

An Overview of Alzheimer's Disease

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Abstract—More than twenty different human proteins can fold abnormally resulting in the formation of pathological deposits and several feared degenerative diseases. These proteins lack primary sequence homology, yet they can self-assemble into fibrils with a characteristic cross β -sheet structure. Among them, β -amyloid of Alzheimer's disease is the best characterized. β -amyloid is the principal protein component of senile plaques seen in the brains of individuals diagnosed with Alzheimer's disease and is implicated in the neurotoxicity associated with the disease. Although Alzheimer's disease has been the center of intense research, much remains to be learned concerning the role of β -amyloid and the toxicity mechanisms that mediate its biological responses.

In the current review, the general background information on Alzheimer's disease and β -amyloid are first presented. Next, attention is focused on the relevant research works regarding structural aspect and molecular features of $A\beta$ species as well as β -amyloid fibrillogenesis/aggregation process. Importantly, an emerging issue that an oligomeric intermediate is the primary toxic β -amyloid species is also discussed. Lastly, several β -amyloid-induced toxicity mechanisms are proposed and reviewed. It is our belief that the advances in basic understanding of the conformational changes as well as biological functions of β -amyloid and β -amyloid-elicited toxicity mechanisms will shed light on the development and/or design of potential interfering agents against amyloid formation associated with Alzheimer's disease.

Key Words : Amyloidosis, Alzheimer's disease, β -amyloid, Fibril, Aggregation

AMYLOIDOSIS AND AMYLOID

The amyloidoses are a group of protein conformational or misfolding diseases which arise when a constituent protein or peptide undergoes a fluctuation in shape or change in size, with resultant protein self-assembly and tissue deposition. These amyloidogenic diseases are indeed of enormous importance in the context of present-day welfare and human health. At least twenty different human proteins and peptides, including transthyretin, α -synuclein, calcitonin, β_2 -macroglobulin, gelsolin, amylin, atrial natriuretic peptide, and β -amyloid, have been isolated as the fibrillar components of disease-associated amyloid deposits (Kelly, 1998b; Lansbury, 1999; Murphy, 2002; Dobson, 2004; Ross and Poirier, 2004; Uversky and Fink, 2004). These conformational diseases individually have their unique clinical, neuropathological, and biochemical characteristics and their corresponding amyloidogenic precursor proteins have unrelated functions and share no sequence homology (Table 1). However, the molecular

events underlying these disease processes appear to be the same. The mechanism involves an aberrant structural transition in a normally innocuous and functional protein (Kelly, 1998a; Lansbury, 1999; Taylor *et al.*, 2002; Dobson, 2004; Ross and Poirier, 2004; Uversky and Fink, 2004).

The pathological conformers in these protein structural diseases are called amyloids. Amyloid is considered a general term delineating protein aggregates and structures of amyloids are recognized to possess several specific tinctorial and physicochemical features in common: exhibition of β -sheet rich secondary structure, a fibrillar morphology, birefringence upon staining with Congo red dye, insolubility in most solvents, and protease-resistance. Extensive protein fibrillogenesis or aggregation often occurs leading to an accumulation of the abnormally folded proteins that damages cells. The formation of the pathological conformers has been shown to be influenced by genetic mutations, protein concentration, chaperones, and environmental factors (*i.e.* the presence of salt, metal ion concentration, and pH of solu-

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Table I. A listing of some common amyloidogenic proteins and corresponding diseases.

Disease Type	Key Protein Involved
Alzheimer's disease	Amyloid- β protein
Primary systemic amyloidosis	Immunoglobulin light chain
Senile systemic amyloidosis	Transthyretin
Familial amyloid polyneuropathy I	Transthyretin
Familial mediterranean fever	Serum amyloid A
Secondary systemic amyloidosis	Serum amyloid A
Hemodialysis amyloidosis	β_2 -Microglobulin
Finish hereditary systemic amyloidosis	Gelsolin
Type II diabetes	Islet amyloid polypeptide (IAPP)
Medullary carcinoma of the thyroid	Calcitonin
Hereditary renal amyloidosis	Fibrinogen
Injection-localized amyloidosis	Insulin
Atrial amyloidosis	Atrial natriuretic factor (ANF)
Hereditary non-neuropathic systemic amyloidosis	Lysozyme
Familial visceral amyloidosis	Lysozyme

tion) (Taubes, 1996; Carrell and Lomas, 1997; Carrell and Gooptu, 1998; Kelly, 1998a; Lansbury, 1999; Soto, 1999; Ji *et al.*, 2002). Generally, the content of β -sheet secondary structure increases with lower pH, increasing salt concentration, or rising protein/peptide concentration. However, A β solution exhibits α -helix rich conformation in membranemimicking solvents (Fraser *et al.*, 1991, 1994; Barrow *et al.*, 1992; Talafous *et al.*, 1994; Kohno *et al.*, 1996; Ji *et al.*, 2002; Stine *et al.*, 2003; Petkova *et al.*, 2004; Beking *et al.*, 2005).

ALZHEIMER'S DISEASE

Alzheimer's disease (AD) was first described by German neurologist Alois Alzheimer nearly a century ago (Alzheimer, 1907). AD is the most common cause of dementia and also the fourth leading cause of death in the developed countries. It is estimated that approximately 18 million people worldwide suffer from AD and, tragically, nearly thirty-four million people worldwide will be afflicted by AD before 2025 (American Health Assistance Foundation, 2005).

AD is a disease characterized by progressive dementia, gradual memory loss, and decline in cognitive functions and functional capacity. It is considered one of the major diseases of dementia in the western world. The progression of AD is often variable but ultimately leading to death due to infections approximately 10 years after symptoms first appear. Histopathology of the disease consists of senile plaques of β -amyloid accumulation, neurofibrillary tangles, cerebrovascular amyloid deposits, neuronal damage, and loss of synapses (Terry and Katzman, 1983; Selkoe, 1989). AD is an age-dependent disorder that increases in prevalence with age. Currently no effective treatments are directed toward curing

this debilitating disease.

Forms of AD

AD is divided into early-onset ('presenile') dementia affecting individuals below 65 years of age and accounting for 25% of cases and late-onset ('senile') dementia (Terry and Katzman, 1983). The disease is also divided into familial and sporadic forms of disease according to family history. Early-onset familial cases make up 10% of all AD patients while late-onset familial cases make up 30% of all AD patients (American Health Assistance Foundation, 2005). Early-onset Alzheimer's has been clearly shown to be genetic in origin. While a mutation on chromosome 19 (where the ApoE gene is located) has been correlated with late-onset AD (the most common form), not everyone having the mutation develops the disease. The relationship between genetics and late-onset Alzheimer's is not fully known (American Health Assistance Foundation, 2005). The mutation of APP on chromosome 21 is linked to early-onset AD (Lendon *et al.*, 1997; Saunders, 2001; Zekanowski *et al.*, 2004), while presenilin 1 (PS1) gene (chromosome 14) and PS 2 gene (chromosome 1) are responsible for 50% of early-onset familial AD (Rogaev *et al.*, 1995; Saunders, 2001; Zekanowski *et al.*, 2004).

Symptoms and diagnosis

Progressive memory loss, problem with adjustment, change in personality, difficulties in communication, and abnormal behaviors are key clinical symptoms of AD. The diagnostic procedure for AD consists of taking a thorough medical history, conducting the Mini Mental State Examination, and checking family members (Alzheimer's Association, 2005).

Until the accomplishment of effective cure for AD, available treatments currently are aimed mainly at retarding the disease progression not reversing the process or halting it completely. Probing the disease in early stages has been a major focus of a number of neuroimaging techniques. One of these techniques is magnetic resonance imaging (MRI), which can be used to detect the size change of some structures in the AD brain, the hippocampus shrinkage in particular. Researchers are exploring exactly how early this shrinkage in hippocampus can be probed. Another set of neuroimaging techniques, such as positron emission tomography (PET) scans and single photon emission computed tomography (SPECT) scans, provides a means to visualize the activity and interactions of some certain brain areas during neural cognitive operations. This window on the living brain can aid in probing early alterations in brain function or structure and further identifying those individuals who are at risk of AD even prior to the development of the symptoms of the disease (Burggren and Bookheimer, 2002; Petrella *et al.*, 2003; Masdeu *et al.*, 2005; Villemagne *et al.*, 2005). Although most of these neuroimaging techniques are currently utilized primarily as research tools, they certainly hold great promise, combined with other diagnostic measures, for the identification of persons at risk of developing AD at early stages.

