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Etiology, Genetics, and Pathogenesis of Alzheimer's Disease

I. Amyloid Hypothesis

Alzheimer's disease (AD) is an age-related neurodegenerative disease that causes a global loss of cognitive function and behavioral deficits. Although cholinesterase inhibitors can improve cognitive function slightly (Knopman and Morris, 1997), truly efficacious drugs for AD treatment and/or prevention are not yet available. However, the etiology of AD is beginning to yield to scientific inquiry. Plausible strategies for treatment and/or prevention have been formulated, but await further research. In the United States, AD afflicts four million individuals and imposes an annual tab of \$80–100 billion (Hoyert and Rosenberg, 1999). Thus, one can readily appreciate the importance of recent progress in AD research. This chapter summarizes the current understanding of AD etiology and pathogenesis.

AD cases can be classified as “familial” or “sporadic.” Familial AD occurs in both early-onset (before age 65) and late-onset kindreds. In 1990, a mutation in the amyloid precursor protein (APP) was reported to cause hereditary cerebral hemorrhage with amyloidosis Dutch type (Levy *et al.*, 1990). This finding linked amyloid deposition to an APP mutation for the first time and enabled investigators to embrace the idea that plaques were an important cause of neurodegeneration, rather than merely end products of a neurodegenerative process. Later, APP mutations were found to cause AD in a small number of early-onset, autosomal-dominant pedigrees (see Table 22.1).

The neuropathological hallmark of AD is the presence of neuritic plaques in brain parenchyma and cerebral blood vessels. Neuritic plaques consist of a protein core, surrounded by degenerating neurites, astrocytes, and activated macrophages. Alzheimer brain is also characterized by the presence of neurofibrillary tangles (NFT; accumulations of paired helical filaments within neuronal cell bodies), the loss of synapses and neurons, and reduced neurotransmitter concentrations. Cholinergic neurons are especially vulnerable to cell death; these neurons arise in the basal forebrain and terminate in the hippo-

campus and cerebral cortex. Neurofibrillary tangles consist primarily of ubiquitin and tau, a microtubule-associated protein.

The core protein of plaques is $A\beta$, a peptide derived from the amyloid precursor protein (APP), which is 39–43 amino acids long (Glennner and Wong, 1984). Plaques also contain numerous other components, including apolipoprotein E (Namba *et al.*, 1991), α_1 -antichymotrypsin (Abraham *et al.*, 1988), serum amyloid P (Coria *et al.*, 1988), interleukin-1 (Griffin *et al.*, 1995), basic fibroblast growth factor (Gomez-Pinilla *et al.*, 1990), α_2 -macroglobulin (Bauer *et al.*, 1991), low-density lipoprotein-related protein (LRP) (Tooyama *et al.*, 1993), and perlecan (a heparin sulfate proteoglycan). Evidence for an inflammatory contribution to AD is provided by the presence of approximately 40 proteins known to play a role in inflammation (McGeer *et al.*, 1996). Plaques are enriched in the small molecules, zinc, copper, and iron (Lovell *et al.*, 1998).

Within plaques, the primary form of $A\beta$ is $A\beta_{42}$, a highly-insoluble peptide that readily adopts a β -pleated sheet conformation (Iwatsubo *et al.*, 1994, 1995; Fukumoto *et al.*, 1996). $A\beta$ molecules assemble into fibrils, which then pack into a highly ordered, crystalline-like lattice known as amyloid. The term “amyloid” can be applied to deposits derived from any protein in which a similar arrangement of molecules occurs. In addition to a core protein, all amyloid deposits are marked by the presence of heparan sulfate proteoglycans. “Diffuse” plaques are those in which $A\beta$ molecules have not assembled into fibrils. Generally speaking, diffuse plaques are not surrounded by dystrophic neurites, activated microglia, or astrocytes. They occur in greater numbers than neuritic plaques and may be neuritic plaque precursors (Mackenzie, 1994). Neuritic plaque formation also occurs in Down syndrome and, to a lesser extent, in normal aging (Selkoe, 1991).

The “amyloid hypothesis” refers to the proposition that events leading to the manifestation of AD originate with the deposition of $A\beta$ in amyloid deposits. Although flawed (or incomplete), this hypothesis is now supported by a large body of experimental work. It is worth noting that amyloid deposition occurs in other disorders such as Down syndrome,

TABLE 22.1 Amyloid Precursor Protein Mutations Associated with AD or Stroke

Pathogenic mutation	Reference
K/M 670/671 N/L (Swedish)	Mullan <i>et al.</i> (1992)
A682G (Flemish)	Hendricks <i>et al.</i> (1992)
E693Q (Dutch)	APP mutation implicated in hereditary cerebral hemorrhage with amyloidosis-Dutch (Levy <i>et al.</i> , 1990)
V715M (French)	Ancolio <i>et al.</i> (1999)
I716V	Eckman <i>et al.</i> (1997)
V717I (London)	Goate <i>et al.</i> (1991)
V717F	Murrell <i>et al.</i> (1991)
V717G	Chartier-Harlin <i>et al.</i> (1991)

Creutzfeldt–Jacob disease, Gertsman–Sträussler–Scheinker disease, type II diabetes, familial amyloid polyneuropathy, and multiple myeloma. Aberrant protein deposition is a common theme in neurodegenerative disease (Kaytor and Warren, 2000). In Parkinson's disease, two mutations in the α -synuclein gene that cause early onset disease also accelerate α -synuclein aggregation (Narhi *et al.*, 1999).

Clearly, both environmental and genetic factors contribute to the risk of AD. Evidence from twin studies supports a role for environmental variables in AD (Breitner *et al.*, 1995; Nee and Lippa, 1999). Among the factors suggested to modify the risk for AD are head injury (Molgaard *et al.*, 1990; Roberts *et al.*, 1994), educational attainment (Stern *et al.*, 1992; Cobb *et al.*, 1995; Callahan *et al.*, 1996; Geerlings *et al.*, 1999), depression (Kokmen *et al.*, 1996; Chen *et al.*, 1999), smoking (Hebert *et al.*, 1992; Lee, 1994; Hillier and Salib, 1997; Merchant *et al.*, 1999), vitamin E consumption (Vatassery *et al.*, 1999), diabetes (Leibson *et al.*, 1997) and hypertension (Skoog *et al.*, 1998; Behl, 1999). A review of the literature cited earlier will reveal that the legitimacy of many so-called environmental risk factors is open to debate. Stronger, but not conclusive, evidence indicates that estrogen replacement (Birge, 1997; Haskell *et al.*, 1997) and the chronic use of nonsteroidal anti-inflammatory drugs may reduce the risk of AD (McGeer *et al.*, 1996). AD and peripheral vascular disease share several risk factors in common; this indicates that impaired cholesterol metabolism may play a role in AD etiology (McKeon-O'Malley *et al.*, 1998). It remains to be determined whether any environmental factor is sufficient to cause AD in the absence of a permissive genotype.

