

**Mechanisms underlying the initiation of cerebral beta-amyloidosis and neurofibrillary tau pathology:
New insights from transgenic mice**

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TABLE OF CONTENTS

ACKNOWLEDGEMENTS

SUMMARY

1.INTRODUCTION

1.1.Protein misfolding and amyloid formation in degenerative disorders

1.2.Alzheimer's disease

1.2.1. Clinical symptoms and diagnosis

1.2.2. Neuropathological phenotype

1.2.2.1. β -amyloid plaques and the A β centric theory of Alzheimer's

1.2.2.2. Neurofibrillary lesions

1.2.3. Epidemiology and genetics of Alzheimer's disease

1.2.4. Origin of A β proteins: cell biology of APP

1.2.5. Human tau gene and protein isoforms

1.2.6. Mouse models of Alzheimer's disease

1.2.7. Treating and preventing Alzheimer's disease

2.ABETA42-DRIVEN CEREBRAL AMYLOIDOSIS IN TRANSGENIC MICE REVEALS EARLY AND ROBUST PATHOLOGY

3.EXOGENOUS INDUCTION OF CEREBRAL BETA-AMYLOIDOGENESIS IS GOVERNED BY AGENT AND HOST

4.NEUROFIBRILLARY PATHOLOGY IS INDUCED IN VIVO BY INTRACEREBRAL INDUCTION OF ABETA-CONTAINING BRAIN EXTRACTS

5.AMYLOID PLAQUE FORMATION LEADS TO A RAPID, ONGOING, AND MODIFIABLE MICROGLIAL RESPONSE

6.CONCLUSION

ABBREVIATIONS

CURRICULUM VITAE

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SUMMARY

Numerous neurodegenerative disorders result from the aggregation of proteins that misfold and accumulate as fibrillar amyloid deposits in selectively vulnerable regions of the central nervous system. Alzheimer's disease (AD) is one of these protein conformational diseases and the leading cause of dementia in the Western world. Postmortem, it is characterized by two major neuropathological features: extracellular deposition of A β peptide and intracellular aggregates of neurofibrillary lesions made of hyperphosphorylated tau protein. The observation that early-onset familial forms of AD are caused by mutations in three genes (the amyloid precursor protein (APP), presenilin-1 (PS1), and presenilin-2 (PS2)), all of which increase the production of A β , led to the so-called amyloid cascade hypothesis. This hypothesis proposed that the aggregation of polymerized forms of A β in soluble multimeric and/or insoluble senile plaque deposits in the brain is an early and critical event that triggers a cascade of pathological events leading to hyperphosphorylation and somatodendritic segregation of tau, formation of neurofibrillary lesions, neuroinflammation, neurodegeneration and, finally, dementia.

The generation of transgenic (tg) mice that exhibit cerebral A β -amyloidosis through expression of mutated human APP gene has provided new opportunities to explore pathogenic mechanisms and treatments of AD. The studies presented below were done in part using the well-established APP23 tg mouse model that carries human KM670/671NL mutated APP under the control of a neuron specific Thy-1 promoter and develops amyloid deposits progressively with age. We also generated and made use of a novel tg model, the APPPS1 mouse. This model coexpresses KM670/671NL mutated APP and L166P mutated PS1 that lead to accelerated cerebral amyloidosis concomitantly with additional AD-like pathologies such as local neuron loss, hyperphosphorylated tau-positive neuritic structures, dystrophic synaptic boutons and robust cortical gliosis. Because of the early onset of amyloid pathology, APPPS1 mice are well suited for studying the mechanism and impact of cerebral amyloidosis and to test therapeutic amyloid-targeting strategies.

The aggregation of A β protein is an established pathogenic mechanism in Alzheimer's disease, however little is known about the initiation of this process *in vivo*. The first set of experiments were therefore performed to characterize the induction of cerebral A β -

amyloidosis *in vivo*, and to clarify which factors are involved in the seeding process. We show that aggregation of A β can be exogenously induced in a time- and concentration-dependent manner by injecting A β -containing brain extracts from humans with Alzheimer's disease or APP23 tg mice into the brains of young APP23 tg host mice. By injecting extracts from APPPS1 tg mice into APP23 hosts and vice versa, our results suggest that characteristics of both the brain extract and the host are important in governing the phenotype of the induced amyloid. Intriguingly, intracerebral injections of synthetic fibrillar A β preparations as well as cell culture-derived A β in concentrations similar to brain extract levels were not able to seed A β aggregation *in vivo*. And yet the seeding requires an aggregated form of A β , because formic acid denaturation and A β -immunodepletion abolished the A β -inducing activity of the extract. Last but not least, we show that β -amyloid-induction is halted by A β -immunization of the host, demonstrating that the earliest stages of cerebral A β -amyloidosis deposition are amenable to therapeutic intervention.

AD presents morphologically with abundant neurofibrillary lesions, but the events that initiate tau pathogenesis *in vivo* remain unclear. Thus, the second series of experiments were performed to characterize the induction of tau pathology *in vivo*, as well as to identify potential tau-inducing candidates. We show that intracerebral injection of A β -containing brain extract from human with AD or β -amyloid-laden APP23 mouse induces neurofibrillary pathology in transgenic mice expressing human tau with the P301L mutation. Importance of soluble A β species for exogenous induction of tau pathogenesis was demonstrated by intracerebral injection of human brain extract with low A β level. Notably, intracerebral injection of brain extract from aged tangle-bearing P301L transgenic mouse induced only limited deposition of tau in brains. Our results show that neurofibrillary pathology is exogenously induced by extracts from A β -containing brains, and provide further support for the hypothesis that A β is a causative pathogenic factor of AD.

It has long been recognized that microglial cells react to β -amyloid deposition as to other brain injuries, but various aspects of their reactive kinetics and ability to phagocytose amyloid *in vivo* remain hypothetical, despite their potential as therapeutic target. To resolve these controversies, we have designed in a third series of experiments a set of robust

analysis tools centered around intracranial multiphoton imaging to characterize the time-course and extend of microglia's response to amyloid deposition in tg mice. By following individual plaques and microglia over time in the living brain, we have shown that plaque formation was accompanied by microglial process extension and subsequent migration to the site of injury where individual microglia then exhibited signs of uptake of the A β peptide. Furthermore, by infusing fluorescent A β -antibody into the brain parenchyma we demonstrated that the interaction of microglia with plaques can be stimulated, leading to further internalization of A β and at least partial clearance of existing dense deposits. Together, these results demonstrate an ongoing dynamic homeostasis between plaques and microglia that is amenable to therapeutic intervention.

In summary, the experiments described herein have increased our understanding of the mechanisms underlying the initiation of cerebral A β -amyloidosis and neurofibrillary pathology *in vivo*. We have shown that cerebral A β -amyloidosis can be induced by exogenous, A β -rich brain extract, and that intrinsic properties of the A β in the extract as well as of the host are crucial for the induction of A β accumulation in brain. We also demonstrated that neurofibrillary pathology can be induced *in vivo* by intracerebral infusion of A β -rich brain extract into a susceptible transgenic host, and that soluble A β species are potent effectors of tau pathology in the brain. Moreover, our observations that interaction of microglial cells with amyloid plaques can be stimulated, such that these cells are induced to clear existing A β deposits, provide the mechanistic clues necessary for development of additional therapeutic targets for amyloid clearance.

1.INTRODUCTION

1.1. Protein misfolding and amyloid formation in degenerative disorders

Proteins are involved in virtually every biological process in a living system. They are synthesized on ribosomes as linear chains of amino acids in a specific order from information encoded within the cellular DNA. In order to perform their biological function these chains of amino acids must fold into the native three-dimensional structures that are characteristic of the individual proteins. How and whether a protein folds is influenced primarily by its amino acid sequence and the cellular environment surrounding the amino acid chain (Anfinsen, 1973; Jackson, 1998; Baldwin and Rose, 1999; Horwich, 1999). Mutations, abnormal physiological concentrations, coupled with prolonged time and certain biochemical conditions are thought to destabilize the native three-dimensional state, or divert soluble proteins from their normal folding pathway, often leading to their aggregation into stable insoluble amyloid deposits. Numerous degenerative diseases arise due to the build up of insoluble misfolded protein deposits (Kelly, 1996; Dobson, 1999; Rochet and Lansbury, 2000; Hetz and Soto, 2003). These proteopathies include neurological disorders such as bovine spongiform encephalopathy and its human equivalent Creutzfeldt-Jakob disease, and also Alzheimer's disease, Parkinson's disease, Huntington's disease, in addition to diverse systemic amyloidosis (Carrell and Lomas, 1997; Prusiner, 1998; Rochet and Lansbury, 2000; Walker and Levine, 2000; Selkoe, 2003) (Table 1).