Treatment

Several acetylcholine esterase inhibitors/drugs such as Cognex, Aricept, and tetrahydroaminoacridine, are designed to fortify the memory and slow the progression of cognitive degeneration in the early stages of AD. These drugs are used to prevent the level of acetylcholine in the brain from dropping acutely. However, the drugs become useless with the disease progression and wasting away of cholinergic neurons. Other potential treatments currently under investigation include: vitamin E (antioxidant), prednisone (targeting inflammatory damage on neurons), premarin (female hormone promoting neuronal survival), calcium channel blockers, and nerve growth factor (Alzheimer's Association, 2002). Although these treatment strategies seem to help a fraction of the patients to some degree, we are currently still far from a real cure (Marx, 1997).

There is a hope that vaccination would serve as a potential treatment for AD. Recent studies showed the deposition of amyloid plaques and associated memory impairment in transgenic mice of AD can be prevented or reversed by active immunization without dramatically changing the total level of A β (Janus *et al.*, 2000; Morgan *et al.*, 2000), while passive immunization with prolonged treatment with anti-A β antibodies in APP-overexpressing mice can

prevent the development of amyloid fibrils (Bard *et al.*, 2000; DeMattos *et al.*, 2001). Since improvement of the disease with immunization/vaccination has been perceived in AD models, it is now considered a potential treatment strategy.

HYPOTHESES OF MAJOR CAUSE OF NEURODEGENERATION IN AD

A β accumulation

It is widely believed that the conversion of A β into amyloid deposits is a causative event in the molecular pathogenesis of AD. This so-called amyloid hypothesis has been buttressed by a number of evidence in animal model, pathological, genetic, epidemiological, and *in vitro* cell culture studies. Generation of amyloid deposits similar to AD pathology and neuronal death in the brains were observed in transgenic mice with overexpression of APP or fragments of APP carrying familial AD mutations (Games *et al.*, 1995; LaFerla *et al.*, 1995; Masliah *et al.*, 1996; Johnson-Wood *et al.*, 1997; Holcomb *et al.*, 1998; Tandon and Fraser, 2002). Additionally, evidence showed that the activation of microglia and significant loss of neurons were associated with the presence of fibrillar A β or A β deposits (Weldon *et al.*, 1998; Bornemann and Staufenbiel, 2000; Nagele *et al.*, 2004), suggesting the central role of A β accumulation in a cascade of events underlying AD pathogenesis.

Pathologically, a strong correlation has been observed between the dementia of a patient in life and the amyloid burden in the autopsy (Cummings *et al.*, 1996). Genetic mutations in APP, PS1, and PS2 genes, which cause the familial AD, result in a rise in A β production (Schellenberg, 1995; Selkoe, 1996; 1997; Holcomb *et al.*, 1998; Kowalska *et al.*, 2004). Evidence from numerous *in vitro* studies has demonstrated the toxicity of aggregated form of A β to cultured nerve cells (Pike *et al.*, 1993; Seilheimer *et al.*, 1997; Hartley *et al.*, 1999; Ward *et al.*, 2000; Small *et al.*, 2001; Wang *et al.*, 2001; Plant *et al.*, 2003; Ciccosto *et al.*, 2004; Michaelis *et al.*, 2005). While there is some disagreement concerning the exact identity of the A β aggregated species (Lambert *et al.*, 1998; Hartley *et al.*, 1999; Ward *et al.*, 2000; De Felice *et al.*, 2004; Klein *et al.*, 2004), the toxicity is associated with the species that are part of the A β accumulation or aggregation process.

Tau hyperphosphorylation and paired helical filaments

Neurofibrillary tangles form intracellularly in neurons. They appear as dense and insoluble clots

found in or around damaged hippocampal cells (Hyman *et al.*, 1984). The chief component of neurofibrillary tangles is paired helical filaments consisting of the hyperphosphorylated isoform of the microtubule-associated protein tau, which are typical histological lesions found in AD brains (Hyman *et al.*, 1984; Iqbal *et al.*, 2003). The correlation between A β deposition and paired helical filament formation has been reported to be responsible for the onset and progression of AD (Gotz *et al.*, 2001; Lewis *et al.*, 2001). Such a correlation suggests a potential link between aggregation state, cytoskeletal abnormalities and cell death. However, the details of the mechanism remain to be further explored.

AD is an inflammatory disorder

Involvement of inflammatory processes in the etiology of AD has recently received considerable attention (Bamberger and Landreth, 2001; Meda *et al.*, 2001; Barger, 2004; Brodyman and Malter, 2004; Zhang *et al.*, 2004). Senile plaques contain a variety of inflammatory molecules that are also elements of an inflammatory response, such as heparan sulfate proteoglycan, thrombin (Akiyama *et al.*, 1993), α 1-antichymotrypsin (Aisen, 1996), and a few complement components (Rogers *et al.*, 1992). These inflammatory components are produced principally by activated microglia, the brain's version of macrophage. Microglia originate from myeloid lineage and serve as the key immune effector cells in the brain. They are observed to be clustered within and adjacent to senile plaques.

Many lines of evidence showed that microglia exhibit an activated, reactive phenotype and extend ramified processes into the senile plaques in AD brains as compared to the controls (Akiyama *et al.*, 1993; Le Prince, 1993) and that A β is responsible for the elevated level of activation. Alternatively, A β has been shown to be a chemoattractant for microglia (Davis *et al.*, 1992). In both cases, activated microglia could either phagocytose A β or stimulate an inflammatory response that over a period of time could lead to the destruction of surrounding tissue.

Numerous complement components, one type of proinflammatory molecules, have been detected with senile plaques in the AD brain. Typically, classical complement action is initiated via the binding to an activator, including amyloid fibrils. After binding of the first complement protein C1, a cascade of autocatalytic or proteolytic cleavage reactions take place, resulting in the formation of biological active complement proteins. A β was shown to bind C1 and activate complement in a number of tests (Rogers *et al.*, 1992; Emmerling *et al.*, 1997; Webster *et al.*, 1997) and this amyloid-dependent activation of the complement cascade eventually culminating in the

formation of a membrane attack complex (MAC) (Emmerling *et al.*, 1997; Bradt *et al.*, 1998). In senile plaques, all complement components, including the MAC, can be detected, suggesting that the full classical complement cascade has been activated. Binding interaction between complement components and A β fibrils could either up-regulate phagocytosis of A β or lead to nonspecific cell lysis.

Clinically, non-steroidal anti-inflammatory drugs (NSAIDs) such as aspirin, ibuprofen, and naproxen commonly used in patients with rheumatoid arthritis, have been shown to significantly ameliorate symptoms of AD (Lim *et al.*, 2000; Yan *et al.*, 2003; Cole *et al.*, 2004; Imbimbo, 2004). The involvement of complement in AD progression is plausible due to increasing experimental support; however, it remains unclear whether this mechanism accounts for the specificity of the disease to given areas of the cortex. Presumably, an immune response to A β deposition would occur, but it is unlikely to serve as a primary event of neuronal loss in AD brains.

β -AMYLOID SPECIES

Generation of A β

β -amyloid (A β) is the principal proteinaceous constituent of senile plaques (amyloid plaques) and vascular amyloid of AD. An increase in production and abnormal accumulation of A β in the brain is implicated in the etiology of AD. A β is a peptide of 39 to 43 amino acid derived from a much larger integral protein, the amyloid precursor protein (APP) (Haass *et al.*, 1993), which appears to have a membrane spanning region and resembles a glycosylated cell-surface receptor (Kang *et al.*, 1987). Cloning studies (Kang *et al.*, 1987) and biochemical studies (Dyrks *et al.*, 1988; Selkoe *et al.*, 1988) showed that the APP gene encodes at least four alternatively spliced products ranging from 695 to 770 amino acids. These four types of human APPs have 695, 751, 770, and 714 residues, in which the first three are the major isoforms of APPs. Both APP751 and APP770 carry a domain that includes a 56 and 75-amino acid insert with high homology to the Kunitz-type protease inhibitor sequence (KPI) (Kitaguchi *et al.*, 1988) which is capable of inhibiting the proteolytic degradation of A β (Naidu *et al.*, 1995). The A β domain is composed of 28 extracellular and 12 to 14 transmembrane amino acids of APP (Martins *et al.*, 1991). The combined activities of β - and γ -secretases are required for generating the A β protein. Once formed, A β is immediately secreted into the culture medium or biological fluids including plasma and cerebrospinal fluid (Haass *et al.*, 1993). The normal processing

of the APP involves cleavage predominately by the secretase enzyme, γ -secretase, which cuts APP in the middle of the β -amyloid sequence and thus prevents the formation of A β (Ishiura, 1991). Ninety percent of A β in the brain consists of A β (1-40) while the remaining ten percent is the more fibrillogenic species A β (1-42).

