

Amyloid Oligomer Structures and Toxicity

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Abstract: Amyloid accumulation is commonly associated with a number of important human degenerative diseases and recent findings indicate that soluble amyloid oligomers may represent the primary pathological species in degenerative diseases. Amyloid oligomers are structurally and morphologically diverse, raising the question on whether this diversity is pathologically significant and whether different types of oligomers may have different toxic activities. Many of the amyloids associated with neurodegenerative diseases form three immunologically distinct types of oligomers. Fibrillar oligomers are structurally related to fibrils and may represent small pieces of fibrils or fibril protofilaments. Prefibrillar oligomers are kinetic intermediates in fibril formation and annular protofibrils that resemble membrane pores. These three classes of oligomers share common structures and toxic activities. Focus on these common mechanisms of toxicity provides a means of simplifying the list of primary disease mechanisms and opens the possibility of developing broad spectrum therapeutics that target several amyloid related degenerative diseases.

Keywords: Amyloid structure, amyloid toxicity, amyloid oligomers, amyloid disease, pathogenesis.

INTRODUCTION

The accumulation misfolded proteins as amyloid fibrils is a key pathognomonic feature of many age-related degenerative diseases, including Alzheimer's (AD), Parkinson's, Huntington's diseases, type II diabetes and prion diseases. In most of these diseases, the end stage aggregation products that accumulate are amyloid fibers. Amyloids have traditionally been defined by their solubility, morphology and ability to bind dyes, like Congo red and thioflavin dyes. Although the common association of amyloids with neurodegenerative disease is a compelling argument for their causal association with pathogenesis, in many cases the presence of these fibrillar deposits is not obligately associated with disease. In AD, non-demented individuals have been reported that have same amount of insoluble amyloid deposits. This has led to a modification of the amyloid hypothesis to state that amyloid oligomers are causally related to disease [1]. There has been an increasing amount of evidence to support the hypothesis that amyloid oligomers represent the primary toxic species and that fibrils may be either inert, protective or toxic by distinct mechanisms.

AMYLOIDS HAVE COMMON, GENERIC STRUCTURES

Advances in our understanding of the structure of amyloid fibrils indicate that many of them share a common structural motif: Intermolecularly hydrogen bonded parallel strand where the sequence of the strands above and below are in register [2-8]. This structural motif gives rise to homogeneous tracts of amino acid side chains, known as "steric zippers" running up and down the β sheets. Since the 20 amino acids are well distributed among various sequences,

amyloid fibrils formed by different sequences will all display the same steric zippers, although the arrangement of the zippers will vary with the sequence. Amyloid oligomers also have common structures [9]. Conformation dependent, aggregation specific antibodies suggest that there are 3 general classes of amyloid oligomer structures than many types of amyloidogenic sequences form [10, 11]. These include "fibrillar oligomers", which may represent small pieces of fibrils or fibril protofilaments [12], "prefibrillar oligomers", which are kinetic intermediates that precede fibril formation [9, 13] and "annular protofibrils", which are pore like structures [11, 14] (Fig. 1).

Fibrils and fibrillar oligomers react with the fibril specific antibody, OC [12]. This antibody recognizes a generic fibril epitope, as it reacts with several types of amyloid fibrils, including amyloid beta peptide ($A\beta$), alpha synuclein, islet amyloid polypeptide and poly Q. This antibody also recognizes a number of natural peptide hormones stored as functional amyloids in pituitary secretory granules [15]. Monoclonal antibodies with similar generic fibril immunoreactivity have also been reported [16, 17]. OC stains all types of amyloid deposits in AD and islet amyloid in transgenic mouse models of type II diabetes, but it does not react with prefibrillar oligomers or annular protofibrils [11, 12]. A11 recognizes a generic epitope associated with prefibrillar oligomers, but it does not react with amyloid fibrils [9]. This indicates that prefibrillar oligomers have a common structural motif that is distinct from that displayed by fibrils. Anti-annular protofibril antibody recognizes a generic epitope that is specific to annular protofibrils [9]. This antibody also recognizes heptameric pores, but not monomers from the bacterial toxin, alpha hemolysin, suggesting that it recognizes a beta barrel motif. The fact that these antibodies recognize common structural features that are unique to specific amyloid aggregation states suggests that the aggregates may share a common mechanism of toxicity and pathogenesis. Indeed, amyloid oligomers from non-disease related proteins and peptides are intrinsically