No sequence or structural similarities are apparent between any of the proteins that display the ability to form amyloids. Despite these differences, the fibrils formed by different polypeptides share a number of structural characteristics (Serpell et al., 1997; Sunde et al., 1997; Dobson, 2003). For example, X-ray fiber diffraction studies indicate that the peptide backbone of the fibers adopts a cross β -structure (Sunde and Blake, 1997; Blake and Serpell, 1996; Guijarro et al., 1998; Chiti et al., 1999). In this structure, the individual β -strands are oriented perpendicular to the long axis of the fiber, while the hydrogen bonds are oriented parallel with the long axis of the fiber (Blake et al., 1996; Wetzel, 2002). Amyloid fibers are also resistant to proteolysis, and display characteristic apple-green birefringence when stained with the histological dye Congo red and seen under polarized light (Sunde et al., 1997). There are also striking similarities in the aggregation behavior of many misfolded proteins, even if their propensity to aggregate can vary markedly between different sequences (Chiti et al., 2003). Amyloid fibrils are thought to form through self-assembly of protein monomers via a nucleation dependent pathway initiated in partially

	<i>Disease</i>	<i>Protein Involved</i>	
<i>Organ-limited extra cellular amyloidoses</i>	Alzheimer's disease	Amyloid β -peptide	
	Spongiform encephalopathies	Prion protein	
	Hereditary cerebral hemorrhage with amyloidosis	Amyloid β -peptide or cystatin C	
	Type II diabetes	Amylin (Islet amyloid polypeptide)	
	Medullary carcinoma of the thyroid	Procalcitonin	
	Atrial amyloidosis	Atrial natriuretic factor	
<i>Systemic extra cellular amyloidoses</i>	Primary systemic amyloidosis	Intact Ig light chains or fragments	
	Secondary systemic amyloidosis	Fragments of serum amyloid A protein	
	Familial Mediterranean fever	Fragments of serum amyloid A protein	
	Familial amyloidotic polyneuropathy I	Mutant transthyretin and fragments	
	Senile systemic amyloidosis	Wild-type transthyretin and fragments	
	Familial amyloidotic polyneuropathy II	Fragments of apolipoprotein A-I	
	Haemodialysis-related amyloidosis	2-Microglobulin	
	Finnish hereditary amyloidosis	Fragments of mutant gelsolin	
	Lysozyme amyloidosis	Full-length mutant lysozyme	
	Insulin-related amyloid	Full-length insulin	
	Fibrinogen α -chain amyloidosis	Fibrinogen α -chain variants	
		Alzheimer's disease	Amyloid β -peptide, Tau
		Frontotemporal dementia with parkinsonism	Tau
<i>Intracellular amyloidoses</i>	Parkinson's disease; dementia with Lewy bodies	α -Synuclein	
	Creutzfeldt-Jakob disease	Prion protein	
	Polyglutamine expansion diseases	Long glutamine stretches within certain proteins	
	Amyotrophic lateral sclerosis	Superoxide dismutase	

Table 1. List of diseases resulting from amyloid formation (adapted from Selkoe, 2003)

denatured states of amyloidogenic proteins (Jarret et al., 1993; Jarrett and Lansbury, 1993; Harper and Lansbury, 1997; Kelly, 1998; Kaye et al., 1999; Scherzinger et al., 1999; Wood et al., 1999; Maioli et al., 2000; Yao et al., 2003; Dobson, 2004). However, even though the formation of fibrils via a nucleation-dependent pathway seems to be generic, most of the studies to date have been done *in vitro* and may not mimic the situation in human diseases (Wetzel, 2002; Buxbaum, 2003). The nucleation-dependent polymerisation mechanism is similar to the highly ordered process of protein crystallization (Harper et al., 1997). This mechanism dictates that aggregation is dependent on protein concentration and time, and consists of an initial nucleation (or lag) phase followed by an elongation (or growth) phase and a steady state phase in which the protein aggregates and monomer are at equilibrium (Harper and Lansbury, 1997). In a typical nucleation-dependent polymerization, oligomerization is not observed until the monomer concentration exceeds a certain level known as the critical concentration. During the lag phase protein associates in a supersaturated solution to form ordered soluble oligomeric nuclei, but no detectable fibers

are formed. Addition of preformed protein nuclei during the lag time results in immediate polymerization, a process known as seeding (Harper et al., 1997). Once the oligomeric nuclei are formed, the aggregates grow rapidly (elongation phase) until a thermodynamic equilibrium between the aggregate and monomer is reached (Harper et al., 1997; Walsh et al., 1997).

Alzheimer's disease is a member of the amyloid disease group, wherein two major kinds of protein aggregates are key contributors to the pathogenesis (Hardy et al., 1998; Hardy and Selkoe, 2002). Extracellular aggregates known as neuritic plaques have their major constituent the A β peptide, which is derived from proteolytic processing of the amyloid precursor protein (APP). The A β -containing aggregates have β -sheet structure and Congo red and thioflavin-T reactivity characteristic of amyloid (Serpell and Smith, 2000). The aggregation process that converts soluble A β into amyloid fibrils *in vitro* is thought to be a nucleation-dependent process (Harper and Lansbury, 1997). In AD, there are also intracellular aggregates of the microtubule-associated protein tau, called neurofibrillary lesions. The molecular structure of tau filaments has been controversial but there is consensus now that tau fibrils in AD fit the amyloidosis definition (Berriman et al., 2003). Kinetics data support the view that tau fiber may also form via a nucleation-dependent mechanism, tau oligomerization and nucleation events being the rate-limiting step in filament formation (Friedhoff et al., 1998; King et al., 1999). Nevertheless, the major caveat remains that we have yet to learn how these aggregational events begin *in vivo* and how their development lead to the progressive behavioral and cognitive demise that characterizes the human disease.

1.2. Alzheimer's disease

Alzheimer's disease (AD) is a neurodegenerative disease characterized by progressive cognitive deterioration together with declining activities of daily living and neuropsychiatric symptoms or behavioral changes. The symptoms of the disease as a distinct entity were first identified by Emil Kraepelin, and the characteristic neuropathology first observed by Alois Alzheimer, a German psychiatrist, in 1906.

1.2.1. Clinical symptoms and diagnosis

Alzheimer's original patient (Alzheimer, 1907) exemplified several cardinal features of the disorder that we still observe in most patients nowadays. One of the first noticeable symptoms is short-term memory loss, which usually manifests as minor forgetfulness that becomes more pronounced with illness progression, with relative preservation of older memories (Morris et al., 1989; Petersen et al., 1999). It is difficult to distinguish these earliest disease-related cognitive changes of AD from those associated with normal aging (Small, 2001; Collie et al., 2001; Morris et al., 2001). As the disorder progresses, cognitive impairment extends to the domains of language, skilled movements, recognition, and executive functions (Morris et al., 1989; Morris, 1996). As subjects continue to lose ground cognitively, slowing of motor functions such as gait and coordination often lead to a picture resembling extrapyramidal motor disorders (Selkoe, 2001). In the final stages, patients become immobile and die of respiratory difficulties such as pneumonia (Fotstl and Kurz, 1999). Average duration of the disease is approximately 7-10 years, although cases are known where reaching the final stage occurs within 4-5 years, or up to 15-20 years (Fotstl and Kurz, 1999).

Although definitive diagnosis requires a postmortem neuropathological examination, neurologists and neuropsychologists have now developed clinical criteria that often lead to ~90% accuracy in diagnosing AD. To make the diagnosis of AD and to exclude other causes of dementia, clinicians rely on histories from patients and informants; physical, neurological, and psychiatric examinations; neuropsychological testing; laboratory assessments; and a variety of other diagnostic tests including neuroimaging (Clark and Karlawish, 2003). Biochemical changes that reflect the presence of disease-related pathology also have the potential to serve as diagnostic biomarkers of Alzheimer disease (Growdon, 1999). To date, the most extensively studied biochemical markers are the cerebrospinal fluid proteins tau and β -amyloid (Andreasen et al., 2001; Knopman, 2001). Both are particularly relevant to the pathology of Alzheimer disease and thus may provide diagnostically useful information.

1.2.2. Neuropathological phenotype

The classical pathophysiology of AD includes extensive neuronal degeneration and synapse loss resulting in marked atrophy of brain regions critical for learning and memory (Fig. 1, A), together with an inflammatory response to the deposition of senile plaques and neurofibrillary lesions (Fig. 1, B and C, respectively) (Terry et al., 1991; West et al., 1994; Gomez-Isla et al., 1996, Selkoe, 2001). The interaction between amyloid plaques, neurofibrillary tangles, their constituent molecules and the neuronal and synaptic losses that characterize the disease has been the subject of speculations for many years and still remains an unresolved issue.

