

Molecular basis of Alzheimer's disease

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Abstract. Despite an exponential production of data, Alzheimer's disease (AD) remains an enigma. Unresolved questions persist in the face of the heterogeneity of this neuropathology. Recent progress in understanding mechanisms for AD results from the study of amyloid precursor protein (APP) metabolism and the involvement of senile plaque-associated proteins. In addition to the amyloid cascade hypothesis, alternative schemes emerge, in which the amyloid peptide is not the

primary effector of the disease. Perturbations of vesicular trafficking, the cytoskeletal network, and membrane cholesterol distribution could be central events. Furthermore, since the physiological role of APP, presenilins, and apolipoprotein E in the central nervous system are not completely understood, their involvement in AD etiology remains speculative. New actors have to be found to try to explain sporadic cases and non-elucidated familial cases.

Key words. Amyloid- β peptide; presenilin; Alzheimer's disease; apolipoprotein E; cholesterol homeostasis.

During the past 20 years, knowledge about the pathology of Alzheimer's disease (AD) has been accumulating. Despite an exponential production of data, which is often controversial, this neuropathology remains hazy and patchy. The absence of an early diagnosis and the lack of an animal model render it difficult to establish an order of events and to explain the molecular mechanisms leading to neuronal loss. In a first stage, hypotheses focused on the amyloid β peptide ($A\beta$) as the major actor in AD. But, the amyloid cascade hypothesis now appears to be sufficient and complementary hypotheses are required to fully explain the heterogeneous Alzheimer's pathology.

Why is AD still an enigma?

Identification of the actors

AD has been characterized by postmortem histopathological studies, genetic linkage, and epidemiological studies [1]. The three main characteristics of AD are amyloid deposits surrounding dying neurons (senile

plaques), neurofibrillar degeneration with tangles, and cerebrovascular angiopathies. These events are associated with gliosis and neuronal loss, particularly of cholinergic neurons, and are localized in some specific brain areas. On the basis of epidemiological studies, AD cases have been classified according to age at onset (early: < 60 years; late: > 60 years) and mode of occurrence (familial transmission or sporadic cases). Extracellular senile plaques contain numerous components, but much fibrillar $A\beta$. $A\beta$ is the result of the cleavage of the amyloid precursor protein (APP) at three sites, α , β , and γ , yielding short peptides of 4 kDa, with heterogeneous amino- and carboxy-terminal ends. Amyloid plaques differ according to pathologies and topologies, either as congophilic fibrillar deposits made of $A\beta$ (1–40) and (1–42) peptides in cerebral parenchymal areas or as amorphous deposits made of non-fibrillar $A\beta$ (17–42) in the cerebellum. Mutations in genes of APP and presenilins (PSs) are linked to familial early-onset cases of AD, in which transmission is autosomal dominant [2, 3]. Mutations in the PS-1 gene, located on chromosome 14, are linked to more than 40% of early-onset cases, whereas APP (chromosome 21) and PS-2 (chromosome 1) mutations are far less common, as low as 1% [4].

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Apolipoprotein (apo) E and, recently, α 2-macroglobulin (α 2-MG) have been identified as risk factors [5]. Indeed, allele ϵ 4 of apoE and deletion in exon 18 of α 2-MG both confer an increased risk of sporadic AD. In addition, apoE allele 4 accelerates the age of onset. These two factors are localized in senile plaques along with other components such as apoA-I and apoJ, heparan sulfate proteoglycans (HSPGs), and elements of the immune system [6].

The neurofibrillary tangles are constituted mainly of paired helical filaments (PHFs). The formation unit of a PHF is the hyperphosphorylated and ubiquitinated form of tau, a microtubule-associated protein (MAP) [7, 8]. When hyperphosphorylated, tau loses its capacity to bind tubulin and stabilize microtubule assembly. Even if the degree of dementia correlates with the localization and severity of PHFs, the exact role of tangles in the development of AD remains unclear and controversial.

Open questions

Faced with these hallmarks of AD, a number of crucial questions arise. Is neurodegeneration induced by $A\beta$? How does $A\beta$ act? What intracellular toxic mechanisms are induced by $A\beta$? Do the molecular factors binding to $A\beta$ play a passive or active role? What are the effects of the accumulating intracellular pool of insoluble $A\beta$? How are glial cells involved in AD? Does apoE act as a protein chaperone and/or a neurotrophic factor in the homeostasis of cholesterol?