On the genetic front, the identification of several AD-linked genes has yielded important insights into the etiology of AD, and steady progress continues to be made in this area. Female gender is a risk factor for AD, even when the longer life span of females is taken into account (Letenneur *et al.*, 1999). Almost all individuals with Down syndrome (trisomy 21) develop AD in midlife (Katzmann, 1986), presumably due to the overexpression of the APP gene on chromosome 21. The linkage of specific genes to AD risk is discussed in the following section.

II. Genetic Contributions to the Etiology of AD

To date, seven of the genes linked to AD include: the amyloid precursor protein (Chartier-Harlin *et al.*, 1991; Goate *et al.*, 1991; Murrell *et al.*, 1991), presenilin 1 (PS1) (Sherrington *et al.*, 1995), presenilin 2 (PS2) (Levy-Lahad *et al.*, 1995b), apolipoprotein E (Corder *et al.*, 1993), α_2 -macroglobulin (Blacker *et al.*, 1998; Liao *et al.*, 1998), LRP (also known as the α_2 M receptor) (Kang *et al.*, 1997; Wavrant-DeVrièze *et al.*, 1997; Hollenbach *et al.*, 1998), and tau (Lilius *et al.*, 1999; Bullido *et al.*, 2000). Importantly, four of these proteins are related to each other: APP, ApoE, and α_2 -macroglobulin are ligands for LRP.

Preliminary evidence has been presented for the involvement of other genes with AD (see Table 22.2). However, data do not permit firm conclusions to be drawn about other genes at this time. Deterministic mutations (i.e., mutations that can cause AD with 100% penetrance) occur in the genes for the amyloid precursor protein, presenilin 1 and presenilin 2, but these mutations account for only a small percentage of total AD cases. Mutations in APP and the presenilins cause AD by increasing the extracellular load of $A\beta_{42}$ (Scheuner *et al.*, 1996). Polymorphisms in the genes for apolipoprotein

TABLE 22.2 Genes in Which Mutations or Polymorphisms May Modify the Risk of AD^a

Gene	Reference
Angiotensin 1-converting enzyme	Alvarez <i>et al.</i> (1999)
α_1 -Antichymotrypsin	Haines <i>et al.</i> (1996); Talbot <i>et al.</i> (1996)
Bleomycin hydrolase	Farrer <i>et al.</i> (1998); Montoya <i>et al.</i> (1998)
Butyrylcholinesterase K	Brindle <i>et al.</i> (1998); Crawford <i>et al.</i> (1998); Hiltunen <i>et al.</i> (1998); Singleton <i>et al.</i> (1998); Tilley <i>et al.</i> (1999)
Cathepsin D	Papassotiropoulos <i>et al.</i> (1999)
Dihydrolipoyl succinyltransferase (DLST)	Sheu <i>et al.</i> (1999)
Estrogen receptor α gene	Brandi <i>et al.</i> (1999)
HLA	Ballerini <i>et al.</i> (1999)
Lipoprotein lipase	Baum <i>et al.</i> (1999)
Mitochondrial genome	Davis <i>et al.</i> (1997); Egensperger <i>et al.</i> (1997); Chagnon <i>et al.</i> (1999)
Myeloperoxidase	Reynolds <i>et al.</i> (1999)
Neurotrophin-3	Kunugi <i>et al.</i> (1998)
Nitric oxide synthase 3	Dahiyat <i>et al.</i> (1999)
Serotonin transporter gene	Oliveira <i>et al.</i> (1998, 1999); Li <i>et al.</i> (1999)
Very low density lipoprotein receptor	Okuizumi <i>et al.</i> (1995, 1996); Pritchard <i>et al.</i> (1996)

^aThe genes may be associated with AD. Cited references include articles that report the association of a particular gene with AD, or a lack of such an association.

E, α_2 -macroglobulin, LRP, and tau are known to increase the risk of AD. A brief description of each of these genes is given.

A. Amyloid Precursor Protein

As indicated earlier, the core protein of neuritic plaques, A β , is derived from APP. The APP gene is located at the boundary of 21.q.3 and 21.q22.1 (Kang *et al.*, 1987) and is widely expressed in human tissues (Tanzi *et al.*, 1988). Ten transcripts can be produced by alternative splicing of 19 exons (Wisniewski *et al.*, 1994). However, A β cannot be generated by alternative splicing (Lemaire *et al.*, 1989). Three major transcripts contain the A β sequence, and these encode proteins with 695, 771, or 770 amino acids (APP₆₉₅, APP₇₅₁, APP₇₇₀). The expression of APP₆₉₅ is confined to the brain (Sola *et al.*, 1993). APP₇₅₁ and APP₇₇₀ contain a region with 50% homology to a Kunitz protease inhibitor domain.

The APP gene lacks a TATA box and has a high GC content, features characteristic of a housekeeping gene (Salbaum *et al.*, 1988). Gene expression produces a protein with the following domains: a signal peptide for transport of APP into the endoplasmic reticulum, a cysteine-rich sequence, a sequence including many negatively charged residues (glutamic acid and aspartic acid), and an uninterrupted stretch of seven threonine residues (Kang *et al.*, 1987) (see Fig. 22.1). A zinc II-binding site is located between the cysteine-rich domain and the negatively charged region (Bush *et al.*, 1993). Two consensus sequences for N-linked glycosylation are located at amino acids 467–469 and 496–498. APP also contains a potential heparin-binding site (Small, 1994). APP is modified by post-translational mechanisms including N- and O-glycosylation (Weidemann *et al.*, 1989; Pahlsson *et al.*, 1992), sulfation (Weidemann *et al.*, 1989), and phosphorylation (Oltersdorf *et al.*, 1990). APP matures in the endoplasmic reticulum and the Golgi and then becomes inserted into the plasma membrane (Weidemann *et al.*, 1989).