1.2.2.1. β -amyloid plaques and the $A\beta$ centric theory of Alzheimer's

Neuritic or senile plaques are one of the histopathological hallmarks of AD. Senile plaques are extracellular deposits primarily composed of β -amyloid ($A\beta$) protein that are surrounded by dystrophic axons as well as the processes of astrocytes and microglia (Arai et al., 1990, 1992; Schmidt et al., 1991; Masliah et al., 1992; Trojanowski et al., 1993; Dickson, 1997; Selkoe, 1999, 2001; Masters et al., 2006). In addition and at least to some

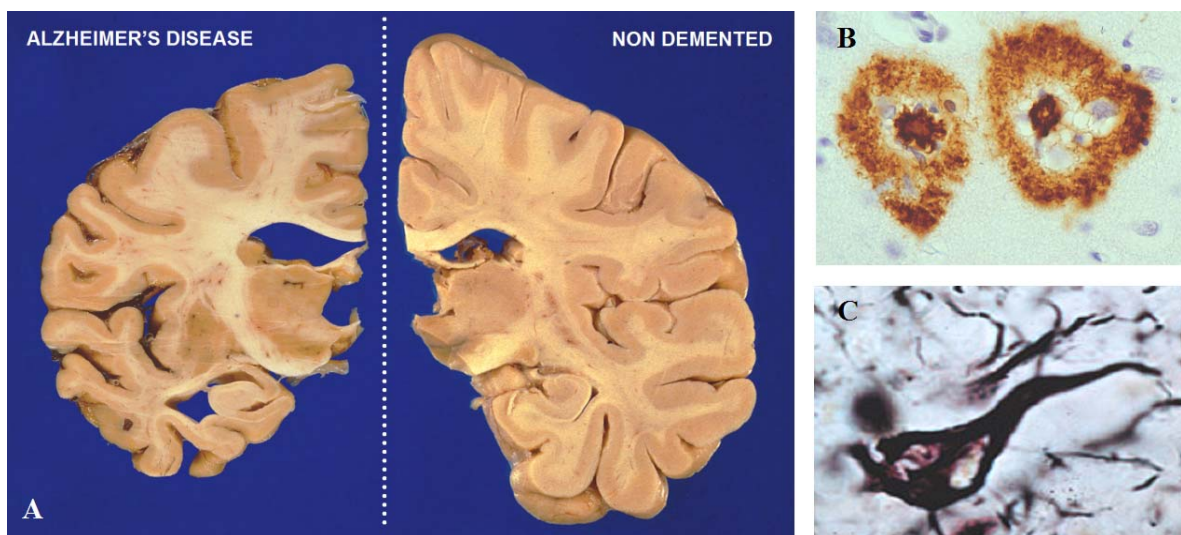


Figure 1. The neuropathological hallmarks of AD. Characteristic pathophysiological changes include loss of neurons, neuronal processes and synapses in the cerebral cortex and certain subcortical regions. These changes are associated with gross atrophy of the affected regions and enlargement of the lateral ventricles (A). Histological stainings of senile plaques (B) and neurofibrillary tangles (C) in an AD brain.

degree, A β deposits are also apparent within the walls of leptomeningeal and cerebral vessels (Selkoe et al., 1987; Vinters, 1987; Yamada et al., 1987; Martin et al., 1991; Jellinger, 2002). The evolution of A β deposits in the brain follows a distinct sequence in which the regions are hierarchically involved (Thal et al., 2002). The first phase is the neocortical phase 1, followed by the allocortical phase 2. In phase 3, the diencephalic nuclei, the striatum and the cholinergic nuclei of the basal forebrain develop A β deposits, and in phase 4 several brainstem nuclei become additionally involved. Finally, phase 5 is characterized by cerebellar A β deposition.

The principal constituent of plaques is A β (Glennner and Wong, 1984; Masters et al., 1985; Selkoe et al., 1986), a 4 kDA protein fragment of 39-43 amino acids which is formed after sequential cleavage of the amyloid precursor protein (APP) by the β - and γ -secretases (see section 1.2.3.) (Cappai and White, 1999; Selkoe, 2001). Much of the fibrillar A β found in the neuritic plaques is the species ending at amino acid 42 (A β 42), the slightly longer, less soluble form that is particularly prone to aggregation (Jarrett et al., 1993b; Harper et al., 1997c). However, the A β species ending at amino acid 40 (A β 40), which is normally more abundantly produced by cells than A β 42, is usually colocalized with A β 42 in the plaque (Iwatsubo et al., 1994). Within amyloid deposits and immediately surrounding them, neurites are marked by ultrastructural abnormalities that include enlarged lysosomes, numerous mitochondria, and paired helical filaments (PHFs) (Arai et al., 1990; Schmidt et al., 1991; Masliah et al., 1992; Trojanowski et al., 1993; Dickson, 1997; Selkoe, 2001). Senile plaques are also surrounded by reactive astrocytes displaying abundant glial filaments, and are also intimately associated with microglia expressing surface antigens associated with activation, such as CD45 and HLA-DR (Itagaki et al., 1989; McGeer and McGeer, 1995; Rogers et al., 1996). Microglia represent the macrophage-derived cells in the nervous system that are capable of responding rapidly to various types of insults (Nimmerjahn et al., 2005; Davalos et al., 2005). Thus, these cells represent reasonable candidates for early cellular respondents of β -amyloid deposition. Nevertheless, microglia and astrocytes are also involved in the overproduction and release of various inflammatory mediators, leading to profound inflammatory disturbance in limbic and association cortices observed in AD (Abraham et al. 1988; Griffin et al., 1989; Rogers et al., 1992; Itagaki et al., 1994).

Many of the plaques found in limbic and association cortices but also thalamus, caudate, putamen, and cerebellum, show relatively light, amorphous A β immunoreactivity that occurs without a compacted fibrillar center (Yamaguchi et al., 1988; Joachim et al., 1989). These lesions that are referred to as “diffuse” plaques, contain mainly A β 42 species with little or no A β 40 (Gowing et al., 1994; Iwatsubo et al., 1994, 1995; Lemere et al., 1996) and lack neuritic dystrophy, glial changes and PHFs (Selkoe, 1991; Dickson, 1997; Selkoe, 2001). In contrast to the A β deposited in compact senile plaques, diffuse deposits are not detected with Congo red or other dyes, such as Thioflavin S, that bind amyloid. Moreover, they are also observed in normal ageing individuals, but the density is lower than in AD patients (Perry et al., 1978). It has been suggested that diffuse plaques may represent precursors to the classical neuritic plaques (Tagliavini et al., 1988; Yamaguchi et al., 1988; Iwatsubo et al., 1996; Lemere et al., 1996; Masters et al., 2006). This hypothesis is best illustrated by studies of Down's syndrome. Here, patients have little or no A β deposition in the first decade of life, but by around 12 years, one begins to see diffuse plaques containing A β 42 (not A β 40), and more and more Down's subjects develop such plaques during the second and third decade of life (Lemere et al., 1996). Then, after the age of 30 years, one begins to see amyloid fibril formation in plaques and there is associated microgliosis, astrocytosis and some neuritic dystrophy. These neuritic plaques become then more prevalent over the next 2 decades of life. A model for the deposition of A β in amyloid plaques consistent with the view that diffuse plaques represent immature precursors to the plaques with surrounding cytopathology is illustrated in the Figure 2.

It has been more than 15 years since it was first proposed that the neurodegeneration in Alzheimer's disease (AD) may be caused by deposition of A β peptide in plaques (the amyloid cascade hypothesis) (Hardy and Allsop, 1991). According to this hypothesis, accumulation of A β fibrils in the brain is the primary influence driving AD pathogenesis. The rest of the disease process, including formation of neurofibrillary lesions containing tau protein, microgliosis, synaptic dysfunction and neuronal loss is proposed to result from an imbalance between A β production and A β clearance. The pathogenic role of β -amyloid deposition in AD is underscored by the evidence that each of the disease-causing mutations in familial AD results in enhanced production of amyloidogenic A β peptides (Hardy and Selkoe, 2002). Although the large A β aggregates present in plaques were initially regarded as the culprits responsible for neurodegeneration, the distribution and density of both

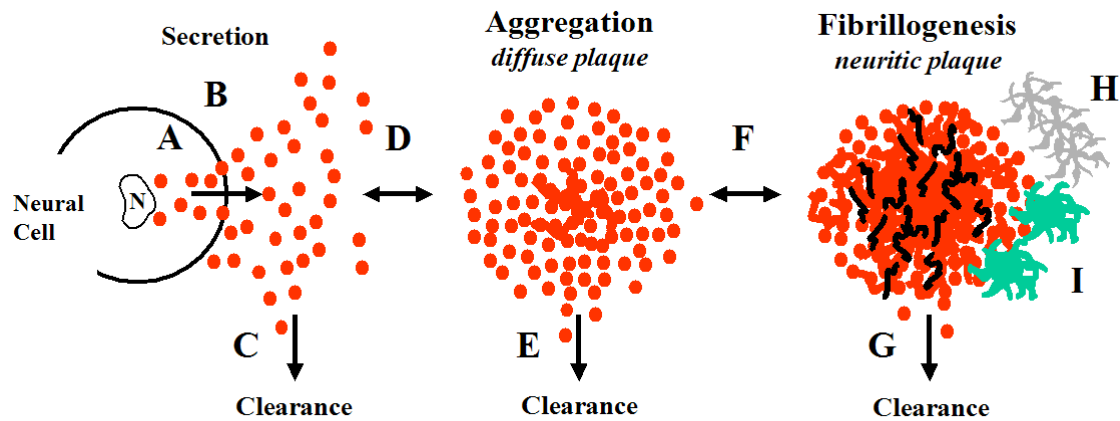


Figure 2. Hypothetical mechanism for the deposition of A β in amyloid plaques. Soluble A β peptides (depicted by the red filled circles) are produced in neurons (N=nucleus of a cell) and secreted (A) into the extracellular space (B) from whence they are cleared in the brains of normal young individuals (C). With advancing age, soluble A β aggregates into diffuse plaques (closely packed filled circles to the right of the D). Some aggregated soluble A β also may be cleared from these plaques (E). In AD, soluble A β in diffuse plaques may be induced to form fibrillar A β aggregates that lead to the formation of mature senile plaques (to the right of the F) which accumulate many additional components including more soluble A β , PHFs (curvilinear black profiles), in addition to microglial cells (I) and reactive astrocytes (H). Nonfibrillar or soluble A β might be cleared from senile plaques (G), but the continued presence of factors that induce the fibrillogenesis and insolubility of soluble A β would favour the persistence of amyloid in the AD brain.