The amyloid cascade hypothesis

Under this hypothesis, the change of conformation and fibrillar aggregation of $A\beta$ result in extracellular deposits, which interact with cells and might lead to neuronal death (fig. 1). This has been confirmed by many studies using cerebral cells in primary culture or neuronal cell lines. This model would target the over-

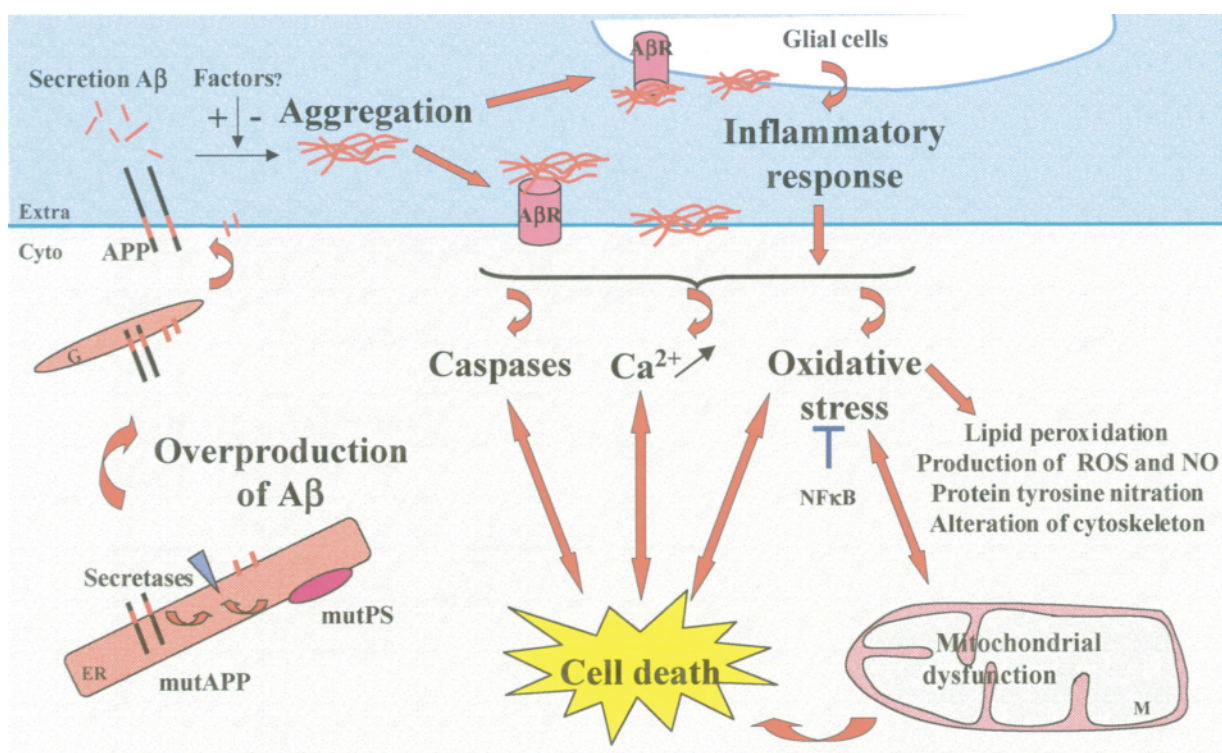


Figure 1. Amyloid cascade hypothesis. Mutated proteins, APP or PSs, increase membrane cholesterol content to alter APP processing, leading to an overproduction of $A\beta$. An increase in $A\beta$ secretion may favor fibrillation and subsequent aggregation, which may be modulated by extracellular factors. Through receptor or direct interactions with neuronal membrane, or through the activation of glial cells, aggregated $A\beta$ triggers a general toxic pathway. The identity of all effectors and the chronology of events are still unclear. It appears that $A\beta$ -induced toxicity involves an oxidative stress, severe mitochondrial dysfunction, the activation of caspases, and an increase in cytosolic calcium. $A\beta$ R, $A\beta$ receptor; mutAPP and mutPS, mutated APP and PS; G, Golgi apparatus; ER, endoplasmic reticulum; M, mitochondrion; extra and cyto, extracellular and cytoplasmic compartments; ROS reactive oxygen species; NO, nitric oxide.

production of A β and/or a deficiency in the clearance of the peptide as the main cause(s) of the disease.

The majority of studies conducted in this area have tried to determine the precise molecular mechanisms involved in the amyloid cascade hypothesis. These include characterization of A β -induced neurotoxicity, causes of peptide overproduction or accumulation in critical areas of the brain, molecular factors that could modify the accumulation, and aggregation and clearance of the A β peptide by neuronal and non-neuronal cells.

