REVIEW

# Variations in the neuropathology of familial Alzheimer's disease

Claire Shepherd · Heather McCann · Glenda Margaret Halliday

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Abstract Mutations in the amyloid precursor protein (APP), presenilin 1 (PSEN1) and presenilin 2 (PSEN2) genes cause autosomal dominant familial Alzheimer's disease (AD). PSEN1 and PSEN2 are essential components of the  $\gamma$ -secretase complex, which cleaves APP to affect A $\beta$ processing. Disruptions in AB processing have been hypothesised to be the major cause of AD (the amyloid cascade hypothesis). These genetic cases exhibit all the classic hallmark pathologies of AD including neuritic plaques, neurofibrillary tangles (NFT), tissue atrophy, neuronal loss and inflammation, often in significantly enhanced quantities. In particular, these cases have average greater hippocampal atrophy and NFT, more significant cortical Aβ42 plaque deposition and more substantial inflammation. Enhanced cerebral A $\beta$ 40 angiopathy is a feature of many cases, but particularly those with APP mutations where it can be the dominant pathology. Additional frontotemporal neuronal loss in association with increased tau pathology appears unique to PSEN mutations, with mutations in exons 8 and 9 having enlarged cotton wool plaques throughout their cortex. The mechanisms driving these pathological differences in AD are discussed.

**Keywords** Alzheimer's disease · Presenilin · Amyloid precursor protein · Neuropathology · Familial

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#### Introduction

Alzheimer's disease (AD) is a slowly progressive degenerative dementia accounting for about one-third of the number of demented persons worldwide [222] and 6–10% of the North American population [80]. The inexorable decline in cognitive abilities usually occurs 32 months prior to diagnosis at an average age of 72 years [94]. Institutionalisation occurs on average at the age of 78 years and death intervenes approximately 8.5 years after the disease onset [94]. At autopsy, many cases with AD also have other coexisting pathologies such as Lewy bodies and Pick bodies, although these pathologies will not be considered in the current review.

## **Genetics of AD**

Most of the AD cases are 'sporadic' with a disease onset after the age of 65 years (late-onset AD), although several susceptibility gene alleles confer an increased risk of late-onset AD, with the most well-established being the apolipoprotein E (ApoE) *e*4 allele [163]. In addition, environmental interactions increase the risk of sporadic disease, including increased cardiovascular risk (high cholesterol, hypertension, atherosclerosis, coronary heart disease, and diabetes [18]) and obesity (both abdominal and body mass index-calculated [218–220]). These factors will not be considered in this review, but rather genetic effects shown to cause AD will be discussed.

Dominant genetic abnormalities that cause AD are largely due to fully penetrant, autosomal dominant mutations in 3 genes: the amyloid precursor protein (APP) gene on chromosome 21, presenilin 1 (PSEN1) on chromosome 14 and presenilin 2 (PSEN2) on chromosome 1. Mutations in PSEN1 account for the majority of autosomal dominant

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cases with 173 mutations described to date, compared to 30 and 14 mutations in APP and PSEN2, respectively (http://www.molgen.ua.ac.be/ADMutations). More recently an extra copy of the APP gene has also been identified in families with AD [170, 171]. In the majority of autosomal dominant cases, these mutations occur before the age of 65 years (early-onset AD), although rare mutations have been identified in families with late-onset AD.

#### **Common pathogenic mechanisms**

The pathological hallmarks of both sporadic and familial AD are extracellular senile plaques made up of A $\beta$  peptides and intracellular neurofibrillary tangles (NFT) made up of hyperphosphorylated tau.

#### A $\beta$ production and toxicity

A $\beta$  peptide formation occurs through proteolysis of the amyloid precursor protein (APP) via the action of  $\alpha$ -,  $\beta$ - and  $\gamma$ -secretases [56, 178, 187, 228]. These secretases normally process APP through two mutually exclusive pathways to produce various peptides, including A $\beta$  [70, 177]. The nonamyloidogenic pathway occurs when membrane-associated  $\alpha$ -secretase cleaves within the A $\beta$  domain, thus precluding A $\beta$  formation, and an intramembrane cleavage by the  $\gamma$ -secretase complex produces soluble APP $\alpha$ , a shortened fragment called p3 [71] and a cytoplasmic fragment identified as the APP intracellular domain (AICD) [173] (Fig. 1). In contrast, the amyloidogenic pathway initially cleaves APP at the N-terminus of the A $\beta$  domain by  $\beta$ -secretase then cleaves by  $\gamma$ -secretase [62, 169] to generate soluble APP $\beta$  and the A $\beta$ 40 and A $\beta$ 42 peptides [70] (Fig. 1). Recently a new cleavage site for  $\gamma$ -secretase has been described which cleaves between the AICD ( $\epsilon$ -cleavage) and  $\gamma$ -secretase site and generates longer A $\beta$  forms, including A $\beta$ 42, A $\beta$ 45, A $\beta$ 46 and A $\beta$ 48 [231] (Fig. 1).