diffuse and senile plaques at the light microscopic level have not been consistently shown to correlate well with the degree of cognitive impairment that the patient experienced in life (Terry, 1991; Berg et al., 1998; Hardy et al., 1998; McLean et al., 1999; Wang et al., 1999). Moreover, abundant cortical A β deposits may also be found in cognitively intact elderly subjects (Dickson et al., 1991; Arriagada et al., 1992). The best correlation with the degree of dementia occurs with soluble levels of A β , measured biochemically (Lue et al., 1999; McLean et al., 1999; Wang et al., 1999; Naslund et al., 2000). In accordance with these observations, several lines of evidence have recently converged to demonstrate that soluble oligomeric assemblies of A β , but not insoluble amyloid fibrils, may be responsible for the loss of neurons and synaptic dysfunction observed in AD (Klein et al., 2001; Kirkitadze et al., 2002; Selkoe, 2002). Importantly, such oligomeric forms of A β have been shown to be neurotoxic both *in vitro* and *in vivo* (Oda et al., 1995; Walsh et al., 1997; Lambert et al., 1998; Hartley et al., 1999; Walsh et al., 1999; Nilsberth et al., 2001, Walsh et al., 2002) and to inhibit long-term potentiation (Walsh et al., 2002). These evidence supports a revision of the amyloid cascade hypothesis such that A β assembly into neurotoxic oligomers, and not into amyloid fibrils, is the seminal event in AD pathogenesis (Klein et al., 2001, 2004;

Kirkitadze et al., 2002; Walsh et al., 2002b). It might well be that fibrillar amyloid acts as a reservoir for the soluble oligomers, or represent the sequestered pool of soluble and now precipitated A β , therefore fulfilling a protective function, or just the end stage of the A β cascade (Masters et al., 2006).

1.2.2.2. Neurofibrillary lesions

The second histopathological hallmark of AD is the neurofibrillary lesions (NFLs). NFLs are intracellular filamentous deposits largely composed of microtubule-associated protein tau in a hyperphosphorylated and abnormally phosphorylated state (Brion et al., 1985; Grundke-Iqbal et al., 1986; Nukina and Ihara, 1986; Wood et al., 1986; Kosik et al., 1988; Goedert, 1993; Lee, 1995; Morishima-Kawashima et al., 1995). There are three main types of NFLs according to their localizations in nerve cells: (i) neurofibrillary tangles (NFTs) in the cell body and apical dendrites of neurons, (ii) neuropil threads (NTs) in distal dendrites and (iii) dystrophic neurites associated with neuritic plaques (Tolnay and Probst, 1999). Ultrastructurally, NFLs contain bundles of abnormal fibers that consist of pairs of ~10nm filaments wound into helices (paired helical filaments or PHFs) as a major fibrous component and straight, 10- to 15-nm filaments (or SFs) as a minor component (Selkoe, 2001). Most of these filaments are highly insoluble and resistant to detergent such as sodium dodecyl sulfate (Selkoe et al., 1982). Tau proteins are the major, if not the sole, building block of PHFs in the major NFLs of the AD brain. However, immunohistochemical studies have demonstrated that PHFs also contain neurofilament proteins (Anderton et al., 1982; Perry et al., 1985; Sternberger et al., 1985; Miller et al., 1986), actin (Vogelsang et al., 1988), ubiquitin (Mori et al., 1987; Perry et al., 1987), MAP2 (Yen et al., 1987) and A β protein (Kidd et al., 1985; Masters et al., 1985). Although very poorly documented, the appearance and development of NFLs is associated with an inflammatory response, indicated by a progressive microglial and astrocytic reaction to tau deposition (Perlmutter et al., 1992; Sheng et al., 1997).

The manner in which neurofibrillary pathology spreads to various brain areas during the course of AD is not random but follows a stereotyped pattern which has been used to define six neuropathological stages, the Braak stages (Braak and Braak, 1991). On the basis of cross-sectional analysis of unselected cases coming to post-mortem, Braak and Braak have

reported that neurofibrillary tangles are first observed in the transentorhinal and entorhinal cortex (stages I and II or transentorhinal stages). A more extensive involvement of the entorhinal cortex and the formation of NFTs in sector CA1 (Cornu Ammonis 1) of the hippocampus correspond to stages III and IV or to limbic stages. Pathology then spreads into sectors CA2, 3 and 4 of the hippocampus, the subiculum, and into isocortical areas, particularly the temporal and parietal cortices (Stage V). The final stage VI is characterized by more extensive spread in neocortical areas, with relative sparing of primary motor and sensory areas. There is a close correlation between the burden of NFTs and the degree of dementia in AD, at least in some cortical and subcortical regions (Bondareff et al., 1989; Arriagada et al., 1992; Holzer et al., 1994; Bierer et al., 1995). At Braak stages I and II, patients are cognitively unimpaired whereas subjects with limbic stages III and IV usually present with mild cognitive impairment. Subjects with stages V and VI are severely demented and meet the neuropathological tau criteria for the diagnosis of AD.

Morphologically, three main subtypes of NFTs can be distinguished, corresponding to different evolutionary stages of this lesion (Tolnay and Probst, 1999). The earliest stage, also termed pretangle stage, is characterized by the accumulation of hyperphosphorylated tau protein in the somatodendritic domain of affected neurons without formation of PHFs and SFs (Baner et al., 1989; Braak et al., 1994). Therefore pretangle neurons are only detectable with anti-tau antibodies in contrast to the later stage of classical NFT formation wherein tau aggregates are identified with silver staining techniques such as Bielschowsky and Gallyas stains. The third stage of NFT formation corresponds to extracellular NFTs or “ghost” tangles (Tolnay and Probst, 1999; Baner et al., 1989). It has been proposed that the release of NFTs from dying neurons could result in interactions between aggregated tau and the soluble A β normally secreted by neurons or other brain cells (Seubert et al., 1992; Shoji et al., 1992; Wertkin et al., 1993; Trojanowski et al., 1993; Trojanowski and Lee, 1994). Thus, the chronic but progressive degeneration of neurons in the AD brain may release NFTs into the extracellular space, which then are able to recruit or immobilize soluble A β into deposits. These same neuronal debris also may play a role in inducing aggregated A β to undergo fibrillogenesis and the formation of neuritic amyloid plaques (Shin et al., 1993, 1994). These data intersect well with the work of Braak and Braak (1991) who stated that initial NFTs predate morphologically detectable amyloid plaques. However, as Hardy and Selkoe (2002) point out, the postmortem cases used to establish the Braak stage I neuropathology criteria were non-demented older individuals, in whom it is

impossible to conclude that they would all have developed AD if they had survived longer. Second, the Braak analysis cannot exclude a toxic effect of any soluble oligomeric forms of A β that have not yet reached the stage of microscopically visible amyloid plaques. Moreover, in patients with the rare presenilin 1 mutations or individuals with Down's syndrome who died prematurely from other diseases, the presence of A β (either as diffuse deposits or typical plaques) precedes the appearance of neurofibrillary tangles (Lemere et al., 1996; Lippa et al., 1998).

PHFs resembling those of AD have been assembled from recombinant tau *in vitro*. This process is usually very slow (days or weeks), corresponding to the highly soluble nature of tau. Several principles have emerged from these *in vitro* studies over the past few years; the repeat domain of tau is important for PHF aggregation (Wille et al., 1992; Wilson and Binder, 1995; DeTure et al., 1996); aggregation is strongly enhanced by oxidation (Wille et al., 1992; Schweers et al., 1995) or in the presence of polyanions such as heparin, ribonucleic acids, or acidic peptides (Perez et al., 1996; Goedert et al., 1996; Kampers et al., 1996); mutations of tau found in hereditary frontotemporal dementia and parkinsonism linked to chromosome 17 (FTDP-17) favor tau aggregation and PHF formation (Barghorn et al., 2000; Goedert et al., 1999; Gamblin et al., 2000; Hong et al., 1998). The reasons for this may be heterogeneous, depending on the type of mutation but at least in the cases of P301L they can be traced back to an enhanced propensity for β -structure, a feature common to many pathological amyloids (Fraser et al., 1994; Pike et al., 1995; Lansbury, 1997). In AD, PHF formation is not due to mutations in the tau gene but rather to some cellular cascade triggered by A β that results in abnormal phosphorylation of tau proteins that causes them to assemble into filaments. This statement intersects well with the observation that A β in the vicinity of neurons enhanced tau phosphorylation *in vitro* and *in vivo* (Busciglio et al., 1995; Geula et al., 1998). This is further supported in a recent article showing that double transgenic mice expressing mutant human tau (P301L) and mutant APP developed enhanced neurofibrillary pathology and degeneration in cortical and subcortical brain regions (Lewis et al., 2001). Moreover, recent work has indicated that direct intracranial injection of synthetic A β peptide increases tau phosphorylation and NFT formation in transgenic mice expressing the P301L tau mutant (Gotz et al., 2001). Although the molecular mechanism by which the extracellular accumulation of A β peptides promotes the intracellular assembly of pathologic tau filaments *in vivo* remains poorly understood, a

mechanistic link between the two is emerging. Exposure of primary neurons to A β activates the tau kinase GSK3 β (glycogen synthase kinase β), increases tau phosphorylation, and leads to cell death (Takashima et al., 1998; Zheng et al., 2002). The tau kinase cdk5 (cyclin-dependent kinase 5) is also activated by A β in cultured neurons and in AD (Dhavan and Tsai, 2001). The activity of the cdk5 kinase is regulated by a 35-kDa myristoylated membrane-attached protein, p35 (Zheng et al., 2002b). When p35 undergoes calpain-mediated cleavage to p25, kinase activity is greatly enhanced. The cdk5/p25 complex appears to be delocalized from the plasma membrane, leading to nonphysiologic phosphorylation of tau, its dissociation from microtubules and self-assembly into insoluble filaments (Michealis, 2002).