Amyloid precursor protein (APP)

The function of APP or its role in the pathogenesis of AD is less than clear. APP is a highly conserved protein that is produced in most of the tissues throughout the body. It has been reported that protein kinase C can enhance APP secretion via the phosphorylation of an undetermined protein (Buxbaum *et al.*, 1992; Caporaso *et al.*, 1992) and decrease the production of A β (Buxbaum *et al.*, 1992; Gabuzda *et al.*, 1993). In addition, persistent depolarization of neurons results in APP cleavage and secretion, implying that APP processing is modulated by neuronal activity (Nitsch *et al.*, 1993). Large numbers of extracellular neuritic amyloid plaques or senile plaques, cerebrovascular amyloids, and to a lesser extent, intracellular neurofibrillary tangles, are the traditional molecular hallmarks found in the brains of AD patients (Selkoe, 1991). Transgenic mice expressing APP gene or fragments of APP gene carrying familial AD mutations exhibit many characteristics of the disease including amyloid plaques, cognitive deficits, and neuronal cell death (Games *et al.*, 1995; LaFerla *et al.*, 1995; Masliah *et al.*, 1996; Kowalska *et al.*, 2004). Genetic and epidemiological observations suggest that mutations in three genes (amyloid precursor protein, presenilin 1, presenilin 2) which cause the relatively rare familial forms of AD that affect the production and amyloidogenicity of A β (Selkoe, 1996; Kowalska *et al.*, 2004).

Pathologically, a strong correlation between the dementia experienced by patients in life and the amyloid burden detected upon autopsy was concluded in some careful studies (Cummings *et al.*, 1996). Although, up to date, the precise cause of AD and the mechanisms leading to the formation of these abnormal protein clusters remain unclear, they are believed to be involved in the pathogenesis of AD. Numerous lines of supporting evidence has pointed to the amyloid cascade hypothesis of A β formation, specifically highly ordered A β plaques (fibrils), as the central player in the molecular pathogenesis of AD.

BIOLOGICAL EFFECTS OF A β : A β -INDUCED NEUROTOXICITY

Accumulating evidence has demonstrated that

A β is toxic to nerve cells both *in vivo* and *in vitro* (Delobette *et al.*, 1997; Nitta *et al.*, 1997; Shin *et al.*, 1997; Giovannelli *et al.*, 1998; Wang *et al.*, 2001, 2002; Plant *et al.*, 2003; Ciccotosto *et al.*, 2004; Michaelis *et al.*, 2005). The majority of toxicity studies have been performed on primary cultures of rat hippocampal neurons typically obtained from fetal tissue. However, studies have found that in mouse model of AD, AD-like symptoms do not develop in young animals (Games *et al.*, 1995). Developmental differences in tissues may bias the results from these toxicity studies. Rat PC12 and human SH-SY5Y cells, two neuron-like cell lines, have also been widely used in toxicity studies and were found to be susceptible to A β -induced neurotoxicity (Iversen *et al.*, 1995; El-Agnaf *et al.*, 2000; Blanchard *et al.*, 2002; Datki *et al.*, 2003; Sung *et al.*, 2003; Datki *et al.*, 2004; Wang *et al.*, 2005a). It has been suggested that microglial cells kill neurons upon activation by A β (Roher *et al.*, 1996; Wegiel *et al.*, 2000). In the past, with the exception of studies on transformed cell lines, microglia cells may or may not be present and have generally been ignored in *in vitro* cultures. Thus, the correlation between *in vitro* assays of toxicity and the *in vivo* disease process remains open to question.

Different A β peptide fragments have been used in these studies. In general, A β (1-16) was thought to be too short to aggregate. A β (1-28) is less toxic than other longer sequences. A β (25-35) was found to aggregate readily and elicit neurotoxic effects in many (Pike *et al.*, 1993; Weiss *et al.*, 1994; Xu *et al.*, 2001) but not all of the studies (Games *et al.*, 1992; Stein-Behrens *et al.*, 1992). The full-length sequence, A β (1-40), is capable of forming aggregates and the its aggregation is positively correlated with A β -induced toxicity (Pike *et al.*, 1993; Tomiyama *et al.*, 1994; Roher *et al.*, 1996; Cribbs *et al.*, 1997; Wang *et al.*, 2001, 2005; Xu *et al.*, 2001; Schuster *et al.*, 2005).

It should be pointed out that some recent studies demonstrated the toxic effect of smaller A β oligomeric species on neurons (Lambert *et al.*, 1998; Hartley *et al.*, 1999; Ward *et al.*, 2000; Klein *et al.*, 2001, 2004; De Felice *et al.*, 2004), suggesting an important and surprising concept that fibrillar species might not be the only neurotoxic form of A β and perhaps not even the most significant form for AD.

MOLECULAR AND STRUCTURAL ASPECTS OF A β SPECIES AND FIBRILLOGENESIS

Because aggregation or deposition of A β has been reported to be closely related to the biological effects or pathology of AD, understanding the aggregation of A β on a molecular basis might aid in the

development of new approaches to eliminate or reduce the destructive effects of A β (Jarrett *et al.*, 1993; Soreghan *et al.*, 1994; Shen and Murphy, 1995; Lomakin *et al.*, 1996).

Structure and conformation of A β species

The sequence of soluble (monomeric) A β peptides can be generally divided into four regions, two hydrophobic segments from 17-21 and 29-42, and two hydrophilic segments from 1-16 and 22-28. Two turns are predicted between residues 6 and 8, and residues 23 and 27 (Lynn and Meredith, 2000; Serpell, 2000).

Secondary structure or conformation of A β has been suggested to be the key determinant of structure changes in the peptide that would accompany the aggregation process (El-Agnaf *et al.*, 1998; Frears *et al.*, 1999; Demeester *et al.*, 2000, 2001; Festy *et al.*, 2001). As opposed to α -helix and random coil, the β -sheet secondary structure has been found to be associated with insolubility and protease resistance (Nordstedt *et al.*, 1994; Jacchieri 1998). Generally, soluble A β species has predominately a random coil or α -helical structure, aggregated A β species adopts a higher degree of β -sheet content, which has been suggested to correlate with neurotoxicity of A β (Simmons *et al.*, 1994). The secondary structure or conformation of A β peptide has proven to be exquisitely sensitive to its environment, including ionic strength, temperature, concentration, pH, and solvent components. In addition, different portions/primary sequences of A β peptide may exhibit different conformations even though those external environmental factors stay the same. Fraser *et al.* (1991) reported the pH-dependent behavior in A β conformational transition. Their results in A β (1-28) showed that largely random coil conformations were observed at either acidic or basic pH, while β -sheet assemblies dominated in the intermediate range. It has been shown that A β (1-42) were primarily β -sheet (~90%) in phosphate-buffered saline at pH 7.4. Under the same experimental condition, A β (1-39) adopted a mix of 50% random coil and 50% β -sheet conformation, while A β (1-28) peptide was virtually in 100% random coil conformation (Barrow and Zagorski, 1991). Similar dependency of pH on A β conformation was also observed in other studies (Ji *et al.*, 2002; Stine *et al.*, 2003).

A β conformation has been shown to be dependent of salt concentration. It was found that A β peptide fragments were soluble in water and adopted a dimeric form (Hilbich *et al.*, 1991). The secondary structure of the peptide was primarily β -sheet conformation. Upon addition of salt, large fraction of precipitates and small fraction of soluble peptide retained β -sheet and random coil conformations, re-

spectively. A β secondary structure was also demonstrated to be concentration-dependent. Results from a thermodynamic study revealed that A β (25-35) underwent a reversible transition between monomeric random coil and oligomeric β -sheet in a concentration-dependent manner (Terzi *et al.*, 1994). It was observed in A β (1-28), A β (1-39), and A β (1-42) that a decreased percentage of intermolecular β -sheet content and an increased percentage of α -helical content as the concentrations of fluorinated alcohols such as trifluoroethanol or hexafluoro-2-isopropanol (Barrow and Zagorski, 1991; Barrow *et al.*, 1992; Sticht *et al.*, 1995) increased. In addition, previous studies of A β (1-40) showed that α -helix was the major structural motif in dimethyl sulfoxide (DMSO) (Snyder *et al.*, 1994) and sodium dodecyl sulfate (SDS). It was also reported that the percentage of β -sheet content of A β peptides varied in different solvents (Shen and Murphy, 1995; Crescenzi *et al.*, 2002).

Factors of aggregation process

A β is secreted as a monomer *in vivo*. Under either *in vivo* or *in vitro* environment, A β spontaneously self assembles into fibrils. It has been shown that A β aggregation process depends on pH of solution, temperature, A β peptide concentration, the presence of salt, and mixing protocol (Fezoui and Teplow, 2002; Kawooya *et al.*, 2003; Stine *et al.*, 2003). Stable monomers of A β can be formed, *in vitro*, by dissolving the peptide in 8M urea, 100% (v/v) DMSO, TFE, HFIP or in detergents such as SDS (Coles *et al.*, 1998; Szabo *et al.*, 1999; Gursky and Aleshkov, 2000). When dissolved in water, A β is observed to undergo a random coil to β -sheet conversion that can be controlled by temperature, pH, and peptide concentration (Szabo *et al.*, 1999; Gursky and Aleshkov, 2000). At low temperatures (0°C), the transition to β -sheet is not accompanied by dimerization or aggregation of the peptide (Gursky and Aleshkov, 2000). At low concentrations (10 μ M) and in 10% DMSO, formation of stable A β dimers occurs (Garzon-Rodriguez *et al.*, 1997). Whether in water or physiological buffers, under higher concentrations and/or high temperature, reversible aggregation into higher molecular weight species may occur (Shen and Murphy, 1995; Gursky and Aleshkov, 2000). Moreover, the effect of dissolving solvents on the kinetic behavior of A β aggregation/fibril formation was quantitatively examined (Wang *et al.*, 2005c).