Overproduction, aggregation, and fibrillar-modulating factors

All events in favor of fibrillogenesis, namely fibrillation, overproduction of A β (1–42), decreased clearance of secreted A β (sA β), and involvement of aggregating factors, might lead to neurodegeneration. Soluble A β peptides have been detected in cerebrospinal fluid (CSF) in normal and AD brains, mainly as A β (1–40). Biochemical studies have demonstrated the propensity of A β (1–42) to self-aggregate and facilitate nucleation-dependent polymerization of the shorter form, A β (1–40) [1]. Mutations in APP or PSs have been shown to modify the processing of APP, through modulation of secretase activities. This altered processing leads to an increase in A β , and particularly A β (1–42). It might trigger aggregation and induce the neurodegenerative process [9].

Numerous biochemical and cellular studies have shown that the aggregation might be modulated by some of the proteins present in senile plaques. apoE and apoJ, laminin, α 2-MG, and α ₁-antichymotrypsin (α 1-ACT) inhibit fibrillogenesis [10]. Conversely, aggregation is accelerated by acetylcholinesterase (AChase) and perlecan [11, 12]. ApoE, α 2MG, and α 1-ACT which prevent fibrillation of A β , protect against neurotoxicity [13]. Indeed, the 'sticky' nature of the peptide A β results in the association of numerous proteins, eventually found in the senile plaques. Therefore, it precludes determining the chronology of their association and whether one protein or another plays an active role in the constitution of senile plaques. Factors responsible for or inducing aggregation of the peptide, as well as the cellular context in which it occurs, have yet to be established. A disequilibrium in the metabolism, not only of APP, but also of an extracellular factor(s), could prime aggregation and fibrillation of A β peptide. In hereditary cerebral hemorrhage with amyloidosis, Dutch type (HCHWA-D), patients develop cerebrovascular amyloidosis with non-fibrillar A β deposits. After injection in rat brain, soluble A β (1–40) formed fibrillar aggregates, whereas the A β (1–42) deposit contained non-fibrillar amorphous material [14]. These results

strengthen the hypothesis of the intervention of more than one factor in the aggregation of A β .

Interaction with a specific receptor or with the plasma membrane?

Cross-linking, membrane binding, or double-hybrid studies have revealed a direct interaction of fibrillar A β with the p75^{NGF} receptor, scavenger receptor and RAGE receptor [15–17]. The scavenger receptor of class A and RAGE receptor are expressed by glial cells and could mediate A β toxicity, leading to activation of microglia and production of reactive oxygen species (ROS) [18]. Binding of A β to p75^{NGF} receptor has recently been reported to activate NF- κ B in human neuroblastoma [19].

Another potential mechanism for inducing toxicity is by direct interaction with the membrane. In biochemical studies, soluble and fibrillar A β peptides have exhibited disrupting membrane properties, particularly at acidic pH [20–22]. Other studies have shown that A β is able to form ionic pores, perturbing membrane permeability. Thus, A β peptides could insert in plasma or intracellular membranes, inducing cell death and/or leading to peptide clearance.

A β toxicity pathway

The pathway by which A β induces neuronal cell death has been investigated and various mechanisms have been proposed, including intracellular calcium accumulation, nitric oxide (NO) and peroxide production, membrane lipid peroxidation, decreased membrane fluidity, and alteration of the cytoskeleton and nucleus. All of these intracellular events converge to the ubiquitous pathways of necrosis or apoptosis.

In neuronal cell lines, A β toxicity induces the production of ROS and NO. The production of these toxic compounds is accompanied by depletion in glutathione peroxidase (GSH), activation of inducible NO synthase (iNOS), accumulation of mitochondrial peroxynitrite, tyrosine nitration, and membrane lipid peroxidation. Bcl2 expression, sAPP α , tumor necrosis factor- α (TNF- α) and C2-ceramide pretreatment protect neurons against A β -induced oxidative stress, associated with increased expression of GSH and manganese superoxide dismutase (Mn-SOD) [23–25]. The protective mechanism involves the activation of NF- κ B [26]. In some cases, however, A β treatment activates NF- κ B, leading to an increased expression of iNOS in rat astrocytes [27], and to cell death in neuroblastoma [19]. Although several studies have reported the production of ROS by A β , antioxidant molecules do not appear to attenuate A β toxicity [28]. ROS production might be a secondary event in the A β -induced cell death.

A substantial cytosolic increase in calcium can induce cell death. Data on the calcium flux involved in $A\beta$ -induced toxicity are contradictory. Two phases have been described upon $A\beta$ exposure: an early Ca^{2+} -independent phase and a late Ca^{2+} -dependent phase involving the voltage-dependent calcium channel (VDCC), such as the L-type VDCC, and intracellular flux from the endoplasmic reticulum through the InsP3 receptor or ryanodine receptor [29]. In some studies, no variation in intracellular calcium leading to $A\beta$ toxicity has been measured [30].