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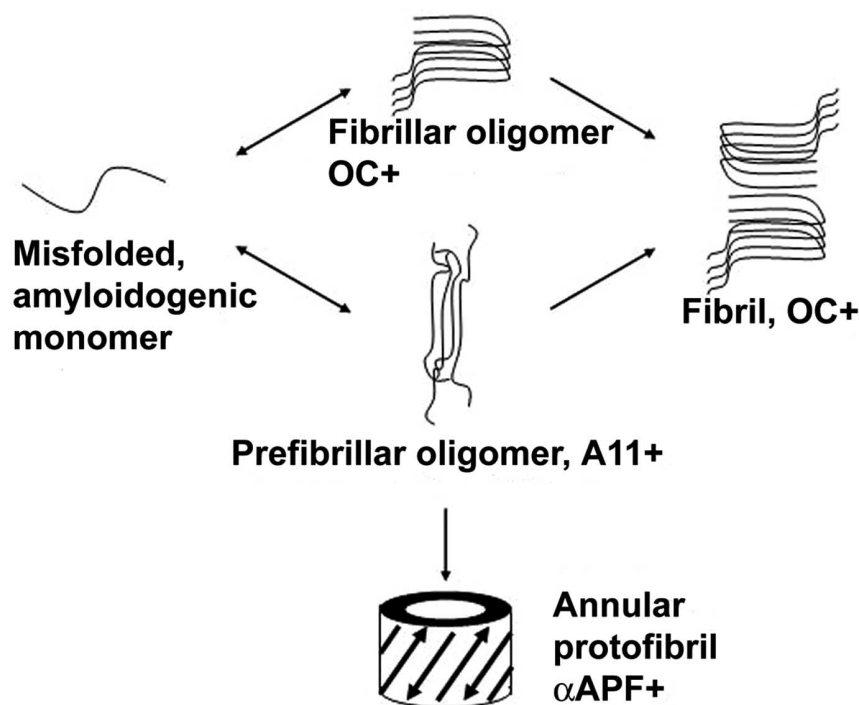


Fig. (1). Distinct assembly states of amyloids. Misfolded amyloidogenic monomers can adopt a fibrillar lattice structure that is recognized by the fibril specific antibody, OC. Fibrillar oligomers represent small pieces of a fibril protofilament, but they share immunoreactivity with OC. Alternatively, monomers may assemble into prefibrillar oligomers that are A11 positive and OC negative. Prefibrillar oligomers are precursors for the formation of annular protofibrils. Annular protofibrils are recognized by aAPF antibody.

toxic [18] and the toxicity shares features with disease related amyloid toxicity [19]. The fact that fibrils, prefibrillar oligomers and annular protofibrils display distinct generic epitopes suggests that they have fundamental differences in the structural organization of their polypeptide backbones. If fibrils are parallel, in-register structures and annular protofibrils are beta barrels, prefibrillar oligomers may be antiparallel beta sheets or alpha extended sheets [20, 21]. Alpha sheets are characterized by a unique pattern of bifurcated hydrogen bonding and can transition back and forth between β -sheet through individual transitions of backbone ϕ, ψ angles [21]. If fibrils, prefibrillar oligomers and annular protofibrils have distinct structures, their toxic activities may also be distinct.

AMYLOIDS ARE GENERIC TOXINS

Although disease associated amyloids have received the most attention, it has become increasingly apparent that the ability to form amyloid fibrils and oligomers is a widespread consequence of protein misfolding [22]. The SH3 domain of phosphatidylinositol 3' kinase and the N-terminal domain of HypF protein form amyloid fibrils and prefibrillar oligomers and the oligomers form by these non-disease related proteins display equivalent toxicity to disease related oligomers like A β [13, 23]. Amyloid oligomers derived from cytosolic proteins and peptides, like alpha synuclein and polyQ are toxic to cells when they are applied externally, indicating that their toxicity does not depend on specific intracellular targets. The toxicity of amyloid does not appear to be stereospecific as the amyloid aggregates derived from D-amino acid peptide, like D-A β 42 are as toxic as the normal

L-amino acid peptides [24, 25], although a more recent report indicates that D-A β 42 aggregates are not toxic [26]. The finding that amyloid oligomers are generically toxic is consistent with the observation that they form common generic structures, since one of the canons of biochemistry is that the structure of proteins determines their function.

WHY ARE AMYLOID OLIGOMERS MORE TOXIC THAN AMYLOID FIBRILS?