A $\beta$ 40 and A $\beta$ 42 exist in different conformational states anywhere from monomers to dodecamers or even higher molecular weight complexes that remain soluble after highspeed centrifugation. Anything larger than a monomer can be referred as an oligomer. Oligomers may then grow in size and form insoluble fibrils, which the A $\beta$ 42 alloform is more inclined than A $\beta$ 40 [17, 76, 215]. Due to their greater aggregation capabilities [17], longer forms of the A $\beta$  peptides, particularly Aβ42, are considered more neurotoxic, although it is the oligomeric rather than the fibrillar nonsoluble amyloid forms which appear most damaging [50, 77, 98, 151, 214, 215]. There is a robust correlation between soluble oligomeric  $A\beta$  levels and the extent of synaptic loss and severity of cognitive dysfunction in AD, with these correlations being limited for fibrillar A $\beta$  [124, 135]. These data support the amyloid cascade hypothesis of AD [75]. Direct binding of oligomeric A $\beta$  to synapses [103] with the resultant disruption of long-term potentiation [114, 214, 216] has been shown experimentally, although other mechanisms of oligomeric AB toxicity have also been described. These include  $A\beta$ 's ability to generate oxidative stress, mitochondrial damage, inflammation, and pore formation in membranes [44, 84, 121, 212]. In addition,  $A\beta$ is capable of altering tau phosphorylation, cleavage and aggregation [39, 45] providing a link between the two major pathological hallmarks of the disease.

Fig. 1 Proteolytic processing pathways of APP. The non-amyloidogenic pathway occurs when cleavage of APP by *a*-secretase yields soluble APPa, thus precluding A β production. Further processing by  $\gamma$ -secretase within its transmembrane domain leads to generation of the p3 peptide and the amyloid intracellular domain (AICD). The amyloidogenic pathway occurs via β-cleavage of APP, yielding soluble APP $\beta$  and a C terminal fragment, which undergoes further cleavage by  $\gamma$ -secretase leading to generation of the  $A\beta$ peptide, predominately AB40 and A<sub>β42</sub>



#### Tau production, phosphorylation and toxicity

Tau is a microtubule-associated protein that stabilises the cytoskeleton, constantly undergoing phosphorylation and dephosphorylation to achieve this. In adult human brain, six isoforms of tau ranging from 352 to 441 amino acids are produced from a single gene by alternative splicing. These

isoforms differ by the presence of one or two amino-terminal inserts and either three or four microtubule binding domains. All six isoforms can be phosphorylated through the action of several kinases, including glycogen synthase kinase- $3\beta$  (GSK- $3\beta$ ), cyclin-dependent kinase-5 (Cdk5) and other tau kinases [6, 123].

In normal ageing, AD and other neurodegenerative diseases, natively unfolded tau becomes hyperphosphorylated and folds into a  $\beta$  conformation, forming abnormal filaments which become the paired helical filaments of NFT and neuritic infiltrates in plaques [27, 126]. In AD, tau neurotoxicity is, at least in part, due to an increase in the phosphorylation of all six isoforms causing hyperphosphorylation and leading to reduced microtubule binding, destabilization of the cytoskeleton, reduced axonal transport [4, 194] and insoluble intracellular fibril formation [5, 8, 104]. Classical NFT are flame-shaped and situated in cell bodies and apical dendrites while tau-positive neurites are found in distal dendrites. Once a neuron dies NFT can persist in an extracellular (or ghost) form due to their intense hyperphosphorylation and insolubility, although the precise role of tau fibrils in cellular toxicity is currently under debate [86]. NFTs are required for the clinical expression of AD, and in related tauopathies leading to dementia in the absence of amyloid plaques. In AD, neuronal loss occurs in brain regions depositing tau fibrils [227] but experimentally suppressing the mutant P301L tau transgene in a model that exhibits neurofibrillary pathology halts neuronal loss but not tau fibril formation [190]. Recent research points to a potential toxic form of soluble tau as necessary for neuronal death, as soluble tau is more toxic to neurons than aggregated, paired helical filament forms [65] and removal of soluble tau is required to achieve a therapeutic benefit with A $\beta$  immunisation [155]. The precise molecular mechanisms of such toxicity have not been fully elucidated, as tau is modified posttranslationally by a series of complex methods, including hyperphosphorylation, glycosylation, ubiquitination, glycation, polyamination, nitration, and truncation [3]. Hyperphosphorylated tau can exist as soluble oligomeric aggregates being considered as the toxic species [86], although overexpression of an A $\beta$ -induced, caplain-mediated cleavage of tau has also been proposed as this accelerates apoptosis and fibril formation through hyperphosphorylation [39]. Treatment of wild-type neurons with a caplain inhibitor prevents tau truncation and Aβinduced neuronal death [159].

#### **Common AD pathologies**

Pathologies required for diagnosis

A $\beta$  plaques and NFT are required for the diagnosis of AD. The plaque type used to diagnose AD is neuritic rather than diffuse plaques. Neuritic plaques are associated with fibrillar A $\beta$  and dystrophic tau-positive neurites with or without a central A $\beta$  neuritic core [15]. These plaques are smaller in size to diffuse plaques but, in contrast to diffuse plaques (which predominantly contain A $\beta$ 42), they contain both Aβ40 and Aβ42 peptides. Regions where neuritic and cored plaques are commonly found in AD include the middle frontal, superior and middle temporal, inferior parietal and entorhinal cortices and the hippocampus, which are the areas proposed for examination according to the CERAD criteria [138]. Predilection sites for tau neuritic and NFT pathology in AD are described in the Braak staging criteria. Using both the anatomical location and density of NFT formation with age, Braak and colleagues developed six stages of NFT formation with four of these stages occurring prior to the development of dementia [26]. NFT stages I/II occur in the entorhinal region, stages III/IV infiltrate into limbic regions and stages V/VI include the neocortex with these three groups corresponding to normal cognition, some cognitive impairment and frank dementia [26]. It is currently recommended that for diagnostic assessment Braak staging in conjunction with the assessment of plaque distribution, type and number from the CERAD protocol is used [138]. However, none of the neuropathological criteria set have been uniformly accepted by neuropathologists and variability and overlap in pathologies can lead to difficulties in diagnosis [92].