Necrosis or apoptosis?

Although the data remain controversial, evidence is accumulating for two types of cell death in AD: apoptosis and necrosis. Necrosis is reported to be induced by $A\beta$ in PC12 cells [31], and by an inflammatory response of glial cells. Morphological changes, characteristics of apoptosis (membrane blebbing, nuclear chromatin condensation, DNA fragmentation), modulation of expression of apoptotic genes (decreased expression of Bcl2 and increased expression of Bax, cFos, cJun, p53, and Fas) are all induced by $A\beta$ in neuronal primary culture and AD postmortem tissue [32–34].

However, determining whether $A\beta$ directly triggers neuronal cell death or whether its effects are relayed by activated microglia is difficult. Furthermore, the properties of neurons and cell lines tested intervene in the type of cell death.

Several mechanisms for a multifactorial pathology?

This dramatic accumulation of data does not clarify the confusing picture of AD. The classical amyloid hypothesis cannot explain all the molecular and cellular events occurring in the different forms of AD. In the last few years, mechanisms have emerged in which the fibrillar amyloid deposit does not act as the primary effector of this neurodegeneration (fig. 2). There is no strong evidence pointing to toxicity of the $A\beta$ deposit in vivo [for a review see ref. 35]. No correlation has been reported between the distribution and number of senile plaques and neurodegeneration or synaptic loss. Neither has any correlation been found between senile plaques and the degree of dementia, whereas neurofibrillary tangles were correlated with dementia. Moreover, amyloid deposits have been found in normal brain of non-demented elderly individuals.

Familial and sporadic cases require alternative hypotheses, as AD is clearly a heterogeneous disease. The mutations found in the three genes, APP, PS-1, and PS-2, lead to an overproduction of $A\beta$ and are linked to around half of the familial cases. The etiology of the

remaining familial cases and the sporadic cases has yet to be determined. All of the histologic studies have been conducted on postmortem slices from brain of individuals with AD. Thus, the impossibility of detecting early the neurological insults accentuates the difficulty in understanding the mechanisms of AD. In particular, trying to establish the chronology of events is hazardous, since distinguishing between early or secondary events with any degree of certainty is impossible.

$A\beta$ deposit: a primary or secondary event in AD?

Most of the experiments conducted on $A\beta$ toxicity have been performed with a suspension of fibrils, but deposits of $A\beta$ fibrils are not always toxic per se. Indeed, a matrix of soluble or fibrillar $A\beta$ has been reported to allow the adherence and development of cell line cultures or neuronal primary culture cells, which express integrins [36]. The fixation of $A\beta$ peptide to integrins occurs through an $A\beta$ sequence homologous to fibronectin [37]. Soluble $A\beta$ is partially internalized and degraded via an $\alpha 5\beta 1$ -integrin-mediated pathway, without inducing toxicity. Furthermore, immunohistochemistry studies of labeled $A\beta$ deposits have established the existence of neuronal cell death prior to the deposition of fibrillar $A\beta$ [38].

Accumulation of an intracellular insoluble pool has been reported, occurring over time or during internalization and degradation of $A\beta(1-42)$. Soluble or fibrillar $A\beta$ present membrane-perturbing properties, which could induce membrane damage and leakage of the intracellular $A\beta$ pool. An amyloid deposit might be seeded with $A\beta$ derived locally from disintegrating neuronal membrane or from the insoluble pool rather than from diffuse $A\beta$ deposits or from secreted $A\beta$ [39]. Thus, internalization could lead either to a protection of the cells against $A\beta$ peptide by its total clearance, or to cell death through long-term intracellular aggregation.

Other factors in AD neuronal insults PSs, tau, APP, and others

PS-1 and PS-2 genes encode proteins that share 63% overall identity. Located mainly in the endoplasmic reticulum membrane, the PSs are membrane-bound proteins with six to eight transmembrane domains and are structurally homologous to G protein. PS-1 and PS-2 proteins undergo endoproteolytic processing to yield two stable fragments [40]. In recent years, a growing list of proteins interacting directly or indirectly with PSs have been established: tau and one of its kinases, glycogen synthase kinase 3β (GSK3 β), filamin, an actin-binding protein, β -catenin, Go protein, calsenilin, and μ -calpain (fig. 3) [41–46]. From these results, two main aspects of PS function emerge: cell survival and