A number of studies have provided evidence that soluble A β oligomers are more toxic to cells than mature fibrils [9, 18, 27-31]. In some cases, fibril formation may actually be neuroprotective [32]. Although amyloid fibrils have also been reported to be toxic [33], there is evidence that fibrils and oligomers are toxic by distinct mechanisms [34]. The fact that prefibrillar oligomers and annular protofibrils have generic structures that are distinct from fibrils is consistent with the idea that they have distinct mechanisms of toxicity. For example, prefibrillar oligomers have been reported to permeabilize cell membranes while fibrils lack this activity [31, 35]. Prefibrillar oligomers can also bind to membranes and convert into annular protofibrils that may represent β -barrel membrane pores [11]. It is more difficult to rationalize the differential toxicity of A β fibrillar oligomers and A β fibrils, as they share the same generic epitope recognized by fibril specific antibodies [12] and they exhibit the same parallel, in-register structure as fibrils [36]. One possibility is that fibrillar oligomers may be small pieces of a single protofilament and that they may have hydrophobic surfaces exposed on the surface of the β -sheets that would otherwise be hidden by sheet stacking interactions between the

protofibrils in the mature fibril [37]. Another possibility is that the ends of fibrils and fibrillar oligomers are toxic and therefore the oligomers would be more toxic in relationship to the amount of A β because the fibrils are considerably longer. Fibrillar oligomers may also be more toxic than fibrils because they are smaller and more capable of diffusing throughout the tissue than the fibrils that accumulate as insoluble deposits [27].

POTENTIAL MECHANISMS OF AMYLOID TOXICITY AND PATHOGENESIS

Many different mechanisms have been proposed for amyloid toxicity. Indeed, the pathogenic mechanism landscape is beginning to look like the elephant viewed by blind men, with many different and seemingly incompatible parts and functions. Soon after the identification of A β as the major component of amyloid plaques in AD, reports of both toxicity and trophic activity appeared [38-40]. The toxicity was reported to be related to the aggregation state of A β , with aggregation being required for toxicity [41, 42]. Several potentially pathogenic alterations were soon reported to be associated with A β toxicity. A partial list includes elevated intracellular calcium [43], activation of complement [44], induction of apoptosis [45], formation of ion channels [46], altered ion channel function and oxygen radical production [47], potentiation of cytokine secretion [48], induction of tau phosphorylation [49], tau dependent microtubule disassembly [50], modulation of signal transduction pathways [51], binding of A β to the receptor for advanced glycation end products (RAGE) [52], binding to synapses and inhibition of LTP [27, 29], binding to APP [53], binding to alpha7 nicotinic acetylcholine receptors (α 7nAChR) [54], inhibition of synaptic function [55], loss of excitatory synapses [56], binding to mitochondrial alcohol dehydrogenase and mitochondrial dysfunction [57], endocytosis of N-methyl-D-aspartate (NMDA) receptors [58], membrane permeabilization [59] and loss of neuronal spines [60]. With so many different ways of damaging neurons and interfering with their function, A β starts looking like the Swiss army knife of AD. These potential mechanisms are not mutually exclusive. Some of them may be proximal to A β and some may be downstream events in a causal cascade. Understanding which of these mechanisms is the primary effect of amyloid oligomers is important for developing therapeutic strategies that target amyloid toxicity, but it also presents a serious experimental challenge in view of the many deleterious functions ascribed to amyloids.

WHICH MECHANISMS ARE PROXIMAL TO AMYLOID?

Understanding the primary pathogenic properties of amyloids is also critical for understanding how all the pathogenic pieces fit the puzzle. What does amyloid actually interact with and are these interactions specific to a particular amyloid sequence or are they specific to a particular assembly state or conformation? A β oligomers are known to bind to cells and in neuronal cells, it binds to both synaptic and non-synaptic sites [27, 61]. The binding of A β oligomers is restricted to a subset of 30-50% of neurons, suggesting that the binding is specific for certain types of neurons [62].

Some of the neuronal binding sites are sensitive to trypsin digestion, suggesting that they are proteins [27] and a variety of cell surface proteins have been reported to bind aggregated A β , including amyloid precursor protein (APP) [53, 63], NMDA-receptors [64], integrins [64], RAGE [52], the α 7nAChR [54] and the prion protein (PrP) [65]. If A β does indeed bind to all of these different cell surface proteins, this would be an unusual specificity unlike typical ligands for cell surface receptors.

