Review Article

β-Amyloid Degradation and Alzheimer’s Disease

Deng-Shun Wang,1 Dennis W. Dickson,2 and James S. Malter1,3

1 Department of Pathology and Laboratory Medicine, School of Medicine, University of Wisconsin, Madison, WI 53705, USA
2 Departments of Pathology (Neuropathology) and Neuroscience, Mayo Clinic College of Medicine, Jacksonville, FL 32224, USA
3 Waisman Center for Developmental Disabilities, School of Medicine, University of Wisconsin, Madison, WI 53705, USA

Received 18 November 2005; Revised 18 January 2006; Accepted 1 February 2006

Extensive β-amyloid (Aβ) deposits in brain parenchyma in the form of senile plaques and in blood vessels in the form of amyloid angiopathy are pathological hallmarks of Alzheimer’s disease (AD). The mechanisms underlying Aβ deposition remain unclear. Major efforts have focused on Aβ production, but there is little to suggest that increased production of Aβ plays a role in Aβ deposition, except for rare familial forms of AD. Thus, other mechanisms must be involved in the accumulation of Aβ in AD. Recent data shows that impaired clearance may play an important role in Aβ accumulation in the pathogenesis of AD. This review focuses on our current knowledge of Aβ-degrading enzymes, including neprilysin (NEP), endothelin-converting enzyme (ECE), insulin-degrading enzyme (IDE), angiotensin-converting enzyme (ACE), and the plasmin/uPA/tPA system as they relate to amyloid deposition in AD.

Copyright © 2006 Deng-Shun Wang et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

INTRODUCTION

Alzheimer’s disease (AD) is the commonest cause of senile dementia and increases in frequency with age. Clinically, AD is characterized by early and progressive memory loss due to neuronal and synaptic loss in the cortex and limbic structures, including the hippocampus and amygdala. In later stages of the disease process, the extensive involvement of cortical and subcortical regions results in loss of higher cognitive abilities, including speech and praxis, and in impaired motor abilities. Grossly, AD brains show global atrophy and reduced weight and volume. Histologically, AD is characterized by amyloid plaques, neurofibrillary tangles, dystrophic neurites, extensive neuronal loss, and gliosis.

Although beta-amyloid (Aβ) accumulation and senile/neuritic plaque formation are striking morphological hallmarks of AD and widely used in the neuropathologic diagnosis of AD, it is clearly recognized that amyloid deposition in the brain parenchyma and in vessels also is common for non-demented individuals in advanced age. Many possible explanations for excessive Aβ deposition have been put forward, including increased production, decreased degradation, and abnormal transport between brain parenchyma and plasma or CSF [1–3]. Although overproduction of Aβ is critical to the pathogenesis of some forms of familial AD, there is still little evidence to suggest that increased Aβ production is important in amyloid deposition in aging and sporadic AD. Recently, the role of degradation has been increasingly recognized in Aβ homeostasis. Several enzymes have been described with a range of abilities to degrade Aβ. This review will focus on enzymes capable of degrading Aβ and their potential significance to the pathogenesis of AD.

THE AMYLOID CASCADE HYPOTHESIS

The mechanisms underlying the pathogenesis of AD remain unclear and are hotly debated. One proposal focuses on Aβ production and deposition, the so-called amyloid cascade hypothesis (Figure 1) [4–6]. This hypothesis posits that increased Aβ production and deposition plays the key role in triggering neuronal dysfunction and death in AD. Evidence, including Aβ deposition in AD brain, the toxic properties of Aβ to neurons in vitro, and the identification of mutations in amyloid precursor protein (APP) in familial early onset AD have supported the amyloid cascade hypothesis. Based on this theory, tremendous efforts had been made during the last decade to uncover the mechanisms underlying the production of Aβ. From these studies it has been shown that sequential cleavage of APP by β-secretase and γ-secretase generates Aβ peptides (Figure 2) [7, 8]. Indeed, pharmacologic intervention targeted at Aβ generation through inhibitors of β-site cleaving enzyme (BACE) and γ-secretase is being
widely pursued [9, 10]. Attempts to block or regulate those two enzymes together with immunotherapy aimed at reducing brain Aβ have been or will soon be tried in AD patients [9, 11–13].

