & Glabe, 2004	Hirakura <i>et al.</i> 2000b
	SHa PrP (90-232)	Baskakov <i>et al.</i> 2002; Lu & Chang, 2002; Vendrely <i>et al.</i> 2005		Sokolowski <i>et al.</i> 2003	Bahadi <i>et al.</i> 2003b, c
	PrP (23-231)				
Huntington's disease	(polyglutamine)	Poirier <i>et al.</i> 2002a		Kayed & Glabe, 2004	Hirakura <i>et al.</i> 2000a; Kagan <i>et al.</i> 2001; Monoi <i>et al.</i> 2000 Demuro <i>et al.</i> 2005; Kayed <i>et al.</i> 2004
Amyotrophic lateral sclerosis	Superoxide dismutase-1 (WT & A4V, G37R, G85R)	Chung, 2003; Rakhit <i>et al.</i> 2002, 2004; Ray <i>et al.</i> 2004	Turner <i>et al.</i> 2003	Chung, 2003; Ray <i>et al.</i> 2004	
Senile & familial amyloidosis	Transthyretin	Cardoso <i>et al.</i> 2002a, b; Kayed <i>et al.</i> 2003, 2004; Lashuel <i>et al.</i> 1998, 1999	Sousa <i>et al.</i> 2001, 2002; Teng <i>et al.</i> 2001	Kayed & Glabe, 2004	Azimov <i>et al.</i> 2001
Type II diabetes	IAPP	Anguiano <i>et al.</i> 2002; Green <i>et al.</i> 2003; Green, 2004; Kayed & Glabe, 2004; Kayed <i>et al.</i> 2003; Porat <i>et al.</i> 2003; Rhoades & Gafni, 2003	Butler <i>et al.</i> 2003; de Koning <i>et al.</i> 1994; Janson <i>et al.</i> 1996; O'Brien <i>et al.</i> 1994	Janson <i>et al.</i> 1999; Anguiano, 2002; Kayed & Glabe, 2004; Porat <i>et al.</i> 2003	Anguiano <i>et al.</i> 2002; Harroun <i>et al.</i> 2001; Hirakura <i>et al.</i> 2000b; Kawahara <i>et al.</i> 2000; Mirzabekov <i>et al.</i> 1996; Porat <i>et al.</i> 2003
	P53	Ishimaru <i>et al.</i> 2003		Ishimaru <i>et al.</i> 2003	
	Equine lysozyme	Malisauskas <i>et al.</i> 2003		Malisauskas <i>et al.</i> 2003	
	Insulin	Dzwolak <i>et al.</i> 2005		Dzwolak <i>et al.</i> 2005	

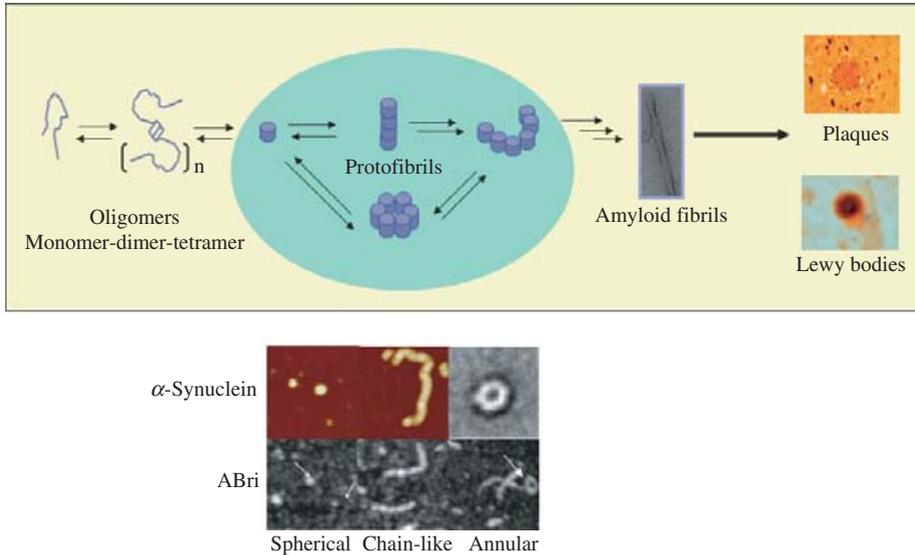


Fig. 1. *In vitro* fibril formation involves transient population of ordered aggregates, or protofibrils. Schematic representation summarizing the quaternary structural species populated during amyloid fibril formation *in vitro* and are thought to form during protein fibrillogenesis and deposition *in vivo*. For simplicity, only the most commonly observed (globular, chain-like and annular structures) protofibrillar structures are shown. (The ABri images were kindly provided by Dr Michael Zagorski.)

raised against the fibrillar form of the amyloidogenic protein amyloid- β ($A\beta$) recognize amyloid fibrils derived from other amyloid-forming proteins (O’Nuallain & Wetzel, 2002). The shared conformational epitopes have not been identified, but may be involved in pathogenesis. Moreover, the structural similarities suggest a shared mechanism of amyloid fibril formation.

2.1 Mechanism of amyloid fibril formation *in vitro*

2.1.1 *In vitro* fibril formation involves transient population of ordered aggregates of intermediate stability, or protofibrils

In order to form an amyloid fibril, proteins must adopt a β -sheet rich conformation(s). This may involve induction of structure in a disordered monomer, or the partial unfolding of a β -sheet-containing globular protein. The β -sheet-rich species has a high propensity to aggregate/fibrillize (Kelly, 1998). *In vitro* amyloid fibril formation does not proceed via a simple two-state, ‘intermediate-less’ mechanism akin to microtubule formation from tubulin (these processes have evolved to be efficient and non-toxic), although that model can be instructive (Jarrett & Lansbury, 1993). Rather, discrete β -sheet rich oligomeric intermediates appear before fibrils form and disappear upon fibril formation (Harper *et al.* 1997a; Walsh *et al.* 1997; Lambert *et al.* 1998) (Fig. 1). These are collectively designated protofibrils. Protofibrils are more stable than the monomer, but less stable than the fibrillar product. They appear to be obligate intermediates in fibril formation; the transient formation of protofibrils has been observed in every well-characterized *in vitro* case, suggesting that they are obligate intermediates that are likely to exist, albeit transiently, *in vivo*.

3. Toxic properties of protofibrils

3.1 Protofibrils, rather than fibrils, are likely to be pathogenic

The presence of amyloid fibrils in the post-mortem brains of demented patients led to the first description of AD and resulted in the hypothesis that fibrils themselves are the primary pathogenic species. This hypothesis fails to explain several important pathological and clinical characteristics of AD, raising the possibility that a species other than amyloid fibrils could be the toxic species (Goldberg & Lansbury, 2000). First, there is no correlation between the amounts of fibrillar $A\beta$ deposits at autopsy and the clinical severity of AD (Lemere *et al.* 1996; Terry *et al.* 1991). Such a correlation does exist between ‘soluble $A\beta$ ’ (monomers plus protofibrils) in the brain and early cognitive dysfunction (Lue *et al.* 1999; McLean *et al.* 1999; Naslund *et al.* 2000). Second, transgenic animals that overproduce APP exhibit neuronal and behavioral abnormalities before amyloid plaques can be detected (Chui *et al.* 1999; Hsia *et al.* 1999; Moechars *et al.* 1999; Mucke *et al.* 2000). Third, inhibiting $A\beta$ amyloid fibril formation does not necessarily attenuate $A\beta$ -associated toxicity towards cultured neurons (Aksenova *et al.* 1996; Stege *et al.* 1999). Fourth, one autosomal dominant form of AD results from a mutation [APP (E693G) = $A\beta$ (E22G)] that decreases $A\beta$ production *in vivo* and promotes protofibril formation and toxicity *in vitro* (Nilsberth *et al.* 2001; Lashuel *et al.* 2003; Whalen, 2005). Fifth, in some AD transgenic mice, vaccination with an $A\beta$ -directed antibody prevented or reversed age-dependent memory decline without reducing the amyloid burden (Morgan *et al.* 2000) [in other cases, vaccination has been shown to reduce behavioral and cognitive deficits *and* the amyloid burden (Janus *et al.* 2000; Morgan *et al.* 2000)]. Finally, $A\beta$ aggregates with properties that are indistinguishable from $A\beta$ protofibrils formed *in vitro* have been found in human CSF, human cerebral cortex (McLean *et al.* 1999), and in neuritic amyloid plaques from AD brains (Roher *et al.* 1996), raising the possibility that soluble prefibrillar oligomeric species, rather than the fibrils, could be the pathogenic species in AD and related amyloid diseases. Consistent with this hypothesis, oligomeric (dimer, trimers and tetramers) low-molecular-weight oligomers (Walsh *et al.* 2002; Wang *et al.* 2004; Cleary *et al.* 2005; Townsend *et al.* 2006) and protofibrillar forms of $A\beta$ altered neuronal function and/or caused neuronal death in culture (Lambert *et al.* 1998; Hartley *et al.* 1999; Walsh *et al.* 2002; Whalen *et al.* 2005).

