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CHAPTER · JANUARY 2012

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# Chapter 1

## Overview of Fibrillar and Oligomeric Assemblies of Amyloidogenic Proteins

Farid Rahimi and Gal Bitan

**Abstract** Aberrantly folded proteins are implicated in over 40 human diseases, including neurodegenerative diseases such as Alzheimer's, Parkinson's, Huntington's, and Creutzfeldt–Jakob diseases; diseases of particular organs, including desmin-related cardiomyopathy or type-2 diabetes mellitus; and systemic diseases, such as senile systemic amyloidosis or light-chain amyloidosis. Although the proteins involved in each disease have unrelated sequences and dissimilar native structures, they all undergo conformational alterations and “misfold” to form fibrillar polymers characterized by a cross- $\beta$  structure. Fibrillar assemblies build up progressively into intracellular or extracellular proteinaceous aggregates generating the pathognomonic amyloid-like lesions *in vivo*. Substantial evidence accumulated in the last decade suggest, that in many amyloid-related diseases, the lesions containing the protein aggregates are the end state of aberrant protein folding whereas the actual culprits causing the disease are soluble, non-fibrillar assemblies preceding the insoluble aggregates. The non-fibrillar protein assemblies are diverse and range from small, low-order oligomers to large assemblies, including spherical, annular, and protofibrillar species. Oligomeric species with different degrees of structural order are believed to mediate various pathogenic mechanisms that may lead to

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cellular dysfunction, cytotoxicity, and cell loss, eventuating in disease-specific degeneration. The particular pathologies thus are determined by the afflicted cell types, organs, systems, and the proteins involved. In many cases, the structure–function interrelationships amongst the various protein assemblies described *in vitro* are still elusive. Moreover, structural and mechanistic studies of amyloid proteins have been challenging due to the dynamic and metastable nature of the non-fibrillar oligomers and the non-crystalline nature of fibrillar protein aggregates. These factors have confounded the development and potential *in vivo* application of specific detection tools for non-fibrillar amyloid assemblies. Nevertheless, evidence suggests that non-fibrillar amyloid assemblies may share structural features and possibly common mechanisms of action as assessed *in vitro* or *in situ*. Deciphering these intricate structure–function correlations will help in understanding a complex array of pathogenic mechanisms, some of which may be common across different diseases albeit affecting different cell types or systems. This prefatory chapter aims to give an overview of historical definitions of amyloid along with a general discussion of fibrillar and non-fibrillar amyloid assemblies and their toxicity. The chapter also discusses some methodological challenges, which often are overlooked.

**Keywords** Amyloid, Cytotoxicity, Degeneration, Oligomer, Protein misfolding, Amyloid fibrils

## 1.1 Etymology of the Term “Amyloid”

The term “amyloid”, in fact a misnomer, has been used in the context of histopathology since its neologism in 1838. Its first use then was by a German botanist, Matthias Schleiden (Schleiden 1838), who described amylaceous constituents of plant cell walls (reviewed in Kyle 2001; Steensma and Kyle 2007). Later in 1854, Rudolph Virchow, a German physician-scientist, used this term when examining the brain *corpora amylacea*, which stained pale blue upon treatment with iodine and violet when subsequently treated with sulfuric acid (Virchow 1854a, b) (reviewed in Kyle 2001; Sipe and Cohen 2000; Steensma and Kyle 2007). Because these staining characteristics are similar to those of starch, Virchow concluded that *corpora amylacea* were essentially cellulose and described the lesions as amyloid (i.e., starch-like). The term amyloid is derived from the Latin *amylum*, a transliteration of the Greek *amylon*, which was a term meaning “not ground at the mill” and referring to fine grains, especially starch (Steensma and Kyle 2007). At that time, the distinction between starch (in animals) and cellulose (in plants) was unclear (Sipe and Cohen 2000; Steensma and Kyle 2007).

In 1859, based on the high nitrogen content of amyloid lesions, Carl Friedreich and August Kekulé reported that the amyloid lesions contained albuminoid material and nothing chemically corresponding to *amylon* or cellulose (Friedreich and Kekulé 1859) (reviewed in Kyle 2001; Sipe and Cohen 2000; Steensma and Kyle 2007). They finally established the proteinaceous nature of amyloid lesions.

A century later, electron microscopic (EM) studies of human or animal amyloid lesions allowed observation of the fibrillar ultrastructure of amyloid (Cohen and Calkins 1959). Further progression of biochemical and biophysical techniques facilitated isolation of amyloid fibrils from tissue amyloid lesions in 1964 (Cohen and Calkins 1964) and their characteristic structure was determined by X-ray fiber diffraction in 1968 (Eanes and Glenner 1968). By then, the term amyloid had survived the test of time and was no longer a misnomer.

In the nineteenth and twentieth centuries, extensive studies have focused on deciphering the molecular and pathological mechanisms of protein misfolding, amyloid formation, amyloid-associated toxicity, and disease. This book provides a compendium of chapters describing these studies, with each chapter focusing on a particular protein, a particular disease, or a particular aspect of the relationship between protein misfolding and disease. Our opening chapter gives an overview of amyloids and different assemblies of amyloid proteins. The following chapter describes the pathologic lesions found in certain common amyloid diseases. All other chapters discuss structures of different amyloidogenic proteins and mechanisms mediated by these proteins involved in individual diseases. The final chapter outlines current therapeutic opportunities targeting these diseases and the associated amyloidogenic proteins.

## 1.2 Amyloid and Disease

To date, 27 human diseases are defined as classic amyloidoses (Westermarck et al. 2007; Harrison et al. 2007; Sipe et al. 2010). These diseases are classified also as proteopathies (Walker et al. 2006), degenerative diseases (Dickson 2009), and conformational, protein-misfolding, protein-aggregation, or protein-deposition diseases (Surguchev and Surguchov 2010; Dobson 2004; Eisenberg et al. 2006). More than 40 human diseases collectively fall under the abovementioned classifications (Chiti and Dobson 2006). Of these, several neurodegenerative diseases, including Alzheimer's (AD) (Kril and Halliday 2001; Mayeux 2010; Aguzzi and O'Connor 2010; Lublin and Gandy 2010; Querfurth and LaFerla 2010), Parkinson's (PD) (Bagetta et al. 2010; Halliday and McCann 2010; Obeso et al. 2010; Pahwa and Lyons 2010; Postuma and Montplaisir 2009; Shulman 2010), Huntington's (HD) (Bauer and Nukina 2009; Cardoso 2009; Pfister and Zamore 2009; Rozas et al. 2010; Sassone et al. 2009), and prion diseases (Frost and Diamond 2010; Aguzzi and Calella 2009; Kupfer et al. 2009; Mallucci 2009; Sharma et al. 2009) are characterized pathognomonically by intracellular or extracellular microscopic lesions containing the proteinaceous amyloid aggregates. These diseases are characterized also by extensive neuron loss and atrophy in selected, vulnerable cerebral regions (Double et al. 2010), determining clinical presentations and outcomes. Amyloid-related diseases such as amyotrophic lateral sclerosis (ALS) (Cozzolino et al. 2008; Eisen 2009), non-neuropathic systemic diseases, e.g., light-chain and senile systemic amyloidoses (Comenzo 2006, 2007; Sancherawala 2006), and other organ-specific diseases, such

as dialysis-related amyloidosis (Dember and Jaber 2006; Kiss et al. 2005; Yamamoto et al. 2009), hereditary renal amyloidosis (Hawkins 2003; Kissane 1973; Eshaghian et al. 2007; McCarthy and Kasper 1998), atrial amyloidosis (Eshaghian et al. 2007; McCarthy and Kasper 1998; Goette and Rocken 2004; Rocken et al. 2002; Benvenga and Facchiano 1995; Looi 1993), and type-2 diabetes mellitus (Hayden et al. 2005; Khemtouri et al. 2008; Li and Holscher 2007; Scheuner and Kaufman 2008) also are characterized by extracellular deposition of aberrantly folded, insoluble amyloid proteins.