APP is a member of a family of highly conserved proteins. Other members of this family include amyloid precursor pro-

tein-like protein (APLP1) and APLP2 (Sprecher *et al.*, 1993; Wasco *et al.*, 1993), but the two latter proteins do not encode A β . APP plays a role in many normal functions, including wound healing (Smith *et al.*, 1990; Van Nostrand *et al.*, 1990), proliferation (Saitoh *et al.*, 1989; Ninomiya *et al.*, 1993), adhesion (Schubert *et al.*, 1989; Breen *et al.*, 1991; Chen and Yankner, 1991; Ghiso *et al.*, 1992), neurite extension (Araki *et al.*, 1991; Milward *et al.*, 1992; Small, 1994), survival under stress (Mattson *et al.*, 1993; Yamamoto *et al.*, 1994), and synaptic plasticity (Mattson, 1994). Processes involved in the production of A β from APP are discussed under Section III.

B. Apolipoprotein E

Apolipoprotein E is a 34 kDa (299 residues) protein known primarily for its role in lipid transport (Mahley and Huang, 1999). The gene for ApoE has been mapped to chromosome 19 (Das *et al.*, 1985). Three polymorphic alleles, ϵ 2, ϵ 3, and ϵ 4 (corresponding to the proteins ApoE2, ApoE3, and ApoE4), occur at frequencies of 8, 75, and 15%, respectively. ApoE3 has Cys¹¹² and Arg¹⁵²; in ApoE2, Arg¹⁵⁸ is replaced by cysteine, and in ApoE4, Cys¹¹² is replaced by arginine. In the periphery, ApoE is synthesized primarily in the liver. ApoE cannot penetrate the blood–brain barrier, but is manufactured within the brain by astrocytes (Pitas *et al.*, 1987). Apolipoprotein E is a ligand for three cell surface receptors: the low-density lipoprotein (LDL) receptor, the low-density lipoprotein-related protein, and the very-low-density lipoprotein (VLDL) receptor.

The ϵ 4 allele of apolipoprotein E increases the risk of AD in a dose-dependent manner and lowers the age at onset (Corder *et al.*, 1993). This finding has been confirmed repeatedly in a host of ethnic groups around the world. However, it is clear that apolipoprotein E alone does not cause AD because a proportion of elderly homozygotes are unaffected (Roses *et al.*, 1994). Interestingly, the ϵ 4 allele has also been shown to increase the risk of cardiovascular disease as well as AD (Lambert *et al.*, 2000). Mutations occurring in noncoding regions of the ApoE gene are also associated with AD (see Table 22.3). In

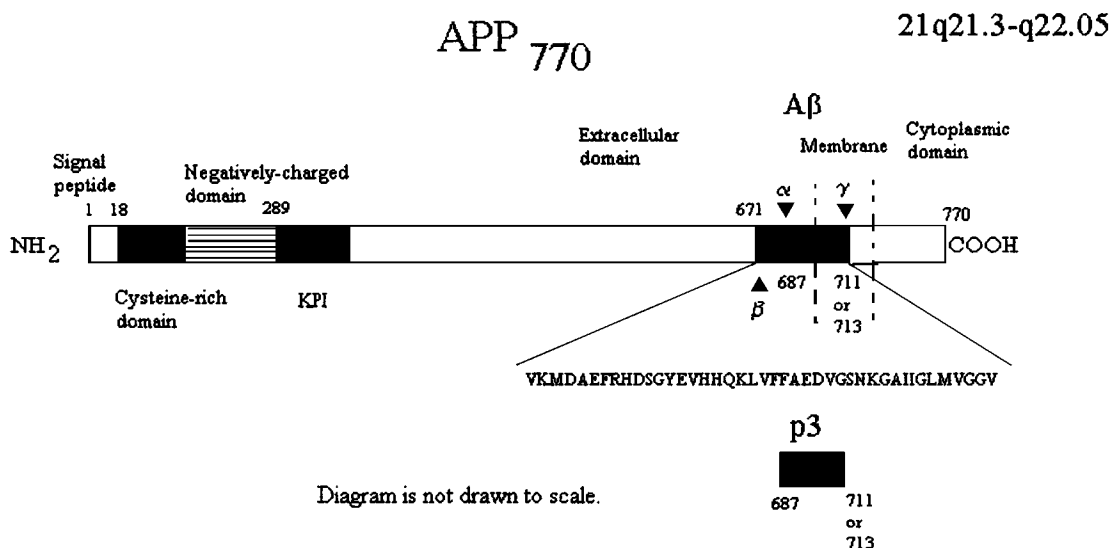


FIG. 22.1. Schematic diagram of APP (not drawn to scale).

TABLE 22.3 Apolipoprotein E Polymorphisms Associated with AD

Polymorphism	Reference
$\epsilon 2/\epsilon 3/\epsilon 4$ polymorphism	The $\epsilon 4$ allele is associated with sporadic and late-onset AD. This finding has been confirmed in more than 100 studies (Corder <i>et al.</i> , 1993)
APOE*4 Pittsburgh (APOE*4P) (this is a missense mutation, L28P, caused by a T \rightarrow C substitution in exon 3)	All APOE*4P carriers identified thus far also carry $\epsilon 4$. However, the risk of AD is five-fold greater in $\epsilon 4$ carriers who also carry APOE*4P than in those who bear the $\epsilon 4$ allele alone (Kamboh <i>et al.</i> , 1999)
Th1/E47 cs polymorphism: G to mutation occurs at -186 bp in relation to the TATA box; this polymorphism is located in a consensus sequence for the transcription factor Th1E47	The presence of at least one T allele increases the risk of AD (Lambert <i>et al.</i> , 1998)

contrast to the $\epsilon 4$ allele, the $\epsilon 2$ allele decreases the risk of AD (Corder *et al.*, 1994; Talbot *et al.*, 1994).