The toxic protofibril hypothesis also explains features of PD and other neurodegenerative diseases that are inconsistent with the fibril being the pathogenic species (Goldberg & Lansbury, 2000; Caughey & Lansbury, 2003; Silveira *et al.* 2005). In PD, fibrillar intraneuronal inclusions comprising α -synuclein, known as Lewy bodies (LBs), are an invariant feature of sporadic and autosomal dominant forms of PD, but are absent in autosomal recessive juvenile Parkinsonism (AJRP) (Shimura *et al.* 2001). It is likely that AJRP brains have such high levels of protofibrils that complete neurodegeneration occurs before LBs have a chance to form [AJRP results from a deletion in the parkin gene; point mutations produce a later-onset form of PD that is characterized by LBs (Kitada *et al.* 1998)]. Elevated levels of soluble oligomeric forms of α -synuclein have been detected in plasma samples of PD patients compared to controls (El-Agnaf *et al.* 2006). Similarly, transgenic mice that overexpress the human α -synuclein protein become symptomatic (movement disorder plus dopaminergic abnormalities) but do not produce fibrillar deposits (Masliah *et al.* 2000). Furthermore, virus-mediated overexpression of human α -synuclein into the substantia nigra of rats (Kirik *et al.* 2002; Lo Bianco *et al.* 2002) and primates (Kirik *et al.* 2003) results in selective dopaminergic neuronal death with non-fibrillar, α -synuclein-containing inclusions. *In vitro* studies of α -synuclein aggregation provide possible hints as to the underlying

situation: mixtures of human and mouse α -synuclein (as exist in the transgenic mouse brain) accumulate protofibrils, but fibrillize very slowly (Rochet *et al.* 2000). Interestingly, virus-mediated expression of rat α -synuclein in rat brain results in aggregation, but no neurodegeneration (Kirik *et al.* 2002; Lo Bianco *et al.* 2002). Further characterization of the aggregates formed by human and rat α -synuclein could provide important insights into the role of α -synuclein aggregation in the degeneration of dopaminergic neurons.

Other neurodegenerative diseases fail to support the proposal that amyloid fibrils are pathogenic. Prion protein (PrP) fibrils are observed in some prion diseases, but are not an invariant feature (Chiesa & Harris, 2001). In yeast and mouse models of prion disease, toxicity was produced in the absence of the stable, protease-resistant aggregated form of the prion protein (PrP-Sc) (Ma & Lindquist, 2002; Ma *et al.* 2002). A transgenic mouse model of a familial prion disease became symptomatic before PrP-Sc could be detected (Chiesa *et al.* 2003). Recent studies by Caughey and co-workers suggest that the most infectious PrP particles represent protofibrillar particles with molecular masses ranging from 300–600 kDa (corresponding to 14–28 PrP molecules) (Silveira *et al.* 2005). Finally, in systemic amyloid diseases, where amyloid was thought to produce disease by physically interfering with organ function, studies by Reixach *et al.* suggest a primary pathogenic role for protofibrils in initiating cytotoxicity and organ dysfunction (Reixach *et al.* 2004). For example, non-fibrillar aggregates of transthyretin (TTR), a protein associated with systemic amyloidosis and familial amyloid polyneuropathy (FAP), have been detected in transgenic mice expressing wild-type and mutant TTR (Teng *et al.* 2001) and in the nerves of FAP patients (Sousa *et al.* 2001, 2002). These aggregates were linked to significant clinical pathology early in the disease before the fibrillar deposits could be detected.

3.2 The toxic protofibril may be a mixture of related species

In an effort to more precisely identify the neurotoxic protein aggregate, cell culture models of extracellular toxicity have been utilized. Although these simplified models allow more detailed analysis, their relevance to AD is debatable. Given that caveat, as well as the fact that $A\beta$ oligomers added to cell culture media are heterogeneous (Lashuel *et al.* 2003; Goldsbury *et al.* 2005) and are likely to change during the course of an experiment, there is remarkable agreement among these studies that the protofibril, and not the monomer or the fibril, is a toxic entity (Lambert *et al.* 1998; Hartley *et al.* 1999; White *et al.* 2005; Townsend *et al.* 2006). In the case of $A\beta$, the amyloid protein of AD, globular oligomers (designated ADDLs) were toxic to cultured neurons (Lambert *et al.* 1998) and inhibited hippocampal long-term potentiation (LTP) when introduced to brain slices (Wang *et al.* 2002a). Globular oligomers of similar sizes (based on AFM and EM measurement) have been described by other research groups and were shown to be toxic to cultured neurons (Barghorn *et al.* 2005). In a related study, small spherical and chain-like $A\beta$ protofibrils (but not monomer, dimer, trimer) induced acute electrophysiological changes and progressive neurotoxicity in cortical neurons (Hartley *et al.* 1999). Large spherical aggregates of $A\beta$ (average diameter of >10 nm), termed amylospheroids, exhibited significantly higher toxicity than small spherical $A\beta$ oligomers (<10 nm) (Hoshi *et al.* 2003). $A\beta_{42}$ forms spherical aggregates (diameter >10 nm) more rapidly and exhibits significantly more (>100 -fold) toxicity to neuronal cultures than those formed by $A\beta_{40}$. Similar, apparently spherical structures with diameters ranging from 8–24 nm have also been observed as transient intermediates during the fibrillogenesis of the arctic variant (E22G) of $A\beta_{40}$ and $A\beta_{42}$ (Lashuel *et al.* 2003), α -synuclein (Lashuel *et al.* 2002a) and mutant SOD1 (Ray *et al.* 2004). The toxicity of TTR towards cultured

cells is also linked to a non-fibrillar oligomeric species, possibly an octamer (Reixach *et al.* 2004). Finally, it is probable that the protofibril structure, rather than the protein primary sequence, produces toxicity. For example, small spherical protofibrils, formed *in vitro* by an amyloidogenic SH3 domain from bovine phosphatidylinositol-3 kinase (which is not linked to any disease) are toxic to cultured cells (Bucciantini *et al.* 2002).

3.3 Morphological similarities of protofibrils suggest a common mechanism of toxicity

The shared morphological and toxic properties of amyloid protofibrils suggest that toxicity depends on shared structural features. Consistent with this hypothesis, antibodies raised against protofibrillar A β were reported to recognize protofibrillar species derived from other amyloidogenic proteins (e.g. α -synuclein, polyglutamine, TTR, IAPP, lysozyme, human insulin, and PrP106-126), but not monomeric or fibrillar forms of these proteins (Kayed *et al.* 2003). These antibodies also inhibit the toxicity of these proteins. These findings support detailed structural studies of protofibrils, some of which are summarized below. Furthermore, These observations raise the possibility that these diverse (with respect to sequence, at least) structures may exert their toxicity through common mechanisms. It may be that an intermediate on the assembly pathway that is in equilibrium with the protofibril could be the toxic species. The most likely candidates are low-molecular-weight oligomers (e.g. dimers, trimers or tetramers) or a high-molecular-weight protofibrillar species, most likely the 4 nm (± 1 nm) spherical species. This is consistent with biophysical studies (AFM and EM) demonstrating that these spheres are the precursors to the chain-like and annular protofibrillar structures and appear to exist in equilibrium with the large spherical aggregates (8–70 nm). Several laboratories have demonstrated that these species are capable of self-assembling into pore-like structures on artificial or biological membranes (Lin *et al.* 2001; Ding *et al.* 2002).