Although the proteins contributing to different amyloidoses may have dissimilar sequences or unrelated native tertiary structures, they all form insoluble amyloid fibrils, ultimately lose their soluble, functional states, and deposit as amyloid, or amyloid-like lesions (Sipe and Cohen 2000). Extracellularly deposited amyloid material can be distinguished from non-amyloid deposits by: (1) characteristic straight, unbranched fibrillar morphology; (2) a typical cross- $\beta$  pattern, in which  $\beta$ -strands run perpendicularly to the fiber axis; and (3) characteristic tinctorial properties, particularly binding of the dyes Congo red and thioflavin S. The cross- $\beta$  pattern consists of two characteristic fiber-diffraction signals located on axes perpendicular to one another, a sharp, intense meridian reflection (parallel with the fiber axis) at  $\sim 4.7\text{--}4.8\text{ \AA}$  and an equatorial signal at  $\sim 10\text{ \AA}$  (Sunde et al. 1997). Binding of Congo red gives rise to characteristic blue-green birefringence under polarized light (Harrison et al. 2007; Merlini and Westermark 2004; Westermark et al. 2007; Frid et al. 2007), and binding of thioflavin S results in a hyperchromic shift in thioflavin-S fluorescent emission spectrum compared with free thioflavin S (Khurana et al. 2005; LeVine 1999). In addition to their major, fibrillar proteinaceous component, amyloid deposits contain metal ions, glycosaminoglycans, serum amyloid P, apolipoprotein E, collagen, nucleic acids, and other components (Hirschfield and Hawkins 2003; Alexandrescu 2005; Ginsberg et al. 1999, 1998; Marcinkiewicz 2002; Liao et al. 2004; Kahn et al. 1999).

Besides extracellularly deposited amyloid lesions in amyloidoses, many different intranuclear/intracytoplasmic amyloid-like aggregates (inclusion bodies) also have been associated with specific diseases. The term inclusion body or “inclusion” is used frequently in the context of protein misfolding and aggregation (Kopito 2000; Cruts et al. 2006). Inclusion bodies in the latter context are distinct from bacterial inclusion bodies. Aggresomes are inclusion bodies formed by retrograde transport of aggregated proteins on microtubules (Kopito 2000). They contain a major aggregated protein and are also enriched in various molecular chaperones (Kopito 2000). Bacterial inclusion bodies typically are highly enriched for a single protein species and isolation of bacterial inclusion bodies is usually the first step in purification of heterologous proteins recombinantly expressed in bacteria. Aggresomes share certain properties with amyloid fibrils but some of them do not meet all the characteristics required by the classic definition of amyloid (Westermark et al. 2007; Sipe et al. 2010). Biochemists and biophysicists formally call the latter “amyloid-like,” “amyloid-related,” or “amyloidogenic” proteins. For instance, in PD and HD, protein aggregates accumulate intracellularly, generating disease-

specific aggresomes—Lewy bodies and Huntington bodies, respectively. These structures have been excluded from the classification of amyloid by the Nomenclature Committee of the International Society of Amyloidosis (Westermarck et al. 2007; Sipe et al. 2010) despite the fact that fibrils derived from the respective proteins,  $\alpha$ -synuclein (Chap. 6) and polyglutamine-expanded huntingtin (Chap. 11), show all the characteristic features of amyloid (Conway et al. 2000a; Scherzinger et al. 1997; Chen et al. 2002; McGowan et al. 2000). A recent exception is the intracellular neurofibrillary tangles in AD. The main component of the neurofibrillary tangles is the microtubule-associated protein  $\tau$  in a hyperphosphorylated form (Ihara et al. 1983; Joachim et al. 1987; Kosik et al. 1986; Nukina et al. 1987; Perl 2010; Steiner et al. 1990; Goedert et al. 1988). Despite their predominantly intracellular location, neurofibrillary tangles are now regarded as true amyloid (Sipe et al. 2010; Westermarck et al. 2007) because of their fibrillar structure, cross- $\beta$  X-ray diffraction pattern, and typical amyloid staining with Congo red (von Bergen et al. 2001; Giannetti et al. 2000; Berriman et al. 2003; Inouye et al. 2006).

### 1.3 Fibrillar Assemblies of Amyloid Proteins

In an Editorial in *Accounts of Chemical Research*, Ronald Wetzel once used the term “common threads” to allude to the common morphology of amyloid fibrils (Wetzel 2006). These fibrils revealed by transmission-electron microscopy (TEM) usually consist of 2–6 protofilaments each with diameter of 2–5 nm (Serpell et al. 2000). The protofilaments intertwine and form thread-like fibrils that are typically 7–13 nm wide (Serpell et al. 2000; Sunde and Blake 1997) or associate laterally to form long ribbons typically 2–5 nm thick and up to 30 nm wide (Bauer et al. 1995; Saiki et al. 2005). X-ray fiber-diffraction data indicate that in individual protofilaments the polypeptide chains are arranged in  $\beta$ -strands running perpendicular to the long axis of the fibril, forming the cross- $\beta$  pattern (Sunde and Blake 1997).

The presence of highly organized and stable fibrillar deposits in affected organs in amyloid-related diseases long was viewed as a common causative link between aggregate formation and pathological symptoms. This had led to postulations such as the “amyloid cascade hypothesis” in the AD field. Originally, this hypothesis stated that deposition of amyloid  $\beta$ -protein ( $A\beta$ ), the main component of amyloid plaques in AD-afflicted brains, was the cause of AD. This view was later reinforced by findings that  $A\beta$ -derived fibrils were neurotoxic (Pike et al. 1991; Lorenzo and Yankner 1994) and caused both membrane depolarization and alterations in the frequency of action potentials (Hartley et al. 1999). It was shown also that microinjection of fibrillar, but not soluble,  $A\beta$  into cerebral cortex of aged rhesus monkeys (*Macaca mulatta*) resulted in pathological events associated with AD, including profound neuronal loss,  $\tau$  phosphorylation, and microglial proliferation (Geula et al. 1998). Similarly, monosialoganglioside GM1, a neuronal membrane component that is released from damaged neurons and is found in

higher levels in cerebrospinal fluid from patients with AD than from age-matched controls, was found to enhance formation of A $\beta$  fibrils with cytotoxicity and cell affinity much stronger than those of A $\beta$  fibrils formed in phosphate-buffered saline (Okada et al. 2007).