Is the binding of A β to these cell surface receptors stereospecific according to peptide sequence? Stereospecific binding would be very desirable from a therapeutic standpoint, as many drugs have been developed that are receptor antagonists. The typical controls used to demonstrate specificity include scrambled peptides and the reverse A β sequence and the lack of binding or activity of these control peptides is often interpreted as a reflection of the specificity of the interaction. However, these peptides do not aggregate and it is known for most of these binding interactions that the binding depends on the aggregation state of A β . Fibrillar prion peptide 106-126 and islet amyloid polypeptide bind to APP as well as A β fibrils, so this binding interaction is independent of the amino acid sequence [66]. In addition, the all D amino acid variant of A β 42 binds to neuronal cell bodies, axons and dendrites to the same extent as L-A β 42, indicating that this binding interaction is not stereospecific [26]. In the cases where it has specifically been examined, the binding has been found to be aggregation specific, rather than sequence specific.

Membrane permeabilization is another fundamental and widely reported property of amyloid oligomers. The earliest findings reported the formation of ion channels in lipid bilayers [46, 67]. Later work reported the formation of pores [14, 68] and non-selective permeabilization of lipid bilayers and cell membranes caused by altering the dielectric properties of the membrane [35, 59, 69]. Regardless of the precise mechanism, the experiments with lipid bilayers demonstrate that amyloid oligomers interact with membranes and cause the dysregulation of ion homeostasis. Membrane permeabilization is also a common and generic property of many different types of amyloid oligomers including A β , alpha synuclein, polyQ and IAPP have been widely reported to permeabilize membranes [70, 71]. Amyloid oligomers specifically increase lipid bilayer conductance regardless of the sequence, while fibrils and soluble low molecular weight species have no observable effect [19, 72]. Like toxicity, membrane permeabilization is a generic property of amyloid oligomers that may reflect their common structural foundations.

COMMON MECHANISMS OF AMYLOID OLIGOMER TOXICITY AND DISEASE PATHOGENESIS

One way of evaluating the potential significance and relationships of these mechanisms is to examine which of these mechanisms are specific to A β and AD and which of the mechanisms are common to many amyloid related degenerative diseases. Since amyloids are believed to be causally related to pathogenesis in many degenerative diseases and they share common structural features, mecha-

nisms that are shared by these diseases have a broader base of experimental support. Of the mechanisms listed above, calcium dyshomeostasis, has been widely reported in other neurodegenerative diseases. As noted above elevated intracellular calcium levels may be the direct result of amyloid oligomers permeabilizing membranes [35, 59], forming ion channels or pores [67, 73] or activating endogenous calcium channels [74, 75]. Mitochondrial dysfunction, the production of oxygen radicals and apoptosis are also widely reported to be associated with amyloid-related degenerative diseases and are known to be caused by accumulation of excess Ca^{+2} in the mitochondrial matrix, so these common disease features may be downstream of elevated cytosolic Ca^{+2} levels [76]. Since elevated intracellular Ca^{+2} levels have been widely reported in neurodegenerative disease and it can regulate several of the key down stream pathological events, it is worth considering as a central mechanism.

CONCLUSIONS

The case for a common, shared mechanism of amyloid toxicity and pathogenesis is compelling. The accumulation of amyloids as fibrils or oligomers is commonly associated with neurodegeneration. Amyloid oligomers have common, intramolecularly hydrogen bonded β structures that give rise to repetitive patterns of amino acid side chains on their surfaces. Amyloid oligomers are toxic *in vitro* and *in vivo* by a variety of mechanisms. Since structure determines the function of biological molecules, this common structure implies that amyloids have common toxic activities. Of the many mechanisms that have been proposed for amyloid toxicity, elevated cytosolic Ca^{+2} , production of reactive oxygen species and mitochondrial dysfunction have been widely reported to be associated with amyloid toxicity. These may represent key features of a common mechanism of amyloid pathogenesis in neurodegenerative disease. Targeting this common pathway may lead to the development of effective therapeutics for a broad spectrum of neurodegenerative diseases.

ACKNOWLEDGEMENT

This work was supported by a grant from the NIH AG00538 and grants from the Cure Alzheimer Fund and The Larry L. Hillblom Foundation. C.G. is a consultant for Kinexis, Inc.

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Received: April 30, 2009

Revised: July 03, 2009

Accepted: July 07, 2009

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