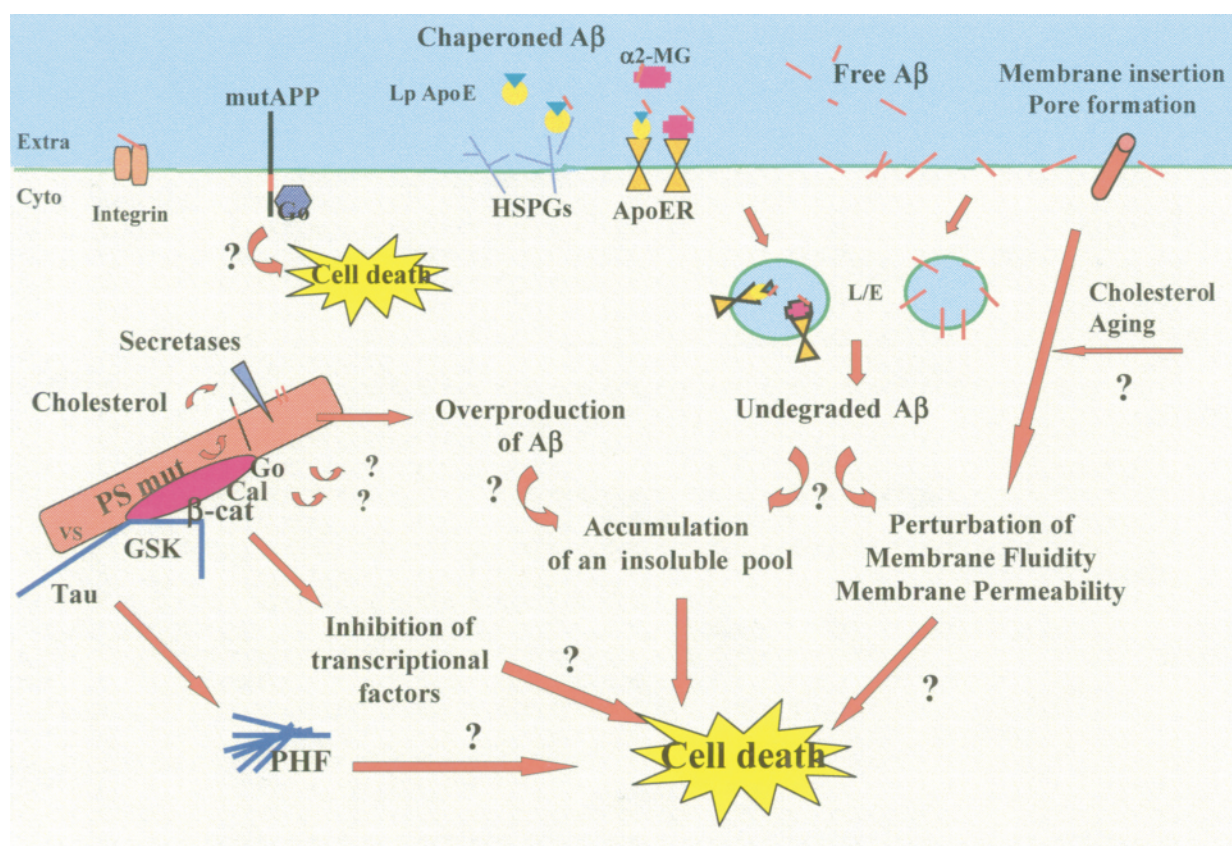


Figure 2. Alternative hypotheses. Different A β cytotoxic pathways could be elaborated from studies in vitro, in which deposition of fibrillar A β does not form the central event. The pathological role of A β might be caused via resistance to catabolism and accumulation of an insoluble intracellular A β pool, via perturbation of membrane properties, by insertion of peptide inside the lipid structure, or by ionic pore formation. Independently of the overproduction of A β , mutAPP and mutPSs may induce cell death through interaction with a Go protein and through phosphorylation of β -catenin and tau by activated glycogen synthase kinase (GSK). The involvement of the other proteins binding to PS, such as Go, calsenilin and filamin, has yet to be established in the pathological mechanism of AD. ApoER, apoE receptors; Lp ApoE, lipoprotein containing apoE; β -cat, β -catenin; Cal, calsenilin; VS, vesicular structures; L/E, lysosomal/endosomal compartments.

fate, notably through the Notch pathway, and vesicular trafficking.

Expression of mutated PS and overexpression of PSs in transfected cells have been reported to increase sensitivity to apoptosis [47, 48]. PS-2 appears to play a direct role in Fas-mediated apoptosis. PS-1 might regulate the JNK pathway, maybe by acting as an anchor protein that directs the activity of related kinases and phosphatases [47]. PS-1 and PS-2 contain a site recognized by caspase-3 close to the proteolytic site of cleavage [49]. This carboxy-terminal fragment resulting from the cleavage of pS-2 by caspase-3 inhibits apoptosis induced by Fas and TNF- α .