C. Presenilin 1 and Presenilin 2

Mutations occurring within the homologous, transmembrane proteins PS1 and PS2 cause early-onset familial AD with 100% penetrance. About 70 such mutations have been identified in PS1, whereas only 5 have been observed in PS2 (see Tables 22.4 and 22.5; Table 22.4 includes only a partial list of all PS1 mutations). Remarkably, mutations in PS1 and PS2 increase the $A\beta_{42}/A\beta_{40}$ ratio, or total $A\beta$ both *in vitro* and *in vivo* (Borchelt *et al.*, 1996; Lemere *et al.*, 1996; Mann *et al.*, 1996; Scheuner *et al.*, 1996; Citron *et al.*, 1997, 1998; Tomita *et al.*, 1997). The presenilins may be γ -secretases, the enzymes that generate final cleavage in the release of $A\beta$ from APP (Wolfe *et al.*, 1999).

PS1 and PS2 share a similar pattern of gene expression. Both proteins are expressed primarily within neurons and are localized to the endoplasmic reticulum and Golgi (Kovacs *et al.*, 1996; Blanchard *et al.*, 1997).

The gene for PS1 is located on chromosome 14q24.3 and encodes a 43 to 45 kDa protein, 467 amino acids long (George-Hyslop *et al.*, 1992; Schellenberg *et al.*, 1992). The PS2 gene has been mapped to chromosome 1q42.1 and encodes a 53 to 55 kDa protein, 448 amino acids long (Levy-Lahad *et al.*, 1995a,b; Takano *et al.*, 1997). The presenilins are predicted to contain six (Lehmann *et al.*, 1997), seven (Dewji and Singer, 1997), or eight (Li and Greenwald, 1998) transmembrane domains and a large hydrophilic loop. The N-terminal, C-terminal, and the large hydrophilic loop of PS1 protrude from the endoplasmic reticulum membrane into the cytoplasm (Doan *et al.*, 1996).

The presenilins are cleaved endoproteolytically to produce N-terminal fragments and C-terminal fragments, with approximate molecular masses of 30 and 20 kDa, respectively (Thinakaran *et al.*, 1996). This cleavage occurs at a site within the large hydrophilic loop. N- and C-terminal fragment associate with one another in a 1:1 ratio, forming a stable complex (Capell *et al.*, 1998). Measurable quantities of the full-length proteins are difficult to detect by conventional methods, strongly suggesting that the cleavage products are the physiologically relevant entities.

Potential roles for the presenilins have been suggested in protein processing, Notch signaling and development, and

apoptosis (Mattson *et al.*, 1997, 1998; Guo *et al.*, 1998a,b). Mice homozygous for a null mutation in the murine homologue of PS1 (i.e., PS1 knockout mice) die within minutes of birth (Shen *et al.*, 1997). These animals exhibit gross skeletal defects, cerebral hemorrhage, and massive neuronal loss. The lethal phenotype of these animals indicates that PS1 plays an essential role in normal development.

D. α_2 -Macroglobulin

α_2 -Macroglobulin (α_2 M) is a "pan-protease" inhibitor involved in the clearance of proteins from the blood via endocytosis (Borth, 1992). α_2 M is composed of four identical subunits (180 kDa), each of which contains a 25 residue "bait region," a cytokine-binding domain, and a receptor-binding domain. The bait region contains an internal cyclic thiol ester that is cleaved when a protease binds to α_2 M. This cleavage provokes a conformational change in α_2 M that permits it to enclose or "capture" the protease and to make its cytokine-binding and receptor-binding domains accessible for ligand binding. Activated α_2 M binds to its plasma membrane receptor, LRP, to deliver its captured protease. Ligand-LRP complexes are internalized via clathrin-coated pits and are then directed into an endosomal/lysosomal compartment (Kowal *et al.*, 1989). There, ligands are released from LRP and degraded; LRP is recycled to the plasma membrane.

The gene for α_2 M is located on chromosome 12 (Fukushima *et al.*, 1988). An AD-linked polymorphism is located in the 5' splice site of exon 18. Two polymorphisms, occurring in this locale, α_2 M-2 and α_2 M-1, specify the presence or absence of a pentanucleotide deletion. Inheritance of a single α_2 M-2 allele increases the risk of AD three- to fourfold, but does not change the age at onset (Blacker *et al.*, 1998). To date, it is not known whether the risk of AD increases with α_2 M-2 dosage. AD is also associated with a second polymorphic site, Val1000(GTC)/Ile1000(ATC), located near the cyclic thiol ester (Poller *et al.*, 1992). AD risk is increased by the presence of a valine residue at this site (Liao *et al.*, 1998). The risks conferred by the Val1000(GTC) allele of α_2 M, and the $\epsilon 4$ allele of ApoE, are independent and additive.

E. Lipoprotein-Related Protein

As described previously, LRP is a plasma membrane receptor for APP, ApoE, and α_2 M. Importantly, an $A\beta$ -serine