3.4 Are the amyloid diseases a subset of a much larger class of previously unrecognized protofibril diseases?

The hypothesis that small protofibrillar aggregates are pathogenic has an interesting corollary: there may be many other diseases that, like ARJP, are not characterized by easily detected protein aggregates. Unlike ARJP, which is genetically and clinically linked to the amyloid disease PD, these diseases may not be recognized as involving protein aggregation at all. In contrast to our expectation that the primary sequence efficiently directs protein folding, a significant portion of newly synthesized proteins ($\sim 35\%$) are not correctly folded *in vivo* (Schubert *et al.* 2000). We expect that many more protein aggregation-driven pathologies remain to be discovered.

3.5 Fibrils, in the form of aggresomes, may function to sequester toxic protofibrils

According to the toxic protofibril hypothesis, the role of the amyloid fibril is uncertain; it could have some greatly reduced toxicity, it could be inert, or it could protect neurons by sequestering toxic protofibrils and/or by consuming protein monomers, inhibiting continued protofibril formation (Caughey & Lansbury, 2003). There is circumstantial evidence that fibrils may have a protective function. In PD brains, dopaminergic neurons that contain LBs appear to be 'healthier' than neighboring neurons based on morphological and biochemical criteria (Tompkins & Hill, 1997). Several transgenic models of polyglutamine diseases are characterized

by polyglutamine inclusions in healthy neuron populations, but not in vulnerable neurons (Kuemmerle *et al.* 1999). In a transgenic mouse model of one polyglutamine disease, spinocerebellar ataxia-type1 (SCA1), there was a direct correlation between the ability of neurons to sequester ataxin-1 into inclusions and their resistance to cell death (Watase *et al.* 2002). Taken together, these observations suggest that formation of fibrillar inclusions may protect neurons against protofibril-induced neurotoxicity. There is mounting evidence that the sequestration process may be an active one. Expression of any one of the four disease-associated proteins; cystic fibrosis transmembrane conductance regulator (CFTR, associated with cystic fibrosis) (Johnston *et al.* 1998), SOD1 (amyotrophic lateral sclerosis) (Johnston *et al.* 2000), the androgen receptor (AR, X-linked spinobulbar muscular atrophy) (Taylor *et al.* 2003), or Parkin (Junn *et al.* 2002) in cultured cells under conditions of oxidative stress or proteasome impairment leads to sequestration of the mutant protein within multicomponent proteinaceous inclusions known as aggresomes. Sequestration is actively mediated by microtubules (Johnston *et al.* 1998). In the case of Parkin, these inclusions exhibit morphological and immunohistochemical features similar to LBs (Junn *et al.* 2002). In addition to sequestering toxic protein aggregates, aggresomes may play an active role in facilitating the clearance of these toxic species by lysosomal mediated degradation mechanisms (Taylor *et al.* 2003).

4. Amyloid pores, a common structural link among protein aggregation neurodegenerative diseases

4.1 Mechanistic studies of amyloid fibril formation reveal common features, including pore-like protofibrils

The convergent circumstantial evidence implicating protofibrils as pathogens has motivated a more detailed analysis of protofibril structure and formation *in vitro*. These studies are briefly summarized below and in Table 1, grouped according to the amyloid disease to which they are relevant. Similar pathways are followed by other fibrillogenic proteins that are not known to be related to disease (see Table 1 and below).

4.1.1 Amyloid- β ($A\beta$) (Alzheimer's disease)

Alzheimer's disease (AD) is characterized by the presence of extracellular fibrillar amyloid plaques and intraneuronal neurofibrillary tangles in brain areas associated with memory and learning. The main fibrillar constituent of amyloid plaques is amyloid- β (β) (Glenner & Wong, 1984), a 39-42 amino acid peptide that is produced by endoproteolytic processing of the APP (Selkoe, 1994). A central role for $A\beta$ amyloid fibril formation in the etiology of AD is supported by extensive genetic and biochemical evidence (Hardy & Selkoe, 2002). In solution, $A\beta$ is unstructured, but $A\beta$ protofibrils, including spherical (average diameter of 2.4–4.5 nm, containing ~40 monomers) and chain-like protofibrils and are rich in β -sheet structure (Fig. 1) (Harper *et al.* 1997a, b; Walsh *et al.* 1997; Lambert *et al.* 1998; Parbhu *et al.* 2002; Stine *et al.* 2003). Smaller oligomers (e.g. dimers, trimers and tetramers) likely exist, but are not populated in solution (they can only be observed by SDS-PAGE). Once the critical concentration of the spherical and later chain-like species is reached, they are rapidly converted into amyloid fibrils. In addition to the globular and chain-like protofibrils, annular structures with variable diameters (outer diameter 6–9 nm, inner diameter 1.5–2 nm) have also been observed during the

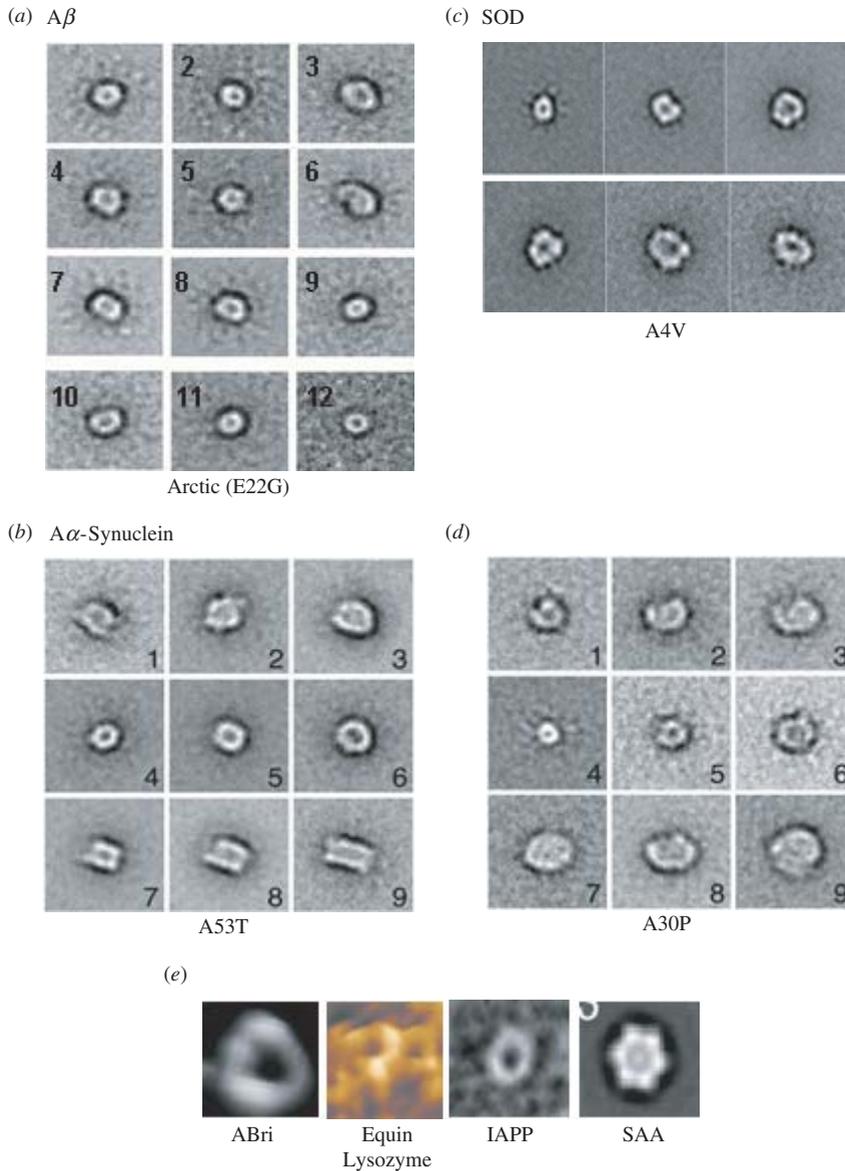


Fig. 2. Many amyloid proteins form annular pore-like protofibrils and have channel- or pore-like properties *in vitro*. Annular pore-like structures with variable diameters form during the *in vitro* fibrillogenesis of disease associated mutants of $A\beta$ [Arctic variant (E22G) of $A\beta_{40}$] (a, f), α -synuclein (A53T & A30P) (b, d), and SOD1 (A4V) (c), and other amyloid-forming proteins (e).