A similar fibril-centered hypothesis was thought to apply contextually to all amyloidoses. For example, cytotoxic effects have been reported for fibrillar prion protein (Novitskaya et al. 2006) and lysozyme (Gharibyan et al. 2007). Insulin aggregation has been associated with rare injection-related amyloidosis (Swift 2002). In addition, insulin aggregation has been studied *in vitro* by multiple groups as a convenient model of protein fibrillogenesis (Murali and Jayakumar 2005; Dzwolak et al. 2007, 2006; Grudzielanek et al. 2007a). Biophysical investigations of insulin fibrillogenesis have identified oligomeric populations with conformations distinct from those of natively folded insulin dimer and hexamer (Ahmad et al. 2005). In a recent study combining structural characterization and cytotoxicity experiments, Grudzielanek et al. found no toxicity for low-order insulin oligomers whereas substantial toxicity was measured for high-order,  $\beta$ -sheet-rich aggregates that displayed either fibrillar or amorphous morphology (Grudzielanek et al. 2007b). Other studies using primates and transgenic murine diabetes models have shown the importance of islet amyloid in the pathogenesis of type-2 diabetes. It was thought that amyloid fibrils preceded formation of islet amyloid deposits and that fibrils derived from islet amyloid polypeptide (IAPP) were likely toxic to  $\beta$ -cells, thereby causing islet dysfunction (Lorenzo et al. 1994). Similarly, deposition of islet amyloid was considered an early event in type-2 diabetes and its progressive accumulation as the cause for parenchymal mass reduction and dysfunction (Westermarck and Wilander 1978; Clark et al. 1988). This was thought to lead to progressively deficient insulin secretion, reduced glucose tolerance, and eventual emergence of fasting hyperglycemia (Kahn et al. 1999). Studies in mice harboring the human IAPP transgene suggested that not only hyperglycemia was associated with the development of islet amyloid, but that amyloid contributed to generation of hyperglycemia due to loss of  $\beta$ -cells (Hoppener et al. 2000).

One of the factors responsible for fibril-induced cytotoxicity is thought to be the physicochemical compositions of the surface of amyloid fibrils (Yoshiike et al. 2007). Significant morphological variations exist among different fibrils derived from the same peptide or protein, e.g., calcitonin (Bauer et al. 1995), SH3 domain of phosphatidylinositol-3'-kinase (Jiménez et al. 1999), insulin (Jiménez et al. 2002), A $\beta$  (Petkova et al. 2005; Paravastu et al. 2006; Wetzel et al. 2007), and IAPP (Goldsbury et al. 1997; Radovan et al. 2008). Even single-residue alterations have been shown to affect fibril structure profoundly. For example, the substitution of D23 by N in A $\beta$ , linked to severe cerebral amyloid angiopathy in an Iowa kindred (Van Nostrand et al. 2001), causes formation of A $\beta$ 40 fibrils considerably faster than wild-type A $\beta$ 40 (Tycko et al. 2009). At the molecular level, D23N-A $\beta$ 40 fibrils are arranged predominantly in an anti-parallel array, in contrast to the in-register, parallel  $\beta$ -sheet structure commonly found in wild-type A $\beta$ 40 fibrils and most other amyloid fibrils (Tycko et al. 2009). Despite these differences in molecular arrange-



ment, the gross morphology, X-ray diffraction pattern, and dye-binding properties of amyloid fibrils appear to be universal amongst fibrillar structures of amyloid proteins.

Morphological differences in amyloid fibrils are governed also by conditions used for fibril preparation. For example, EM and nuclear magnetic resonance (NMR) enable visualization of polymorphic structure of A $\beta$ 40 fibrils prepared under agitated or quiescent conditions (Petkova et al. 2005). Seeding experiments may facilitate detailed structural characterization of amyloid fibrils developing *in vivo* and elucidate the controversial role of fibrils (Hardy and Selkoe 2002) in human amyloidoses. To study fibril polymorphism *in vivo* and based on the ability of pre-formed amyloid fibrils to propagate their structures through seeded growth *in vitro* (Petkova et al. 2005), fibrils extracted from AD brain tissue were used to seed growth of synthetic A $\beta$ 40 fibrils (Paravastu et al. 2009). This allowed Paravastu et al. to deduce putative structures of fibrils extracted from AD brain by recapitulating these structures using seeded fibrillar growth of synthetic A $\beta$ 40. Paravastu et al. showed that fibrils grown after being seeded with material extracted from two separate AD patients' brains had predominantly the same two fibril structures (Paravastu et al. 2009). These predominant fibril structures differed from the two previously described, purely synthetic A $\beta$ 40 fibril structures (Paravastu et al. 2008; Petkova et al. 2006), indicating that seeded growth combined with structural studies may determine the molecular structures of fibrils developing in AD brain or in fibrils involved in other amyloid diseases *in vivo*. The results described above suggest that each amyloid protein potentially forms a spectrum of structurally distinct fibrils, and that kinetic and microenvironmental factors determine which of these alternatives predominate under given circumstances, which can differ considerably *in vitro* and *in vivo*.

Direct correlation between specific molecular organization and fibril toxicity may be important where pathogenic mechanisms of sporadic and genetic forms of amyloid diseases are studied. For example, some genetic cases of AD (Taddei et al. 1998; Miyoshi 2009; Moro et al. 2010; McDonald et al. 2010) and PD (Dawson 2007; Gasser 2009; Inzelberg and Polyniki 2010; Schiesling et al. 2008; Houlden et al. 2001) have an earlier onset and a faster progression than sporadic forms of these diseases suggesting potentially different underlying molecular mechanisms. Studies similar to those of Paravastu et al. could be extended to compare fibril structures of A $\beta$  in sporadic *versus* genetic, early-onset forms of AD. Such studies will potentially delineate correlations between protein structure and disease severity or progression at the molecular level. Aging-induced spontaneous chemical modifications, such as amino-acid racemization or amino-acid isomerization—e.g., involving aspartate and asparagine residues—may affect A $\beta$  production, polymerization, and clearance, potentially playing a pivotal role in the pathogenesis of sporadic and genetic forms of AD (Moro et al. 2010). Therefore, studies linking fibril morphology with aging-induced posttranslational protein modifications in AD may unravel correlations between fibril structure and pathogenesis. This example is potentially applicable and relevant to other amyloidoses, for example PD.



## 1.4 Non-fibrillar Assemblies of Amyloid Proteins

Contrary to the original amyloid cascade hypothesis (Hardy and Higgins 1992), substantial evidence suggests that fibrillar aggregates are the end state of aberrant protein folding and eventuate as potentially protective sinks for the cytotoxic, oligomeric, non-fibrillar protein assemblies. The transient, non-fibrillar assemblies likely are the actual culprits. These assemblies are believed to initiate the pathogenic mechanisms that lead to cellular dysfunction, cell loss, loss of functional tissue, and disease-specific regional or organ-specific atrophy (Kirkitadze et al. 2002; Gurlo et al. 2010; Haataja et al. 2008; Luibl et al. 2006; Meier et al. 2006).