TABLE 22.4 A Partial List of Presenilin 1 Mutations Associated with AD

Mutation	Reference	Mutation	Reference
A79V	Cruts <i>et al.</i> (1998)	A231V	Cruts <i>et al.</i> (1998)
V82L	Campion <i>et al.</i> (1995)	M233L	Aldudo <i>et al.</i> (1999)
V96F	Kamino <i>et al.</i> (1996)	M233T	Kwok <i>et al.</i> (1997)
F105L	Finckh <i>et al.</i> (2000)	L235P	Campion <i>et al.</i> (1996)
Y115H	Campion <i>et al.</i> (1995)	A246E	Sherrington <i>et al.</i> (1995)
Y115C	Cruts <i>et al.</i> (1998)	L250S	Harvey <i>et al.</i> (1998)
T116N	Romero <i>et al.</i> (1999)	A260V	Rogaev <i>et al.</i> (1995)
P117L	Wisniewski <i>et al.</i> (1998)	L262F	Forsell <i>et al.</i> (1997)
E120D	Poorkaj <i>et al.</i> (1998b)	C263R	Wasco <i>et al.</i> (1995)
Q120D	Reznik-Wolf <i>et al.</i> (1996)	P264L	Campion <i>et al.</i> (1995)
E120K	Reznik-Wolf <i>et al.</i> (1998)	P267S	Alzheimer's Disease Collaborative Group (1995)
E123K	Yasuda <i>et al.</i> (1999)	R269G	Perez-Tur <i>et al.</i> (1996)
N135D	Crook <i>et al.</i> (1997)	R269H	Gomez-Isla <i>et al.</i> (1997)
M139K	Dumanchin <i>et al.</i> (1998)	E273A	Kamimura <i>et al.</i> (1998)
M139T	Campion <i>et al.</i> (1995)	R278T	Kwok <i>et al.</i> (1997)
M139I	Boteva <i>et al.</i> (1996)	E280A	Alzheimer's Disease Collaborative Group (1995)
I143F	Rossor <i>et al.</i> (1996)	E280G	Alzheimer's Disease Collaborative Group (1995)
I143T	Cruts <i>et al.</i> (1995)	L282R	Aldudo <i>et al.</i> (1998a)
M146I	Jorgensen <i>et al.</i> (1996)	A285V	Aoki <i>et al.</i> (1997)
M146L	Sherrington <i>et al.</i> (1995)	L286V	Sherrington <i>et al.</i> (1995)
M146V	Alzheimer's Disease Collaborative Group (1995)	E318G	Reznik-Wolf <i>et al.</i> (1998); Aldudo <i>et al.</i> (1998b); Mattila <i>et al.</i> (1998)
T147I	Campion <i>et al.</i> (1999)	G378E	Besançon <i>et al.</i> (1998)
H163R	Sherrington <i>et al.</i> (1995)	G384A	Cruts <i>et al.</i> (1995)
H163Y	Perez-Tur <i>et al.</i> (1995); Axelman <i>et al.</i> (1998)	S390I	Campion <i>et al.</i> (1999)
W165C	Campion <i>et al.</i> (1999)	C410Y	Sherrington <i>et al.</i> (1995)
S169P	Ezquerro <i>et al.</i> (1999)	L424R	Kowalska <i>et al.</i> (1999)
S169L	Taddei <i>et al.</i> (1998)	A426P	Poorkaj <i>et al.</i> (1998b)
L171P	Ramirez-Duenas <i>et al.</i> (1998)	P436Q	Taddei <i>et al.</i> (1998)
L173W	Campion <i>et al.</i> (1999)	To to G at intron 9	Nishiwaki <i>et al.</i> (1997)
E184D	Yasuda <i>et al.</i> (1997)	Intronic polymorphism located 3' to exon 8	Wragg <i>et al.</i> (1996); but see Cai <i>et al.</i> (1997), Tysoe <i>et al.</i> (1997), Sorbi <i>et al.</i> (1997)
G209R	Sugiyama <i>et al.</i> (1999)	Deletion Delta9Finn	Crook <i>et al.</i> (1998); Prihar <i>et al.</i> (1999)
G209V	Poorkaj <i>et al.</i> (1998b)	58304G>A Delta9	Sato <i>et al.</i> (1998)
I213T	Kamino <i>et al.</i> (1996)	58304G>T Delta9	Perez-Tur <i>et al.</i> (1995)
A231T	Campion <i>et al.</i> (1995)	A deletion of G from the intron four splice donor consensus sequence	Tysoe <i>et al.</i> (1998); PS1 truncating mutation

TABLE 22.5 Presenilin 2 Mutations Associated with AD

Pathogenic mutation	Reference
T122P	Finckh <i>et al.</i> (2000)
N141I	Levy-Lahad <i>et al.</i> (1995a)
M239I	Finckh <i>et al.</i> (2000)
M239V	Rogaev <i>et al.</i> (1995)
Splice variant: mRNA lacks exon 5	Sato <i>et al.</i> (1999)

protease- α 2M pathway is one of several mechanisms by which $A\beta$ is cleared (Qiu *et al.*, 1999). LRP belongs to a family of proteins that includes the LDL receptor, megalin (also known as gp330), the VLDL receptor, and the vitellogenin receptor (Krieger and Herz, 1994).

F. Tau

The diagnosis of AD in postmortem brain requires the presence of both NFT and neuritic plaques. Unlike plaques, NFT are not specific to AD; these entities occur in many neurodegenerative disorders, including supranuclear palsy, dementia pugilistica, corticobasal degeneration, and fronto-temporal dementia with parkinsonism linked to chromosome 17 (FTDP-17) (Goedert *et al.*, 1997). However, NFT density correlates well with dementia severity, whereas plaque density does not (Braak and Braak, 1991).

The primary protein component of NFT is tau (45–60 kDa), a protein that promotes the stabilization of microtubules (Weingarten *et al.*, 1975). In the central nervous system, alternative splicing of the tau gene results in the expression of six isoforms primarily (see Fig. 22.2). A seventh isoform containing a “big tau insert” is expressed prominently in the peripheral nervous system and to a much lesser extent in the central

nervous system (Georgieff *et al.*, 1993). Each isoform possesses either three or four microtubule-binding domains (repeat units of 31 amino acids, encoded by exon 10) and 0, 1, or 2 different amino-terminal inserts. Differential expression of tau isoforms occurs during development (Couchie *et al.*, 1988; Kosik *et al.*, 1989). Within NFT, tau is hyperphosphorylated (Grundke-Iqbal *et al.*, 1986), which prevents its binding to microtubules (Bramblett *et al.*, 1993).

The finding made in 1991 that mutations in the amyloid precursor protein gene can cause AD with 100% penetrance focused attention on the role of $A\beta$ in AD. Lately, there has been a resurgence of interest in tau. Tau mutations have been linked to frontotemporal dementia with parkinsonism (FTDP-17; previously known as Pick disease) (Poorkaj *et al.*, 1998a; Hutton *et al.*, 1998; Spillantini *et al.*, 1998; Iijima *et al.*, 1999) and to supranuclear palsy (Chambers *et al.*, 1999). Because plaque deposits are largely absent in FTDP-17 tauopathies, the latter findings indicate that tau aggregation is sufficient for neurodegeneration (Ghetti *et al.*, 1999).

Several groups have searched for AD-linked mutations in the tau gene without success (Crawford *et al.*, 1999; Roks *et al.*, 1999). However, two reports indicate that polymorphisms in the tau gene may increase the risk for AD when found in combination with the ApoE ϵ 4 allele (Lilius *et al.*, 1999; Bullido *et al.*, 2000).