fibrillogenesis of $A\beta$ *in vitro* (Fig. 2a) and during the reconstitution of $A\beta$ in lipid bilayers (Fig. 3a) (Hafner *et al.* 2001; Lin *et al.* 2001; Chromy *et al.* 2003; Klug *et al.* 2003; Lashuel *et al.* 2003; Kaye & Glabe, 2004). The similar heights of the spheres, chain-like and annular protofibrils suggests that the spheres are the precursors of the others (Lashuel *et al.* 2003). Formation of annular protofibrils is promoted by a pathogenic mutation [APP (E693G) = $A\beta$ (E22G)] that is linked to familial AD and accelerates the oligomerization of $A\beta$ *in vitro* (Nilsberth *et al.* 2001; Lashuel *et al.* 2002a, b). Annular protofibrils represent only a small fraction of the total population of $A\beta$

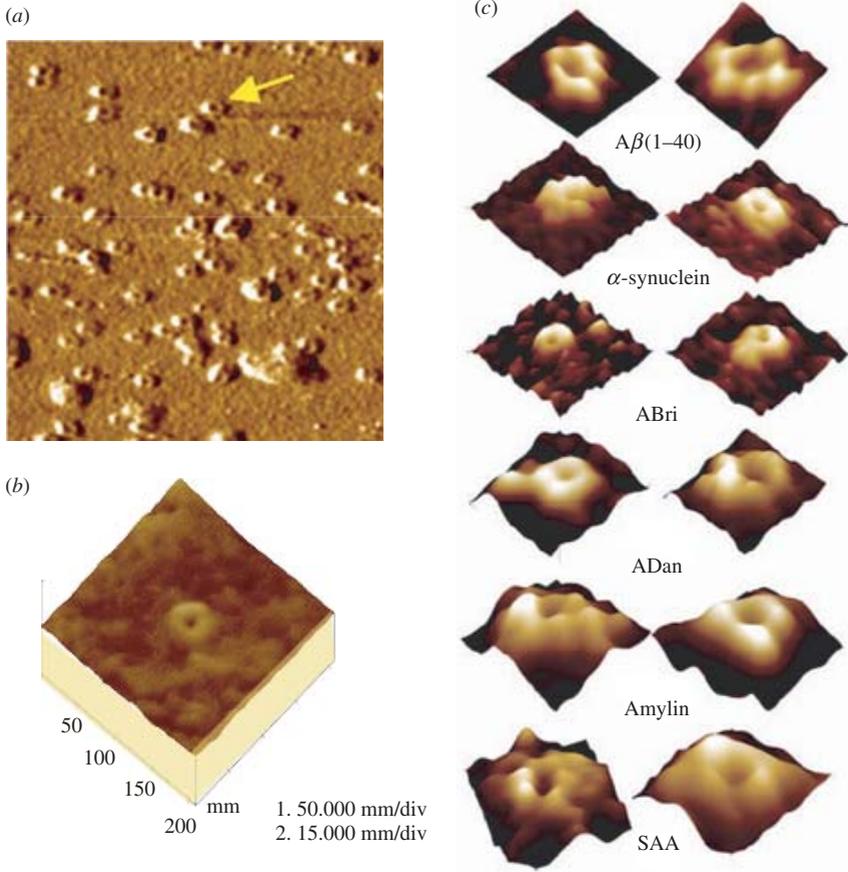


Fig. 3. Amyloid forming proteins form pore-like/channel structures on artificial as well as biological membranes. (a) AFM images of pore-like structures formed during the reconstitution of $A\beta$ in lipid bilayers (adapted from Lin *et al.* 2001). (b) Pore-like structures that were obtained by incubating predominantly spherical α -synuclein protofibrils (WT and A53T) with brain-derived vesicles (adapted from Ding *et al.* 2002). (c) Amyloid-forming proteins/peptides reconstituted in lipid bilayers form pore/channel-like structures (adapted from Quist *et al.* 2005).

protofibrils at any given time, which explains why these structures were missed or ignored in previous studies.

4.1.2 α -Synuclein (PD and diffuse Lewy body disease)

PD is associated with the formation of intraneuronal fibrillar inclusions (LBs) (Pollanen *et al.* 1993; Shults, 2006). α -Synuclein is the primary component of LBs in all PD patients (Spillantini *et al.* 1998b) and is strongly implicated as a cause of PD by biochemical (Cookson, 2005) and genetic studies of familial forms of PD (Polymeropoulos *et al.* 1997; Kruger *et al.* 1998; Singleton *et al.* 2003; Zarranz *et al.* 2004) and by mouse (Masliah *et al.* 2000) and *Drosophila* (Feany & Bender, 2000; Chen & Feany, 2005) modeling studies. Three different α -synuclein missense mutations (A30P, A53T and E46K) are associated with rare, autosomal dominant forms of early-onset PD (Polymeropoulos *et al.* 1997; Kruger *et al.* 1998; Zarranz *et al.* 2004). In addition, triplication of the wild-type α -synuclein gene causes autosomal dominant PD in an Iowan

kindred (Singleton *et al.* 2003). Transgenic mice (Masliah *et al.* 2000) expressing human wild-type α -synuclein and *Drosophila* (Feany & Bender, 2000; Chen & Feany, 2005) expressing WT, A30P, or A53T are characterized by α -synuclein non-fibrillar (mice and fly) or fibrillar (Flynn & Theesen, 1999) inclusions and a Parkinsonian phenotype. Like $A\beta$, α -synuclein is not folded under 'native' conditions (Weinreb *et al.* 1996), but will form β -sheet rich protofibrils and amyloid fibrils *in vitro*. Three mutations (A53T, E46K and A30P) linked to early-onset PD promote the formation of α -synuclein protofibrils, but the A30P mutation was shown to form fibrils more slowly than WT α -synuclein, suggesting that α -synuclein protofibrils may cause neurodegeneration in PD (Conway *et al.* 1998; Conway *et al.* 2000; El-Agnaf *et al.* 1998; Li *et al.* 2001; Pandey *et al.* 2006). Amyloid fibril formation by α -synuclein occurs by a hierarchical assembly mechanism (random coil \rightarrow spheres \rightarrow chain-like and annular protofibrils \rightarrow fibrils) similar to that observed for $A\beta$ in AD (Conway *et al.* 2000; Ding *et al.* 2002). The PD-linked mutations promote formation of annular and tubular protofibrillar structures (wild-type α -synuclein forms annular protofibrils after extended incubation) (Conway *et al.* 2000; Ding *et al.* 2002; Lashuel *et al.* 2002a,b) (Fig. 2*b,d*). The diameter of α -synuclein annular protofibrils detected *in vitro* is similar to that of the α -synuclein fibrils. Zhu and colleagues observed the formation of α -synuclein annular protofibrils during drug-induced disaggregation of α -synuclein fibrils *in vitro* (Zhu *et al.* 2004), suggesting that a direct relationship between the two structures may exist. These observations are consistent with cross-sectional analysis of *ex vivo* amyloid fibrils demonstrating that amyloid fibrils have an electron-lucent center, indicative of the presence of a hollow center (Serpell *et al.* 2000).

4.1.3 ABri (familial British dementia)

ABri is the major component of amyloid deposits in the brain of patients with familial British dementia (FBD). FBD is an autosomal dominant neurodegenerative disorder associated with a stop codon mutation in the BRI gene that results in the production of ABri (Vidal *et al.* 1999; Ghiso *et al.* 2000). *In vitro* fibrillogenesis of ABri produced protofibrils and subsequently, amyloid fibrils (El-Agnaf *et al.* 2001a,b; Srinivasan *et al.* 2003, 2004), by a mechanism that is reminiscent of that of $A\beta$ and α -synuclein, including the formation of spherical, chain-like and annular protofibrillar intermediates. Spherical protofibrils exhibited more toxicity to cultured neurons than chain-like protofibrils and fibrils (El-Agnaf *et al.* 2001a). Annular ABri protofibrils have been characterized *in vitro* (see Fig. 2*e*) (Srinivasan *et al.* 2004; O. M. El-Agnaf, personal communication) but their toxicity has not been determined.