#### Atrophy and neuronal loss

Although not required for a definitive diagnosis of AD, the degeneration of brain structure is assumed to be the main substrate for the precipitation of AD dementia. While brain volume can be easily measured using MRI techniques, the identification of atrophy is more difficult due to considerable inter-individual variation in brain shape and size as well as some atrophy of white matter (less than 0.25% per year) as a normal consequence of age [57, 162]. In older individuals with mild cognitive impairment this rate of atrophy doubles in posterior cingulate, temporoparietal and medial temporal regions [57, 93]. Once clinical AD commences, progressive atrophy and neuronal loss particularly affect the hippocampus [19, 20, 91, 106] correlating with Braak staging [167, 221]. Mean brain atrophy rates for well-established clinically diagnosed AD are 2.4% per annum, with a widespread and symmetrical generalised volume loss [35, 58] with more concentrated atrophy in fusiform and inferior temporal gyri, the temporal pole,

superior and middle frontal gyri, amygdala, entorhinal cortex and hippocampus. Regions unaffected by neuronal loss include orbital, inferior frontal and postcentral gyri and the posterior hippocampus [73].

In the hippocampus atrophy relates to the degree of neuronal loss [105], a concept that may be extrapolated to other brain regions. Until recently the molecular mechanism leading to neuronal loss was considered to be the deposition of fibrillar forms of hyperphosphorylated tau (see above), although evidence for other cellular mechanisms cannot be ignored. It has been suggested that apoptosis might be the primary mechanism underlying AD neurodegeneration [40] and there is substantial evidence demonstrating that at least some cells in sporadic AD die via apoptosis [29, 41, 191, 195]. Other characteristic signs of apoptosis observed in AD include mitochondrial dysfunction, caspase activity, nuclear abnormalities, DNA damage and altered activity of apoptosis-related genes, such as p53 and Bax [29, 133, 196]. A $\beta$  can induce apoptosis by downregulating Bcl-2 and upregulating Bax [157] and by inducing oxidative stress and lipid peroxidation [44], which are the common features of AD brain [33, 144, 154, 196]. Apoptotic neuronal death has also been linked with failed attempts to reenter the cell cycle leading to abortive apoptosis [147], a theory which is supported by the presence of DNA replication in vulnerable neurons in AD [229].

Atrophy may occur because of cell shrinkage and/or synaptic loss. Decreased neuronal size (rather than neuronal loss) has been demonstrated in a recent study of AD where there was a marked decrease in the size of large neurons from layers II and III of the middle temporal cortex accompanied by an increase in the numbers of small neurons, suggesting that these supragranular layer neurons become atrophic in AD [208]. Neuronal atrophy could occur either because of reduced neurotrophic support or signalling in AD [175], or because of oligomeric A $\beta$  induced synaptic changes [111, 140], resulting in synaptic degradation and remodelling of dendritic spines [112, 179]. Such changes are thought to occur prior to the complete loss of neurons in AD.

## Inflammation

Alzheimer's disease is also characterised by a chronic inflammatory response, possibly initiated by deposited fibrillar A $\beta$  fragments binding to C1q receptors on microglia [55]. Increased numbers of activated microglia associate particularly with neuritic plaques [60, 165, 180, 184], even though they rarely contain phagocytosed A $\beta$  and degrade it exceedingly slowly [59, 158]. Activated microglia directly produce toxic oxygen species and destructive enzymes that damage neurons [60, 95] and cause neurite retraction [143]. Microglial activation or the presence of A $\beta$  deposits also cause astrocyte recruitment in order to facilitate A $\beta$  clearance. Indeed, astrocytes in the entorhinal cortex of AD cases have been shown to contain A $\beta$ 42 in amounts proportionate to the severity of regional AD pathology [146]. However, astrocytes can also potentially act as a source of A $\beta$  by overexpressing BACE1 when chronically stressed [168]. The degree of inflammation correlates with brain atrophy [34] and the severity of dementia [156] in early AD.

## Pathogenic mechanisms of genetic forms of AD

Mutations in APP, PSEN1 and PSEN2 have all been shown to affect APP processing to alter the levels and/or length of A $\beta$  produced, consistent with the amyloid cascade hypothesis [75]. Different APP mutations cause neuronal death via different pathogenic mechanisms [78], although all APP mutations cluster around the  $\beta$ - and  $\gamma$ -secretase cleavage sites to increase the overall production of A $\beta$  by enhancing  $\beta$ -secretase cleavage [38], or modifying  $\gamma$ -secretase processing [193]. Some APP mutations also increase production of the AICD and other C-terminal APP fragments [102]. These fragments have been shown to play a direct role in modulating gene expression, cytoskeletal dynamics and apoptosis [61, 99, 142, 148]. Other APP mutations affect alternate intracellular mechanisms to increase cellular vulnerability to oxidative stress and death [54].