1.2.3. Epidemiology and genetics of Alzheimer's disease

AD is the most common cause of dementia (Table 2) and affects approximately 7% of people older than 65 and perhaps 40% of people over the age of 80 (McKhann et al., 1984; Evans et al., 1989; Rocca et al., 1991; Ebly et al., 1994; Lautenschlager et al., 1996; Lobo et al., 2000). Because of increased life expectancy and the post-World War II baby boom, the elderly is the fastest growing segment of our society (Olshansky, 1993). More than twelve million people worldwide now suffer from AD, a striking figure that is predicted to almost triple by 2050 (Hebert et al., 2003). Thus, AD is one of society's major public health problems.

The vast majority of AD cases are sporadic and occur late in life with no clearly defined etiology. However, genetic factors are known to be important and, in fact, after age, family history is the second greatest risk factor for AD (Selkoe, 1999). Autosomal dominant mutations in three different genes (amyloid precursor protein, presenilin 1 and presenilin 2) have been identified that account for a small number of cases of familial, early-onset AD (FAD) (Schellenberg, 1995; Kim and Tanzi, 1997). The first genetic mutation associated with FAD was in the APP gene. Suspicion of the involvement of APP in FAD arose since the gene resides on chromosome 21 (Kang et al., 1987) and people with Down's syndrome (who have an extra copy of chromosome 21) develop neuropathological attributes of AD by age 40 (Wisniewski et al., 1985). Genetic linkage studies also suggested the involvement of a locus near the APP gene on chromosome 21 in FAD (Tanzi et al., 1987; Goate et al.,

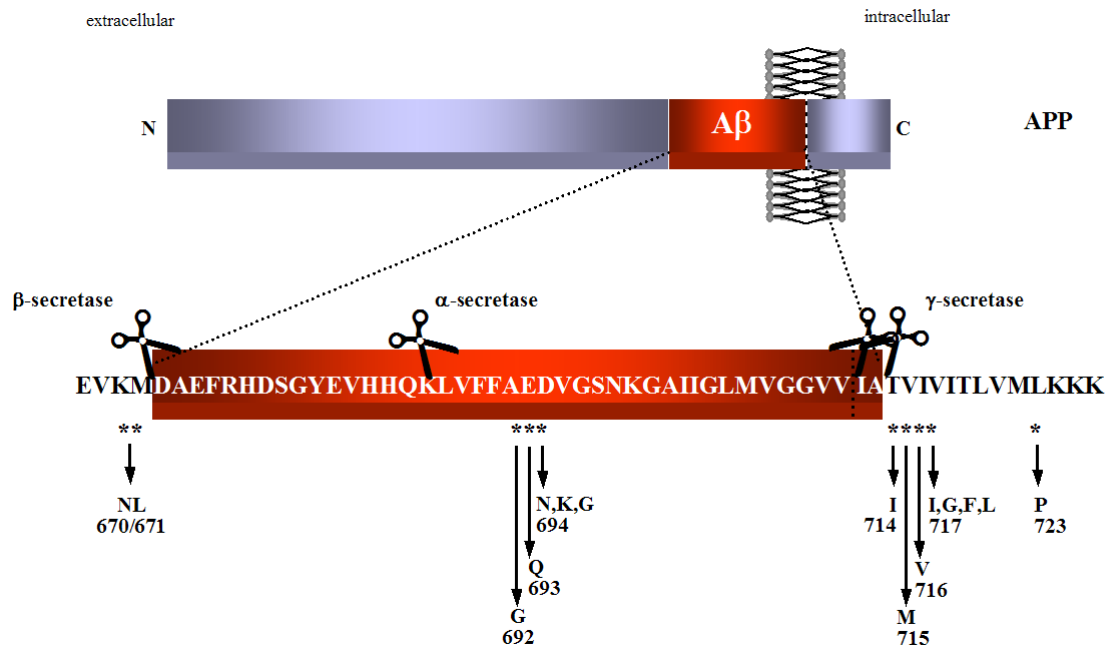


Figure 3. Structure of the β-amyloid precursor protein (APP, in blue), the β-amyloid (Aβ, in red), and missense mutations located within APP. APP is proteolytically cleaved by sequential actions of α-, β-, and γ-secretases (indicated by the scissors). The location of APP mutations associated with early-onset familial AD (FAD) and/or cerebrovascular pathology are marked by asterisks and the amino acid substitutions are indicated.

1989). In 1991 the first genetic linkages of AD were identified as missense mutations in the APP gene located on chromosome 21 (Naruse et al., 1991; Goate et al., 1991). Since then, more than 20 pathological mutations in APP have been identified (Figure 6). Most of these are near the proteolytic cleavage sites involved in Aβ production (Goate et al., 1991; Hendriks et al., 1992; Mullan et al., 1992; Ghiso and Frangione, 2002). Mutations in APP do not account for all cases of FAD. In the mid 1990s, further genetic linkage studies uncovered mutations in presenilin 1 on chromosome 14 (St George-Hyslop et al., 1992; Sherrington et al., 1995) and presenilin 2 on chromosome 1 (Levy-Lahad et al., 1995; Rogaev et al., 1995). Presenilin forms the active site of the γ-secretase complex involved in the production of Aβ (De Strooper, 2003). To date there are more than 120 different mutations identified in the PS1 gene, while only 8 missense mutations have been identified in PS2. FAD mutations in PS1, PS2 and APP result in overproduction of total Aβ and/or lead to an increase of secreted Aβ₄₂, the primary component of β-amyloid plaques in the brain (Tamaoka et al., 1994; Hardy, 1997; Price and Sisodia, 1998; Selkoe, 1999; Haass and DeStrooper, 1999).

In addition to the mutations that have been associated with early-onset FAD, other genetic factors have been identified that increase the risk of developing sporadic AD. These include the $\epsilon 4$ allele of the apolipoprotein E (ApoE) gene (Strittmatter et al., 1993) on chromosome 19 (Olaisen et al., 1982), the proteinase inhibitor $\alpha 2$ -macroglobulin gene (Blacker et al., 1998) on chromosome 12 (Pericak-Vance et al., 1997), insulin degrading enzyme gene on chromosome 10 (Vekrellis et al., 2000), low density lipoprotein receptor-related protein (Olson, 1998) or angiotensin converting enzyme (Kehoe et al., 1999).

At present, no mutations in the tau gene have been identified in AD. Nevertheless, several mutations in human tau on chromosome 17 result in a cluster of neurodegenerative diseases, termed FTDP-17, that are characterized by the accumulation of neurofibrillary tangles in affected brain regions (Hutton et al., 1998; Poorkaj et al., 1998; Spillantini et al., 1998). They include missense mutations in coding regions of the tau gene in exons 9, 10, 12 and 13, silent mutations as well as a deletion mutation in exon 10, and intronic mutations located close to the splice-donor site of the intron following exon 10. These pathogenic mutations either reduce the ability of tau to bind to microtubules or alter the splicing of exon 10 resulting in increased 4 repeat tau isoforms (Hutton et al., 1998). To date more than 20 different tau gene mutations have been identified in a large number of FTDP-17 families. The identification of these mutations provided direct evidence that tau dysfunction per se is sufficient to cause neurodegeneration (Hutton et al., 1998; Poorkaj et al., 1998; Spillantini et al., 1998; Clark et al., 1998), presumably due to failure of the self-assembled tau to regulate the microtubule dynamics essential for cell survival (Lee et al., 2001). Notably, the exact form of tau which causes neuronal degeneration is now being re-examined (Duff and Planel, 2005), with data emerging that the soluble aggregated species, akin to soluble A β oligomers, might represent the best target.