Amyloid  $\beta$ -protein ( $A\beta$ ), the causative agent in AD, is considered an archetypal amyloidogenic protein. The multitude and variety of structural, functional, and pathophysiological studies of  $A\beta$  exemplify the complexity of research findings covering non-fibrillar assemblies of amyloidogenic proteins. Extensive biophysical studies in the  $A\beta$  field have led to functional and structural descriptions of non-fibrillar and pre-fibrillar  $A\beta$  assemblies. For example, the discovery of  $A\beta$  protofibrils (Walsh et al. 1997; Harper et al. 1997) and other toxic non-fibrillar  $A\beta$  assemblies, including low-order oligomers,  $A\beta$ -derived diffusible ligands, and paranuclei (reviewed in Rahimi et al. 2008) have led to a paradigm shift (Kirkitadze et al. 2002; Haass and Selkoe 2007; Glabe 2006; Glabe and Kaye 2006) in AD research, challenging the original, fibril-centered, amyloid cascade hypothesis (Hardy and Higgins 1992). An updated version of the hypothesis presented a decade after the original one (Hardy and Selkoe 2002) emphasizes that early, pre-fibrillar  $A\beta$  assemblies or  $A\beta$  assemblies unrelated to fibrils are the primary cytotoxins in AD pathogenesis leading to synaptic dysfunction and neuron loss (Sakono and Zako 2010; Gong et al. 2003; Klein 2002a; Cleary et al. 2005; Lambert et al. 1998). This paradigm shift and the centrality of non-fibrillar  $A\beta$  assemblies in AD research have led to a search for similar non-fibrillar protein assemblies in other amyloid-related diseases. To date, at least 40 different proteins have been identified as causative agents of amyloidoses (Bellotti et al. 2007; Chiti and Dobson 2006). In most cases, including prion proteins (Simoneau et al. 2007, also discussed in Chaps. 9 and 10), transthyretin (Sorgjerd et al. 2008 and Chap. 13),  $\alpha$ -synuclein (van Rooijen et al. 2010 and Chap. 6), apolipoprotein C-II (Ryan et al. 2008),  $\tau$  (Peterson et al. 2008; Sahara et al. 2008; Kaye et al. 2009 and Chap. 5), superoxide dismutase (Cuzzolino et al. 2009 and Chap. 8), polyglutamine-expanded proteins (Legleiter et al. 2010 and Chap. 11), and islet amyloid polypeptide (Haataja et al. 2008 and Chap. 7), non-fibrillar protein assemblies have been found and shown to exert adverse biological effects similar to those of non-fibrillar  $A\beta$  oligomers (Kirkitadze et al. 2002; Caghey and Lansbury 2003; Ferreira et al. 2007; Glabe 2006; Jellinger 2009; Kitamura and Kubota 2010; Sakono and Zako 2010; Roychaudhuri et al. 2009 and Chaps. 3, 4, 5).

Before the focus in the amyloid field shifted from fibrils to non-fibrillar assemblies, it was known that despite sequence dissimilarity among amyloidogenic proteins, amyloid fibrils were largely similar in the core regions (Eisenberg

et al. 2006; Serpell 2000). The realization that the non-fibrillar oligomeric structures may be the proximate disease-causing agents in the amyloidoses related to these proteins raised the question of whether oligomeric structures were also similar. High-resolution microscopic studies of oligomeric structures, mostly by TEM and AFM, have demonstrated that in most cases the morphologies observed were spherical, annular, or protofibrillar (worm-like). Despite morphological similarities, studies have demonstrated that small structural changes may have a large impact on the oligomer populations formed by the same protein (Bitan et al. 2003a, b, c).

Protofibrils, the penultimate precursors of fibrillar assemblies, are curvilinear, fibril-like structures of 4–8 nm diameter,  $\leq 200$  nm length (Walsh et al. 1997), and may have an axial twisting periodicity of 20 nm (Hartley et al. 1999). They have been described as spherical beads of 2–5 nm diameter arranged as beaded chains in linear, curvilinear, or annular arrangements in studies originally reporting them (Harper et al. 1997; Walsh et al. 1999, 1997). The annular protofibrils have been the predominant structures found in several studies (Caughey and Lansbury 2003; Lashuel et al. 2002a, b; Ding et al. 2002; Kaye et al. 2009). However, as discussed elsewhere (Bitan et al. 2005), it is important to note that in many cases the term protofibril has been used even though the morphologies of the assemblies under study were distinct from those originally defined as protofibrils. It is also important to distinguish between protofibrils and protofilaments, which are the constituent units of mature fibrils (Serpell et al. 2000; Teplow 1998).

One of the most-studied amyloidogenic proteins is  $\alpha$ -synuclein (Chap. 6).  $\alpha$ -Synuclein, first characterized in zebra finch (*Taeniopygia guttata*) (George et al. 1995) (under the UniProt accession number Q91448, the organism described is *Serinus canaria* (Island canary) or *Fringilla canaria*), was thought to be important in neural plasticity during vertebrate development. The exact function of  $\alpha$ -synuclein still is not clear though it is thought to be part of the proteasomal system (reviewed in Layfield et al. 2003; Betarbet et al. 2005), vesicle trafficking and endocytosis (Varkey et al. 2010), and/or SNARE complex assembly (Burré et al. 2010).  $\alpha$ -Synuclein has been shown to form  $\alpha$ -helical structures when interacting with artificial (Jao et al. 2008; Trexler and Rhoades 2009; Georgieva et al. 2008) or biological membranes (Kim et al. 2006). As discussed earlier,  $\alpha$ -synuclein is the predominant component in Lewy bodies, the pathological hallmarks in PD brains. It has been implicated also in other degenerative disorders (synucleinopathies), including dementia with Lewy bodies and multiple-system atrophy (Ian et al. 2001; Jellinger 2009; Chiti and Dobson 2006). Similar to A $\beta$ ,  $\alpha$ -synuclein belongs to a growing family of “intrinsically disordered” proteins (Tomba 2002; Dyson and Wright 2005), a characteristic that perhaps renders these proteins more prone to undergoing amyloidogenic assembly because of their structural instability. Mutant  $\alpha$ -synuclein alloforms linked to familial PD were found to oligomerize faster than the wild-type protein, whereas the rate of fibril formation did not correlate with the presence of disease-causing mutations (Conway et al. 2000b). Non-fibrillar assemblies of both wild-type and mutant  $\alpha$ -synuclein included spherical oligomers, protofibrillar structures, and most abundantly, annular protofibrils (Ding et al. 2002; Lashuel et al. 2002b). The latter morphology suggested that the

mechanism whereby  $\alpha$ -synuclein induces toxicity is pore formation in cell membranes. In agreement with this idea, protofibrillar  $\alpha$ -synuclein was found to permeabilize synthetic vesicles (Volles et al. 2001). Interestingly, this effect was increased by the familial PD-linked mutants A30P and A53T (Volles and Lansbury 2002), but not by the mutant E46K (Fredenburg et al. 2007). Thus, although pore formation may be involved in  $\alpha$ -synuclein-induced toxicity, other mechanisms also have been implicated, but these are not understood well (Takeda et al. 2006).

IAPP aggregation is thought to cause type-2 diabetes. IAPP is a 37-residue peptide hormone produced in pancreatic  $\beta$ -cells and co-secreted with insulin. Early stages of type-2 diabetes are characterized by insulin resistance followed by increased insulin and IAPP secretion. Elevated IAPP levels lead to its assembly into toxic, soluble oligomers and insoluble aggregates (Marzban et al. 2003). Oligomeric and protofibrillar IAPP were shown to interact with synthetic membranes (Anguiano et al. 2002), a characteristic that decreases with further aggregation, providing a clue for the mechanism of IAPP toxicity (Porat et al. 2003). Similar to  $\alpha$ -synuclein, interaction with biological membranes may induce a transient  $\alpha$ -helical conformation in IAPP, presumably facilitating penetration of the oligomers into the membrane resulting in solute leakage across the membrane (Jayasinghe and Langen 2005; Knight et al. 2006). Strong evidence for the cytotoxic role of IAPP oligomers in type-2 diabetes was given in a study in which rifampicin, an inhibitor of IAPP fibril, but not oligomer, formation, did not protect pancreatic  $\beta$ -cells against apoptosis induced by either exogenous or endogenously expressed IAPP (Meier et al. 2006). More recent data have suggested that *in vivo*, toxic IAPP oligomers are formed intracellularly and therefore, oligomer-specific antibodies do not prevent cell death *in vitro* or *in vivo* (Lin et al. 2007).