**CANDIDATE ENZYMES FOR Aβ DEGRADATION**

Altering catabolism is another way to reduce Aβ levels in the brains of AD. Many proteases or peptidases have been reported with the capability of cleaving Aβ either in vitro or in vivo. These include neprilysin (NEP) [14–16], endothelin-converting enzyme (ECE)-1 [17], insulin-degrading enzyme (IDE) [18–20], angiotensin-converting enzyme (ACE) [21], uPA/tPA-plasmin system [22, 23], cathepsin D [24, 25], gelatinase A [26], gelatinase B [27], matrix metalloendopeptidase-9 [28], coagulation factor Xla [29], antibody light chain c23.5 and hk14 [30], and α2-macroglobulin complexes [31]. Many of them have more than one cleavage site in the Aβ peptide (Figure 3). The basic biological features of these enzymes are summarized in Table 1. There are probably other proteases with potential to cleave Aβ if all peptide bonds are taken into consideration, but only those physiologically or pathologically relevant are discussed. Among them, NEP, IDE, ECE, ACE and plasmin, tissue plasminogen activator (tPA), and urokinase-type plasminogen activator (uPA) system are the most promising Aβ-degrading candidates.

**NEPRILYSIN (NEP)**

NEP is also known as neutral endopeptidase-24.11, EC 3.4.24.11, enkephalinase, neutrophil cluster-differentiation antigen 10 (CD10), or common acute lymphoblastic leukemia antigen (CALLA) [32–38]. In humans, the NEP gene is located on chromosome 3q21–q27 and contains 24 exons [39, 40]. NEP is composed of 750 amino acids with a calculated molecular weight of approximately 86 kDa [41]. Because of abundant posttranslational modifications, especially glycosylation [42], NEP from human brain tissues migrates between 97–110 kDa on denaturing gel electrophoresis. As a plasma membrane-bound glycoprotein, NEP is composed of a short N-terminal cytoplasmic tail, a membrane-spanning domain, and a large C-terminal extracellular catalytic domain. The latter contains a HEXXH zinc-binding motif [43, 44], which facilitates the hydrolysis of extracellular oligopeptides (<5 kDa) on the amino side of hydrophobic residues, such as the small, hydrophobic Aβ40 and Aβ42 peptides.

NEP is widely expressed in many normal tissues including the brush-border of intestinal and kidney epithelial cells, neutrophils, thymocytes, lung, prostate, testes, and brain [45–49]. In the brain, it is expressed on neuronal plasma membranes, both pre- and postsynaptically [50, 51], and is most abundant in the nigrostriatal pathway, as well as in brain areas vulnerable to amyloid plaque deposition, such as the hippocampus [43, 52].
Table 1: Features of selected Aβ-degrading enzymes.

<table>
<thead>
<tr>
<th>Protease</th>
<th>a.k.a.</th>
<th>Class</th>
<th>Subcellular location</th>
<th>Substrates in addition to Aβ</th>
</tr>
</thead>
<tbody>
<tr>
<td>Neprilysin</td>
<td>CD10, CALLA, EC 3.4.24.15</td>
<td>M</td>
<td>Cellular &amp; intracellular membrane including presynaptic membrane</td>
<td>Enkephalin, cholecystokinin, neuropeptide Y, substance P, opiod peptides, atrial natriuretic peptides, bombesin-like peptides, chemotactic peptides, adrenocorticotropin homone (ACTH)</td>
</tr>
<tr>
<td>Insulin-degrading enzyme</td>
<td>EC 3.4.24.56 Insulysin, IDE</td>
<td>M</td>
<td>Cytosol, cellular, and intracellular membrane extracellular space</td>
<td>Insulin, glucagon, atrial natriuretic factor, β-endorphin amylin, APP intracellular domain TGFα</td>
</tr>
<tr>
<td>Endothelin-converting enzyme</td>
<td>EC 3.4.24.71 ECE</td>
<td>M</td>
<td>Trans-Golgi network cell surface</td>
<td>Big endothelin, substance P, bradykinin, oxidized insulin B chain</td>
</tr>
<tr>
<td>Angiotensin-converting enzyme</td>
<td>EC 3.4.15.1; ACE, dipeptidyl carboxypeptidase</td>
<td>M</td>
<td>plasma membranes perinuclear region</td>
<td>Angitensin-I, enkaphalins, bradykinin</td>
</tr>
<tr>
<td>Plasmin/uPA/tPA</td>
<td>EC 3.4.21.31 tissue plasminogen activator for tPA; urokinase-type plasminogen activator for uPA</td>
<td>S</td>
<td>Extracellular space</td>
<td>fibrin, plasminogen, &amp; other matrix proteins</td>
</tr>
</tbody>
</table>