PSEN1 and PSEN2 are alternate subunits of the  $\gamma$ secretase protein complex with mutations directly affecting A $\beta$  peptide metabolism through  $\gamma$ -secretase cleavage to increase A\u00f342 production [22, 32, 37, 139, 176]. However, experimental loss of PSEN1 and PSEN2 results in an age-related, progressive neurodegeneration characterised by synaptic loss, neuronal death, astrogliosis and tau hyperphosphorylation [13, 174] but virtually no A $\beta$  production [47, 81]. In fact some PSEN1 mutations cause severe neurodegeneration in the absence of A $\beta$  pathology as evidenced by the identification of a number of families with mutations in PSEN1 and frontotemporal dementia [49, 164], although further evidence for mutation segregation in these families is necessary. This has lead to the hypothesis that PSEN mutations give rise to AD through an additional partial, or in some instances a complete, loss of function [224]. The  $\gamma$ -secretase protein complex interacts with a large number of substrates [205] and mutations in PSEN have been shown to reduce its proteolytic activity towards several substrates [14] while enhancing APP metabolism to increase A $\beta$ 42 production [22, 32, 37, 139, 176]. Given that the  $\gamma$ -secretase protein complex has a large number of substrates, either a shift in substrate specificity or a partial loss of function may result in a diverse spectrum of toxicity.

The increase in A $\beta$  peptide production of these mutations is thought to produce quantitative differences in the diagnostic pathologies (namely plaques and NFT) between genetic and sporadic forms of AD. Many studies have reported an increase in overall AB plaque pathology in APP, PSEN1 and PSEN2 cases compared to sporadic AD (Table 1) [63, 64, 88, 89, 108, 128, 130, 131]. However, most studies show considerable overlap with a recent report showing no statistical difference between plaque loads in PSEN1 and sporadic AD [226], similar to reports in PSEN2 Volga German families [127] and in other studies of PSEN1 and APP AD cases [122, 131, 153]. In contrast, all studies appear to agree on the fact that the majority of plaques contain A $\beta$ 42 in genetic forms of AD, often with no increase in Aβ40 compared to sporadic AD cases (Table 1) [63, 90, 127, 128, 131]. However, an increase in the mean area of cortex occupied by A $\beta$ 40 positive plaques has been reported in one of the largest studies of PSEN1 AD [89]. The reason for the discrepancy between studies is unclear, although mutation position is likely to account for some of the variations reported, at least in the PSEN1 cases [128]. It should also be noted that dramatic quantitative variations in neuropathology can exist in subjects with identical PSEN1 mutations, even when they are members of the same family [63].

Unfortunately, there are only limited studies describing the effect of PSEN or APP mutations on oligometric  $A\beta$ concentrations, with most studies including very small numbers of cases [83, 108, 136, 149, 200-202, 210] and no studies on PSEN2 AD. These studies have largely shown increases in both soluble, and to a greater extent, insoluble A $\beta$ 42 in genetic compared to sporadic AD brain tissue (Table 2). This is consistent with the increased  $A\beta 42$ plaque burden described above. The data concerning Aβ40 appear more variable with some studies showing no change or a decrease compared to sporadic AD [136, 149, 200, 201] while others have shown increases [83, 108, 136, 200, 202], consistent with some immunohistochemical findings [89]. While these data support a growing body of literature demonstrating an increase in A $\beta$ 42 in genetic forms of AD, it is not easy to reconcile the variable reports concerning A $\beta$ 40, especially in light of in vitro and in vivo studies demonstrating mutation-specific decreases in Aβ40 [22, 51, 85, 108, 201, 213, 224]. However, there is also variability among these studies, with some mutations failing to demonstrate any change in A $\beta$  [12, 185], while others report a decrease in Aβ42/Aβ40 ratio, suggesting a relative increase in A $\beta$ 40 [2], although additional studies to determine the pathological relevance of this mutation is required. Indeed, discrepancies between in vitro and human brain measurements of Aβ40 have also been observed in a single study using the same gene mutation [108]. Some of these studies have also found decreased levels of AB40 and AB42 in controls compared to sporadic AD cases, indicating that enhanced A $\beta$ 42 production driven by  $\gamma$ -secretase activity is not a feature of sporadic AD [200, 201].

## Vascular Aß

Amyloid precursor protein mutations are often associated with severe cerebral amyloid angiopathy (CAA) (Fig. 2v) and consequent cerebral haemorrhage or stroke, in addition to the conventional neuritic pathology (neuritic plaques, neuropil threads, NFT) [42, 107]. The type of A $\beta$  deposited in vessels in CAA is A $\beta$ 40 (Fig. 2v), while plaques contain both A $\beta$ 40 and A $\beta$ 42 [166]. In some APP mutation cases, CAA dominates and there is little to no coexisting AD pathology or progressive dementia [107]. This is particularly observed in Dutch APP mutation carriers where the cognitive impairment is mostly due to recurrent vascular events, as AD pathology is rarely present [23, 150]. CAA is also found in some PSEN1 and PSEN2 mutations. There is evidence that mutations occurring in the PSEN1 gene after codon 200 have a higher incidence of severe CAA and more plaque formation [128]. Assessment of a single case with a novel L282V PSEN1 mutation agrees with this observation, finding significant AB40 in the vessels and plaque cores and N-truncated A $\beta$ 42 in diffuse plaques [48]. Neuropathological examination of a family carrying a PSEN2 mutation identified five of six demented members fulfilling the pathological criteria for AD and four of these had mild to severe CAA with evidence of a vascular event in one [152].