III. Pathogenesis

A. Fundamental Questions in AD Research

Most of the current research in AD is designed to address one of the following questions:

What factors regulate the cleavage of $A\beta$ from APP, and $A\beta$ assembly into fibrils?

How does $A\beta$, alone or in combination with other plaque components, cause neuronal cell death?

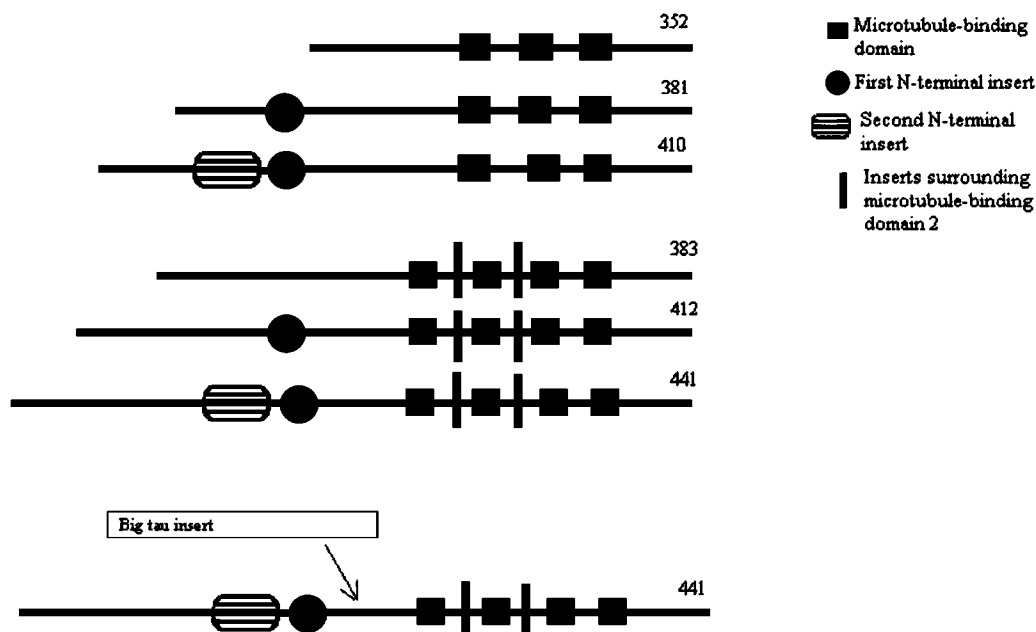


FIG. 22.2. Schematic diagram of tau protein isoforms.

What is the role of inflammation in the maturation of neuritic plaques?

What is the role of tau in AD?

A thorough discussion of last three questions is beyond the scope of this chapter (see Tolnay and Probst, 1999, for a review of the role of tau in AD.) This chapter concentrates, how $A\beta$ is produced from APP, and on $A\beta$ fibrillogenesis.

B. Amyloid, Neuritic Plaques, and Paired Helical Filaments

Within specific brain locale, certain conditions (as yet undefined) permit soluble $A\beta$ molecules to adopt a high degree of β -pleated sheet conformation; this alteration facilitates the rearrangement of $A\beta$ molecules into fibrils. Fibrils pack in cross- β conformation to form amyloid, a highly ordered arrangement of protein molecules that can be detected using Congo Red or Thioflavin S (Kirschner *et al.*, 1987). Neuritic plaques, but not diffuse plaques, are visualized using these stains. Fibril stability is critically dependent on the primary structure of the peptide. This is exemplified by the fact that an APP mutation associated with early-onset FAD, $A\beta_{E22Q}$, increases the stability of $A\beta$ fibrils dramatically (Fraser *et al.*, 1992).

Within plaques, $A\beta$ molecules differ in length, exhibiting heterogeneity at both amino (Tekirian *et al.*, 1998) and carboxyl termini (Jarrett *et al.*, 1993a). Plaques contain a mixture of $A\beta$ molecules; $A\beta_{42}$ and $A\beta_{40}$ are the predominant species in extracellular neuritic plaques, whereas the vascular amyloid consists primarily of $A\beta_{39-40}$ (Dickson, 1997). As indicated earlier, a highly amyloidogenic form of $A\beta$, $A\beta_{42}$, is the initial $A\beta$ species deposited in neuritic plaques (Iwatsubo *et al.*, 1995). Diffuse plaques contain $A\beta_{42}$, but not $A\beta_{40}$ (Cummings *et al.*, 1996). Plaque enlargement requires a nidus for further protein deposition; $A\beta_{42}$ may serve as a "seed," which permits the deposition of $A\beta_{40}$ (Jarrett *et al.*, 1993b). $A\beta_{40}$ constitutes the bulk of the $A\beta$ produced by normal metabolism (Haass *et al.*, 1992; Seubert *et al.*, 1992).

Neuritic plaques can be surrounded by dystrophic neurites or by neurites containing paired helical filaments (PHF-type neurites). [PHF occurring within neurites are essentially equivalent to those found in neuronal cell bodies. In AD, PHF occur in three locations: within plaques, neurites, or neuronal cell bodies (Braak *et al.*, 1986). PHF-type neurites found in the absence of plaques are known as "neuropil threads" (Dickson, 1997).] Among dystrophic neurites, diverse neuronal types are represented (Struble *et al.*, 1987). In contrast, there is a hierarchy of neuronal types that are susceptible to PHF formation (Price *et al.*, 1991). Both dystrophic neurites and PHF-type neurites are recognized by ubiquitin-specific antibodies, but only the latter are recognized by the Alz-50 antibody.

C. $A\beta$ Formation, Aggregation, and Clearance

1. APP Cleavage Sites

APP is cleaved within $A\beta$ at Lys⁶⁸⁷-Leu⁶⁸⁸ (APP₇₇₀ numbering), by one or more " α -secretases." This cleavage generates a soluble N-terminal fragment (sAPP _{α}) and a membrane-associated C-terminal fragment. Thus, α -secretase-mediated cleavage of APP precludes the production of $A\beta$. The amino and carboxy termini of $A\beta$ are produced by the actions of " β -secretase" and " γ -secretase," respectively. As in the case of α -secretase, β -secretase-mediated cleavage of APP produces an amino-terminal fragment (sAPP _{β}) and a membrane-associated C-terminal fragment. The "p3" peptide (3 kDa) is created when the C-terminal fragment produced by α -secretase cleavage becomes a substrate for γ -secretase (Haass *et al.*, 1993). The p3 sequence may be amyloidogenic (Lalowski *et al.*, 1996; Dickson, 1997). The cleavage of APP by γ -secretase is unusual in that it occurs within the transmembrane domain of APP. $A\beta$ and p3 are normal constituents of biological fluids (Shoji *et al.*, 1992). Secreted sAPP _{α} protects cells from toxic insults (Goodman and Mattson, 1994; Furukawa *et al.*, 1996). In this regard, it may be much more effective than sAPP _{β} (Barger and Mattson, 1996).