Several studies have focused on identifying certain primary sequences or particular amino acids that are critical to A β aggregation. The C-terminus of A β has been shown to play a role in rate of aggregation. Studies using variants with different C-termini showed that shorter C-terminus slowed the aggregation process (Burdick *et al.*, 1992; Jarrett *et al.*, 1993;

Walsh *et al.*, 1997). Several lines of evidence indicate that the central hydrophobic cluster region Leu17-Ala21 is important for β -sheet formation as well as A β aggregation (Wood *et al.*, 1995; Tjernberg *et al.*, 1996; Mansfield *et al.*, 1998; Frears *et al.*, 1999; Pallitto *et al.*, 1999). Introduction of substitutions of two hydrophobic phenylalanine residues in positions 19 and 20 (Hilbich *et al.*, 1991; Esler *et al.*, 1996; Mansfield *et al.*, 1998) or Lys16 (Hilbich *et al.*, 1991) produced a peptide with high solubility in aqueous buffers and no propensity for aggregation. Substitution of V18 in A β (1-40) led to an enhanced propensity for α -helical conformation and a decreased ability to aggregate (Soto *et al.*, 1995). Abolished aggregation was observed in A β (15-23) and A β (12-26) as the replacement of a single amino acid with proline within the region 17-23 (Wood *et al.*, 1995). Furthermore, the segment ranging from 17 to 21 has been proposed to be a potential target for aggregation inhibitors (Pallitto *et al.*, 1999). Residues 14-23 are necessary for long fibril formation (Tjernberg *et al.*, 1999).

It has been suggested that not all N-terminal region of A β is necessary for aggregation (He and Barrow, 1999). Truncated peptide fragments from N-terminus of A β indicated that residues 1-9 were not necessary for aggregation (Hilbich *et al.*, 1991). However, residues between 11 and 16 are probably critical to the conformation stability responsible for aggregation (Mansfield *et al.*, 1998; He and Barrow, 1999).

Mechanisms of aggregation process/ fibrillogenesis

Nucleation-dependent growth

In vitro work has led to the proposal of nucleation-dependent pathway in amyloid fibrillization (Jarrett and Lansbury, 1992; Jarrett *et al.*, 1993; Lomakin *et al.*, 1996). This mechanism primarily involves three main steps: (1) a slow nucleation phase, in which A β undergoes a series of thermodynamically unfavorable association steps to generate an ordered oligomeric nucleus, (2) a growth phase, involving the nucleus which readily grows to form larger polymeric species, and (3) a steady state phase, where the ordered aggregated species and the monomeric species are at equilibrium. Results showed that no detectable turbidity was perceived after a few days (with a longer lag time) with A β (1-39) or A β (1-40) at 20 μ M (below the critical concentration), whereas A β (1-42) solution with identical concentration formed aggregates or fibrils readily. Other sedimentation results also supported this point (Burdick *et al.*, 1992). Apart from the elimination of lag time, the elongation rate of A β (1-39) or A β (1-40) was drastically enhanced and the aggregation kinet-

ics of these fragments were observed to follow the first order kinetics as seeded with a trace of A β (1-42). A similar conclusion was also established by others (Esler *et al.*, 1996; Naiki and Nakakuki, 1996).

Other researchers (Snyder *et al.*, 1994) have also found that the aggregation kinetics of A β (1-40) and A β (1-42), alone and in combination, were tremendously different. The aggregation rate of A β (1-42) was retarded by adding monomeric A β (1-40) as compared with A β (1-42) alone. However, the mixture of A β (1-40) and A β (1-42) was still aggregated faster than A β (1-40), suggesting that aggregation kinetics was determined by A β (1-40).

Amyloid fibril formation model

The model is proposed in the work of Shen and Murphy (1995). Fibrils are initiated from nuclei formed by monomers of A β and could either elongate by adding of partial fragments (*i.e.* entire nuclei, small fibrils), or dimers to lengthen the fibril ends. The same research group (Tomski and Murphy, 1992; Shen and Murphy, 1995) has quantified changes of fibril dimensions with time, and also developed mathematical models to verify this mechanism of amyloid fibrillization. Other investigators have proposed conceptually somewhat similar models, but did not account for the fibril-fibril interactions, or reactions among the variety of known oligomeric species in existence. Only one other investigator has constructed a mathematical model of fibril assembly (Lomakin *et al.*, 1996), in which monomers of A β form a micelle, from which nuclei are spontaneously released. Monomers of A β then add to the nuclei, resulting in fibril elongation. The model, although capable of describing the sedimentation data on which it was based, still does not explain the fibril elongation observed during light scattering experiments (Shen and Murphy, 1995).

Micelle formation

Other investigators proposed a micelle formation hypothesis to describe the mechanism of amyloid aggregation (Soreghan *et al.*, 1994). They found that A β displayed properties commonly associated with surfactants or detergents that form micelle in solution and also lowered the surface tension of water. Different degrees of surface tension reduction were observed in various A β analogs, depending on whether these analogs contained the hydrophobic residue 29-43. In addition, based on the SDS-PAGE and gel filtration analyses, the results showed that, with the exception of A β (1-40), A β (1-41), A β (1-42), A β (1-43) formed SDS-resistant aggregates with mass of about 16 kDa. On the other hand, A β (1-40) exhibited higher molecular weight aggregates in gel filtration results. Furthermore, two populations, a

dimer species and a larger aggregate species, were observed in both A β (1-40) and A β (1-42) solutions at concentrations above the critical concentration of 25 μ M.

This model postulates that A β peptide was organized into a "tubular micelle", known as a hexagonal I type phase. The polar domain (approximately the first 28 residues) forms the outer wall of the amyloid fibril, while the hydrophobic domain forms the inner wall surrounding the center of the fibril. This tubular micelle model, although consistent with the β -crystallite model deduced from X-ray fiber diffraction (Inouye *et al.*, 1993), does not explain the cross β -sheet conformation.

Advanced glycation modification

Vitek *et al.* (1994) postulated that the deposition and the accumulation of A β in AD might be triggered by the formation of advanced glycation end products (AGEs), which have been implicated in amyloidogenesis of β 2-microglobulin associated with hemodialysis-associated amyloidosis (Miyata *et al.*, 1994). The thioflavin T fluorescence results indicated that aggregation rate induced by AGE-A β (1-40) was about ten times faster than that induced by preformed aggregated A β (1-40). Based on this AGE modification model, A β aggregation can be induced by chemical modification of the peptide.

While numerous models have been proposed, the great detail of the aggregation process remains to be unequivocally discovered. Exploring, at the amino acid residue level, which parts of monomeric, oligomeric, and fibrillar A β species are accessible to the environment media/solvent will aid in recognizing a critical contact sites that are pivotal to aggregation. Additionally, elucidating, at the residue level, how A β -A β interaction or A β self-associate in the aggregation event will certainly provide new targets for the development of aggregation modifiers that could potentially inhibit the neurotoxicity elicited by A β . Hydrogen/deuterium exchange (HX) technique provides significant insight into structure information by determining the portions of the peptide backbone that are protected from H/D exchange. Hydrogen/deuterium exchange along with mass spectrometry (MS) or nuclear magnetic resonance spectroscopy (NMR) has proven to be a relatively powerful tool for mapping residue-level aggregation of A β (Kheterpal *et al.*, 2000, 2001, 2003a, 2003b; Wang *et al.*, 2003b; Whittemore *et al.*, 2005; Williams *et al.*, 2005). Wetzel and coworkers reported that HX-MS was able to demonstrate the structural difference(s) among monomeric, protofibrillar, and fibrillar A β species by their different protection patterns. Their results further showed that, relative to A β monomer, approximately 40% and 60% of the backbone amide hydrogens resistant to H/D ex-

change in protofibrillar and fibrillar species, respectively (Kheterpal *et al.*, 2000, 2003a). In order to reveal the degrees of protection from exchange in different regions of the full-length A β , the proteolytic digestion was employed after HX. Wang *et al.* (2003b) found that the N-terminus (residues 1-4) was completely unprotected from exchange and the fragment containing residues 5-19 was over 50% protected from exchange while the C-terminal segment was approximately 35% protected in the fibrillar A β . However, recent HX-NMR data presented a good solvent accessibility of the C-terminus of A β (Whittemore *et al.*, 2005). Further investigations are needed to strengthen our knowledge concerning the amyloid fibril structure and the fibril formation process.