Note: a.k.a. is also known as M: metalloproteases and S: serine.

The first clue that NEP was involved in Aβ degradation was provided by Howell et al [14]. Using high-performance liquid chromatography (HPLC) combined with mass spectroscopic analysis, they found that NEP cleaved Aβ between residues Glu3-Phe4, Gly9-Trp10, Phe19-Phe20, Ala30-Ile31, and Gly33-Leu34. The true breakthrough demonstrating the importance of NEP was demonstration that NEP was the rate-limiting enzyme for Aβ degradation in vivo made by Iwata et al in 2000 [15]. After injecting radio-labeled Aβ peptides into rat hippocampus in the presence or absence of various protease inhibitors, the resultant Aβ fragments were analyzed by HPLC equipped with flow scintillation. Iwata and coworkers found that Aβ42 was degraded in the hippocampus, with a half-life of 17.5 minutes and with Aβ10–37 as the major catabolic intermediate. Infusion of thiorphan, a specific NEP inhibitor [53], directly into rat hippocampus for 3 days elevated endogenous Aβ levels, and infusion for 30 days resulted in further endogenous Aβ accumulation and accumulation of extracellular Aβ deposits resembling amyloid plaques [15, 54]. They also found that almost all radio-labeled Aβ42 could be recovered from the hippocampus 1 hour after the injection, which suggested that Aβ clearance depends predominantly on local proteolysis, rather than transport across the blood brain barrier into the blood or into the cerebrospinal fluid [15]. Interestingly, in another independent study, it was found that radio-labeled Aβ40 injected into mouse brain was more readily transferred to blood, compared with Aβ42, suggesting that the relative contributions of degradation and transport to brain Aβ clearance might be different for these two peptides [55]. Furthermore, it had been found that NEP was able to degrade not only monomeric, but also oligomeric forms of both Aβ.
that even partial down-regulation of NEP activity could contribute to $\beta$-amyloid accumulation. These studies also established that NEP is a physiologically relevant $\beta$-degrading enzyme [16]. On the other hand, overexpression of NEP by gene transfer in amyloid-depositing transgenic mice slowed, and in some cases reversed $\beta$-amyloid deposition [54, 58–60].

Studies in human subjects have also supported the notion that NEP plays a key role in brain $\beta$-metabolism and AD pathogenesis. As mentioned above, aging is one of the most important risk factors for AD [61] and is associated with the accumulation of $\beta$-amyloid even in cognitively normal elderly [62, 63]. Although systematic study of the relationship between NEP and aging in humans remains to be done, aging mice show region selective decreases in NEP mRNA expression [52, 64, 65]. These changes occurred despite maintenance of synaptic and neuronal numbers suggesting gene specificity. Immunohistochemical studies on AD brains have revealed NEP immunoreactivity in senile plaques [49]. Quantitative analysis showed that both NEP mRNA and protein were significantly lower in AD than in age-matched normal control brains [65–68]. Reductions occurred selectively in the regions most vulnerable to AD pathology, but not in other brain areas such as cerebellum or in peripheral organs [65, 66]. NEP was also decreased in the cerebrospinal fluid (CSF) of prodromal Alzheimer’s disease patients [69], consistent with cause and effect. Interestingly, an inverse relationship between NEP and $\beta$-levels in AD brain vasculature has been reported. These data suggested that NEP may play a role in cerebral amyloid angiopathy (CAA), another very common pathological change found in AD brains [70]. Consistent with these findings, $\beta$-mutations identified in familial AD found in Dutch, Flemish, Italian, and Arctic families do not increase $\beta$-production, but rather cause presenile amyloidosis and CAA [71].