### ***1.4.1 Analytical Challenges in Studies of Amyloid Protein Oligomers***

Structural studies of oligomers of amyloidogenic proteins have been challenging because these assemblies typically are metastable and comprise heterogeneous mixtures of species. Immunological insights have been obtained by Glabe and co-workers, who developed antibodies that bound specifically to oligomers but not to the monomeric or fibrillar forms of proteins of unrelated sequences (Kayed et al. 2003). The first polyclonal antibody, A11, and similar antibodies developed in follow-up studies (Kayed and Glabe 2006; Georganopoulou et al. 2005; Lafaye et al. 2009), showed remarkable ability to bind to oligomers formed by proteins as diverse as A $\beta$ ,  $\alpha$ -synuclein, IAPP, lysozyme, insulin, polyglutamine, and prion fragments (Kayed et al. 2003). In a recent study, iterative immunization of aged beagles with an aggregated A $\beta$  preparation (Head et al. 2008) was shown to produce antibodies specific for monomeric, non-fibrillar, or fibrillar A $\beta$ 42 preparations (Vasilevko et al. 2010). However, dot-blotting results in this study were not conclusive enough to designate the canine antibodies as purely oligomer-specific anti-A $\beta$

antibodies because some degree of cross-reactivity (50% by densitometry) was evident and the results were not complemented by structural studies of A $\beta$  preparations used for antibody-specificity assays.

As discussed above, recent studies by Paravastu et al. (2009) showed that the dominant structure of A $\beta$  fibrils grown by A $\beta$  fibril seeds derived from AD-afflicted brains differed from that in fibrils derived from purely synthetic A $\beta$ 40, suggesting that fibrillization conditions *in vitro*, and by inference, oligomerization conditions, differ from conditions *in vivo*. Findings based on the above studies by Paravastu et al. (Paravastu et al. 2009) and others (Petkova et al. 2005; Inaba et al. 2005; Lee et al. 2007; Kaye et al. 2009; Nekooki-Machida et al. 2009) argue against the idea, based on immunoreactivity data, TEM, and AFM studies, that non-fibrillar or pre-fibrillar amyloid assemblies are structurally similar. Although *in vitro* studies provide valuable insight into the structure and activity of non-fibrillar amyloid assemblies, these studies must be interpreted carefully because: (1) the conditions *in vivo* differ from those *in vitro* due to the complexity of cellular and tissue milieus; (2) mutations, amino-acid substitutions, or amino-acid modifications can result in different oligomer populations, different levels of oligomer toxicity or different fibrillar structures with different toxic properties (Bitan et al. 2003b; Yoshiike et al. 2007; Hung et al. 2008); and (3) fibrils grown in the presence of monosialoganglioside GM1 released from damaged neurons are more toxic than those prepared in buffer alone (Okada et al. 2007). Conclusively, non-fibrillar amyloid structures and compositions *in vivo* likely differ, at least to some degree, from those produced, analyzed, and studied *in vitro*. Some of the confounding factors in these cases involve post-extraction or post-analysis sample handling (e.g., freeze–thaw cycles, transportation, etc.). For examples, it was initially shown that A $\beta$  dimers isolated from human brain tissue inhibited long-term potentiation (LTP), enhanced long-term depression, and reduced dendritic spine density in rodent hippocampal neurons (Shankar et al. 2008). However, these toxic activities were ascribed later to A $\beta$  protofibrils, which formed readily from covalently stabilized A $\beta$  dimers (O’Nuallain et al. 2010). These data suggest that by the time the activity of a certain A $\beta$  preparation is measured, potentially inert A $\beta$  species (e.g., dimers) may have converted to toxic species (e.g., protofibrils).

The same argument may apply to studies whereby non-fibrillar amyloid assemblies were extracted and studied *in vitro* (Shankar et al. 2008, 2007; Paleologou et al. 2009; Klucken et al. 2006; Sharon et al. 2003; Lesné et al. 2006; Head et al. 2010). Many extraction procedures use detergents, such as sodium dodecyl sulfate (SDS), which are known to disrupt the structure of non-fibrillar amyloid assemblies (Bitan et al. 2005; Hepler et al. 2006). Although electrophoretic separation of proteins in the presence of SDS (SDS–PAGE) generally is an excellent analytical method, the effect of SDS on all proteins is not equivalent (Gudiksen et al. 2006). Different proteins, different conformations of the same protein (Leffers et al. 2004), or truncated versions of certain proteins (Kawooya et al. 2003) may not bind stoichiometric amounts of SDS. In addition, in certain cases, SDS can induce or stabilize secondary or quaternary structures rather than denaturing them (Leffers et al. 2004; Montserret et al. 2000; Yamamoto et al. 2004). Further, SDS may cause

dissociation of some protein assemblies or conversely induce protein self-association, depending on the specific protein studied (Yamamoto et al. 2004; Rangachari et al. 2007, 2006; Piening et al. 2006). For example, A $\beta$ 42-derived “globulomers” are oligomeric species produced by incubating A $\beta$ 42 in the presence of 0.2% SDS (Barghorn et al. 2005). Apparent electrophoretic fractionation of monomeric or oligomeric components in a protein mixture does not necessarily indicate existence of such components prior to SDS treatment. Examples of this shortcoming of SDS–PAGE have been reported in its applications to studies of A $\beta$  (Bitan et al. 2005; Hepler et al. 2006) and  $\alpha$ -synuclein (Moussa et al. 2004). A recent example is a study of A $\beta$ 40 dimers stabilized by an intermolecular disulfide bridge, which showed the same SDS–PAGE profile before and after formation of  $\beta$ -sheet-rich protofibrils (O’Nuallain et al. 2010).

Because of the structural instability of amyloidogenic protein oligomers and the abovementioned analytical artifacts, studies reporting on structural properties of amyloidogenic proteins based on SDS–PAGE findings must be interpreted cautiously. This is particularly relevant to those studies, which have reported characterization of antibodies specific for oligomeric assemblies of amyloidogenic proteins relying on SDS–PAGE and western blotting. Recently, an elaborate study using ultrathin array tomography and immunofluorescence showed that senile plaques in brains of a murine model of AD are surrounded by “haloes of oligomeric A $\beta$ ” (Koffie et al. 2009) based on immunoreactivity of an antibody (NAB61), which apparently was reactive to oligomeric A $\beta$  assemblies fractionated by SDS–PAGE (Lee et al. 2006). The original paper, which described this antibody, reported that NAB61 also recognized synthetic A $\beta$  fibrils (Lee et al. 2006). Considering these caveats, one may question the major conclusions drawn by Koffie et al. because of the use of an antibody that was claimed to be specific for SDS–PAGE-fractionated oligomeric A $\beta$  but was also cross-reactive with fibrillar A $\beta$  assemblies. Similar cross-reactivity was apparent in antibodies that were produced and characterized after iterative immunization of beagles (Vasilevko et al. 2010) with an aggregated A $\beta$  preparation (Head et al. 2008). Caveats regarding binding specificity of reagents ostensibly recognizing non-fibrillar amyloid assemblies also are relevant to aptamers. Aptamers are short ribo- or single-stranded deoxyribo-oligonucleotides used as specific molecular recognition tools in research, diagnostics, and therapy. Recently, we have found that aptamers bind fibrillar assemblies of amyloid proteins avidly yet non-specifically (Rahimi et al. 2009). Despite the fact that our aptamers were selected using covalently stabilized oligomeric preparations of A $\beta$ 40, they were found to bind not only A $\beta$ -derived fibrillar structures, but also fibrils of other amyloid proteins (Rahimi et al. 2009). Similar high affinity for fibrils was observed using aptamers selected by multiple rounds of enrichment and two non-enriched, “naïve” RNA libraries demonstrating that fibril binding was a general phenomenon rather than a characteristic of particular RNA sequences (Rahimi et al. 2009). Comparable findings were observed previously with aptamers selected against fibrillar and non-fibrillar  $\beta_2$ -microglobulin (Bunka et al. 2007). Moreover, nucleic acids have been shown to enhance formation of amyloid fibrils and interactions between amyloid-forming peptides and nucleic acids have been shown to cause