Mutated PSs destabilize calcium homeostasis, possibly through calsenilin, a calcium-binding protein [45, 50]. This neuronal protein interacts with the carboxy-terminal end of both PS-1 and PS-2.

Furthermore, neurons in AD brain and mutated PS-1-transfected cells overexpressed Par-4, a protein containing both a leucine zipper and a death domain implicated in apoptosis [51].

Destabilization of the cytoskeleton has been described as a critical step in apoptosis. In AD, this destabilization could occur through PS mutations in two ways: modulation of phosphorylation of tau leading to formation of PHFs, and/or overproduction of A β inducing apoptosis and alteration of the cytoskeleton as a final step. PS-1 and PS-2 immunostaining have been detected in neurofibrillary tangles from sporadic and familial cases of AD, suggesting a possible interaction between PS and tau [52]. These findings are inconsistent with another study which did not report any specific interaction of PS-1 with neurofibrillary tangles or senile plaques [53]. In vitro, PS has been reported to complex

both tau and GSK3 β . Familial AD mutations increase the ability of PS-1 to bind GSK3 β , leading to a modulation of tau phosphorylation, and may favor formation of PHFs [54].

Tau is reported to interact with other cytoskeletal proteins, such as actin and α -spectrin, and with phosphatases and kinases mediated by the anchorage of its N-terminal domain in the plasma membrane. Through all these interactions, tau is implicated in cytoskeletal maintenance and vesicular trafficking. Many studies have focused on the phosphorylation process of tau, but failed to establish the mechanism leading from tau hyperphosphorylation to formation of PHFs. Paradoxically, Canu et al. [55] have shown that induction of apoptosis by serum deprivation of cerebellar cells leads rapidly to the cleavage of dephosphorylated tau and finally microtubule destabilization. The induction of apoptosis by potassium serum deprivation activates caspase-3 and calpain. Calpain induces activation of calcineurin, a tau phosphatase. Dephosphorylation of tau provokes dual effects, increasing its ability to bind microtubules, but also increasing its vulnerability to proteolysis. However, recent studies have demonstrated that the stabilization of microtubules protects neuronal cells against A β -induced toxicity [56].

Thus, the mechanism of protection against apoptosis remains to be explained. Neurodegeneration in AD could involve different types of cytoskeletal damage, particularly in microtubule destabilization, an early pathway implicating cleavage of tau, and another driven by A β -induced toxicity.

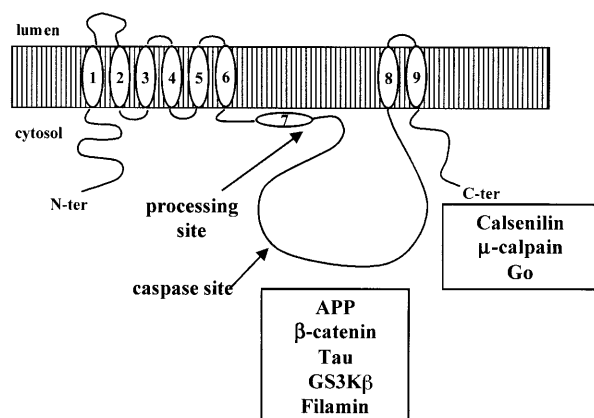


Figure 3. PSs have been localized in endoplasmic reticulum and Golgi membranes. These proteins are constituted of eight transmembrane domains. An enzymatic cleavage site yields two protein fragments, a caspase site being located near this processing site. The central and the carboxy-terminal cytosolic regions interact with APP, β -catenin, tau, GSK3 β , filamin, calsenilin, and Go protein.

Mutations of PSs and APP have also been shown to deregulate vesicular trafficking and signal transduction through GSK3 β , β -catenin, and Go protein. GSK3 β modulates tau phosphorylation and also inactivates pyruvate dehydrogenase (PDH), which could lower acetyl-CoA and ATP levels. In hippocampal primary culture cells treated with A β , GSK3 β is induced, and the acetylcholine level is reduced, whereas choline acetyltransferase and cholinesterase activity are unaffected by A β peptide. In a similar manner, muscarinic M1 receptor agonist enhances processing of APP in non-amyloidogenic products and decreases phosphorylation of tau [7]. All these data correlate with results obtained in AD brain: a considerable decrease in the metabolic rate of glucose, a decrease in PDH activity, and predominant lesions in the cholinergic region. The primary effects of mutated PS may affect GSK3 β , glucose turnover, and acetylcholine-derived products, leading to deregulation of the cholinergic innervated system and neuronal cell death. The overproduction of A β might be a secondary event in PS mutation.