1.2.4. Origin of A β proteins: cell biology of APP

APP is a type-I integral transmembrane glycoprotein that is ubiquitously expressed, and is encoded by a gene located on chromosome 21 (Masters et al., 1985). Alternative splicing of the APP gene gives rise to at least three transcripts that encode proteins of 695, 751 and 770 amino acids (Hardy, 1997; Selkoe, 1999). The two longer isoforms contain a motif which is homologous to the Kunitz-type of serine protease inhibitors (KPI) (Kitaguchi et al., 1988;

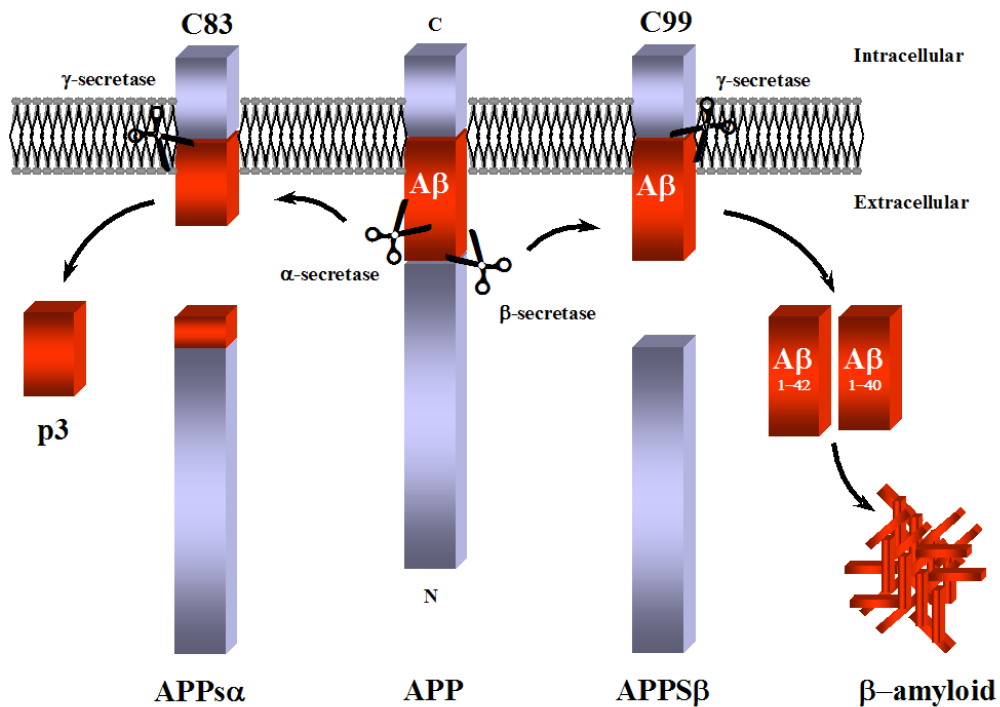


Figure 4. Pathways processing the APP by α -, β - and γ -secretases. Cleavage by α -secretase does not result in A β production but in release of soluble APPs α and retention of a 83-residue C-terminal peptide (C83). Cleavage by β -secretase produces soluble APPs β and a 99-residue C-terminal (C99). Both C83 and C99 are substrates for γ -secretase that yields a 3-kD peptide called p3 from cleavage of C83, and A β from cleavage of C99.

Ponte et al., 1988; Tanzi et al., 1988), whereas the shorter form of 695 amino acids lacks this 56-residue Kunitz domain (Golde et al., 1990). All of the APP isoforms contain the 39-43 amino acids long A β domain. The shorter form of 695 amino acids is the main isoform expressed in neurons (Golde et al., 1990). At present the physiological function of APP in the brain remains unclear, although it has been proposed to have functions in transmembrane signal transduction (Nishimoto et al., 1993), cell proliferation and adhesion (Saitoh et al., 1989), calcium regulation (Mattson et al., 1993) and neurite outgrowth (Milward et al., 1992).

A characteristic feature of APP is its proteolytic cleavage by the α -, β - and γ -secretases (Figure 4) (Selkoe, 2001). The differential actions of these secretases lead either to the non-amyloidogenic or amyloidogenic pathway. α -secretase cleaves APP within the A β region to produce the soluble α -APPs and the 83-residue COOH-terminal fragment C83 (Esch et al., 1990; Sisodia et al., 1990). The α -cleavage pathway is considered as default, non-amyloidogenic pathway. The β -secretase (or BACE for β -site APP-cleaving enzyme)

cleavage corresponds to the alternative, amyloidogenic pathway, that produces a 99-residue COOH-terminal fragment C99 and the soluble β -APPs (Sinha et al., 1999; Vassar, 1999). Both the C83 and C99 fragments remain anchored in the membrane where they are processed by γ -secretase to produce p3 from C83 or A β from C99. γ -secretase cleavage is not sequence specific resulting in A β peptides of varying length (Selkoe, 2001).

1.2.5. Human tau gene and protein isoforms

Tau proteins belong to the microtubule-associated proteins family (MAP) and are abundant in both central and peripheral nervous system neurons, although reports have suggested that tau can be expressed in other cell types (Weingarten et al., 1975; Schoenfeld and Obar, 1994; Tucker, 1990; LoPresti et al., 1995; Wakabayashi et al., 2006). As part of the cytoskeleton, tau proteins bind to microtubules and function to stabilize microtubules in the polymerized state as well to facilitate the polymerization of tubulin subunits (Drechsel et al., 1992; Cassimeris, 1993; Ludin and Matus, 1993; Goode and Feinstein, 1994). The human tau gene is located on the chromosome 17 (Neve et al., 1986) and contains 16 exons (Figure 5, A) with the major tau protein isoforms being encoded by 11 of them (Andreadis et al., 1992; Buee et al., 2000). Through alternative messenger RNA splicing of exons 2, 3 and 10 (Figure 5, B) a set of six isoforms ranging from 352 to 441 amino-acids are generated in adult human brain (Figure 5, C) (Himmler et al., 1989; Kosik, 1989). Exons 9-13 encode four microtubule-binding motifs which are imperfect repeats of 31 or 32 amino acids in the carboxy terminal half of the tau molecule. The alternative splicing of exon 10 thus generates tau protein isoforms with either three (3R) or four (4R) microtubule-binding repeats. Further, the 6 isoforms differ by alternative splicing of exons 2 and 3 resulting in the absence (0N) or presence of one (1N) or two (2N) 29 amino acid inserts in the amino-terminal half of the tau molecule. Thus, alternative splicing of exons 2, 3 and 10 allows for six combinations: the longest 441-amino acids (4R2N), 410-amino acids (3R2N), 412-amino acids (4R1N), 381-amino acids (3R1N), 393-amino-acids component (4R0N) and the shortest 352-amino acids isoform (3R0N). Each of these isoforms is likely to have particular physiological roles since they are differentially expressed during development (Kosik et al., 1989). Also, the degree of phosphorylation is developmentally regulated. Thus, tau from fetal brain is phosphorylated at more sites than tau from adult brain (Buee et al., 2000).

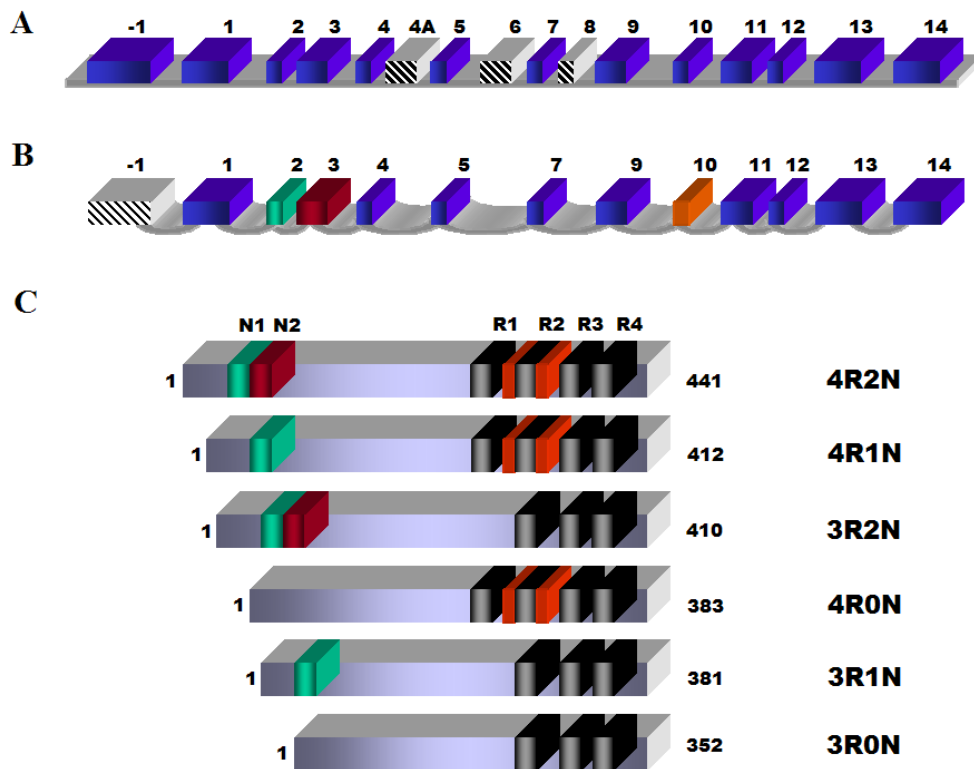


Figure 5. Schematic representation of the human tau gene (A), the tau primary transcript (B) and the six tau isoforms (C). The human tau gene is located on the long arm of the chromosome 17 at position 17q21 and contains 16 exons, with exon -1 is a part of the promoter. (B) The Tau primary transcript contains 13 exons, since exons 4A, 6 and 8 are not transcribed in human. (C) Through alternative messenger RNA splicing of exons 2, 3 and 10 a set of six isoforms ranging from 352 to 441 amino-acids are generated in adult human brain. The six tau isoforms differ by the absence or presence of one or two 29 amino acids inserts encoded by exon 2 (green box) and 3 (dark red boxes) in the amino-terminal part, in combination with either three or four repeat-regions (black boxes) in the carboxy-terminal part. The fourth microtubule-binding domain is encoded by exon 10 (orange box).

Tau proteins contain two functional domains (Buée et al., 2000). The amino-terminal part of tau proteins, referred to as projection domain, interacts with cytoskeletal elements to determine spacings between microtubules in axons (Brandt et al., 1995; Hirokawa et al., 1988). The amino-terminal part is also involved in signal transduction pathways by interacting with proteins as phospholipase C- γ (Hwang et al., 1996). The carboxy-terminal part, referred to as microtubules binding domain, regulates the rate of microtubules polymerization (Butner and Kirschner, 1991; Goedert and Jakes, 1990). It is also involved in the binding with functional proteins as protein phosphatase 2A (Sontag et al., 1999) or presenilin-1 (Takashima et al., 1998).