After its synthesis on ribosomes, APP is directed into the endoplasmic reticulum by its signal peptide (Kang *et al.*, 1987). During its transit through the constitutive secretory pathway (endoplasmic reticulum, Golgi, and *trans*-Golgi network), APP is phosphorylated on its ectodomain. A small percentage of total holoprotein is inserted into the plasma membrane, where it is subject to cleavage by α - or β -secretases (Selkoe, 1998). Uncleaved holoprotein and the C-terminal fragments remaining in the plasma membrane after α -secretase or β -secretase cleavage (C83 and C99, respectively) are reinternalized via clathrin-coated vesicles. The latter molecules can be recycled to the cell surface or enter an endosomal/lysosomal pathway.

2. α -Secretase-Mediated Cleavage of APP

APP has a hydrophobic sequence near its carboxyl terminus (about 23 residues long), which directs its insertion into the plasma membrane and internal membranes of the endoplasmic reticulum, Golgi, and *trans*-Golgi network (Selkoe, 1998). α -Secretase-mediated cleavage of APP occurs both at the cell surface and within the constitutive secretory pathway. This cleavage does not depend on a specific sequence of amino acids; rather, it cuts APP at a specific distance from the plasma membrane (Maruyama *et al.*, 1991).

2. α -Secretase-Mediated Cleavage of APP

Total α -secretase activity can be divided into PKC-independent and PKC-dependent components (Buxbaum *et al.*, 1994), which represent basal and stimulated α -secretase activity, respectively. PKC-independent regulation of α -secretase activity involves the elevation of intracellular calcium (Buxbaum *et al.*, 1994). Several metalloproteases belonging to the ADAM family have been shown to possess α -secretase-like activity; among these are TACE (tumor necrosis factor _{α} converting enzyme, also known as ADAM-17), MDC9, and ADAM-10. ADAM metalloproteases are membrane-anchored proteins that contain a catalytic domain, an autoinhibitory domain, a disintegrin-like domain, a cysteine-rich sequence, and epidermal growth factor-like sequence. TACE, MDC9, and ADAM-10 also possess a consensus sequence (HEXXH) for a zinc-binding domain. TACE mediates most cellular PKC-dependent α -secretase activity (Buxbaum *et al.*, 1998; Lammich *et al.*, 1999). MDC9 mediates both basal and PKC-induced cleavage of APP₆₉₅ at the α -secretase site, and inhibition of MDC9 increases β -secretase cleavage (Koike *et al.*, 1999).

Overexpression of ADAM-10 in HEK 293 cells stimulates both basal and PKC-dependent α -secretase activity (Lammich *et al.*, 1999).

3. Cleavage of A β from APP

There are several pathways for the production of A β_{42} and A β_{40} . A β_{40} is generated in recycling endosomes following reinternalization from the cell surface (Koo and Squazzo, 1994). Both peptides are produced in the secretory pathway (Chyung *et al.*, 1997; Wild-Bode *et al.*, 1997), but the primary site for A β_{42} production is the endoplasmic reticulum, whereas the primary site for A β_{40} production is the *trans*-Golgi network (Hartmann *et al.*, 1997). Intracellular production of A β may be unique to neurons because nonneuronal cells produce significant amounts of A β_{42} and A β_{40} only at the cell surface (Hartmann *et al.*, 1997).

Four groups independently identified an unusual membrane-bound aspartyl protease as the elusive β -secretase (Hussain *et al.*, 1999; Sinha *et al.*, 1999; Vassar *et al.*, 1999; Yan *et al.*, 1999). This enzyme has been named BACE (β -site APP-cleaving enzyme) by one group and Asp2 by another group. Although other proteases, such as cathepsin D, can cleave APP at the β -secretase site, BACE meets all the requirements of a true β -secretase. BACE is located within the Golgi and endosomes and has a pH optimum of 5–5.5.

To date, γ -secretase has not been identified. Because inhibition of γ -secretase activity is a prime therapeutic major therapeutic target, the identity of this enzyme may be known by the time this chapter is published. Clearly, presenilin 1 is implicated in γ -secretase cleavage, either as an essential cofactor or as the enzyme itself (Wolfe *et al.*, 1999).

4. Regulation of APP Processing

The regulation of APP processing is extremely complex. It varies across species and also differs between neuronal and nonneuronal cell types. In nonneuronal cell lines or nonhuman cell lines, acetylcholine binding to muscarinic receptor subtypes concurrently increases sAPP $_{\alpha}$ production and *inhibits* A β production (Buxbaum *et al.*, 1992; Hung *et al.*, 1993; Jacobsen *et al.*, 1994). This effect can be mimicked by phorbol ester, indicating the involvement of PKC in signal transduction. However, in cultures of primary human cerebral neurons, PKC activation increases the rate of sAPP $_{\alpha}$ release and *increases* the production of A β (LeBlanc *et al.*, 1998). The latter finding, in conjunction with others, indicates that distinct pathways exist for α - and β -secretase-mediated cleavage of APP (Dyrks *et al.*, 1994). PKC-induced α -secretase cleavage is regulated by protein phosphorylation, but does not depend on the phosphorylation of APP (Jacobsen *et al.*, 1994). The *trans*-Golgi network is the site of regulated, intracellular α -secretase cleavage (Skovronsky *et al.*, 2000).