Role of size/aggregation state of A β species in the A β -induced neurotoxicity

The relationship between structure and toxicity has been well documented for β -amyloid of AD. In aggregated solutions (containing fibrils, protofibrils, and low molecular weight species) A β has been consistently shown to be toxic to different cultured nerve cells such as PC12 cells, primary mixed brain cells and B12 cells (Yankner *et al.*, 1990; Busciglio *et al.*, 1993; Howlett *et al.*, 1995; Seilheimer *et al.*, 1997; Ward *et al.*, 2000). While there has been some disagreement as to the exact structure of the aggregated species associated with toxicity, whether it be a protofibril (Hartley *et al.*, 1999; Ward *et al.*, 2000), a diffusible, non-fibrillar ligand (Lambert *et al.*, 1998; Klein *et al.*, 2001), some other low molecular weight intermediate (Hartley *et al.*, 1999), or spherical aggregates (Hoshi *et al.*, 2003), it is certain that toxicity is associated with peptide structures that are part of an aggregation pathway associated with amyloid fibril formation.

Several investigators have attempted to characterize the size of the toxic A β species (Lambert *et al.*, 1998; Hartley *et al.*, 1999; Walsh *et al.*, 1999; Ward *et al.*, 2000; Klein *et al.*, 2001, 2004; Hoshi *et al.*, 2003). Toxicity was attributed to a non-fibrillar species with molecular weight ranging from 17 to 42 kD (Lambert *et al.*, 1998; Klein *et al.*, 2001, 2004) or with hydrodynamic radii between 3 and 8 nm (Chromy *et al.*, 2003). These oligomers, referred to as the slowly sedimenting A β -derived diffusible ligands (ADDLs), were formed via incubation of A β (1-42) with clusterin (Apo J) or via incubation at low temperatures, and were not associated with A β fibril formation or an aggregation pathway. ADDLs were showed to be toxic at nanomolar doses, when bound to cell surface toxin receptors and Fyn, a non-receptor protein tyrosine kinase overly expressed in AD, leading to a disruption in long-term potentiation

(LTP) and synaptic plasticity.

Other researchers further confirmed the nature of toxic A β oligomers in the brain (Walsh *et al.*, 2002). Their results showed that these A β oligomeric species were produced soon after generation of the peptide within certain intracellular vesicles and are subsequently secreted from the cell. Microinjection of cell medium containing both A β oligomers and monomers markedly blocked hippocampal LTP in rats *in vivo*. Immunodepletion from the culture medium of all A β species entirely prevented the inhibition of LTP. Cell medium treated with insulin-degrading enzyme, which selectively degraded monomeric A β , did not prevent the block of LTP, suggesting the toxic effect of these low molecular weight A β oligomers (Walsh *et al.*, 2002). Besides, Ward and coworkers have performed fractionation of aggregated (fibrillar) A β and then measured its biological activity (Ward *et al.*, 2000). They used density-gradient centrifugation to isolate different fibrillar forms of A β including protofibrils, fibrils, and low molecular weight oligomers. The hydrodynamic radii of the protofibrillar species were characterized by photon correlation spectroscopy to be on the order of 22-35 nm and 97-367 nm, whose corresponding molecular weights would be significantly greater than 42 kD. The species were found to be toxic as determined via a 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) reduction assay. It was concluded that the detectable effects on cell viability were found to correspond to the presence of protofibrillar and fibrillar structures, but not to the monomeric species.

Walsh *et al.* (1999) used size exclusion chromatography (SEC) to fractionate fibrillar A β into low molecular weight species (LMW), protofibrils, and fibrils, and found that protofibrillar intermediates, not the LMW A β , significantly affected the physiology, as evaluated via the alteration in neuronal MTT metabolism, of the primary rat cortical neurons in a concentration-dependent manner. However, Hartley *et al.* (1999), comparing the biological effects of different A β assemblies on primary mixed brain cultures, suggested that low molecular weight A β (with hydrodynamic radius of 1.5 to 2 nm) and prefibrillar or protofibrillar A β (4 to 100 nm diameter, length under 200 nm) were toxic as assessed via lactate dehydrogenase release after 3 days of exposure, while, only protofibrils induced acute rise in neuron electrical activity, for instance, action potentials and excitatory postsynaptic currents. Authors pointed out that these findings were consistent with the results that some transgenic mice over-expressing human APP have exhibited altered electrophysical responses before or during the initiation of A β fibril formation (Holcomb *et al.*, 1998; Chapman *et al.*, 1999; Hsia *et al.*, 1999).

Other than protofibrils, fibrils, and ADDLs, recent findings showed that spherical aggregates ASPDs with radius of 10-15 nm acquired the highest neurotoxicity (Hoshi *et al.*, 2003). This toxic ASPD species was highly correlated to SDS-resistant oligomeric bands in Western blotting. An elevation in TPKE/GSK-3 β activity was observed on neuronal culture treated with ASPDs. This ASPD-induced TPKE/GSK-3 β activity and resultant cell death were inhibited by lithium in a dose-dependent manner. Additionally, A β -elicited toxicity was still detected even with the addition of the β -sheet breakers, suggesting that the formation route of ASPDs might be different from that of A β fibrils (Hoshi *et al.*, 2003). Recently, using oligomer-specific recognition antibody, an important report demonstrated that the soluble oligomeric species of various amyloid diseases exhibited a unique conformation-dependent structure that was different from those in low molecular weight A β and fibrillar A β species (Kayed *et al.*, 2003). Also, judging from toxicity experiments, the authors commented that the soluble oligomeric species perhaps served as the actual culprit responsible for toxicity mechanism of A β (Kayed *et al.*, 2003).

It should be noted, however, that during the time course of a toxicity experiment, protofibrillar species were observed to convert both into monomeric or dimeric A β species and into fibrillar species (Walsh *et al.*, 1999). Due to the dynamic structure of A β , it has been fairly difficult to determine definitely and precisely which species are toxic. By taking advantages of the plaque-forming assay in virology and the diffusion concept, a new diffusion-based method was developed to simultaneously separate and detect the toxic A β oligomeric species formed during the A β aggregation process (Wang *et al.*, 2002). This method provides a new estimate of the smallest species associated with A β -induced neurotoxicity, a species with hydrodynamic radius of ~10 nm, which are considerably smaller than typical fibrils and protofibrils (Wang *et al.*, 2002).

Most importantly, identifying the size and/or structure of the A β species responsible for toxicity will aid in the development of agents that can intervene the aggregation pathway of A β and prevent the formation of toxic species either from preformed plaques or from newly synthesized and proteolytically cleaved monomeric/dimeric/oligomeric A β species.

MECHANISMS OF A β -INDUCED NEUROTOXICITY

The detailed mechanisms involved in the A β -elicited neurotoxicity remain elusive, but a variety of

hypotheses regarding the mechanisms of the toxicity induced by A β have been proposed in the literature. These mechanisms include membrane depolarization (Whitson *et al.*, 1994), membrane destabilization (Kilsdonk *et al.*, 1995; Neufeld *et al.*, 1996), pore formation (Arispe *et al.*, 1993a, 1993b, 1994a, 1994b), free radical generation (Butterfield *et al.*, 1999; Varadarajan *et al.*, 2000), A β -induced alterations in intracellular signaling (Ferrari-DiLeo *et al.*, 1995; Soomets *et al.*, 1999), ion channel function (Weiss *et al.*, 1994; Good, 1996; Good *et al.*, 1996), and calcium homeostasis (Mattson *et al.*, 1993; Weiss *et al.*, 1994; Good, 1996; Good *et al.*, 1996).

Free radical generation

The over-production of reactive oxygen species (ROS) and free radicals has been widely accepted as one of the key theories underlying the A β -induced toxicity mechanism (Butterfield, 1997; Carr *et al.*, 1997; Markesbery, 1997; Holscher, 1998). A correlation between the A β peptides and the production of ROS and free radicals has been demonstrated in various *in vitro* experiments (Davis, 1996; Pereira *et al.*, 1999), in transgenic mice models of AD (Pappolla *et al.*, 1998), and in AD brain (Yatin *et al.*, 1999a, 1999b).