1.2.6. Transgenic mouse models of Alzheimer's disease

The identification and sequencing of APP and PS genes has provided new opportunities to explore pathogenic mechanisms and treatments of AD using genetically engineered mice. Multiple lines of transgenic mice expressing mutated human APP now exist that develop age-dependent cerebral A β -amyloidosis concomitantly with additional AD-like pathologies such as memory deficits, gliosis, regional neuronal loss, cerebral amyloid angiopathy and dystrophic neurites (Games et al., 1995; Hsiao et al., 1996; Sturchler-Pierrat et al., 1997; Calhoun et al., 1998; Stalder et al., 1999; Moechars et al., 1999; Bronfman et al., 2000; Kumar-Singh et al., 2000; Van Dorpe et al., 2000; Bondolfi et al., 2002; Kelly et al., 2003). In addition to mice expressing mutations in the APP gene, mouse models bearing PS mutations have been generated (Duff et al., 1996; Citron et al., 1997). Except for increased production of A β 42/43, no pathological phenotype could be observed. Other models combine the insertion of mutated APP with an insertion of mutated PS1 that lead to accelerated amyloid plaque deposition (Figure 7) (Borchelt et al., 1996, 1997; Holcomb et al., 1998; Lamb et al., 1999; Chishti et al., 2001; Gordon et al., 2002). Several of these A β depositing mouse models develop hyperphosphorylated tau-positive structures around plaques but all of them consistently fail to show intracellular filamentous deposits of tau protein, which are an essential hallmark of AD. The difference in tau sequence between mouse and humans may explain why despite the progressive and severe A β deposition there are no neurofibrillary tangles and very little neuronal loss in these APP models (Hsiao, 1996; Irizarry et al., 1997).

As APP transgenic models failed to develop insoluble tau aggregates, tau transgenic mice have been developed. The first transgenic tau models expressing wild-type human tau were generated before pathogenic tau mutations had been identified (Gotz et al., 1995; Brion et al., 1999; Spittaels et al., 1999; Probst et al., 2000). Overexpressing the 3 or 4 repeat wild-type human tau in these models resulted in hyperphosphorylation of tau and somatodendritic localization; however, none of these transgenic mice developed neurofibrillary tangles. The discovery of mutations in the tau gene in FTDP-17 has provided the basis for the generation of transgenic mouse models that exhibit age-related filamentous tau deposits through expression of mutant human tau protein (Lewis et al., 2000; Gotz et al., 2001; Hutton et al., 2001). Among others models, Lewis and al. (2000) developed transgenic mice expressing the shortest 4 repeat (4R0N) tau with the P301L

mutation under control of the mouse prion promoter. These mice developed motor and behavioural deficits accompanied by age- and gene dose-dependent accumulation of neurofibrillary tangles (Figure 8) in both brain and spinal cord, with associated neurodegeneration and reactive gliosis (Lewis et al., 2000). Using a transgenic line expressing the longest 4 repeat (4R2N) tau with the same mutation under the mouse Thy1.2 promoter, Götz et al. (2001) reported quite similar results. A recent study also showed a correlation between the number of NFT and decline in performance on the Morris water maze in transgenic mice expressing the P301L mutation, indicating a detrimental effect of NFT on memory (Arendash et al., 2004). The FTDP-17-associated mutation P301S has also been used to make mouse models. P301S mutant tau expressed under the mouse Thy1.2 promoter caused tau hyperphosphorylation and formation of tau filaments in affected brain regions. FTDP-17 mutations V337M (Tanemura et al., 2001, 2002) and G272V (Götz et al., 2001) also were expressed in transgenic mice. Neurofibrillary lesions and associated neurodegeneration were found in neurons of V337M mutant mice (Tanemura et al., 2002), while G272V mutant mice developed prominent oligodendroglial tau filament formation (Götz et al., 2001). None of these tau depositing mouse models developed deposits of amyloid- β protein, suggesting that the neurofibrillary tangles in AD are secondary to A β production (Hardy et al., 1998) and probably triggered by A β (Rapoport et al., 2002).

In an attempt to obtain mouse models that display the entire neuropathological spectrum of AD, APP transgenic mice were bred with mice expressing the P301L mutant tau. Interestingly double mutant mice exhibited substantially enhanced neurofibrillary tangle pathology in limbic areas as compared to single tau mutant mice. Notably, plaque formation was unaffected by the presence of the tau lesions (Lewis et al., 2001). Thus, amyloid plaques can cause tau tangles, but vice versa tangles do not obligate amyloid plaque formation. Recently, triple-transgenic mice harboring mutated PS1 (M146V), APP (Swedish) and tau (P301L) transgenes have been created that develop extracellular A β deposits prior to tangle formation in AD relevant brain regions (Oddo et al., 2003). Moreover, treatment of the amyloid pathology in these triple transgenic mice led to a partial resolution of tau abnormalities (Oddo et al., 2004).

1.2.7. Treating and preventing Alzheimer's disease

At present there is no cure for AD. Present-day therapies focus on treating associated symptoms, such as depression, agitation, sleep disorders, hallucinations, and delusions (Clippingdale et al., 2002). To date, only four medications have been approved for the symptomatic treatment of patients with Alzheimer disease. These are tacrine (Cognex, Warner-Lambert, Morris Plains, New Jersey); donepezil (Aricept, Eisai, Inc., Teaneck, New Jersey, and Pfizer, Inc., New York, New York); rivastigmine (Exelon, Novartis, Basel, Switzerland); and galantamine (Reminyl, Janssen, Titusville, New Jersey). All are cholinesterase inhibitors that are aimed at counterbalancing deficits in the neurotransmitter acetylcholine observed in AD (Emilien et al., 2000). Unfortunately, these drugs induce, at best, a very modest effect on cognitive functions and activities of daily living and do not stop the progression of AD (Grutzendler and Morris, 2001). If the amyloid cascade hypothesis of AD pathogenesis (Hardy and Allsop, 1991) is correct, the most rational strategy to treat the disease would rather involve retarding, halting or even reversing the process that leads to increased production of A β .

With the identification of the α -, β - and γ - secretases, new approaches to treat AD have become possible. Therefore, a promising strategy might be reducing formation of A β by inhibiting either β - or γ -secretases and/or enhancing α -secretase activity (Xia, 2003). There are already potent γ -secretase inhibitors tested in a variety of experimental models (Lanz et al., 2004; Wong et al., 2004). Several classes of inhibitors are showing favourable acute pharmacokinetics with rapid lowering of plasma and CSF A β levels (Anderson et al., 2005; Barten et al., 2005) but are also revealing unanticipated effects on synaptic function (Dash et al., 2005). New classes of γ -secretase inhibitors continue to be disclosed, as part of the attempt to develop compounds that are devoid of side-effects (Gundersen et al., 2005; Lewis et al., 2005). The major concern is the inhibition of signaling in the Notch pathway, which is important for a variety of cell fate decisions during embryogenesis and also in adult tissues (Milner and Bigas, 1999; Doerfler et al., 2001; Sisodia and St George-Hyslop, 2002; van Es et al., 2005). Compounds that inhibit A β formation without affecting Notch cleavage may offer new leads for the design of APP-specific γ -secretase inhibitors. The development of β -secretase inhibitors has been focused on the discovery and design of compounds which target the active site of BACE-1 which is thought to be an ideal

therapeutic target as it catalyses the first step of A β production. Furthermore, β -secretase knockout mice are apparently normal showing no obvious anatomical or physiological abnormalities (Luo et al., 2001; Roberds et al., 2001) except for a dramatic reduction in A β levels. However, one major challenge for the generation of specific inhibitors is the large active site of this secretase (Hong et al., 2000).

A chronic inflammatory response, exemplified by activated microglia, reactive astrocytes, complement factors, and increased inflammatory cytokine expression, is associated with A β deposits in AD brain (Akiyama et al., 2000; Emmerling et al., 2000). Therefore, trials of anti-inflammatories in AD have been conducted, and considerable research efforts undertaken to examine the effects of anti-inflammatories in a variety of experimental models. These include the non-steroidal anti-inflammatory drugs (NSAIDs) (Farias et al., 2005; Morihara et al., 2005), cannabionoids (Ramirez et al., 2005) and glucocorticoids (Boedker et al., 2005). NSAIDs have been suggested to delay the onset and slow the progression of AD by inhibiting the cyclooxygenase, and therefore prostaglandin synthesis, resulting in reduced inflammatory response (Launer, 2003). Besides an anti-inflammatory action, some NSAIDs have also been shown to have direct effects on the cleavage of APP by γ -secretase, an effect that is independent of the drugs' inhibition of cyclooxygenase and other inflammatory mediators (Weggen et al., 2001). Some such drugs reduce cytopathology in APP tg mice (Lim et al., 2001; Jantzen et al., 2002), perhaps by lowering the production of the highly amyloidogenic A β (Weggen et al., 2001). However, although epidemiological studies suggest that NSAIDs reduce the risk of developing AD, clinical trials in patients with mild to moderate AD have been negative (Aisen et al., 2003; Launer, 2003).