4.1.4 Superoxide dismutase-1 (amyotrophic lateral sclerosis)

Amyotrophic lateral sclerosis (ALS), also known as Lou Gehrig's disease (Rosen, 1978; Julien, 2001), is linked to the gene encoding superoxide dismutase-type 1 (SOD1) (Rosen *et al.* 1993; Brown, 1997). Cytoplasmic inclusions containing mutant SOD1 are present in the motor neurons of familial ALS patients (Shibata *et al.* 1996) and transgenic mouse models (Bruijn *et al.* 1998; Watanabe *et al.* 2001). Significantly, these inclusions do not clearly contain fibrillar substructure. SOD1 is a structured homodimer. FALS mutations destabilize the native SOD1 dimer (Nakano *et al.* 1996; Cardoso *et al.* 2002b; Hayward *et al.* 2002; Lindberg *et al.* 2002; Rodriguez *et al.* 2002; Tiwari & Hayward, 2003; Rakhit *et al.* 2004; Ray *et al.* 2004) and promote SOD1 aggregation *in vitro* (Ray *et al.* 2004). Significantly, SOD1 has not been induced to form amyloid

fibrils *in vitro*. Instead, spherical and annular oligomeric structures have been observed (Chung, 2003; Ray *et al.* 2004). As expected, the pathogenic SOD1 mutants aggregate more rapidly than WT SOD1 (Chung, 2003; Ray *et al.* 2004), consistent with what is observed with A β and α -synuclein (Lashuel *et al.* 2003; Lashuel *et al.* 2002a, b). Their findings suggest that common pathogenic assemblies may underlie all of these diseases. In addition to pathogenic mutations, conditions that promote metal depletion or oxidative damage of SOD1 accelerate the formation of annular structures by mutants and wild-type SOD (A4V, H46R, G37R, and G85R) (Chung, 2003; Elam *et al.* 2003; Ray *et al.* 2004). The morphology of these oligomeric forms of SOD1 formed *in vitro* resembles that of protofibrillar species of A β and α -synuclein, in particular the annular and small spherical species (Fig. 2c). Thus, these species have been designated SOD1 protofibrils, yet they do not convert to fibrils over several weeks of incubation (Ray *et al.* 2004).

4.1.5 Prion protein (Creutzfeldt–Jakob disease, bovine spongiform encephalopathy, etc.)

The prion diseases [Creutzfeldt–Jakob disease (CJD), Gertsman–Straussler syndrome (GSS), and fatal familial insomnia (FFI) in humans, bovine spongiform encephalopathy (BSE) in cattle, scrapie in sheep, and chronic wasting disease in elk] are characterized by the presence of an abnormal form of the PrP in the brain. The ability of these diseases to be transmitted, apparently by an abnormal form of the PrP, distinguishes them from the others discussed here, but there are also sporadic forms of human prion disease as well as forms that are purely genetic; caused by mutations in the gene encoding PrP (CJD, GSS, and FFI). The disease-associated form of the PrP, or PrP-Sc, is resistant to proteolysis and rich in β -sheet structure, relative to the normal form of the PrP, PrP-C (Cohen & Prusiner, 1998). PrP-Sc can also be isolated in fibrous form (Rubenstein *et al.* 1987). However, several lines of evidence suggest that PrP-Sc, like other amyloid fibrils, may not be the neurotoxic form of the protein. Transgenic mice that overproduce a disease-associated form of PrP exhibit disease-like phenotypes before PrP-Sc can be detected (Chiesa & Harris, 2001; Harris *et al.* 2003). During this phase, the protease-resistance of PrP gradually increased, suggesting the stepwise formation of structured oligomers of increasing stability. *In vitro* fibrillization of a fragment of PrP (residues 89–231) involves multiple oligomeric species, some of which appear to be off-pathway β -sheet-rich oligomers (Baskakov *et al.* 2002). Truncated variants of PrP form spherical and elongated protofibril-like structures that share properties with PrP-Sc and are capable of seeding the conversion of PrP^C into amyloid fibrils (Lee & Eisenberg, 2003). Finally, a truncated variant of PrP (SHaPrP 90-232) forms spherical and annular oligomeric structures *in vitro*, similar to those formed by A β and α -synuclein (Sokolowski *et al.* 2003). It was estimated that 8 subunits of SHaPrP 90-232 are required to form the β -sheet-rich annular structures (Sokolowski *et al.* 2003).

4.1.6 Huntingtin (Huntington's disease)

Huntington's disease is the most prevalent of a group of purely genetic neurodegenerative movement disorders that are caused by expansions of naturally occurring polyglutamine (polyQ) tracts in several proteins (the normal function of these tracts is not known) (Zoghbi & Orr, 2000). The magnitude of the expansion is related to the age of onset of the disease, with large expansions causing juvenile onset disease. The Huntington's disease brain is characterized by nuclear inclusions comprising the protein huntingtin (htn). Truncated mutant versions of htn with expanded polyQ repeat form spherical (Poirier *et al.* 2002; Wacker *et al.* 2004) chain-like

(Poirier *et al.* 2002), and annular (Wacker *et al.* 2004) protofibrillar structures *in vitro* that closely resemble those discussed above.

4.2 Amyloidogenic proteins that are not linked to disease also form pore-like protofibrils

Several other proteins that are not associated with disease form annular protofibrillar structures during the *in vitro* formation of amyloid fibrils. Conditions required to induce annular protofibrils vary depending on the precursor protein. Under partial denaturing conditions, the calcium-binding protein equine lysozyme (EL) self-assembles into protofibrils and fibrils of various morphologies in a pH and calcium dependent manner (Malisauskas *et al.* 2003). At pH 4.5 and 57° in the presence of 10 mM EDTA, EL forms annular structures with an average diameter of 45 nm (± 5 nm), whereas at pH 2.0 EL forms rings with larger diameters ranging from 70–80 nm. Interestingly, in the presence of calcium at pH 4.5, elongated chain like structures are populated as the major species, but upon removal of calcium, EL forms predominantly annular structures (major species by AFM). Similarly, partial denaturing conditions were sufficient to induce oligomerization and formation of pore-like structures by the core domain of the tumor suppressor protein p53C (Ishimaru *et al.* 2003). Furthermore, Glabe & Kaye reported to have developed conditions for the formation of highly homogeneous preparations of annular protofibrils (outer diameter 8–12 nm, inner diameter 1.8–4.5 nm) from several amyloidogenic proteins, including A β , α -synuclein, IAPP, polyglutamine (KKQ40KK), Prion H1 (106–126), TTR and several A β variants (Kaye & Glabe, 2004). It has been proposed that the ability of a wide range of proteins to form annular protofibrils suggest that these quaternary structures might represent a second generic form of amyloid structures in addition to amyloid fibrils (Malisauskas *et al.* 2003). Furthermore, the ability to populate pore-like structures as the predominant species *in vitro* by manipulating solution conditions, suggest that *in vivo* conditions that promote the formation of these structures could exist.

4.3 Amyloid proteins form non-fibrillar aggregates that have properties of protein channels or pores

Disruption of Ca²⁺ homeostasis and generation of reactive oxygen species have long been recognized to be key events in the pathogenesis of several neurodegenerative diseases, including AD (Hardy & Higgins, 1992). Cellular factors responsible for initiating these events and the mechanism by which they contribute to the neurodegeneration and cytotoxicity remain poorly understood.

Every protein that forms amyloid fibrils *in vitro* does so via the protofibril. Aggregates comprising many of these proteins have channel-like or pore-like properties *in vitro* (the most relevant studies are summarized below). We propose that the pore-like properties arise from the pore-like protofibrillar structures or the ability of a protofibrillar intermediate to form these structures upon interactions with membranes. We prefer the term pore as opposed to channel, because the latter implies selectivity and regulation and we do not expect that either is involved with amyloid associated diseases. However, the terms used in the sections below reflect literature usage.