Butterfield *et al.*, using electron paramagnetic resonance (EPR) and spin trapping techniques, showed that A β generated free radicals in solution. A β (25-35) rapidly quenched spin labels within prepared synaptosomal membranes, but did not quench labels on the surface of the membrane (Butterfield *et al.*, 1994). Subsequent study showed that A β (25-35) produced a detectable free radical in solution within minutes, while full-length peptide A β (1-40) generated free radicals only after 3 to 24 hours, depending on the solvent type. A β (35-25), the non-neurotoxic counterpart of A β (25-35) also produced a comparable EPR signal by an oxygen dependent reaction (Hensley *et al.*, 1994). Mass spectroscopic measurement suggests that the peptide fragmentation occurs along the same time scale as free radical production. The identity of the peptide fragments is still undetermined. ROS generated by A β peptide had a short life-time (Mattson and Goodman, 1995). Pre-incubation of the peptide prior to measurement yielded no ROS production. In addition, different lots of A β (1-40) showed different patterns of free radical formation that correlated with toxicity (Aksenov *et al.*, 1995). Besides A β peptides, other amyloid-forming peptides including amylin and β 2-microglobulin, also caused ROS production and increased the level of intracellular calcium ion [Ca²⁺]_i (Mattson and Goodman, 1995).

Generation of ROS could be associated with increased intracellular concentration of Ca²⁺ (Mark

et al., 1995). It was reported that exposure of rat hippocampal neurons or synaptosomes to A β (25-35) or A β (1-40) led to a reduction in Na/K-ATPase activity and Ca²⁺-ATPase activity, respectively. The decline in ATPase activity in cultured neurons closely paralleled the rise in [Ca²⁺]_i. Impairment of the Na/K exchanger or Ca²⁺ pumps from cells would lead to a loss of intracellular ion gradient, depolarization of the membrane, and increase in concentration of intracellular Ca²⁺. Antioxidants, such as vitamin E and propylgallate, function as free radical scavengers that attenuate the impairment of Na/K-ATPase activity, impede the rise in [Ca²⁺]_i and prevent neurotoxicity induced by A β peptide (Mark *et al.*, 1995), all of which are suggestive of a role for ROS. The conclusion that A β -induced neurotoxicity could be inhibited by free radical scavengers was also suggested in other studies (Goodman and Mattson, 1994a, 1994b; Behl *et al.*, 1995).

Free radical production and ROS may indeed be involved in the pathogenesis of AD (Lockhart *et al.*, 1994). Until further evidence can be found to support these results, there is still too much uncertainty regarding the appropriateness of the findings and their consistency with the pool of literature to consider the free radical hypothesis of A β -mediated toxicity an acceptable proposal.

Membrane perturbation

The importance of the interaction(s) of most amyloid proteins including A β with membranes has been drawing a lot of attentions in the mechanism of A β -induced neurotoxicity. A variety of evidence demonstrates that plasma membrane may play a potential role, either by interaction with or perturbation by A β , in the A β -mediated neurotoxicity associated with AD (Ginsberg *et al.*, 1993; Mason *et al.*, 1993; Roth *et al.*, 1995; Terzi *et al.*, 1997; Wood *et al.*, 2003).

A β has been shown to decrease the fluidity of membranes derived from human lymphocytes, cerebral cortex, hippocampus, striatum, cerebellum and rat cerebellum embedded with DPH in a concentration-dependent fashion (Hartmann *et al.*, 1994; Muller *et al.*, 1995). In addition, immunostaining of cultured neurons incubated with A β by antibodies to β (1-40) and β (1-38) fragments clearly depicted aggregated species at the plasma membrane (Muller *et al.*, 1995). Subsequent study suggested that the longer fragments had greater impact on membrane fluidity than the shorter fragments under the same condition. Furthermore, the effect of A β peptides on the fluidity of phospholipid bilayer was observed to be greater in the hydrocarbon core than the hydrophilic heads (Muller *et al.*, 1998). Kremer *et al.* (2000) examined the size of A β species and its asso-

ciation with aggregation state, hydrophobicity, and changes in the membrane fluidity. Via light scattering and bis-ANS fluorescence, the authors noted that considerably greater aggregation rate and surface hydrophobicity were observed to occur at pH 6.0. Moreover, these two properties were strongly correlated with the extent of reduction in membrane fluidity measured in model lipid vesicles embedded with DPH. Recently, it has been observed that A β perturbed membranes of rat, mouse, and human brain resulted in enhanced membrane-bound DPH anisotropy (inversely correlated with membrane fluidity). They also showed that membrane-disordering or perturbing effect of A β occurred not only on synaptic plasma membranes (SPM) but also on mitochondrial membranes (Muller *et al.*, 2001).

In contrast, other researchers reported a rise in membrane fluidities (annular or bulk) induced by A β (1-40) or A β (25-35) in biological or model membrane embedded with the fluorescent dye pyrene via the fluorescence-based method (Avdulov *et al.*, 1997; Mason *et al.*, 1999; Chochina *et al.*, 2001). The lipid peroxidation was observed to be correlated with the fluidizing action of A β peptides (Avdulov *et al.*, 1997). Mason *et al.* (1999) explored the distribution and fluidizing action of soluble and aggregated A β species in rat SPMs by using small angle X-ray diffraction and fluorescence spectroscopy for quantifying bulk and annular fluidities. The fluorescence anisotropy data presented an increase in both bulk and annular fluidities of SPM induced by both soluble and aggregated A β (1-40). Also, according to the electron density profile, the authors postulated that the soluble species were intercalated into a membrane hydrocarbon core, while aggregated species interacted with membrane bilayer at the headgroup/water interface and thus led to dramatic reorganization of the lipid bilayer.

Consistent with the observation that A β interacts with the hydrophilic headgroups of phospholipid membranes, the interaction between phospholipid membranes and both A β (25-35) as well as A β (1-40) through the electrostatic-mediated force was observed (Terzi *et al.*, 1994, 1995, 1997; Seelig *et al.*, 1995). Using circular dichroism spectroscopy, titration calorimetry, and ultracentrifugation, investigators proposed the role of plasma membrane in the process of aggregation (Terzi *et al.*, 1994, 1995; Seelig *et al.*, 1995). It was hypothesized that both A β (25-35) and A β (1-40) exhibited cooperative and reversible random coil to β -sheet transition. However, the concentration-dependent conformational conversion between random coil and β -sheet structure shifts almost completely toward the β -sheet structure upon the addition/binding of negatively charged, small unilamellar lipid vesicles. The binding isotherms were exothermic and the apparent

binding constants for both peptide fragments were also determined. The authors concluded that the presence of the lipid membrane served as a catalyst to A β aggregation which occurred at the lipid/water interface. The local elevation of peptide concentration was the result of cationic peptide attraction to negatively charged membrane surface (Terzi *et al.*, 1994, 1995; Seelig *et al.*, 1995). Researchers also tested the effects of several membrane process-related compounds on the A β -induced neurotoxicity and demonstrated that polyhydroxylated aromatic dipolar compounds such as phloretin, exifone, and phenolphthalein prevent association of A β to negatively charged lipid vesicles and A β -mediated neurotoxicity (Hertel *et al.*, 1997). All the aforementioned findings implied that there is a nonspecific dipole-dipole interaction between A β and cell membranes (Hertel *et al.*, 1997). Moreover, due to identical maximum chemical shielding anisotropy and similar ordering and average orientation of the labeled headgroup observed with and without A β from phosphorus-31 and deuterium NMR studies, the same authors concluded that A β binds electrostatically to the outer envelope of the polar headgroup region but does not penetrate through the polar groups (Terzi *et al.*, 1997).

However, there have been experiments suggesting that A β might be incorporated into the membrane rather than interacting with the membrane surface or the polar lipid head groups. This idea was supported by the work of Butterfield *et al.* (1994) in which A β (25-35) was found capable of reacting with a spin label, quenching it, when the label was within the membrane, but not when the label was on the surface.

Additionally, there have been other studies suggesting that A β (1-40) formed ion channels in cellular membranes (Arispe *et al.*, 1993a). These experiments proposed that A β inserted into lipid vesicles upon sonication of the vesicles. The liposomes containing A β peptide were then fused with a planar bilayer, and the conductance of the membrane was measured under various conditions. Discrete change in ion channel activity (conductance) was measured a few minutes after the addition of A β -liposome to the planar bilayer. The ion channels formed were permeable to cations including Ca²⁺ (Arispe *et al.*, 1993a; Lin *et al.*, 1999). Researchers also reported giant conductances in cation channels formed by A β and concluded that A β peptide was able to form similar channels irrespective of the mechanism involved in the insertion of A β into cell membrane, providing supportive evidence that cell death might be due to amyloid ion channel activity (Arispe *et al.*, 1993a, 1993b; 1994b, 1996; Pollard *et al.*, 1995). Besides, a study was proposed to describe numerous channel subtypes with properties likely to cause toxicity (Kourie *et al.*, 2001).