Recent data from our study showed that NEP decreased in AD brains, but not in pathological aging (PA), a term to describe neurologically normal individuals with high brain amyloid burden (sufficient to diagnose AD with the Khachaturian criteria), but minimal or no neurofibrillary degeneration (Braak neurofibrillary tangle stages of three or less) [63, 72]. Interestingly, NEP levels were inversely correlated with a range of amyloid measures including senile plaque counts and levels of $\beta$-40 and $\beta$-42 [56], both intracellularly and extracellularly [57].

The role of NEP in $\beta$ degradation was solidified by studies in transgenic mice. In partially NEP-deficient animals, the degradation of both endogenous and exogenous $\beta$-peptides was tightly correlated with gene dose, suggesting that even partial down-regulation of NEP activity could contribute to $\beta$-amyloid accumulation. These studies also established that NEP is a physiologically relevant $\beta$-degrading enzyme [16]. On the other hand, overexpression of NEP by gene transfer in amyloid-depositing transgenic mice slowed, and in some cases reversed $\beta$-amyloid deposition [54, 58–60].

These data support the hypothesis that decreased NEP contributes to $\beta$ deposition in AD, but perhaps in means that are not entirely linked to visible amyloid deposition [72], perhaps implicating failed degradation of toxic soluble intermediates in AD.

Taken together, these data indicate that NEP is an important enzyme that contributes to the normal metabolism, accumulation, and perhaps toxicity $\beta$-amyloid in AD.

ENDOTHELIN-CONVERTING ENZYME (ECE)

Endothelin (ET) is a potent vasoconstrictive peptide produced in vascular endothelial cells [73]. In addition, ET also plays an important role in early development of the neural crest and, thus, organogenesis [74]. Endothelin-converting enzyme (ECE) is a transmembrane metalloprotease that catalyzes the conversion of pro-ET (also referred to big-ET) into vasoactive endothelin. So far, two different isoforms of ECE—ECE-1 and ECE-2—have been cloned in humans [75–77]. It has been estimated that expression of ECE-2 is only 1–2% as much as the more abundant ECE-1 based on comparative mRNA transcript levels in endothelial cells [78]. Studies have suggested that ECE-1, but not ECE-2, is a possible brain $\beta$-degrading enzyme [17].

ECE-1 consists of 758 amino acids [79] and is the major enzyme responsible for specific cleavage of biologically active pro-ET-1 to active ET-1 in vascular endothelial cells. It is a membrane-bound type II metalloprotease and shares significant sequence identity (about 38% homologue at the amino acid level) with NEP. ECE-1 is abundantly expressed in the vascular endothelial cells of all organs and is also widely expressed in nonvascular cells of many tissues, including lung, pancreas, testis, ovary, adrenal gland, and kidney [75, 80–83]. Recent systematic immunohistochemical analyses have shown ECE-1 widely expressed in human brain, including neurons in the diencephalon, brainstem, basal nuclei, cerebral cortex, cerebellar hemisphere, amygdala, and hippocampus [84, 85]. Four isoforms of ECE-1 have been identified to date [75, 86–90]. All of them are encoded by a single gene located on chromosome 1 (1p36), and they differ in their cytoplasmic tail domains through alternative promoter usage. The four isoforms cleave pro-ET with similar efficiency, but they differ in their tissue distribution and subcellular localization [87, 90]. Human ECE-1a is localized predominantly in plasma membrane. Human ECE-1c and ECE-1d have also been reported to be localized in plasma membrane, but also in intracellular compartments. In contrast, human ECE-1b is expressed exclusively intracellularly, particularly in Golgi-like structures and the cytoplasmic face of the plasma membrane [90–92].