formation of combined protein–nucleic-acid fibrils (Braun et al. 2011). These findings suggest that non-specific reactivity with oligonucleotides may be a universal property of amyloid proteins (Rahimi and Bitan 2010; Rahimi et al. 2009; Braun et al. 2011; Ylera et al. 2002; Bunka et al. 2007). Therefore, aptamers developed against non-fibrillar amyloid assemblies or those claimed to be specific for non- or pre-fibrillar amyloid assemblies must be tested for specificity for fibrillar assemblies of amyloid proteins. This is particularly applicable to studies reporting aptamers “specific” for monomeric or oligomeric A $\beta$  (Takahashi et al. 2009) or  $\alpha$ -synuclein (Tsukakoshi et al. 2010). Further delineation of specific mechanisms governing these interactions requires additional studies and will be important in interpretation of structure–function relationships and for designing reagents that recognize non-fibrillar amyloid assemblies specifically or potentially block amyloid-related toxicity. A relevant recent News article in *Nature* (Ledford 2010) has highlighted similar challenges researchers are facing in studying diseases with complex mechanisms and outlined some of the complexities and controversies involved in studies linking the prion protein and A $\beta$  in AD research.

## 1.5 Non-fibrillar and Fibrillar Assemblies of Disease-Unrelated Proteins

The milieu of a polypeptide chain may cause it to adopt a multitude of conformations, or interconvert among many, in a wide temporal range (Dobson 2001; Dzwolak et al. 2007; Frieden 2007; Guijarro et al. 1998; Gursky and Aleshkov 2000; Stefani and Dobson 2003; Kelly 1998; Cruz et al. 2005; De Felice et al. 2004). This complexity is more relevant *in vivo* where interactions amongst proteins and interactions between proteins and other cellular components govern various cellular functional processes (Canale et al. 2006; Kitamura and Kubota 2010; Stefani and Dobson 2003; Zhang et al. 2004). Conformational heterogeneity renders the study of amyloidogenic proteins particularly difficult due to the transient nature of the adopted conformations, which populate closely related minima in the thermodynamic energy landscape (Miller et al. 2010). Besides disease-associated amyloid-forming proteins and proteins that naturally form non-pathological, functional amyloid-like fibrils (reviewed in Chiti and Dobson 2006) (see also Maji et al. 2009a), disease-unrelated proteins (Stefani and Dobson 2003) and artificially designed peptides (Fezoui et al. 2000; Wang et al. 2007; Kammerer and Steinmetz 2006) were shown to form amyloid under particular non-native conditions. The first proteins shown to form amyloid fibrils were reported by (Guijarro et al. 1998 and Litvinovich et al. 1998). The src-homology 3 (SH3) domain of bovine phosphatidyl inositol 3-kinase (PI3K), an 85-residue,  $\beta$ -structured protein, was shown to form amyloid fibrils slowly under acidic conditions (Guijarro et al. 1998). Thenceforth, the disease-unrelated SH3 domain has served as an excellent model system for studies examining structural properties of amyloid fibrils and molecular mechanisms of amyloid formation (Jiménez et al. 1999; Zurdo et al. 2001a, b; Carulla et al. 2005). It was found that the



initial protein aggregates were relatively dynamic and flexible to allow particular interactions guiding formation of the highly ordered fibrils (Polverino de Laureto et al. 2003).

After Litvinovich et al. demonstrated formation of amyloid-like fibrils by self-association of a murine fibronectin type-III module (Litvinovich et al. 1998), others reported that similar conversions in a number of disease-unrelated proteins could be induced *in vitro* by a deliberate, rational choice of experimental conditions (Chiti et al. 2001, 1999; Stefani and Dobson 2003). Formation of fibrils from full-length proteins occurs under solution conditions that partially or completely disrupt the native structure of the protein but do not completely break hydrogen bonds (Chiti et al. 2001). On the other hand, in the aggregation of unstructured proteins, e.g., A $\beta$ , partially structured conformers have been shown to be necessary for fibril formation (Fezoui and Teplow 2002; Kiritadze et al. 2001; Maji et al. 2005). It was shown that proteins with as few as four residues, and amino-acid homopolymers unable to fold into stable globular structures, form fibrils readily (Stefani and Dobson 2003; Tjernberg et al. 2002; Lopez De La Paz et al. 2002). Therefore, it has been suggested that the ability to form amyloid fibrils could be a generic property of polypeptide chains (Stefani and Dobson 2003).

In contrast to the hypothesis that adoption of amyloid or amyloid-like conformation is a generic property of the polypeptide backbone with only a minor contribution by the amino-acid side-chains (Dobson 2001), Maji et al. argued that side-chain interactions are essential in the aggregation process (Maji et al. 2009b) as demonstrated in fibril-related crystal structures (Nelson et al. 2005; Nelson and Eisenberg 2006; Sawaya et al. 2007), in studies showing the sequence-specific nature of amyloid aggregation (Tjernberg et al. 2002; Margittai and Langen 2006; Zanuy and Nussinov 2003), and by the scale of amino-acid aggregation propensities determined experimentally, ranging from aggregation-prone hydrophobic residues to aggregation-interfering, charged side-chains (Fernandez-Escamilla et al. 2004; Tartaglia et al. 2008). These studies suggest that under non-physiological conditions, including acidic pH, extremes of protein concentration, or addition of aprotic solvents (Guijarro et al. 1998; Chiti et al. 1999; Polverino de Laureto et al. 2003; Marcon et al. 2005), the influence of side-chains in the aggregation process can be altered, eventually driving the protein of interest into amyloid fibrils (Maji et al. 2009b).

## 1.6 Studying the Toxicity of Non-fibrillar Amyloid Assemblies

One of the main pathogenic mechanisms (Jellinger 2010) underlying many neurodegenerative diseases is abnormal protein dynamics and protein misfolding (Skovronsky et al. 2006; Herczenik and Gebbink 2008) accompanied by an imbalance between protein production and degradation, proteasomal/autophagy impairment, and dysfunction or mutation of molecular chaperones (Jellinger 2009, 2010). Oxidative stress in the form of reactive oxygen/nitrogen species, free radical formation, and lipid peroxidation also is involved in protein-misfolding diseases



(Butterfield et al. 2010; Kahle et al. 2009; Sesti et al. 2010; Ahmad et al. 2009). Oxidative stress goes hand-in-hand with inflammatory mechanisms and production of cytokines and chemokines in the disease-affected tissues (Ahmad et al. 2009; Lee et al. 2009; Lucin and Wyss-Coray 2009; Sugama et al. 2009; Tansey and Goldberg 2010; Sokolova et al. 2009; Shepherd et al. 2006). Mitochondrial dysfunction, DNA damage, disruption of ion homeostasis, and impaired bioenergetics coincide with oxidative stress and inflammatory conditions (Jellinger 2009, 2010). All these pathogenic mechanisms, inter-related in complex cycles, lead to cellular dysfunction, apoptosis, and/or necrosis. In the central nervous system, depending on the cell populations affected, these pathogenic mechanisms lead to emergence of specific or mixed disease phenotypes and complex clinical presentations and outcomes (Dickson 2009; Boeve 2007; Murray et al. 2005; Pittock and Lucchinetti 2007; Lansbury and Lashuel 2006).