4.3.1 A β 'channels'

In 1993, Arispe and colleagues demonstrated that A β forms calcium channels in lipid bilayers and proposed that channel formation by A β is partially or wholly responsible for A β -induced

toxicity in AD (Arispe *et al.* 1993a, b). This finding has been reproduced many times, in several different laboratories, using many membrane models (Arispe *et al.* 1993b, 1994; Kawahara *et al.* 1997, 2000; Sanderson *et al.* 1997; Rhee *et al.* 1998; Hirakura *et al.* 1999; Lin *et al.* 1999, 2001; Bhatia *et al.* 2000; Kourie *et al.* 2001b; Kagan *et al.* 2002; Lin & Kagan, 2002; Bahadi *et al.* 2003a; Alarcon *et al.* 2006). The form of A β that is closely linked to AD pathogenesis (A β 42) exhibits higher propensity to form channels, consistent with its increased propensity to aggregate and form annular protofibrils *in vitro* (H. Lashuel & P. T. Lansbury Jr., unpublished observations) as compared to A β 40, the predominant form (Jarrett *et al.* 1993). β -sheet formation is also linked to A β -channel formation (and aggregation) (Sanderson *et al.* 1997). When incorporated into artificial lipid bilayers, A β produces uniform pore-like structures with an outer diameter of 8–12 nm and inner diameter of 2 nm (Fig. 3a, c) (Lin *et al.* 2001; Quist *et al.* 2005). These aggregates, formed at the membrane surface, resemble pore-like aggregates formed in solution using A β 42 or the disease-associated mutant form of A β 40 (E22G) (Lashuel *et al.* 2002b, 2003). Addition of A β 40 oligomers to hypothalamic GT1-7 neuronal cells results in simultaneous formation of Ca²⁺ channels and increase in intracellular Ca²⁺ levels, suggesting that A β 40 oligomers is capable of disrupting biological as well as artificial membranes, possibly via pore formation (Kawahara & Kuroda, 2001, 2000; Singer & Dewji, 2006). The nature of the oligomer responsible for this activity was not investigated. AD-derived A β oligomers were observed to exhibit high affinity and selective attachment to membranes, suggesting that AD-derived oligomers are either directly integrated into the membranes or bind tightly to other cell surface molecules of cultured hippocampal neurons (Gong *et al.* 2003). Oligomer-specific antibodies were shown to block their interaction with membranes.

4.3.2 α -Synuclein 'pores'

The α -synuclein protofibril (but not the monomer or the fibril) binds very strongly to vesicle membranes and causes leakage of small compounds (less than ~ 2.5 nm hydrodynamic radius) entrapped within synthetic vesicles (Volles *et al.* 2001; Volles & Lansbury, 2002). This typical pore-like behavior was consistent with the observation that addition of spherical protofibrils of α -synuclein to purified brain-derived vesicle (BDV) fractions resulted in the formation of pore-like structures (Fig. 3b) (Ding *et al.* 2002). Additionally, reconstitution of α -synuclein in lipid bilayers also results in the formation of pore-like structures that exhibit channel-like properties (Quist *et al.* 2005). Mutations linked to familial PD promoted the formation of the β -sheet-rich annular, pore-like ($d = 8\text{--}12$ nm, $2\text{--}2.5$ nm inner diameter) structures in solution (Lashuel *et al.* 2002a, b). These structures resembled in morphology and dimension, membrane-spanning pores that are formed by protein toxins (e.g. hemolysin, latrotoxin, and aerolysin) (Valeva *et al.* 1997; Orlova *et al.* 2000; Wallace *et al.* 2000). Vesicle permeabilization was also demonstrated for protofibrils comprising the congener γ -synuclein, but *not* those comprising β -synuclein (Park & Lansbury, 2003). At the same time, γ -synuclein, but not β -synuclein, produced pore-like structures in solution (H. Lashuel, unpublished results), strengthening the case that the pore-like structures are responsible for the pore-like behavior of α -synuclein.

4.3.3 PrP 'channels'

Aguzzi and colleagues have proposed that the pathogenicity of the PrP may be related to abnormal pore formation (Moore *et al.* 1999; Rossi *et al.* 2001; Behrens & Aguzzi, 2002). This proposal, based on studies of a PrP homolog, Doppel, is supported by circumstantial

experimental evidence. First, an abnormal transmembrane (translocation-incompetent) form of PrP has been linked to disease (Hegde *et al.* 1999). Second, a peptide based on the proposed transmembrane domain of PrP produce non-fibrillar aggregates that disrupt membranes (Pillot *et al.* 1997) and induce toxicity in rat cortical neurons (Pillot *et al.* 2000). Third, several PrP-based peptides interacts with lipid membranes and form ion channels (Lin *et al.* 1997; Kourie & Culverson, 2000; Bahadi *et al.* 2003b, c). Fourth, a truncated form of PrP permeabilizes synthetic vesicles (Sanghera & Pinheiro, 2002). Fifth, when disease-associated mutant forms of PrP were expressed in CHO cells, PrP was found to be very tightly associated with plasma membranes (Lehmann & Harris, 1996).

4.3.4 Polyglutamine 'channels'

Peptides with pathological polyglutamine repeats (>35–40 residues) insert into artificial membranes (Hirakura *et al.* 2000a; Monoi *et al.* 2000; Kagan *et al.* 2001) and also affect mitochondrial Ca^{2+} homeostasis (Panov *et al.* 2002). Furthermore a polyglutamine (Gln40) peptide produced homogeneous pore-like protofibrillar structures *in vitro*, while a shortened peptide did not (Monoi *et al.* 2000). Importantly, β -sheet formation, oligomerization, amyloid pore/channel formation, and fibrillogenesis are also very sensitive to polyGln repeat length (Scherzinger *et al.* 1999). Circumstantial evidence suggests that membrane disruption is mediated by direct interaction between the polyglutamine repeats or an aggregated form of these proteins resulting in the formation of ion channels in lipid bilayers and in mitochondrial membranes. Interestingly, only pathological polyglutamine repeat (>35–40) were observed to insert into artificial membranes and exhibited direct effects on mitochondrial Ca^{2+} homeostasis, reproducing the mitochondrial deficit seen in Huntington's disease patients and in transgenic animals expressing these repeats (Hirakura *et al.* 2000a; Monoi *et al.* 2000; Kagan *et al.* 2001; Panov *et al.* 2002). Furthermore, Kaye & Glabe (2004) reported that a polyglutamine protein containing 40 repeat (KKQ40KK) forms homogeneous annular pore-like protofibrillar structures *in vitro*, suggesting that protofibril formation and channel activity are linked.

Monoi and colleagues proposed that a single chain of poly-glutamine polypeptide is capable of forming cylindrical pores by forming a right handed helix (6.2 residues/turn), termed μ -helix, that is further stabilized by backbone side-chain hydrogen bonding interactions between the amide groups and glutamine side-chain (Monoi, 1995; Monoi *et al.* 2000). What makes this model an attractive one is that it offers an explanation for the requirement of >35 polyglutamine tract to confer pathogenicity in polyglutamine diseases, because 37 residues (each contributing 0.81 Å to the length) would be required to form a μ -helix that spans the hydrophobic region of the bilayer (30 Å). A normal transmembrane domain composed of an α -helix is ~20 amino acids long. However, β -sheet formation, oligomerization and fibrillogenesis by poly-glutamine proteins are highly dependent on the polyQ repeat length with 36 or more glutamines favoring these tertiary and quaternary structure changes (Scherzinger *et al.* 1999). However, further studies are required to elucidate the nature of the membrane active species responsible for polyglutamine membrane disruption properties.