Although both ECE-1 and NEP are metalloendopeptidases and thus subject to competitive inhibition by the metalloprotease inhibitors nanomolar concentrations of thiorphan and phosphoramidon can inhibit NEP, whereas ECE-1 is inhibited only at micromolar concentrations of phosphoramidon, and it is insensitive to thiorphan [53]. Another difference is that ECE-1 is active only at neutral pH, while
NEP is active over a slightly wider pH range (pH 6.5–7.5) [72, 93].

By using HPLC, mass spectrometry, and N-terminal sequence analysis, Eckman and her colleagues provided the first evidence that ECE-1 may be involved in the metabolism of Aβ. They found that ECE-1 expressed in cultured Chinese hamster ovary cells that lack endogenous ECE activity, reduced the concentration of extracellular Aβ by up to 90%. In vitro, recombinant ECE-1 cleaves synthetic Aβ40 in at least three sites, resulting in formation of Aβ fragments Aβ1–16, Aβ1–17, Aβ1–19, and Aβ20–40 [17]. In mice deficient for ECE-1 and the closely related ECE-2, both Aβ40 and Aβ42 levels were significantly higher when compared with age-matched wild-type littermate controls. Taken together, the results suggest that ECE activity might be an important factor involved in Aβ clearance in vivo [94]. How important is ECE-2 in this process is yet to be determined, and direct evidence that ECE contributes to Aβ deposition in human AD brains remains to be determined.

INSULIN-DEGRADING ENZYME (IDE)

IDE is also known as EC 3.4.24.56, insulin protease, insulysin, or insulinase [95, 96]. Cloned human IDE consists of 1019 amino acids [97]. The IDE gene was mapped to chromosome 10q23–q25, which made it a candidate gene for the Alzheimer disease-6 locus (known as AD6) [98, 99]. It is a zinc metalloendopeptidase that hydrolyzes multiple peptides, including insulin, glucagon, atrial natriuretic factor, transforming growth factor-α, β-endorphin, amylin, and the APP intracellular domain. It also participates in the metabolism of angiotensin II [100, 101]. Purified IDE from several mammalian tissues, including blood cells, skeletal muscle, liver, and brain, migrates as a 110 kDa band on denaturing gel electrophoresis, but it migrates as a 300 kDa band under non-denaturing conditions. These results suggest that native IDE exists as a mixture of dimers and tetramers [100, 102]. IDE is active at neutral pH and dimers have greater activity than monomers [96, 103, 104]. Subcellularly, IDE is primarily located in the cytosol, although it also had been found in peroxisomes [105], plasma membrane [106, 107], and in a secreted form [20].

Kurochkin and Goto reported the first evidence that IDE might be involved in Aβ degradation [18]. They found that 125I-labeled synthetic Aβ specifically cross-linked to a single 110 kDa protein, which was shown to be IDE, in cytosol fractions from rat brain and liver. Purified rat IDE effectively degraded synthetic Aβ in vitro. Subsequently, it was shown that an IDE-like activity from soluble and synaptic membrane fractions from postmortem human and fresh rat brain also degraded Aβ peptides [19, 108]. Studies in the cultured cells also proved that IDE could degrade both endogenous and synthetic Aβ in vitro [20, 109]. The overexpression of IDE in Chinese hamster ovary cells resulted in a marked reduction in levels of intracellular detergent-soluble Aβ, as well as reduced levels of extracellular Aβ40 and Aβ42 [110].

Transgenic mice overexpressing IDE showed significant reductions of total amyloid burden and improved survival rates [58], while IDE knockout mice demonstrated a clear elevation of brain Aβ and the APP intracellular domain. Additionally, heterozygous mice exhibited Aβ levels that were intermediate between wild-type controls and knock-out mice, indicating that IDE affected Aβ levels in a gene-dose dependent manner [111, 112].

Immunohistochemical studies showed that IDE was primarily expressed in neurons, but was also located in senile plaques, in AD brain [113]. The finding that IDE mRNA and protein were reduced in the hippocampus of AD patients, especially in APOE e4 carriers, suggested that APOE e4 might be sensitive to IDE expression levels with downstream effects on Aβ metabolism [114]. Like NEP, IDE also showed progressively decreased expression that was age- and region-dependent [65]. Thus, strong evidence exists that IDE is another important Aβ-degrading enzyme that may play a role in the amyloid pathology of AD.