Epidemiological studies suggest that cholesterol-lowering drugs could provide some degree of protection from AD and therefore could be an attractive treatment strategy (Jick et al., 2000; Fassbender et al., 2001). Conversely, high blood cholesterol levels have been correlated with a higher risk of developing AD (Kivipelto et al., 2001) and high cholesterol diets increase A β deposition in transgenic mice and in rabbits (Sparks et al., 1994; Refolo et al., 2000). A molecular explanation might be that high cholesterol favors processing of APP through the amyloidogenic β -secretase pathway *in vitro* and *in vivo* (Simons et al., 1998; Fassbender et al., 2001). Inhibitors of cholesterol synthesis (statins) have been shown to

decrease A β production resulting in reduced pathology in APP tg mice (Fassbender et al., 2001; Refolo et al., 2001). However, while some early phase clinical trials with statins have shown encouraging results (Masse et al., 2005), others have not (Höglund et al., 2005).

Passive immunization with antibodies against A β (Bard et al., 2000; DeMattos et al., 2001; Wilcock et al., 2003), or active immunization with A β (Schenk et al., 1999; Janus et al., 2000) were proven to prevent amyloid deposition in young mice but also cleared plaques and reduced associated glial and neuronal cytopathology in older animals. Moreover, immunization with A β was found to protect against or reverse cognitive deficits in mice (Janus et al., 2000; Morgan et al., 2000; Younkin, 2001; Dodart et al., 2002). Based on these results, Elan Corporation moved into clinical trials with the active A β -vaccination approach. Toxicological testing in several animal species, and Phase I clinical trials in 104 AD cases suggested that the vaccination with aggregated A β ₄₂ was safe (Senior, 2002). Therefore, in June 2001, a Phase II trial was begun with 360 early to moderate stage Alzheimer's patients in the United States and Europe. However, the phase IIa clinical trial for an AD vaccine (AN-1792) was suspended in January 2002 when 6% of the patients developed clinical signs of meningoencephalitis, a potentially deadly inflammation of the brain (Munch and Robinson, 2002; Senior, 2002; Nicoll et al., 2003; Orgogozo et al., 2003). The mechanism of this inflammation is unknown, but the appearance of the inflammatory reaction before anti-A β antibody production in some patients indicates the involvement of a T-cell-mediated immune response to A β (Weiner and Selkoe, 2002). Despite the serious side effects encountered, autopsy evaluation and cognitive assessment of patients involved in the study suggest that immunization might work (Nicoll et al., 2003). The aborted clinical trial with the AN1972 vaccination approach has provided a wealth of clinical information (Gilman et al., 2005; Lee et al., 2005) which will assist further development of strategies designed to avoid the auto-immune adverse events (Lee et al., 2005b; Racke et al., 2005). Chief among these will be avoidance of T-cell-mediated responses (Agadjanyan et al., 2005) and the development of passive immunization protocols (Hartman et al., 2005). Passive immunization clinical trials are currently underway. In the meantime, novel methods of antigen presentation are being tested (Frenkel et al., 2005). Three main possible mechanisms have been suggested to be responsible for A β clearance: (i) A β antibodies enter the CNS and target aggregated A β deposits where they form immune complexes. The Fc-region of the anti-A β antibodies

binds to the Fc-receptors on microglia and induces phagocytosis of the A β peptide. (Bard et al., 2000); (ii) A β antibodies generate a peripheral sink for efflux of A β out of CNS compartments, reducing the potential for aggregation and deposition (DeMattos et al., 2001); (iii) A β antibodies prevent the fibrillar aggregation of A β and/or neutralize A β fibers (Solomon et al., 1996; 1997).

Excessive phosphorylation of the tau protein in AD is thought to cause formation of insoluble tau filaments with resulting neurofibrillary tangles, disruption of microtubules, and subsequent neuronal dysfunction (Trojanowski and Lee, 2002). Thus, drugs targeted to preventing neurofibrillary pathology may help slow progression of cell death. Identification of such agents is still in very early stages, but some efforts are focused on agents that might decrease abnormal phosphorylation of tau and/or prevent the loss of microtubule structure. Inhibition of proline-directed kinases has become a major focus for drug development. Of the proline-directed kinases, glycogen synthase kinase β (GSK3 β) and cyclin-dependent kinase 5 (cdk5) are the primary targets for drug discovery efforts because of their association with microtubules, their phosphorylation of tau at AD-relevant epitopes, and their involvement in apoptotic cascades in various models (Lau et al., 2002a, b). Their inhibition would be expected to decrease tau pathology in AD. The finding that valproate, a well-established epilepsy and mood-stabilizing medication, inhibits GSK3 β (Chen et al., 1999) has led to proposal that this drug might improve symptoms of or slow progression of AD (Loy and Tariot, 2002). Interestingly, lithium, another well-established mood stabilizer, has also been shown to inhibit GSK3 β (Alvarez et al., 2002). Another recent neuroprotective approach emerging from microtubule studies is the development of small molecules that stabilize microtubules such as paclitaxel (Taxol). Down regulation of expression of the tau gene (Santacruz et al., 2005) or changing the alternative splicing (Rodriguez-Martin et al., 2005) could also confer some new strategies.

Although many therapeutic agents are in various stages of development for the treatment of AD, the design of clinical trials has been hampered by the difficulty of identifying patients early enough on the disease continuum to test new drugs for effectiveness in slowing the progression of deterioration. Thus, success in pharmacological interventions hinges on developments in both the diagnostic arena and elucidation of the molecular pathogenesis of nerve cell death. Moreover, it is extremely unlikely that a single class of compound or

targeting a single mechanism of action will be sufficient to treat AD. For this complex disease, it is far more likely that a combination of drugs targeting various aspects of the A β and/or tau pathways will evolve into some form of rational therapy.

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6. CONCLUSION

The objective of this thesis has been to gain new insights into the mechanisms underlying the initiation of cerebral A β -amyloidosis and neurofibrillary pathology using transgenic mouse models of AD.

A major finding of our studies is that cerebral A β -amyloidosis can be induced by exogenous, A β -rich brain extract, and that intrinsic properties of the A β in the extract as well as of the host are crucial for the induction of A β accumulation in brain. The present results indicate that A β plays a crucial role in β -amyloid induction *in vivo*, but the inability of synthetic A β to potently stimulate protein deposition suggests that β -amyloid induction is dependent on a conformation of A β and/or cofactors that are specific to the brain. The identification of potential conditions and chaperones that are necessary to transform synthetic A β into a potent amyloid-inducing agent will be crucial for the understanding of the *in vivo* mechanisms of cerebral A β -amyloidosis. Moreover, our findings demonstrate that the nature of the host is important for the exogenous induction of cerebral A β -amyloidosis and support the possibility that A β can form multiple proteopathic strains reminiscent of prions. Together, this work also adds indirect support to therapeutic efforts targeted at early-stage amyloid formation.

A second important observation is that neurofibrillary pathology, akin to A β -amyloidosis, can also be induced *in vivo* by intracerebral infusion of A β -rich brain extract into a susceptible transgenic host. The finding that human extract with low A β levels had no tau-inducing activity indicates that soluble A β species are potent effectors of tau pathology *in vivo* and further supports the hypothesis that a similar interaction occurs in AD. It remains to be determined whether a particular A β assembly is responsible for the induction of tau phenotype. Moreover, our results do not exclude the possibility that factors other than A β could also induce neurofibrillary pathology in brain, in view of the many tauopathies associated with neurofibrillary lesions in the absence of A β pathology. In this regard, the intracerebral infusion of brain extracts from patients affected by frontotemporal dementia or other demented conditions could help to identify such tau-inducing candidates.

In a third set of experiments, we have provided a thorough characterization of the kinetics of the microglial response to amyloid pathogenesis in the living brain via multiphoton microscopy. The observation that plaque-associated microglia remain very motile at the

plaque-glia interface and exhibit signs of uptake of the A β peptide, provides compelling evidence of a dynamic process of homeostasis. Notably, the interaction of microglia with plaques could be stimulated by intracerebral infusion of A β antibody, such that these cells adopted a more macrophagic morphology and were induced to clear existing amyloid deposits. Together, our results highlight the dynamic nature of microglia surrounding amyloid plaques and indicate that these cells are capable of A β clearance *in vivo*, holding great potential for the fight against AD.

ABBREVIATIONS

A β	beta-amyloid
AD	Alzheimer's disease
ApoE	apolipoprotein E
APP	amyloid precursor protein
BACE	β -site of APP cleaving enzyme
CA	Cornu Ammonis
Cdk5	cyclin-dependent kinase 5
CD	cluster of differentiation molecule
CNS	central nervous system
DNA	deoxyribonucleic acid
FAD	familial Alzheimer's disease
FTDP-17	frontotemporal dementia and parkinsonism linked to chromosome 17
GSK3 β	glycogen synthase kinase β
HLA-DR	human lymphocyte antigen-classII-DR
KPI	Kunitz-type of serine protease inhibitor
MAP	microtubule-associated protein
NFL(s)	neurofibrillary lesion(s)
NFT(s)	neurofibrillary tangle(s)
NSAIDs	non-steroidal anti-inflammatory drugs
NT(s)	neuropil thread(s)
PHF(s)	paired helical filament(s)
PS1	presenilin-1
PS2	presenilin-2
RNA	ribonucleic acid
SF(s)	straight filament(s)

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