In addition to fibrillar CAA deposition in vessel walls (sometimes extending into the lumen and out into the parenchyma), patients with APP mutations often have abnormal A $\beta$  deposits associated with the CAA. Patients with the Flemish APP mutation often form plaques with unusually large, dense and sometimes multiple cores around or adjacent to vessels [30, 42, 107] (Fig. 2v). The Arctic APP mutation causes a more typical CAA of sub-arachnoid and parenchymal vessels, but has an unusual ring-like plaque lacking a central core but staining strongly with A $\beta$ 42 [11]. The Iowa APP mutation has a late age of onset compared with the Italian APP mutation with both exhibiting severe CAA with vessel thickening, calcification and occlusion in addition to vessel-associated dystrophic neurites [67, 209].

# $A\beta$ cotton wool plaques

A $\beta$  cotton wool plaques (CWP) are most often observed in PSEN1 mutations affecting exons 8 and 9 [31, 43, 52, 83, 97, 110, 128, 129, 182, 188, 198, 211] but are also reported in PSEN1 mutations in exons 4 [192], 5, 6 [182], 12 [186] and intron 8 [52]. They occur in addition to the diffuse, neuritic

Table 1 Summary o	of con	nparative studies	investigating con	rtical plaque load	1 (% 0	f cortex occupie	d by plaque) in c	ases with sporadi	ic and genetic f	orms of AD		
References	Con	trol			Spor	adic AD			Genetic AD			
	Ν	Αβ42	Αβ40	Ratio	Ν	Αβ42 (%)	Aβ40 (%)	Ratio Aβ42:40	z	Αβ42 (%)	Αβ40 (%)	Ratio A \$42:40
Iwatsubo [90]	5	Actual values not given	Actual values not given	Actual values not given	10	4.5 (2–8.7)	1.4 (0.2–4.5)	3:1	2 (APP)	9.4 13.2	0.15 0.13	62:1 101:1
Mann [130]	0	I	I	I	16	$5.3 \pm 2.2$	$1.8\pm1.6$	3:1	8 (PSEN1)	$14\pm5.4^*$	$4 \pm 2.5^{*}$	3.5:1
Mann [131]	0	I	I	I	16	$5.3 \pm 2.2$	$1.8 \pm 1.6$	3:1	5 (APP717) 3 (APP670) 2 (APP693)	$15.2 \pm 3.8$ $5.7 \pm 1.1$ $3.7 \pm 0.4$	$0.38 \pm 0.15*$ $1.7 \pm 1.4$ 0	40:1* 3:1 0
Mann [127]	0	I	1	I	16	$5 \pm 2.4$	$2.1 \pm 2.3$	2:1	6 (PSEN2) 8 (PSEN1)	$7.9 \pm 3.1$ $14 \pm 5.4^{*}$	$1.9 \pm 1.4 \\ 4 \pm 2.5^{*}$	4:1 3.5:1
Ishii [88]	0	I	1	I	7	$1.8 \pm 1.38$	$0.4 \pm 0.5$	4.5:1	2 (PSEN1)	$4.74 \pm 0.4$ $6.17 \pm 0.16$	$0.2 \pm 0.04$ $0.9 \pm 0.2$	24:1
Gomez-Isla [64]	0	I	I	I	5	$7.7 \pm 1.8$	$3.82\pm0.73$	2:1	1 (PSEN1)	15.4↑	5.9	3:1
Gomez-Isla [63]	33	Actual values not given	Actual values not given	Actual values not given	51	7 ± 3	$3.3 \pm 2.2$	2:1	7 (PSEN2) 23 (PSEN1)	$11.6 \pm 5.2^{*}$ $12.9 \pm 5^{*}$	$1.3 \pm 1.4$ $2.6 \pm 2.1$	9:1* 5:1*
Ishii [89]					14	$3.3 \pm 1.3$	$0.7 \pm 0.9$	5:1	23 (PSEN1) 6 (APP)	$5.6 \pm 2.7 \Uparrow$ $5.2 \pm 1.4 \Uparrow$	$\begin{array}{c} 1.7 \pm 1.9 \Uparrow \\ 0.7 \pm 0.6 \end{array}$	3:1
Mann [128]	0	I	I	I	25	$7.6 \pm 2.3$	$2.2 \pm 2.2$	3:1	54 (PSEN1)	$13.6\pm6^*$	$2.5 \pm 3.7$	5:1
Kumar-Singh [108]	0	I	1	I	8	Actual values not given	Actual values not given	I	6 (PSEN1)	*	*↓	I
Woodhouse [226]	S	$8.9 \pm 2.1\%$ (tot Pathological co	al plaque) ntrols		2	$7.0 \pm 1.5$ (total	plaque)		8 (PSEN1)	$12.1 \pm 1.0$ (to	otal plaque)	
Ratios provided are . * Significant ( $P \le 0$ . - Not studied	calcul .05) d:	lated from mean ifferences compa	data and rounded ured to sporadic A	up or down D								