ANGIOTENSIN-CONVERTING ENZYME (ACE)

Angiotensin-converting enzyme, also known as EC 3.4.15.1, dipeptidyl carboxypeptidase, or ACE, is a membrane-bound zinc metalloprotease. At least two ACE isotypes (ACE1 and ACE2) had been cloned in humans, thus far [115]. ACE is composed of 732 amino acids [116] and contains two proteolytically active domains that are located at N- and C-termini, respectively [117]. The major function of ACE is to catalyze the conversion of angiotensin I (AngI) to angiotensin II (AngII), which plays an important role in maintaining blood pressure, body fluid, and sodium homeostasis [118].

ACE is also widely expressed both outside and within the CNS. In the brain, ACE was found at highest levels in circumventricular organs such as the subfornical organ, area postrema, and the median eminence [119]. It was detected in other areas as well, including the caudate nucleus, putamen, substantia nigra pars reticularis, nucleus of the solitary tract (NTS), dorsal motor nucleus, median preoptic nucleus, and choroid plexus in rat, human, rabbit, sheep, and monkey [120].

Most of the evidence for the potential relationship between ACE and AD has come from human genetic studies [121–127]. Patients at higher AD risk had an insertion (I) polymorphism within intron 16 of the ACE gene, which was associated with AD [121]. Interestingly, patients with a deletion polymorphism had a lower risk of AD [123, 124]. Genetic analysis of postmortem AD brains showed homozygous I/I was associated with higher brain Aβ levels compared to D/D allele carriers [128]. Results from earlier preclinical and clinical studies suggested that ACE might have a role in the modulation of cognitive memory processes in the rat and in humans [129].

Hu and coworkers provided the first evidence that ACE could significantly inhibit the aggregation, deposition, and cytotoxicity of Aβ in vitro by cleavage of Aβ at Asp7-Ser8. This was a surprising finding given the known specificity of ACE [130] and the failure of ACE inhibitors to alter Aβ degradation in vivo [15, 16]. Whether this discrepancy was due to different experimental systems (eg, in vitro versus in
vivo) is not clear. Further work in other experimental systems such as ACE-deficient or knockout animals is needed to clarify the role ACE might have in amyloid pathology in AD.

A very recent report by Hemming and Selkoe, showed that ACE expression promoted the degradation of endogenous Aβ40 and Aβ42 [131]. Using site-directed mutagenesis, they also showed that both N- and C-terminal proteolytically active domains contributed to Aβ degradation. Captopril, a widely prescribed ACE inhibitor blocked Aβ cleavage in culture medium. This is potentially very important observation because it suggests widely used ACE inhibitors could increase cerebral Aβ levels in patients with hypertension.

Unlike other candidate Aβ-degrading enzymes discussed above, the levels of both ACE protein and activity were elevated in postmortem brains [132–134]. Given that other Aβ-degrading enzymes such as NEP and IDE are decreased in AD brains compared to age-matched healthy controls [65–68, 72], ACE may show compensatory up-regulation in response to accumulating Aβ. Along with concurrent evaluation of NEP, ECE, IDE, ACE, and possibly others in the same panel of postmortem human brains with the spectrum of pathology from normal aging, early and advanced AD will be helpful in clarifying respective functions of these proteases.

PLASMIN, TISSUE PLASMINOGEN ACTIVATOR (tPA), AND UROKINASE-TYPE PLASMINOGEN ACTIVATOR (uPA)

Plasmin is a serine protease important in the degradation of many extracellular matrix components [135]. The principal components of this system include plasminogen/plasmin, tissue plasminogen activator (tPA), urokinase-type plasminogen activator (uPA) [136]. tPA and uPA cleave plasminogen to yield the active serine protease, plasmin. In the nervous system, plasminogen and uPA are expressed in neurons, while tPA is synthesized by neurons and microglial cells [137]. The plasmin system is involved in many normal neural functions, such as neuronal plasticity [138], learning, and memory [139].