Another intracellular disorder related to mutated PS is the instability of the β -catenin-PS complex. PS-1 may sequester cytoplasmic β -catenin in a membrane-associated complex [43, 53, 57]. This interaction has been demonstrated by immunoprecipitation in brain tissue and in neuroblastoma cells. A defect in PS-1 may induce the phosphorylation of β -catenin by GSK3 β , inducing the catabolism of unstable β -catenin by proteasome. The cytoplasmic protein β -catenin is implicated in the Wg/Wnt signaling pathway through the Tcf/Lef family of transcription factors. This pathway is involved in the control of cell survival. The instability of the complex β -catenin/PS could explain the susceptibility of mutated PS neurons to apoptosis. A brain isoform of β -catenin, δ -catenin, has been reported, but its role in the normal and pathologic central nervous system (CNS) has not yet been determined [58].

APP has been implicated in cell adhesion, cell growth, neurite outgrowth, and neuroprotection. It has been suggested that a Go protein, interacting directly with APP, may mediate apoptosis in cells transfected with mutated APP.

Thus, involvement of APP and PS mutations may reflect an intracellular perturbation as the primary cause in AD, independently of A β overproduction.

Not forgetting glial cells

While neuronal loss is the main aspect of AD, the involvement of glial cells should not be forgotten. Neuritic plaques in AD are densely surrounded by reactive astrocytes and microglia. Microglial cells accumulate in dense A β plaques, rather than diffuse deposits, and act

as plaque-attacking scavenger cells. The majority of the internalized A β microaggregates are undegraded after uptake [59]. Microglial cells are activated by fibrillar A β , resulting in the production of reactive nitrogen species and TNF- α , and in a decrease in intracellular calcium. The reactive astrocytes participate in the inflammatory response in AD by secreting proinflammatory cytokines and by expressing iNOS. Fibrillar A β injected into the rat striatum is phagocytized by microglia, whereas nearby astrocytes form a virtual wall between fibrillar A β -containing microglia and neuropils. Astrocytes and microglia near the injected fibrillar A β site show a significant increase in iNOS [60]. Thus, A β neurotoxicity is mediated by factors released from activated microglia and astrocytes.

In addition to being involved in the digestion of plaques, glial cells in the CNS represent the major source of apoE, which modulates A β -induced ROS and is involved in cholesterol homeostasis and A β clearance [61, 62].

apoE: A β 'chaperone,' A β clearance effector and/or neurotrophic factor?

Genetic linkage and immunohistochemistry studies have suggested the involvement of apoE in the onset of AD. Nevertheless, the function of apoE in the normal and AD CNS is still unclear. The brain is the second major site of apoE expression [63]. Glial cells were previously thought to be the sole source of cerebral apoE, but a recent study has suggested that it is also expressed by human neuroblastoma [64]. ApoE acts as a lipid carrier protein and has been suggested to play a role in the transport of phospholipids and cholesterol in the CNS. In neuronal cultures, apoE increases neurite extension in an isoform-specific manner [65, 66]. According to the data, apoE4 has no effect or inhibits neurite outgrowth associated with depolymerization of microtubules [67]. Other studies have reported a toxic effect of unlipidated apoE4 on rat hippocampal neurons [68]. The uptake and internalization of lipidated apoE are mediated by interactions with HSPGs and with several apoE receptors. LDL-R and LRP, both members of the LDL-R family, are expressed in the brain [69]. Other receptors, apoE2 or LR7/8B, and LR11, are mainly expressed in brain, particularly by neurons [70]. LR7/8B binds apoE and α 2-MG as substrates, as does LRP [71]. LR11 is expressed during development, depending on the neural cell type, and may play a role in neural organization and the pathogenesis of degenerative brain diseases.

Histopathological studies of AD brains have revealed apoE labeling in the amyloid deposits. The C-terminal end of truncated apoE appears to be the domain most

frequently detected in deposits [72]. Biochemical tests have confirmed a direct interaction of apoE with A β , and with APP. Complex formation involves the carboxy-terminal domain of apoE and is apoE isoform specific. In vitro, apoE3 and E2 form complexes with A β , unlike apoE4 [73]. The association of apoE and A β inhibits fibril formation, the effect being more marked with free apoE than with lipidated apoE [74]. In neuronal cultures, apoE3 might protect neuronal cells against A β -induced toxicity through complexation and internalization of A β via apoE receptors [68, 75]. apoE has also been detected in neurofibrillary tangles [76]. The cytoplasmic localization of apoE is still unclear. However, biochemical studies have demonstrated an interaction between the isoforms E3 and E2 of apoE and dephosphorylated tau. Neither apoE4 nor the phosphorylated form of tau are involved in the complexes. Treatment of rat primary neuronal cultures by apoE peptides leads to dephosphorylation of tau by Ca²⁺-dependent and G protein pathways [77].