Numerous experimental approaches have facilitated study of cytotoxic mechanisms of non-fibrillar assemblies of amyloidogenic proteins. *In vitro* experiments using cell culture and tissue slices along with biophysical studies have been performed to examine the toxic mechanisms of non-fibrillar amyloid assemblies using recombinant, synthetic, cell-, or tissue-derived variants of the amyloidogenic proteins. As discussed above, a concern in these experimental setups is that only a small proportion of the artificial assemblies may closely resemble non-fibrillar assemblies occurring *in vivo*. Other experimental approaches include the use of animal models, such as insect (Botella et al. 2009; Cowan et al. 2010; Iijima and Iijima-Ando 2008; Iijima-Ando and Iijima 2010; Khurana 2008; Lu 2009; Lu and Vogel 2009; Park et al. 2009; van Ham et al. 2009), *Caenorhabditis elegans* (Johnson et al. 2010), *Brachydanio rerio* (Sager et al. 2010; Ingham 2009; Malaga-Trillo and Sempou 2009), murine (Ashe and Zahs 2010; Dawson et al. 2010; Elder et al. 2010; Guyenet et al. 2010; Park et al. 2010; Taylor et al. 2010), rat (Flood et al. 2009), canine (Barsoum et al. 2000; Green and Tolwani 1999; Lossi et al. 2005; Vasilevko and Head 2009; Woodruff-Pak 2008), and simian models (Yang et al. 2008; Wang and Qin 2006; Qin et al. 2006; Walker 1997) to assess various aspects of etiology and pathogenesis, including genetics, behavior, system functions, or nutritional and therapeutic applications.

Toxicity mechanisms of non-fibrillar amyloid assemblies in various diseases are discussed in detail in individual chapters of this book. Here we highlight a few examples of non-fibrillar amyloid assemblies and their associated toxicity mechanisms. In one prominent example, synthetic A $\beta$  oligomers derived from cells transfected with amyloid precursor protein (Podlisny et al. 1995) were shown to disrupt LTP in hippocampal tissue slices and *in vivo* (Townsend et al. 2006; Walsh et al. 2002), impair the memory of a complex pre-learned behavior (Cleary et al. 2005), memory consolidation, and synaptic remodeling causing loss of functional synapses in rats (Freir et al. 2011).

Another type of oligomer studied extensively is A $\beta$ -derived diffusible ligands (ADDLs), which are synthetic A $\beta$ 42-derived species formed in the presence of apoJ (Oda et al. 1995), in F-12 media (Klein 2002b), or in phosphate-buffered saline (De Felice et al. 2008) as small globules 3–8 nm in diameter (Chromy et al. 2003) in

polydisperse mixtures of 150–1,000-kDa complexes (Hepler et al. 2006). ADDLs have been shown to be highly neurotoxic (Lambert et al. 1998; Xia et al. 1997), inhibit LTP (Lambert et al. 1998), promote oxidative stress and increased  $[Ca^{2+}]_i$  (De Felice et al. 2007), induce  $\tau$  phosphorylation (De Felice et al. 2008), and enhance interleukin-1 $\beta$ , inducible nitric oxide synthase (iNOS), nitric oxide, and tumor-necrosis-factor- $\alpha$  expression in astrocytes (White et al. 2005). Recently, it has been shown that ADDLs are sequestered into, and seed, new amyloid plaques in the brains of a murine AD model (Gaspar et al. 2010). However, the underlying mechanisms of this observation require further studies.

In neurodegenerative diseases characterized by intraneuronal  $\alpha$ -synuclein deposition, even modest  $\alpha$ -synuclein elevations can be toxic, though the precise mechanisms underlying synaptotoxicity in these diseases are unclear. Recently, a quantitative model system was used to evaluate the time-course and localization of evolving  $\alpha$ -synuclein-induced pathologic events using cultured neurons isolated from brains of transgenic mice overexpressing fluorescently labeled human  $\alpha$ -synuclein (Scott et al. 2010). Transgenic  $\alpha$ -synuclein was shown to be altered pathologically over time while overexpressing neurons showed enlarged synaptic vesicles and striking deficits in neurotransmitter release (Scott et al. 2010), a phenotype characteristic of animal models lacking critical presynaptic proteins (Abeliovich et al. 2000; Chandra et al. 2004, 2005). In this model, Scott et al. showed that several endogenous presynaptic proteins were undetectable in a subset of transgenic synaptic boutons, suggesting that such diminutions triggered the overall synaptic pathology due to increased  $\alpha$ -synuclein levels (Scott et al. 2010). Similar alterations in levels of synaptic proteins were retrospectively observed in human pathologic brains (Mukaetova-Ladinska et al. 2009; Bertrand et al. 2003), highlighting potential relevance to human disease.

Another toxic mechanism proposed for non-fibrillar assemblies of amyloid proteins is their pore- or channel-forming capacity that may lead to membrane leakage and increased  $[Ca^{2+}]_i$  (Lashuel and Lansbury 2006; Lashuel et al. 2002a). In lipid bilayers *in vitro*, A $\beta$  was shown to form uniform pore-like structures (Lin et al. 2001; Quist et al. 2005). These are thought to serve as  $Ca^{2+}$  channels and thus have been hypothesized to cause excitotoxicity and mediate A $\beta$ -induced neurotoxicity in AD (Arispe et al. 1993b, a). Reports of various models including artificial phospholipid membrane bilayers, excised neuronal membrane patches, whole-cell patch-clamp experiments, and phospholipid vesicles support a channel-forming property of A $\beta$  (Lin et al. 2001; Arispe et al. 1993b; Kawahara et al. 1997; Kawahara and Kuroda 2000; Sanderson et al. 1997; Rhee et al. 1998; Hirakura et al. 1999; Lin et al. 1999; Bhatia et al. 2000; Kourie et al. 2001; Kagan et al. 2002; Lin and Kagan 2002; Bahadi et al. 2003; Alarcon et al. 2006) and  $\alpha$ -synuclein (Adamczyk and Strosznajder 2006; Di Pasquale et al. 2010; Kim et al. 2009; Tsigelny et al. 2007; Zakharov et al. 2007; Feng et al. 2010). Imaging techniques (Lin et al. 2001, 1999; Rhee et al. 1998; Bhatia et al. 2000), electrophysiological experiments (Arispe et al. 1993b; Kawahara et al. 1997; Sanderson et al. 1997; Rhee et al. 1998; Hirakura et al. 1999; Bhatia et al. 2000; Kourie et al. 2001; Bahadi et al. 2003; Alarcon et al. 2006), or cation-sensitive dyes (Bhatia et al. 2000; Jelinek and Sheynis 2010) were

used to assess channel-like properties of A $\beta$ . However, other studies have reported general disruption of the plasma membrane homeostasis without channel formation (Sokolov et al. 2006; Demuro et al. 2005; Kayed et al. 2004).