5. A β Aggregation

A β aggregation is dependent on concentration, pH, and the length of incubation in aqueous media (Burdick *et al.*, 1992). A β exists in a random conformation at low pH, a β -pleated sheet conformation at pH 4–7, and a random conformation at high pH (Barrow and Zagorski, 1991; Fraser *et al.*, 1992). The

effect of pH on A β conformation indicates that A β aggregation is influenced by the ionization state of key residues. Histidine-aspartic acid/glutamic acid salt bridges stabilize β -pleated sheets, facilitating fibril assembly (Fraser *et al.*, 1991). Due to the presence of hydrophobic residues at its carboxyl terminus, A β_{42} is very insoluble in water at pH 7.4 (Burdick *et al.*, 1992).

Aqueous solutions of A β exhibit kinetic rather than thermodynamic solubility (Jarrett and Lansbury, 1993). In other words, A β will precipitate from apparently soluble solutions, given sufficient time. The rate-limiting step in the formation of amyloid is nucleation, i.e., the formation of a certain sized A β oligomer, which can serve as a scaffold for further aggregation (Jarrett and Lansbury, 1992). Lag time, i.e., the time until a solution exhibiting kinetic solubility precipitates, is directly proportional to the size of the A β oligomer required for nucleation and inversely proportional to peptide concentration.

Biometals can induce A β aggregation *in vitro* (Bush *et al.*, 1994). In AD, concentrations of zinc, copper, and iron are likely to be particularly important (for a review, see Atwood *et al.*, 1999). Submicromolar copper induces the aggregation of A β_{40} at mildly acidic pH values, similar to those that might be encountered during mild acidosis (Atwood *et al.*, 1998). Under acidic conditions, nanomolar concentrations of A β_{40} form aggregates, which can subsequently be dissociated by chelation or alkalization. A β_{42} , but not A β_{40} , is precipitated by copper at pH 7.4.

In vitro, low micromolar concentrations of zinc induce the aggregation of A β_{40} at pH 7.4 (Huang *et al.*, 1997). This reaction is mediated by dimeric A β , potentiated by α -helical-promoting solvents, inhibited by multimeric forms of A β , and requires NaCl. At pH 7.4, zinc-induced aggregation of A β_{40} is reversible by chelation over the course of several precipitation/solubilization cycles. A β aggregation also occurs in acidic solution (pH 5.5), but aggregates formed in this manner cannot be resolubilized by alkalization (Huang *et al.*, 1997). In canine CSF, half-maximal aggregation of endogenous A β is produced by zinc concentrations ranging from 120 to 140 μ M (Brown *et al.*, 1997). The ability of zinc to induce A β aggregation is dependent on the presence of a histidine residue at position 13 (Liu *et al.*, 1999). Neuronal depolarization can trigger the massive release of zinc in response to pathological events (Howell *et al.*, 1984), causing extracellular zinc concentrations to rise dramatically (Tonder *et al.*, 1990; Koh *et al.*, 1996). Thus, elevated zinc concentrations may facilitate A β aggregation *in vivo*.

A β aggregates formed in the presence of zinc are more dense and are solubilized less easily than those formed in the presence of copper (Moir *et al.*, 1999). Apolipoprotein E inhibits zinc-induced A β aggregation, but enhances copper-induced aggregation. Furthermore, the extent to which metal-induced aggregation of A β occurs *in vitro* is altered by specific apolipoprotein E isoforms. Zinc- or copper-induced A β aggregation is greater in the presence of apolipoprotein E4 than apolipoprotein E3. This is consistent with the increased risk for AD conferred by the $\epsilon 4$ allele.

6. A β Clearance

A β clearance is not well understood, but may be critically important to AD pathogenesis. Pathways for A β clearance include, but are not limited to, the following:

In soluble fractions of human and rat brain, maximal clearance of $A\beta$ occurs at pH 4–5 and is mediated by cathepsin D, an aspartyl protease (McDermott and Gibson, 1996, 1997; Hamazaki, 1996a). Because cathepsin D requires a low pH for catalytic activity, $A\beta$ -degradation by cathepsin D must occur in an acidic intracellular compartment. Cathepsin D cleaves a wild-type $A\beta$ sequence 20 times faster than it does a mutant $A\beta$ sequence (a glycine for alanine substitution at position 21) associated with early-onset AD (Hamazaki, 1996b). This suggests that $A\beta$ clearance by cathepsin D may be relevant to AD.

In vitro, $A\beta$ proteolysis by insulin-degrading enzyme occurs at neutral pH (McDermott and Gibson, 1997).

In vivo, microglia cause $A\beta$ degradation by releasing a protease thought to be a member of the disintegrin family (Mentlein *et al.*, 1998).

$A\beta$ can be cleared by a serine protease– $\alpha 2M$ complex (Narita *et al.*, 1997; Qiu *et al.*, 1999). Because polymorphisms in the genes for both $\alpha 2M$ and LRP are associated with AD, it is tempting to speculate that $A\beta$ might compete with other molecules, such as cholesterol, for lysosomal clearance (Kowal *et al.*, 1989).

IV. Therapeutic Strategies

Although AD treatment and prevention are still in the future, many potential therapeutic targets exist, each of which could be implemented via several routes. These include the following:

- Inhibition of $A\beta_{42}$ or $A\beta_{40}$ secretion, with or without concomitant stimulation of sAPP $_{\alpha}$ secretion

- Inhibition of $A\beta$ aggregation or fibril formation

- Resolubilization of plaques

- Limitation of $A\beta$ -induced toxicity

- Stimulation of $A\beta$ clearance

- Prevention or limitation of brain inflammation

- Administration of neurotrophic agents

- Inhibition of neurofibrillary tangle formation

- Inhibition of β -secretase or γ -secretase

For a fuller discussion of potential therapeutic strategies, see McKeon-O'Malley *et al.* (1998).

V. Summary

Tremendous progress has been made in the area of AD genetics. Several other genes, yet to be unidentified, may have a major impact on AD risk. However, it seems likely that many more genes will be discovered, each of which increases AD risk slightly. A poor combination of genetic risk factors may be sufficient to cause disease or to permit detrimental environmental factors to operate. The fact that four genes, which alter AD risk (APP, ApoE, $\alpha 2M$, and LRP), are related to each other indicates that cholesterol and other lipids may play a role in AD etiology. We speculate that AD may be caused by risk factors leading to sublethal vascular disease. If this speculation is substantiated by further research, it may be possible to implement lifestyle alterations for AD prevention. Presenilin research is likely to bring about many important findings in area of development, as well as in AD.

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