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Table 2 Sum	nary of com	parative studies in	vestigating Aβ α	concentrati	ons in brain	tissue extracts from	n cases with sporad	lic and ger	letic forms o	f AD		
References	Control				Sporadic AI	0			Genetic AD			
	N	Αβ42	Aβ40	Ratio Aβ42:40	N	A β42	Aβ40	Ratio Aβ42:40	N	Aβ42	Αβ40	Ratio Aβ42:40
Naslund [149]	$\begin{array}{c} 4\logA\beta\\ 1\ln\betaA\beta\end{array}$	53%/total 12%/total	19%/total 32%/total	3:1 1:3	10	$18 \pm 10\%$ total A $\beta$	$46 \pm 16\%$ /total A $\beta$	1:2.5	2 (APP)	$16 \pm 6\%$ / total A $\beta$	$24 \pm 11\%$ total A $\beta$	1:1.5
Tamaoka [201]	ю	0.38 pmol/100 µl	0.7 pmol/100 µl	1:2	17	143 ± 316 pmol/100 μl	$13 \pm 13$ pmol/100 µl	11:1#	2 (APP)	5 ± 0.4 pmol/100 μl#	$1 \pm 0.2$ pmol/100 µl	5:1#*
Tamaoka [202]	0	I	I	I	∞	32 ± 66 fmol/mg (sol) 4 ± 6 fmol/mg (insol)	25 ± 31 fmol/mg (sol) 1 ± 1 fmol/mg (insol)	1.3:1	1 (APP)	27 fmol/mg (sol) 67 fmol/mg (insol)	250 fmol/mg (sol) 101 fmol/mg (insol)	1:9
Tamaoka [200]	15	$2.2 \pm 0.9 \text{ nmol/g}$	$0.2 \pm 0.1$ nmol/g	11:1	22	9.9 土 2.4 nmol/g#	$7.4 \pm 3$ nmol/g#	1.3:1#	4 (APP) 7 (PSEN1)	19.9 ± 5.7 nmol/g#* 37 ± 7 nmol/g#*	$1.5 \pm 8.8 \text{ nmol/g}$ $11.5 \pm 9 \text{ nmol/g}$	13:1*
Houlden [83]	0	1	I	I	14	3.14 μg/g	1.66 µg/g	2:1	2 (PSEN1)	35.34 µg/g 35.21 µg/g	56.18 μg/g 20.05 μg/g	3:1
Miklossy [136]	e	QN	ŊŊ	I	2 FAD no mutation	8.84 ng/mg ND	4.93 ng/mg 6.28 ng/mg	2:1	3 (PSEN1)	230.1 ng/mg 78.5 ng/mg 12.12 ng/mg	13.56 ng/mg ND ND	17:1*
Verdile [210]	13	Actual values not given	Actual values not given	I	6	Actual values not given	Actual values not given	I	8 (PSEN1)	Actual values not given ↑	Actual values not given ↑	I
Kumar-Singh [108]	0	I	I	I	9	Actual values not given	Actual values not given	I	8 (PSEN1)	¢	¢	I
Ratios provided # Significant dif * Sionificant (P	are calculat ference com < 0.05) diffe	ed from mean data a pared to controls	und rounded up of snoradic AD	r down								

\* Significant ( $P \le 0.05$ ) difference compared to sporadic AD

ND not detected - Not studied



Fig. 2 Representative micrographs of variant pathologies in the inferior temporal cortex of genetic forms of AD. **i** Haematoxylin and eosin stained section of a PSEN1 AD case demonstrating a cotton wool plaque (CWP). Note the lack of cellular infiltrate as indicated by an absence of glial nuclei. **ii** Section of a PSEN1 AD case immunohistochemically stained with an antibody against tau protein (tau-2). Tau-2 immunohistochemistry reveals globular staining in CWP. **iii** Immunohistochemical labelling of an inflammatory plaque (IP) stained with an antibody against Aβ42 and glial fibrillary acidic protein (GFAP) and

and cored AD plaque types, and have been noted infrequently in sporadic AD [118, 230]. To date, 30 PSEN1 families with 25 defined mutations have been identified with CWP pathology [52, 72, 97, 186].

Cotton wool plaques have several characteristic features, notably that they are larger than most diffuse or neuritic plaques (up to 150 µm in diameter), have eosinophilic properties, clearly defined margins and little neuritic or inflammatory infiltrate [43] (Fig. 2i, ii). Staining with thioflavin S to detect fibrillar AB shows only very weak reactivity [43, 192, 198, 211]. When immunostained, CWP display strong positivity for A $\beta$ 42 and weak or little A $\beta$ 40 [129, 137, 186, 192, 198, 207, 211]. Immunohistochemistry also indicates the presence of non-hyperphosphorylated tau-2 [182] (Fig. 2ii) and shows variable positivity for AT8 phospho-tau within [198, 211] and around the margins of the plaques [129, 207]. Very little complement (C1q, C3d and C9) or glial activity [43, 129] is seen around CWP with immunostaining. More recently, the synaptic proteins synapsin-1 and synaptophysin have been found in CWP in the C410Y PSEN1 mutation [72]. The typical distribution pattern of CWP follows that of neuritic and diffuse plaques in AD, which are mainly found in the neocortex, particularly

counterstained with cresyl violet (*purple*) to reveal the unstained core. Abundant GFAP-positive astrocytes surround the A $\beta$ -negative core of IPs. **iv** Immunohistochemical labelling of a classic cored plaque stained with an antibody against A $\beta$ 42 in a sporadic AD case. Unlike IPs, these plaques have a dense A $\beta$ -positive core. **v** Immunohistochemical labelling with an antibody against A $\beta$ 40 in an APP AD case demonstrating severe A $\beta$ 40 cerebral amyloid angiopathy and unusual parenchymal A $\beta$ 40 plaques

the frontal, cingulate and temporal cortices as well as limbic regions and striatum [192, 198, 211]. They extend through all cortical layers, often encroaching into the superficial white matter [186].