In addition to these functions recent data have suggested the involvement of apoE in vasoconstriction and the activity of ciliary neurotrophin factor (CNTF). Vasoactive properties have been reported for both apoE and A β peptide [78]. The A β -apoE4 complex synergistically enhances vasoconstriction [79]. Furthermore, soluble A β -apoE complex has been found in the CSF of AD patients, and was not detected in normal CSF, probably because the levels were too low [80]. The precise effect of vasoactive properties in the development of AD has yet to be explored.

ApoE has recently been reported to bind to and potentiate the survival-promoting activity of CNTF on hippocampal cells. Both proteins are associated with the response to insults in the CNS. Binding of apoE could protect CNTF from oxidation or hydrolysis, and could stabilize complex binding to the receptor [81]. Potentiation of CNTF activity may strengthen the neuroprotective role of apoE in AD pathology.

Control of membrane properties by cholesterol

In AD, the isoform-specific protective role of apoE might occur at two levels. As a protein chaperone, apoE could prevent fibrillogenesis, clear A β peptide, and modulate tau phosphorylation. As a lipoprotein component, it could be involved in cholesterol homeostasis and neuronal development.

An age-related change has been detected in asymmetric membrane cholesterol distribution [82]. Similarly, a progressive increase in phospholipid metabolite formation has been observed during aging, which is accelerated in AD [83]. Elevation of membrane phospholipid metabolites may play a role in the deposition of A β , as some of these metabolites are known to increase the aggregation

of A β . Membrane fluidity is partially controlled by the ratio of cholesterol to phospholipids, and influences the activity of membrane proteins through the modulation of the structural order or degree of lipid packing.

Low concentrations of A β have been reported to slightly decrease the fluidity of brain membranes. However, important local effects of A β occurring in the membrane microdomains may be sufficient to alter the activity of receptors or ionic channels located in such microdomains. These perturbing effects have also been suggested by biochemical studies. A β peptide exhibited fusogenic properties [20]. At high concentrations, A β peptide has more pronounced effects on the membrane, probably by disrupting its structure [21, 22, 84].

The distribution of membrane cholesterol has another effect in AD, namely the modulation of APP processing. A rise in the level of membrane cholesterol decreases cleavage of APP by α -secretase [85], whereas cholesterol depletion leads to an inhibition of β -secretase cleavage and has no effect on α -secretase activity [86, 87]. Several hypotheses could explain this modulation of protease activity by cholesterol. Changes in cholesterol membrane concentration may modulate the vesicular traffic of APP so that the protein does not reach the cellular sites where β -cleavage takes place [88]. The α -secretase activity may depend on membrane fluidity [85]. Correspondingly, A β decreases cholesterol esterification and changes the distribution of free cholesterol in neurons [88].

Control of cholesterol homeostasis involves apoE and its receptors. Although the data are controversial, an LRP polymorphism seems likely to be genetically linked to AD. apoE, RAP and α 2-MG are among the numerous ligands of LRP. α 2-MG has recently been reported to be genetically associated with AD [5]. This major protease inhibitor with broad substrate specificity is detected in amyloid plaques. The association of α 2-MG and A β prevents fibril formation and attenuates neurotoxicity of A β in cortical primary cultures [13, 89]. α 2-MG has been suggested to mediate A β degradation and clearance via endocytosis through LRP or via a serine protease- α 2-MG complex [90].

A conclusion is premature: hypotheses, only hypotheses

Progress in our understanding of AD requires an animal model faithfully reproducing the stigmata of AD, an earlier screening of AD patients, and a more precise delineation of pathological subtypes of AD. Most of the progress already achieved in AD research stems from studies on the role of plaque-associated proteins and APP. But if A β -induced toxicity has been clearly established in vitro, our understanding of the processes affecting the CNS in AD still remains speculative.

Milestones in future research are still the understanding of APP, PS, and apoE functions in normal brain and how these could be altered under pathological situations. Could the role of apoE in cholesterol homeostasis and neuronal development be maintained when apoE is associated with A β ? How does PS act in the development of AD: as a factor promoting the overproduction of A β or as a protein managing the general intracellular pathway?

New actors and/or new hypotheses have to be found to try to explain sporadic cases and non-elucidated familial cases, and the pathways of selective neuronal death in this disease. Less than half familial AD cases are linked to identified loci and the sporadic cases are identified in terms of risk factors. Additional genomic loci and mitochondrial mutations remain to be explored [91]. Although considerable progress has been made in the study of AD, the molecular key(s) of AD is (are) still to be found.

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