It has been shown that directed expression of the molecular chaperone, Hsp70, one of numerous molecular chaperones that guide the correct folding of polypeptides, prevented dopaminergic neuronal loss associated with  $\alpha$ -synuclein in a *Drosophila* model of PD and that interference with endogenous chaperone activity accelerated  $\alpha$ -synuclein toxicity (Auluck et al. 2002). This work, and similar approaches in polyglutamine-related disorders (Warrick et al. 1999; Opal and Zoghbi 2002), indicate that such diseases are indeed disorders of protein folding, suggesting that activation of chaperones and other compensatory mechanisms, such as the ubiquitin–proteasome system, potentially can decrease accumulation of misfolded proteins or enhance their clearance.

In contrast to fibrils of disease-causing amyloidogenic proteins (discussed above), those formed by disease-unrelated proteins do not cause cytotoxicity in cell-culture experiments. For example, fibrils formed by an artificially designed  $\alpha$ -helix-turn- $\alpha$ -helix ( $\alpha\alpha\alpha$ ) peptide displayed no neurotoxicity, even though they were morphologically indistinguishable from A $\beta$  and IAPP fibrils, which were toxic (Fezoui et al. 2000). However, the pre-fibrillar assemblies of PI3K-SH3 and HypF-N were shown to be highly toxic to PC12 cells and murine fibroblasts *in vitro* (Bucciantini et al. 2004). The extent of cellular injury caused by the cytotoxic oligomers was comparable to that by A $\beta$ 42 oligomers, whereas the corresponding fibrils of both PI3K-SH3 and HypF-N were benign.

Early pre-fibrillar HypF-N assemblies were shown to permeabilize artificial phospholipid membranes more efficiently than mature fibrils, suggesting that this disease-unrelated protein shared toxic properties with non-fibrillar assemblies of peptides and proteins involved in pathology (Relini et al. 2004). Further investigation of the cellular effects of HypF-N oligomers revealed that they entered the cytoplasm and caused an acute rise in levels of reactive oxygen species and  $[Ca^{2+}]_i$ , leading to cell death (Bucciantini et al. 2004). In a study in which murine fibroblasts or endothelial cells were treated with pre-fibrillar HypF-N assemblies, the two cell types underwent two different death mechanisms—fibroblasts exposed for 24 h to 10  $\mu$ M HypF-N oligomers underwent necrosis, whereas endothelial cells treated similarly underwent apoptosis (Bucciantini et al. 2005). A similar study comparing cytotoxic effects of pre-fibrillar and fibrillar HypF-N assemblies using a panel of normal and pathological cell-lines showed that cells were variably affected by the same amount of pre-fibrillar aggregates, whereas mature fibrils showed little or no toxicity (Cecchi et al. 2006). Recently, it has been shown that microinjection into rat brain nucleus basalis magnocellularis of non-fibrillar assemblies of PI3K-SH3 or HypF-N, but not the corresponding mature fibrils, compromised neuronal viability dose-dependently (Baglioni et al. 2006). Taken together, these data clearly demonstrate that the non-fibrillar assemblies of disease-unrelated proteins are highly toxic whereas most of the corresponding mature fibrils are not (Baglioni et al. 2006). The toxic effects of the oligomers may arise when these assemblies assume a “misfolded” conformation, which may expose hydrophobic residues that are natively buried within the core

structure. These exposed hydrophobic sequences are aggregation-prone and may interact with membranes and other cellular constituents modifying their structural/functional homeostasis. Interestingly, two types of stable, pre-fibrillar oligomers of HypF-N, which display similar morphologic and tinctorial properties, were shown to differ in their cytotoxic effects (Campioni et al. 2010). The differences in the packing of hydrophobic interactions between adjacent protein molecules in the oligomers determined the ability of the two oligomeric assemblies to cause cellular dysfunction and toxicity. Thus, a lower degree of hydrophobic packing within the oligomer core structure was found to correlate with a higher ability to penetrate the cell membrane and cause  $\text{Ca}^{2+}$  influx (Campioni et al. 2010).

## 1.7 Conclusions

Since the discovery and definition of amyloid lesions, intensive research has led to accumulation of data elucidating the pathogenic mechanisms of protein-misfolding diseases. Initially, pathogenic and toxic primacy was given to fibrillar forms of amyloidogenic proteins as these structures were found to be the major pathological hallmarks in neurodegenerative diseases. As discussed previously, earlier studies attributing toxicity to amyloid fibrils may have found this effect because of the inadvertent use of immature amyloid fibrils or equilibrium mixtures of oligomers and fibrils, which are cytotoxic, rather than pure preparations of mature amyloid fibrils, which often are not (Aksenov et al. 1996; Martins et al. 2008). Importantly, as our understanding of the devastating neurodegenerative and protein-misfolding diseases has been growing, an alternative paradigm has emerged. This paradigm postulates that non-fibrillar protein assemblies rather than mature amyloidogenic fibrils likely are the key neurotoxins responsible for most of the pathogenic mechanisms in protein-misfolding and neurodegenerative diseases. Accordingly, oligomeric species are thought to mediate diverse but interrelated pathogenic mechanisms that may lead to cytotoxicity and cell loss eventuating in organic and systemic involvement. This interrelation may lead to self-promoting and -propagating pathogenic cycles that worsen with age and chronicity. For instance, mechanisms associated with protein-misfolding may cause other events, such as inflammation and oxidative stress, which in turn aggravate misfolding. Overall, it is postulated that the non-fibrillar amyloidogenic proteins are “on path” to fibrillogenesis. The resulting protein fibrils are thought to be the end-stage sinks for the toxic non-fibrillar species. Fibrillar assemblies accumulate progressively into intracellular or extracellular proteinaceous amyloid aggregates generating the disease-specific lesions *in vivo*.

Global research efforts have established a framework for understanding the fundamentals of protein assembly and misfolding. A remaining challenge is to assess how these fundamental structural principles are linked to cellular and tissue microenvironments during progression of disease. Many experimental conditions have been used to study the structure and function of non-fibrillar assemblies; however, due to methodological limitations, regeneration and scrutiny of the actual *in vivo* milieu

and conditions in which protein assembly, oligomerization, fibrillization, and deposition occur are difficult. Similarly, it is extremely difficult to assess all the possible interactions these assemblies may have with various cellular components and organelles in the course of pathogenesis. A multitude of detrimental mechanisms, including disruption of cellular metabolism, deregulation of synapse structure and function, membrane damage, ionic imbalance, oxidative/inflammatory stress, apoptosis, and other cytotoxic effects, have been shown to be mediated by non-fibrillar assemblies of amyloidogenic proteins, emphasizing that a single therapeutic approach likely will be insufficient to prevent or treat the progression of diseases involving protein misfolding. Involvement of complex pathogenic mechanisms in these diseases calls for multifaceted rational diagnostic and therapeutic approaches that could potentially target not only a single assembly or a single mechanism but a multitude of assemblies or mechanisms. Agents that arrest the self-assembly process at the earliest stages or divert the process into formation of non-toxic species likely have the highest chance of success preventing and treating amyloid-related diseases because they inhibit formation and/or toxicity of both initial toxic oligomers and later aggregates.

**Acknowledgements** We thank Drs. D. Teplow and M. Landau for reviewing this book chapter and acknowledge financial support by grants AG027818 and AG030709 from NIH/NIA and grant 07-65798 from California Department of Health Services.

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