## Atrophy and neuronal loss

A recent study has demonstrated greater rates and amounts of atrophy in PSEN1 and APP cases, particularly in the medial temporal lobes, despite similar disease durations [68, 69]. Greater amount and rate of neuronal loss in PSEN1 AD has also been observed in frontal and temporal regions compared to APP and sporadic AD (Table 3) [63, 69, 144, 181]. This effect may be due to the influence of PSEN1 on other substrates of the  $\gamma$ -secretase complex, such as  $\beta$ -catenin, N-Cadherin, GSK-3 $\beta$ , tau, calsenilin, Bcl2 proteins, metalloproteases and Notch to name just a few [205]. All of these substrates have been implicated in AD-related pathologies, such as disturbed calcium homeostasis (calsenilin), apoptosis (Bcl2), abnormal protein aggregation (tau, GSK-3 $\beta$ ) and alterations in the cell cycle  $(\beta$ -catenin). Both in vitro and in vivo studies have demonstrated detrimental effects of PSEN mutations on apoptosis

References	Con	trol	Spor	adic AD	Genetic AD	
	N	Neuronal loss	N	Neuronal loss	N	Neuronal loss
Gomez-Isla [63]	33	$9.42 \pm 1.06$ (neurons × 10 <sup>4</sup> )	51	$4.82 \pm 2.2$ (neurons × 10 <sup>4</sup> ) #	7 (PSEN2) 23 (PSEN1)	$4.45 \pm 1.07 \text{ (neurons } \times 10^4)\text{#}$ $4.98 \pm 1.98 \text{ (neurons } \times 10^4)\text{#}$
Muench [144]	1	AD values expressed as % of controls	2	Actual values not given	4 (PSEN1)	65–80% loss in CA1 compared with controls
Shepherd [181]	23	All AD values expressed as % of controls	13	Frontal 82 $\pm$ 3 Medial temporal 78 $\pm$ 4 Other temporal 71 $\pm$ 4	10 (PSEN1) 3 (APP)	Frontal 71 $\pm$ 4*/57 $\pm$ 15* Medial temporal 56 $\pm$ 6*/36 $\pm$ 4* Other temporal 59 $\pm$ 4*/47 $\pm$ 3*
Gregory [68]	7	$30.4 \pm 1.2$ neurons/field	6	$23.7 \pm 1.2$ neurons/field#	17	19.5 $\pm$ 0.8 neurons/field*#

Table 3 Summary of comparative studies investigating neuronal loss in cases with sporadic and genetic forms of AD

# Significant difference compared to controls ( $P \le 0.05$ )

\*Significant difference compared with sporadic AD ( $P \le 0.05$ )

Table 4 Summary of comparative studies investigating NFT load in cases with sporadic and genetic forms of AD

References	Control		Spora	adic AD	Genetic/familial	Genetic/familial AD	
	N	NFT	N	NFT	N	NFT	
Lantos [115]	0	-	1	Specific values not given	1 (PSEN1)	No difference found	
Nochlin [151]	16	Specific values not given	28	Specific values not given#	32 (mutations not known)	No difference in NFT or neuritic plaques#	
Lippa [122]	0	_	11	Specific values not given	19 (PSEN1) 6 (APP)	No difference in NFT or neuritic plaques	
Gomez-Isla [64]	0	-	5	$10.1 \pm 4.6$ (total NFT × $10^3$ )	1 (PSEN1)	11.41 (total NFT x10 <sup>3</sup> )	
Gomez-Isla [63]	33	-	51	$7.4 \pm 4.6 \text{ (total NFT} \times 10^3)$	7 (PSEN2) 23 (PSEN1)	$7.3 \pm 4.2$ (total NFT × 10 <sup>3</sup> ) 9.6 ± 3.6 (total NFT × 10 <sup>3</sup> )	
Thaker [203]	0	-	109	${\sim}2.5\%$ of total cortical area in cases matched for ApoE	24 (PSEN1) 5 (PSEN2) 6 (APP)	$\sim 2.5\%$ of total cortical area in cases matched for ApoE	
Heckmann [79]	0	_	3	30/mm <sup>2</sup>	1 (PSEN1)	>50/mm <sup>2</sup>	
Sudo [197]	6	Data not shown	26	CA4: 22.4 $\pm$ 3.6/mm <sup>2</sup> CA3: 20.3 $\pm$ 4.3/mm <sup>2</sup> CA2: 36 $\pm$ 6/mm <sup>2</sup> CA1: 82 $\pm$ 8/mm <sup>2</sup> Subiculum: 86 $\pm$ 11/mm <sup>2</sup> Entorhinal: 144 $\pm$ 10/mm <sup>2</sup>	6 (PSEN1) 7 (APP)	CA4: $42 \pm 8/41 \pm 7/mm^2$ CA3: $43 \pm 7.5^*/47 \pm 8^*/mm^2$ CA2: $96 \pm 18^*/96 \pm 23^*/mm^2$ CA1: $168 \pm 15^*/133 \pm 21^*/mm^2$ Subiculum: $47 \pm 6/103 \pm 15/mm^2$ Entorhinal: $89 \pm 11/100 \pm 14/mm^2$	
Woodhouse [226]	0		5	$19.0 \pm 2.4/1{,}000 \ \mu\text{m}^2$	8 (PSEN1)	$17.6 \pm 2.7/1,000 \ \mu m^2$	

\* Significant difference compared with sporadic AD ( $P \le 0.05$ )

- Not studied

[10, 53], cell cycle events [1, 125], oxidative stress [21], mitochondrial dysfunction [99] and calcium dysregulation [134]. Enhanced levels of cyclin D1 indicative of abortive  $\beta$ -catenin regulation of cell cycle re-entry are found in some PSEN1 cases [125] and mutant PSEN can alter calcium signalling [36] and inactivate neuroprotective signalling pathways [9] to enhance neuronal degeneration.