4.4 Nature uses β -strand-mediated protein oligomerization to construct pore-forming toxins

A simple working hypothesis emerging from the studies summarized above holds that five properties of disease-associated amyloid proteins are linked: (1) aggregation, (2) β -sheet formation,

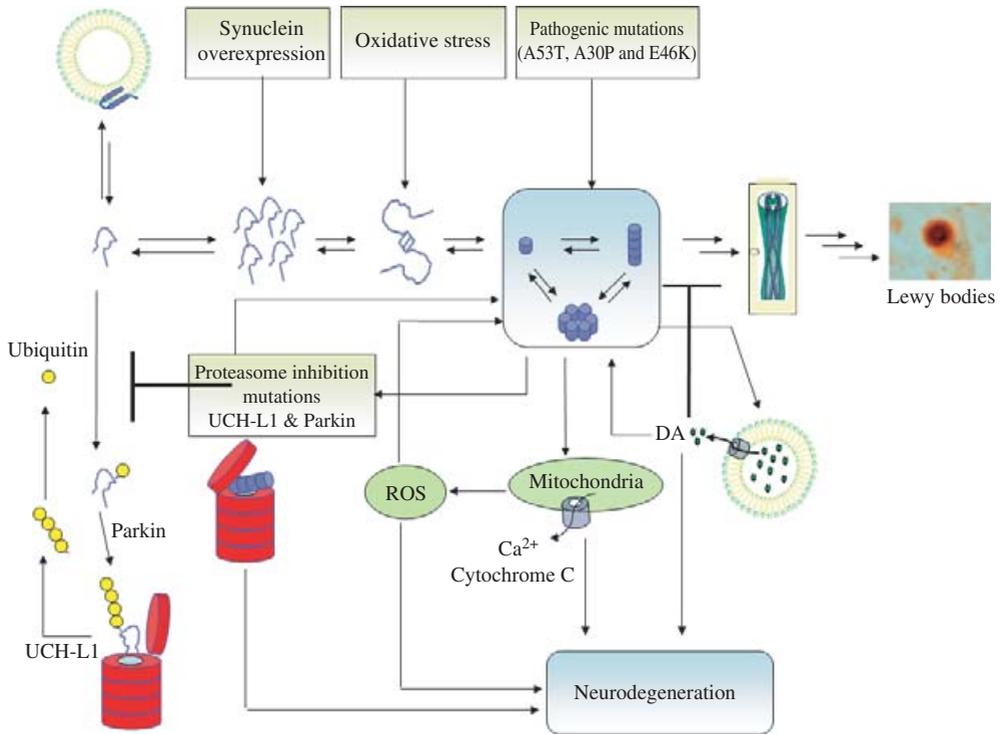


Fig. 4. Schematic depiction of the various steps involved in α -synuclein aggregation and Lewy Body formation and potential mechanisms by which these processes could contribute to the pathogenesis of PD. Several factors have been shown to play a role in initiating and/or accelerating α -synuclein aggregation and fibrillogenesis including, increased protein expression, mutations, oxidative stress induced modifications and crosslinking, and phosphorylation at S129 (Chen & Feany, 2005; Fujiwara *et al.* 2002; Smith *et al.* 2005). The scheme depicts amyloid protofibril as the toxic species and that it may amplify itself by inhibiting proteasome-dependent protein degradation, disrupting dopaminergic vesicles, formation of reactive oxygen species and increased oxidative stress, causing mitochondrial dysfunction (Abou-Sleiman *et al.* 2006), all of which have the affect of increasing levels of α -synuclein and/or accelerating α -synuclein oligomerization and protofibril formation. This hypothesis is supported by the findings that triplication of the α -synuclein gene causes and autosomal dominant PD in Iowan kindred (Singleton *et al.* 2003). Protofibrils may promote their own accumulation and toxicity by inhibiting the proteasome. Two gene products in the protein degradation pathway have been implicated in early onset forms of PD (Lansbury & Brice, 2002). One form is associated with genetic mutations in the gene encoding parkin (a protein with an E3 (ubiquitin ligase)-like activity), where the mutations reduce or abolish parkin's E3-like ligase activity (Kitada *et al.* 1998). A rare point mutation in the gene encoding ubiquitin C-terminal hydrolase (UCH-L1), a neuronal-specific deubiquitinating enzyme, is thought to lead to reduced catalytic activity of UCH-L1, and, thus, indirectly affect the proteasomal function (Leroy *et al.* 1998). Furthermore, reduced expression of UCH-L1 in the substantia nigra of DLB and PD brains suggest that it plays a role in modulating protein aggregation and LB formation (Barrachina *et al.* 2005). In addition to its beneficial hydrolase activity (hydrolysis of C-terminal ubiquityl esters and amides), UCH-L1 exhibits a concentration dependent ubiquityl ligase activity that is thought to be pathogenic for PD. Taking together, these findings demonstrate that accumulation of α -synuclein either due to increased expression or decreased degradation is sufficient to cause PD, as predicted by the amyloid hypothesis.

(3) amyloid pore formation, (4) membrane permeabilization, and (5) toxicity (see Fig. 4). This proposal is more compelling because natural protein toxins utilize an analogous mechanism. Latrotoxin, α -hemolysin, and aerolysin all form well-ordered, oligomeric membrane-spanning pores characterized by β -sheet structure. It is important to remember that while these toxins are

optimized by evolution to permeabilize target membranes, amyloid pore formation is likely to be an accident and will therefore be very inefficient *in vitro*. Pore formation by β -sheet bacterial toxins involves a series of complex events that include membrane association, oligomerization, and insertion of a β -barrel. The pore-forming protein toxins (PFTs) typically exist as structured, water-soluble monomers; conversion into the membrane-inserted pore requires that these proteins undergo oligomerization and a conformational change. In the case of aerolysin, proteolytic processing by the target is required to initiate the formation of the transmembrane β -barrel domain (Abrami *et al.* 1998). The PFT proteins typically aggregate and/or are activated (Walker *et al.* 1992; Song *et al.* 1996; Sellman *et al.* 1997; Heuck *et al.* 2003) at the membrane surface, a feature that promotes membrane selectivity. Up to 100 β -hairpins can be inserted on activation, to produce the transmembrane β -sheet pore (Hotze *et al.* 2001). β -barrels that span the membrane (Valeva *et al.* 1997; Heuck *et al.* 2001) typically comprise 8–22 β -strands (each 10–13 residues long) and have an average diameter of 1.5–3.5 nm (Heuck *et al.* 2001, 2003). In the α -hemolysin barrel, each monomer contributes an amphipathic hairpin to a 14-stranded heptameric β -barrel (Menestrina *et al.* 2001). PFTs form pores ranging in diameter from 1 to 2 nm for staphylococcal α -hemolysin (Fussle *et al.* 1981) and *Vibrio cholerae* cytolysin (Zitzer *et al.* 1995), and from 15 to 45 nm for streptolysin O (Sekiya *et al.* 1993) and perfringolysin O (Olofsson *et al.* 1993). For some PFTs, some degree of heterogeneity (pore size and oligomeric state) has been reported (Sharpe & London, 1999; Tadjibaeva *et al.* 2000). PFT membrane binding and oligomerization are dependent on the membrane composition and microenvironment and, in some cases, are mediated by interaction with receptor molecules. Cholesterol, for example, can play a critical role in PFT insertion (Cabiaux *et al.* 1997), and may also play a role in amyloid pore toxicity (Arispe & Doh, 2002; Curtain *et al.* 2003; Eckert *et al.* 2003).

5. Mechanisms of protofibril induced toxicity in protein aggregation diseases

5.1 The amyloid pore can explain the age-association and cell-type selectivity of the neurodegenerative diseases

Most cases of AD, PD and ALS are sporadic, that is, they do not involve mutant protein, and are strongly age-associated. Any model for pathogenesis must explain these cases. It is important to emphasize that the wild-type proteins will also form amyloid pores *in vitro*, albeit more reluctantly than the disease-associated mutants (Hafner *et al.* 2001; Ding *et al.* 2002; Lashuel *et al.* 2002a, b, 2003; Shtilerman *et al.* 2002; Chromy *et al.* 2003; Chung, 2003; Klug *et al.* 2003; Kaye & Glabe, 2004). Factors other than mutations could trigger pore formation pathogenesis in sporadic disease (Fig. 4). These factors could include (but are not limited to): (1) increased expression of the amyloid-forming protein (Singleton *et al.* 2004; Uryu *et al.* 2003); (2) impaired degradation of the monomeric protein by the proteasome (Giasson & Lee, 2003); (3) impaired degradation of the protofibrils by a lysosome-mediated autophagic process (Lee *et al.* 2004); (4) changes in chaperone activity and/or expression of homologs that act as specific chaperones (Rochet *et al.* 2000; Conway *et al.* 2001; Hashimoto *et al.* 2001; Maslah & Hashimoto, 2002); (5) changes in levels of post-translational modification, both enzymatic (Shimura *et al.* 2001; Fujiwara *et al.* 2002; Chen & Feany, 2005; Smith *et al.* 2005) and non-enzymatic (Conway *et al.* 2001); (6) changes in the pathogenic microenvironment (pH, membrane composition, increased oxidation). Oxidative damage of amyloid-forming proteins increases their propensity to misfold and aggregate *in vitro* (Rakhit *et al.* 2002; Dauer & Przedborski, 2003). Expression of α -synuclein in

cells, under oxidizing conditions, promotes cytoplasmic aggregation and cell death (Kim *et al.* 2003; Smith *et al.* 2005). Many of the factors listed above are ATP-dependent and would therefore be expected to emerge on aging (Heydari *et al.* 1995; Gaczynska *et al.* 2001; Soti & Csermely, 2002; Ferrington *et al.* 2005; Chondrogianni, 2005), when ATP production becomes less efficient. Aging may also affect the susceptibility of membranes to permeabilization; age-dependent changes in the distribution of cholesterol in neuronal membranes can facilitate oligomerization and accumulation of $A\beta$ in plasma membranes (Wood *et al.* 2002) and cholesterol content influences $A\beta$ toxicity in cell culture (Arispe & Doh, 2002). It must be emphasized that of the factors listed above, all except membrane composition can be easily rationalized by other pathogenic mechanisms.