Fragments with neurotoxicity such as A β (1-42) and A β (25-35) were also shown to form Ca²⁺-permeable pores on lipid bilayers (Mirzabekov *et al.*, 1994; Rhee *et al.*, 1998; Hirakura *et al.*, 1999). Both A β (1-42) and A β (25-35) have been demonstrated to readily insert into planar bilayer membranes to establish slightly cation selective, voltage dependent, ion channels. In addition, it has been found that C-terminal fragment of APP was able to change the cellular ionic activity either via interaction with existing channels or through *de novo* ion channel formation (Fraser *et al.*, 1997). It was also found that A β activated a similar conductance, but only upon transition from random coil to β -sheet (Li *et al.*, 1995). If the peptide were over-aged (already β -sheet structure), it could not have caused the conductance, nor would it have caused the conductance if the peptide were freshly prepared and hence random coil in configuration. Only if the peptide underwent the conformational transition from random coil to β -sheet would the conductance occur. Species of A β that were over-aged, and hence not capable of causing the conductance, were still toxic to neurons, which makes the relevance of this A β induced-conductance somewhat ambiguous (Li *et al.*, 1995).

Taken together, based upon the findings in aforementioned studies, there seems to be a link between ion channel formation and AD and A β does interact with cell membranes. However, the detail of this hypothesis of ion channel formation needs to be thoroughly explored.

Role of Cell Membrane Composition in A β -induced Neurotoxicity

Mounting evidence indicates that the neuronal cell membrane constituents, either in the cell membrane or in culture medium, are pivotal to the mechanism of A β toxicity. Studies have indicated that membrane components such as cholesterol and gangliosides altered the affinity of A β or other amyloid proteins for phospholipid membranes (Choo-Smith *et al.*, 1997; Ariga and Yu, 1999; Avdulov *et al.*, 1999; Matsuzaki and Horikiri, 1999; Wang *et al.*, 2005b). Once associated with membranes, negatively charged phospholipids, cholesterol, and gangliosides have been shown to increase the β -sheet content and/or rate of aggregation of A β or bovine calcitonin, another amyloid protein (Choo-Smith *et al.*, 1997; McLaurin *et al.*, 1998; Del Mar Martinez-Senac *et al.*, 1999; Matsuzaki and Horikiri, 1999; Mizuno *et al.*, 1999; Wang *et al.*, 2005b). Both *in vivo* and *in vitro* studies elucidated that the inhibition of cholesterol synthesis led to decreased A β formation (Frears *et al.*, 1999; Simons *et al.*, 1998).

Cholesterol

Generally, cholesterol has a broad variety of effects on the physical properties of cell membranes such as increasing ordering and rigidity, reducing permeability, and decreasing lateral diffusion (Yeagle, 1991). Cholesterol exerts a homogenizing effect in natural membranes and lipid bilayers. It has been shown to be correlated with some membrane proteins and is responsible for specific regulation of membrane-associated protein activity (Sinha *et al.*, 1977; Klein *et al.*, 1978; Mitchell *et al.*, 1990; Bretscher and Munro, 1993; Klein *et al.*, 1995). Cholesterol may serve as a regulator of protease access to its substrate or a structural membrane component of the lipid bilayer that alters the activity of embedded proteins, either by changing membrane fluidity or by a mechanism independent of its membrane-ordering effect (Schroeder *et al.*, 1991).

Epidemiological and genetic studies have supported the fact that cholesterol serves as a *bona fide* risk factor in the pathogenesis of AD. An increased risk of AD has been linked with a natural genetic variant of apolipoprotein E (apoE), a molecule associated with cholesterol metabolism. The apoE-4 allele, the allele involved in increased risk for sporadic and late onset AD (Corder *et al.*, 1993; Saunders *et al.*, 1993; Schmechel *et al.*, 1993; Graham *et al.*, 1999; Sadowski *et al.*, 2004), has been associated with elevated total serum cholesterol levels (Jarvik *et al.*, 1995; Notkola *et al.*, 1998). Demented patients homozygotic for apoE-4 had the highest total plasma cholesterol levels among a referral population of 40 patients with clinically diagnosed AD in comparison to a sample of non-demented elderly controls (Czech *et al.*, 1994). In addition, in a population-based study, the risk of AD has been positively correlated with elevated serum cholesterol levels (Evans *et al.*, 2000).

Alterations in soluble cholesterol and/or cholesterol biosynthesis have also been shown to affect the normal processing of APP in several *in vitro* cell-based studies (Howland *et al.*, 1998; Simons *et al.*, 1998; Frears *et al.*, 1999). Bodovitz and Klein, (1996), using cyclodextrin-solubilized cholesterol as a delivery system, examined the link between cholesterol and the stability of APP in human embryonic kidney 293 cells transfected with APP human plasmid. The results showed that cholesterol solubilized by methyl- β -cyclodextrin or ethanol downregulated the levels of the soluble N-terminal derivative following α -secretase cleavage (sAPP). However, APP holoproteins remained unchanged or increased. In COS-1 fibroblast cells, increasing concentrations of cellular non-esterified cholesterol carried by rabbit β -very low-density lipoprotein or human low-density lipoprotein were found to cause an inhibitory effect on sAPP release in a dose-dependent fashion. This inhibition in sAPP release was observed to be inde-

pendent of receptor-mediated lipoprotein metabolism (Racchi *et al.*, 1997). Simons *et al.* (1998) noted that the production of A β but not the generation of sAPP in transfected hippocampal cells was reduced by cholesterol-depleting drugs such as lovastatin and methyl- β -cyclodextrin, suggesting that cholesterol is essential for A β formation. Via immunoprecipitation, immunofluorescent labeling, and surface-enhanced laser desorption/ionization mass spectrometry, Frears *et al.* (1999) confirmed that cholesterol shifted the APP metabolism from α -secretase pathway to β -secretase pathway. Their results showed that the presence of the β -hydroxy- β -methylglutaryl-CoA (HmG-CoA) reductase inhibitor lovastatin, on human HEK cells transfected with APP, attenuated intracellular cholesterol/protein ratios by one half, and dramatically inhibited β -secretase cleavage of newly synthesized APP. Exogenous water-solubilized cholesterol at 200 μ g/mL concentration increased newly synthesized β -amyloidogenic products four-fold. By examining three different primary cultures including rat neurons, astrocytes, and microglial cells, Galbete *et al.* (2000) demonstrated a reduced secretion of sAPP in glial and neuronal cells induced by cholesterol. In addition, a slight decrease in APP mRNA expression and a substantial effect on protein maturation were observed in neurons. Via cell-surface biotinylation study, the authors concluded that cholesterol interfered with maturation of APP and inhibition of glycosylation of the protein.

Several lines of evidence have also demonstrated a link between A β production and cellular cholesterol levels in regards to *in vivo* animal studies. Durham *et al.* (1998) reported that A β level in the brain was elevated in apo E deficient mice fed cholesterol diet. It has been indicated that A β production and enzymatic processing of APP could be modulated by cellular cholesterol levels. Most importantly, APP gene-targeted mice that lack apoE, and had high serum cholesterol levels, did not show changes in APP processing. Such finding was suggestive of the importance of apoE in this enzymatic processing (Howland *et al.*, 1998). In contrast, one group observed an rise in brain A β level of mice with APP695 Swedish mutation fed with a high cholesterol diet but not wild type mice fed on cholesterol (Shie *et al.*, 1999). In the mouse model that exhibited over-expression of the C-terminal fragment of APP after β -cleavage, a cholesterol diet led to significant accumulation of AD-like pathology (Li *et al.*, 1999). Fishman *et al.* (1999) used mice with APP v717f mutation fed on high fat and cholesterol diet as an animal model and found that these mice exhibited both increased serum lipids and brain A β levels. Several observations were made in transgenic mouse model with diet-induced hypercholesterolemia-dramatic: dramatic rise of A β in the CNS, a strong

correlation between the levels of plasma and CNS total cholesterol, a significant decrease in sAPP, and an increase in C-terminal fragment of APP (Refolo *et al.*, 2000). Finally, recent reports have shown that cholesterol-lowering drugs were capable of decreasing accumulated A β levels in animal models such as guinea pigs fed with high doses of the hydroxymethyl co-enzyme A (HMG-CoA)-reductase inhibitor, simvastatin (Fassbender *et al.*, 2001). Similar results were found in APP/PS1 co-transgenic mice fed with (4-(2-[1-(4-chlorocinnamyl) piperazine-4-yl]ethyl]benzoic acid) (Refolo *et al.*, 2001) or 7-dehydrocholesterol-reductase inhibitor (Golde and Eckman, 2001), suggesting the critical role of cholesterol in A β -induce neurotoxicity responsible for AD.

Gangliosides

While present only in relatively small quantities in most tissues, gangliosides are abundant components of nervous tissues. Gangliosides compose of approximately one-tenth of total neuronal membrane lipids (Wiegandt *et al.*, 1982; Tettamanti and Riboni, 1993), and, specifically, ganglioside GM1 tends to be highly concentrated in certain regions of neurons, especially in pre- and postsynaptic membranes (Hansson *et al.*, 1977). In the respect of functionality, gangliosides have been associated with a number of important neurological events such as neuritogenesis, neurodifferentiation, synaptogenesis, and synaptic transmission.