## Tau pathology

In spite of an increase in neuronal loss in genetic forms of AD (see above), it is not clear whether this is related to a general

increase in NFT. Some studies show an increase in NFT compared to sporadic cases [79, 197] while others report no change [63, 64, 116, 122, 153, 226] (Table 4). This variability may be partly due to variation in the ApoE gene, which appears to affect tau and A $\beta$ 40 load [203]. Sudo and colleagues [197] report that the effects of ApoE on tau pathology is region specific with the entorhinal cortex being the initial site of NFT formation in sporadic AD compared to the CA regions of the hippocampus in APP and PSEN1 AD [197].

A significant increase in plaque-associated tau deposition has been reported in PSEN1 AD with this difference being markedly greater than the difference in A $\beta$  deposition

(6.6-fold versus 2-fold increase, respectively) [182]. A significant increase in phosphorylated tau protein within the neuropil has also been shown in PSEN1 cases [118] with PSEN1 gene mutations increasing total tau protein levels in A $\beta$  treated neurons [161]. Deposition of additional non-fibrillar, non-hyperphosphorylated tau has also been reported in CWP in PSEN1 AD [182] consistent with an accelerated rate of cytoskeletal pathology in these cases [226]. However, a mutational deletion in exon 8 (L271V) of PSEN1 results in a complete absence of neuritic plaque pathology and a decrease in PSEN1 function [110]. Furthermore, in cases with mutations in PSEN1 giving rise to frontotemporal dementia [49, 164] and transgenic mice with common PSEN1 mutations [117] there is significant tau pathology without A $\beta$  deposition indicative of alterations in tau processing and tau kinases [10, 199].

To date several studies have investigated the concentrations of tau in the soluble and PHF protein fractions in sporadic AD cases using biochemical techniques [7, 24, 28, 74, 82, 87, 100, 113, 119, 141, 204, 217, 223]. These studies show a redistribution of soluble tau to PHF consistent with increased NFT pathology in AD [25]. However, only one study has performed a quantitative analysis of the detergent-insoluble tau in PSEN1 and PSEN2 AD compared to sporadic cases and found no increase using a proteomic approach [225]. Further analysis of changes in tau expression, aggregation and phosphorylation in genetic forms of AD is now required in order to elucidate the role of APP and PSEN in tau pathology.

## Inflammation

Imaging studies of sporadic AD demonstrate an association between microglial activation, brain atrophy and clinical progression [34]. However, no microglial imaging studies have been carried out in genetic forms of AD, and only a few studies have described the inflammatory response in these cases [120, 183, 189]. While CWP have consistently been reported as being devoid of cellular infiltrate, PSEN1 cases display a potent inflammatory response around other plaques [183] and have greater levels of inflammatory mediators in soluble brain tissue extracts [189], possibly due to a loss of PSEN regulation of inflammation [13]. These plaques with increased inflammation have been called inflammatory plaques (IP) and are found in cortical regions of both PSEN1 and APP mutation cases [181, 183].

Inflammatory plaques are small (around 25 µm diameter), dense and well-circumscribed with a distinct core and accumulations of surrounding reactive microglia and astrocytes (Fig. 2iii). The plaque core has a particularly curious staining profile, showing positivity with simple histological stains such as silver, haematoxylin and eosin, cresyl violet and thioflavin S (Fig. 2iii), but negativity for many of the components of conventional neuritic plaque cores (Fig. 2iv) such as A $\beta$ , tau, ApoE, ubiquitin, PSEN1, IgG,  $\alpha$ -synuclein, filipin and glial fibrillary acidic protein. HLA-DR, ferritin and glial fibrillary acidic protein immunohistochemistry demonstrate the presence of significant numbers of activated microglia and astrocytes in the areas immediately surrounding IP [183] (Fig. 2iii). While the presence of IP per se are not associated with greater neuronal loss [181], increases in specific inflammatory mediators may play an important role in the disease process and contribute to the greater neurodegeneration observed in genetic forms of AD [189] and in PSEN1/APP transgenic models of AD [66, 109, 160].

## Conclusions

Most PSEN1 and PSEN2 mutations and many APP mutations enhance Aβ42 production over that observed in sporadic AD via changes in  $\gamma$ -secretase processing of APP, thereby supporting the amyloid cascade hypothesis [75]. This is reflected in greater hippocampal atrophy and NFT, and more significant cortical deposition of insoluble fibrillar A $\beta$ 42 plaques, which in PSEN1 cases with mutations in exons 8 and 9 forms enlarged CWP structures. More substantial inflammation is associated with a proportion of plaques (IP) in these cases. AB40-enhanced CAA is a feature of many cases with AD mutations, but particularly those with APP mutations where CAA can be the dominant pathology. Additional frontotemporal neuronal loss in association with tau increases appears unique to PSEN mutations, possibly due to an additional loss of PSEN function. These data indicate that APP and PSEN mutations have widespread effects on a broader range of cellular functions [16, 46, 96, 101, 115, 132, 145, 172, 206] compared to sporadic AD. These important differences need to be carefully considered when using these mutations to model AD. In particular, the enhanced  $\gamma$ -secretase production of A $\beta$ 42 is not a feature of sporadic AD.

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