Another striking feature of the neurodegenerative diseases is that they are selective for certain neuronal populations (hence the clinical diversity). This feature can be explained by an amyloid pore model. It is likely that structural differences among protofibrils formed by the various amyloid-forming proteins would confer some specificity in the way they interact with cellular membranes. In addition, accessory molecules could play a role in modulating pore formation. Finally, conversion of annular protofibrils into amyloid pores may occur at the membrane surface *in vivo*, triggered by specific environmental factors, changes in fluidity of the membrane or interaction with specific proteins. For example, the selective vulnerability of dopaminergic neurons of the substantia nigra to α -synuclein toxicity in PD may be related to (1) the relatively low expression of β -synuclein (Rockenstein *et al.* 2001), a homolog that prevents α -synuclein protofibril formation *in vitro* (Park & Lansbury, 2003), (2) the high concentration of cytoplasmic dopamine (Lotharius & Brundin, 2002; Xu *et al.* 2002) in these cells (some populations of dopaminergic neurons, that have more efficient machinery for removal of cytoplasmic dopamine, are resistant to PD), or (3) highly oxidizing conditions (higher levels of free radical scavengers are expressed in PD-resistant populations of dopaminergic neurons) (Hirsch *et al.* 1997). A combination of the latter two factors may generate dopamine ortho-quinone, which, *in vitro*, covalently modifies α -synuclein and stabilizes protofibrils (Conway *et al.* 2001; Li *et al.* 2004). The extreme sensitivity of dopaminergic neurons to proteasomal inhibition (McNaught *et al.* 2002) may be related to the importance of keeping cytoplasmic α -synuclein levels low in these cells. Second, the differences between cell-types would be expected to influence the specific activity of the amyloid pores in a way that depended on the protein constituent. Microinjection of protofibrillar $A\beta_{42}$ induces death of human neurons, but not neuroblastoma cells, astrocytes or other non-neuronal cell lines (Zhang *et al.* 2002). Decreased susceptibility to intracellular toxicity could arise from the absence of 'receptor' molecules that mediate $A\beta$ toxicity, the presence of neuroprotective factors, or just the changed composition of target membranes.

5.2 Protofibrils may promote their own accumulation by inhibiting the proteasome

Neurons have developed housekeeping systems to avoid misfolded proteins accumulating in the cytoplasm. These include the chaperone system [some of which is ATP-dependent and would be compromised on aging (Heydari *et al.* 1995; Soti & Csermely, 2002)], which prevents aggregation (Muchowski, 2002; McClellan *et al.* 2005) and the proteasomal system, which degrades misfolded and damaged proteins (Berke & Paulson, 2003; Ross & Pickart, 2004). The importance of ubiquitin-dependent proteasomal degradation in PD is illustrated by the fact that parkin and *UCH-L1*, two PD-linked gene products, are involved in this process (Lansbury & Brice, 2002) (Fig. 4). Once protein aggregation has occurred, several backup systems may take over, including

the HSP90 heat-shock protein, that is capable of disaggregating these species (Ben-Zvi & Goloubinoff, 2001; Ben-Zvi *et al.* 2004), the autophagy system, which engulfs and degrades protein aggregates [including protofibrils (Lee *et al.* 2004)] *via* fusion with the lysosome, and the ‘aggresome’ system (Kopito, 2000). Complete or partial failure of any of these systems could have detrimental consequences for the cell. Convergent evidence indicates that the protofibrils themselves could compromise proteasomal degradation. First, overexpression of disease-associated proteins (SOD1 or α -synuclein) in non-neuronal cells resulted in inhibition of proteasome activity (Tanaka *et al.* 2001; Urushitani *et al.* 2002). Second, aggregated (protofibrillar and fibrillar) α -synuclein binds directly to the proteasome and inhibits proteasomal activity (Snyder *et al.* 2003; Lindersson *et al.* 2004). Third, inhibition of the neuronal proteasome causes cytosolic inclusion formation (Ma & Lindquist, 2002) and neuronal death (Ma *et al.* 2002). It is not known whether neuronal death is a result of an increase in protein aggregation due to decreased degradation or of another proteasome-mediated event (Bennett *et al.* 2005). The former scenario offers a mechanism whereby toxicity can amplify itself.

6. Testing the amyloid pore hypothesis by attempting to disprove it

In the past 4 years, 18 different amyloid-forming proteins have been reported to form prefibrillar intermediates with pore-like morphologies (Table 1), supporting the notion that formation of the pore and formation of the fibril are tightly linked. However, whether the pore has any relevance to disease, as proposed here, is not at all clear. It must be emphasized that there is a much work to be done to strengthen the case, which must, by definition, be based on circumstantial evidence. A goal of this review is to encourage experiments designed to disprove the hypothesis. In closing, we make three points, each based on different experimental approaches:

- (1) *Detection of amyloid pores in tissue from patients or animal models does not support the hypothesis nor does the failure to detect these structures disprove it.* This point is illustrated by the flawed logic that led to the toxic fibril hypothesis. However, one could argue that, in the absence of evidence for the existence of pores in tissue, there is no proof that they are able to form under physiological conditions. Several studies of α -synuclein aggregates extracted from brains affected by rare neurodegenerative diseases related to PD, provide tantalizing evidence that pore-like structures do exist *in vivo*. Several studies of α -synuclein fibrils from diffuse Lewy body disease (DLBD) reveal pore-like structures that co-purify with α -synuclein fibrils (Spillantini *et al.* 1998a; Fujiwara *et al.* 2002). The resemblance of these structures to the amyloid pores produced from α -synuclein *in vitro* (Lashuel *et al.* 2002a) is striking. Direct evidence for the existence of amyloid pore-like structures *in vivo* has been provided by the extraction of annular α -synuclein structures, similar to those seen in *in vitro* preparations, from inclusions from post-mortem brain tissues of a multiple system atrophy (MSA, another α -synuclein aggregation disease) patient (Pountney *et al.* 2004).
- (2) *Evidence for membrane abnormalities is consistent with the amyloid pore, but these abnormalities could easily have arisen by another mechanism.* Formation of unregulated pores at the mitochondrial membrane could result in altered Ca^{2+} homeostasis, the release of cytochrome *c* and other proapoptotic molecules, ultimately causing increased oxidative stress and apoptosis. These are features that are clearly seen in the motor neurons of the post-mortem ALS brain, where mitochondrial swelling and cytochrome *c* release are invariant features (Menzies *et al.* 2002). In cellular models of PD, Golgi fragmentation, which is a common feature of human

neurodegenerative diseases, including PD, AD, ALS, CJD, is specifically linked to protofibril formation (Gosavi *et al.* 2002).

- (3) *Determination of the toxicity of a mutant protein that efficiently forms very stable pores would be very informative.* According to the amyloid pore hypothesis, mutations in amyloid proteins that stabilized pores to a great extent may have been disfavored by natural selection, since they would have led to juvenile-onset disease. If one could discover a mutation that had this effect *in vitro*, one could then determine its toxicity relative to disease-linked mutants in cellular and/or animal models of disease. If such a mutant lacked *in vivo* toxicity, then the amyloid pore hypothesis would be untenable. If such a mutant was extremely toxic, the circumstantial case would be considerably stronger. We are working hard to find such a mutant. Hopefully, the identification of the pathogenic species will motivate drug discovery efforts aimed at treating the neurodegenerative processes that underlie these devastating diseases.

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