Several lines of evidence implied the importance of gangliosides in pathology of AD. Working with isolated ganglioside-bound A β (1-42), Yanagisawa and coworkers (Yanagisawa *et al.*, 1995, 1996) reported that brain tissue which contained increasing levels of diffuse plaques also included increased amounts of ganglioside-bound A β (1-42). They also suggested that some of the A β peptides in diffuse plaques were bound to GM1 or its related members. The same research group, via different anti-A β monoclonal antibodies such as BC05 (specific for A β (1-42)), BAN50 (raised against A β (1-16)), BAN052 (raised against A β (1-16) and specific for N-terminus), and 4G8 (specific for A β (17-24)) along with immunoprecipitation, noted that A β bound to a GM1 ganglioside in a certain way that the bound A β could only be characterized by BAN052 monoclonal antibody. They proposed a possible mechanism whereby the membrane-bound A β species might be shed into the extracellular space and served as a "seed" for fibril formation (Yanagisawa and Ihara, 1998). Large body of data suggested that gangliosides might play a role in A β fibrillogenesis after binding to membranes or in acceleration of A β fibril formation *in vitro* (Choo-Smith *et al.*, 1997; McLaurin *et al.*, 1998; Matsuzaki and Horikiri, 1999; Ariga

et al., 2001; Kakio *et al.*, 2001, 2002; Tashima *et al.*, 2004; Yamamoto *et al.*, 2004; Wakabayashi *et al.*, 2005).

Cholesterol and/or gangliosides have been linked to certain biological activities of A β (Wang *et al.*, 2001). Investigations showed that cholesterol reduction and depletion of membrane associated sialic acid residue both not only significantly reduced the A β -induced GTPase activity but also protected cells from A β -induced toxicity, indicating the importance of A β -membrane interactions in the mechanism of A β toxicity. Similar results have also been observed with other amyloid-forming peptides such as bovine calcitonin (Wang *et al.*, 2005a).

G-protein activation (GTP hydrolysis)

G-protein-linked receptors influence the concentration of second messengers and thereby affect the behavior of other target proteins in cells. In most cases, the interactions between the receptors and second messengers in the signal transduction cascade are mediated via enzymes or ion channels activated by GTP-binding or G-proteins. G-proteins are the membrane bound proteins and provide the site for the exchange between GDP and GTP. Signal transduction is typically initiated by the binding of a ligand, hormone, or neurotransmitter to a G-protein-linked receptor located in the membrane. This binding stabilizes the conformation of the receptor, transmits information across the membrane, and stimulates G-proteins (Gilman, 1987; Bourne *et al.*, 1990a, 1990b; Simon *et al.*, 1991; Linder and Gilman, 1992). On the other hand, signal transduction can also be started by directly activating G-protein through external stimuli. Upon activation, the α -chain of G-protein exchanges GDP for GTP, and α -GTP complex dissociates from the rest of the G-protein due to the lower affinity for the G $\beta\gamma$ subunit. It diffuses along the inner surface of plasma membrane to bind and activate an effector. Different types of effectors such as adenylyl cyclase, phospholipase C, and ion channels have been discovered. The signal terminates when the α -bound GTP hydrolyze to GDP and the α subunit reassociates with the rest of the G-protein (G $\beta\gamma$ subunit).

Increasing evidence suggests that G protein activation and other signal transduction events such as phospholipase D and adenylyl cyclase activation are associated with the biological activity of A β (Schnecko *et al.*, 1994; Singh *et al.*, 1998; Soomets *et al.*, 1999; Jonsson *et al.*, 2000; Zambrzycka *et al.*, 2000; Vaudry *et al.*, 2004). A report showed that G-protein activation and A β aggregates were capable of upregulating tyrosine phosphorylation of focal adhesion kinase (FAK Tyr(P)) through a mechanism associated with protein kinase C and F-actin (Zhang *et al.*, 1996). After one day of incubation with aggre-

gated A β (1-42), cellular FAK Tyr(P) level was elevated on immunoblots; however, this stimulation was blocked by cytochalasin D, an F-actin disrupting drug. Furthermore, the toxicity of A β (1-42) was inhibited by the addition of bisindolylmaleimide, suggesting the role of protein kinase C in the stimulation of FAK Tyr(P) by A β fibril. Soomets *et al.*, found that GTPase activity was upregulated by A β (25-35) and A β (1-42) in ventral hippocampal and cortical membranes. The effect of on GTPase activity followed a dose dependent manner and exhibited a bell-shaped curve for A β (1-42) case. The bell-shaped concentration-dependent effect on adenylyl cyclase activity was observed for both A β (1-42) and A β (25-35). At high concentrations of A β (25-35) the GTPase activity was pertussis toxin sensitive, suggesting the involvement of a G $_{i/o}$ G protein (Soomets *et al.*, 1999). Their study implied that the G protein and adenylyl cyclase response to A β was associated with A β neurotoxicity (Soomets *et al.*, 1999).

It was observed that, in reconstituted phospholipid vesicles containing G $_0$ and APP, the turnover rate of G $_0$ GTPase activity was elevated when a monoclonal antibody (22C11) against N-terminal domain was added (Okamoto *et al.*, 1995). Authors concluded that the mode of G $_0$ activation by APP was highly similar to that of receptor-stimulated G protein activation suggested by others (Nishimoto *et al.*, 1993). However, a proposal has been made stating that the intracellular interaction between APP and G $_0\alpha$ can be regulated by extracellular signals and the high-affinity G $_0$ GTPase activity reduced upon incubating neuronal membranes with N-terminal APP recognition antibody (Brouillet *et al.*, 1999). It was found that G $_0\alpha$ interacted with APP, especially the C-terminal part of APP, in axonal microdomain. Moreover, in COS cell NK1 clone the activation of G $_0$ in reconstituted vesicles by the familial AD-associated APP mutant, V642I APP in particular, led to pertussis toxin-sensitive apoptosis and the impairment of cAMP response element via G $\beta\gamma$ -protein complex and G $_0\alpha$ -related mechanisms respectively (Giambarella *et al.*, 1997).

It has been previously shown that aggregated A β (25-35 and 1-40 fragments, but not 1-16 fragment) was able to increase GTP hydrolysis in membranes derived from PC12 cells while inhibition of GTPase activity attenuated the toxicity of the A β peptides (Rymer and Good, 2001). Similar results were shown for bovine calcitonin; only when in an amyloidogenic form, bovine calcitonin increased GTP hydrolysis, and inhibition of the GTPase activity attenuated the toxic effects of calcitonin (Rymer and Good, 2001). An A β -induced increase in GTPase hydrolysis was observed with purified G $_i$ and G $_0$ alpha subunits reconstituted in liposomes, and with cell membranes in which the receptors had been proteolytically removed. These results sug-

gested that the G protein activation observed upon incubation with A β was receptor-independent and was probably membrane-mediated. Recent evidence pointed that the mixtures of A β (25-35) and A β (1-42) or A β (1-40) induced an increase in GTP-binding several-fold higher than A β alone (Molnar *et al.*, 2004). This GTP-associated potentiation was found to be accompanied with the secondary structure of A β peptide mixtures, revealing that structural alterations are behind the enhanced biological activity (Molnar *et al.*, 2004).

While the link between G protein activation and A β actions was observed, the issue regarding how the activation of G protein occurs remains largely unclear. The kinetic analysis on A β -induced GTP hydrolysis was performed to achieve the above goal (Wang *et al.*, 2003a). Further mechanistic understanding of reaction pathways/cascades of the interaction between A β and G protein remains to be examined.

In summary, it is unequivocal that A β triggers adverse impacts on cellular function via interactions with cell membranes. Given the ample of aforementioned evidence describing the possible actions of A β , there might be more than one mechanism involved in the interaction between A β and neurons as well as the A β -induced neurotoxicity. Therefore, it is most likely that AD is a heterogeneous disease. However, the underlying mechanism(s) of A β -membrane interaction remain to be investigated. Is the mechanism governed by the electrostatic interaction, dipole-dipole interaction, or membrane fluidity alteration? Closer examinations on the mechanism(s) of this interaction will certainly provide an exploratory guide for rational design of potential inhibitor molecules.

CONCLUSION

In the present review, the general background information on Alzheimer's disease and β -amyloid are first presented. Next, attention is focused on the relevant research updates regarding structural aspect and molecular features of A β species as well as β -amyloid fibrillogenesis/aggregation process. Importantly, an emerging issue that an oligomeric intermediate is the primary toxic β -amyloid species is also discussed. Finally, a number of β -amyloid-induced toxicity mechanisms are proposed and discussed. It is our belief that further knowledge on novel approaches for the understanding of the conformational changes as well as biological functions of β -amyloid and β -amyloid-elicited toxicity mechanisms will shed light on the development and/or design of potential therapeutic strategies for Alzheimer's disease.

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