Several studies showed that Aβ aggregates could substitute for fibrin aggregates in activating tPA, and suggested that tPA may be activated by Aβ in AD [140, 141]. Later, it was reported that brain plasmin enhanced Aβ degradation [142, 143], while plasmin and its activity were decreased in AD brains [142, 144]. In cultured cells purified plasmin significantly decreased the level of neuronal injury induced by aggregated Aβ, presumably by degrading Aβ [143, 145]. However, the in vivo effect of plasmin could be very different given that serum amyloid P, that is associated with amyloid pathology in AD brain, is able to prevent proteolysis of purified cerebral Aβ [146]. Indeed, plasminogen deficient mice did not show increased Aβ in the brain or in the plasma and suggested that plasmin does not regulate steady-state Aβ levels in nonpathologic conditions [147], although it might be involved in the degradation of pathological Aβ aggregates.

OXIDATIVE DAMAGE TO Aβ-DEGRADING ENZYMES

Some studies have indicated that genetic polymorphisms of Aβ-degrading enzymes including NEP, IDE, ACE might be associated with AD [122, 125, 127, 148–155], although these results remain controversial [128, 156–161]. Further clinical and pathologic studies of large numbers of individuals carrying various mutations in possible Aβ-degrading enzymes are needed to clarify this issue.

In addition to genetics, many environmental factors such as oxidative stress can potentially impair the activity of Aβ-degrading enzymes [162–164]. Recent data showed that NEP and IDE might be substrates for oxidative damage during aging and in AD [65, 68]. Both NEP and IDE from AD brain tissues could be modified by 4-hydroxy-nonenal (HNE), a by-product of lipid peroxidation [165]. The ratio of oxidized NEP from frontal cortex [68] and IDE from hippocampus [65] was greater in AD brains than in age-matched controls. Studies reported by Russo et al failed to confirm these findings [166]. In their study, they found that NEP mRNA from AD brains was significantly lower than in controls, but not NEP protein [166], which was contradictory to several previous reports [65–68]. One possible reason for such a discrepancy might be purely technical, reflecting different immunoprecipitation protocols and incomplete antigenic recovery [166]. Although very recent data confirmed that both recombinant IDE and the extracellular domain of NEP were modified by HNE in vitro [167], additional, in vivo studies of neuronal proteases are needed to clarify this potentially very important mechanism for Aβ deposition in AD development.

SUMMARY

Since the majority of AD cases are sporadic without clear genetic causes, and that even a large percentage of familial cases cannot be explained by the overproduction of Aβ, multiple factors are likely involved in the pathogenic metabolism of Aβ in AD (Figure 4). Exploration for possible mechanisms underlying Aβ accumulation in AD is crucial to resolve these issues. There are growing and compelling data now available to implicate Aβ degradation in AD pathogenesis. Aβ is a substrate of a wide range of proteases, which are likely to contribute to the accumulation of Aβ in AD. Both enzymatic loss through genetic mutations and nongenetic factors, such as direct oxidative damage or enhanced production of inhibitors, may contribute to aberrant Aβ catabolism. Current results from in vitro and animal models support NEP, IDE, ECE, and ACE as probable enzymes for Aβ degradation, but data from humans remain largely missing. Due to clear limitations of animal models, validation in human subjects with AD will be critical to establish the physiologic significance of these proteases. Measurement of brain Aβ levels, amyloid pathology and clinical cognitive performance with enzyme activity, location and expression will help to clarify which of these many enzymes that are capable of cleaving Aβ are actually key players in human disease.
**ACKNOWLEDGMENTS**

The authors express their thanks for the financial support from the Research Fund of the Department of Pathology and Laboratory Medicine, University of Wisconsin School of Medicine, Madison to Deng-Shun Wang, NIH-RO1AG10675 and P30HD63352 to James S. Malter, and NIH-P01-AG03949, 5P01AG003949, 5P01AG014449, and 5P50NS040256 to Dennis W. Dickson.

**REFERENCES**


[17] Eckman EA, Reed DK, Eckman CB. Degradation of the Alzheimer’s amyloid beta peptide by endothelin-converting...


