



Amyloid-clearing proteins and their epigenetic regulation as a therapeutic target in Alzheimer's disease

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Abnormal elevation of amyloid β -peptide ($A\beta$) levels in the brain is the primary trigger for neuronal cell death specific to Alzheimer's disease (AD). It is now evident that $A\beta$ levels in the brain are manipulable due to a dynamic equilibrium between its production from the amyloid precursor protein (APP) and removal by amyloid clearance proteins. Clearance can be either enzymic or non-enzymic (binding/transport proteins). Intriguingly several of the main amyloid-degrading enzymes (ADEs) are members of the M13 peptidase family (nepriylisin (NEP), NEP2 and the endothelin converting enzymes (ECE-1 and -2)). A distinct metallopeptidase, insulin-degrading enzyme (IDE), also contributes to $A\beta$ degradation in the brain. The ADE family currently embraces more than 20 members, both membrane-bound and soluble, and of differing cellular locations. NEP plays an important role in brain function terminating neuropeptide signals. Its decrease in specific brain areas with age or after hypoxia, ischaemia or stroke contribute significantly to the development of AD pathology. The recently discovered mechanism of epigenetic regulation of NEP (and other genes) by the APP intracellular domain (AICD) and its dependence on the cell type and APP isoform expression suggest possibilities for selective manipulation of NEP gene expression in neuronal cells. We have also observed that another amyloid-clearing protein, namely transthyretin (TTR), is also regulated in the neuronal cell by a mechanism similar to NEP. Dependence of amyloid clearance proteins on histone deacetylases and the ability of HDAC inhibitors to up-regulate their expression in the brain opens new avenues for developing preventive strategies in AD.

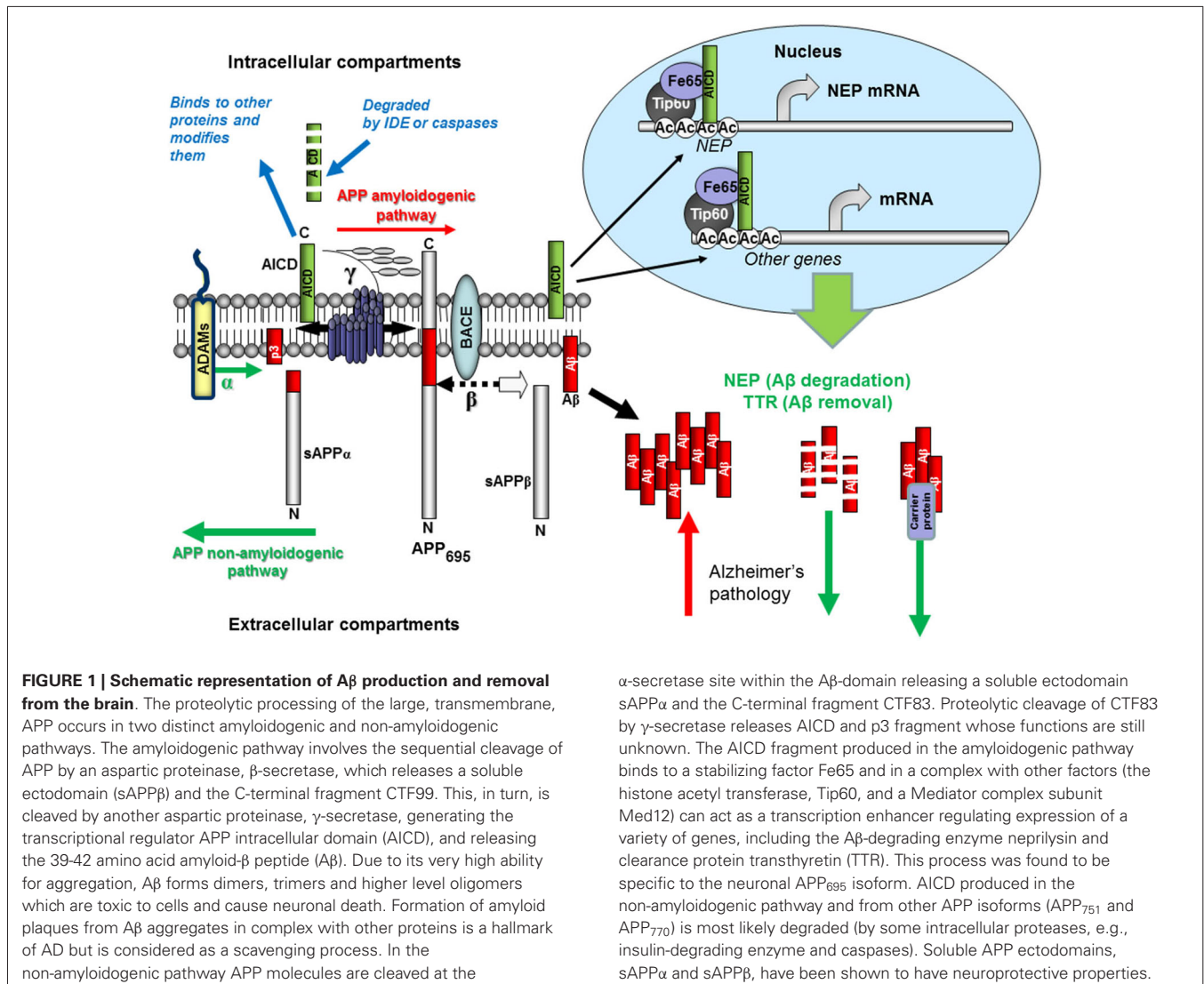
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INTRODUCTION

Overproduction and accumulation in the brain of abnormally high concentrations of the amyloid- β ($A\beta$) peptide and its oligomers causing synaptic loss and neuronal cell death are considered among the principal pathological events underlying neurodegeneration and Alzheimer's disease (AD; Hardy and Higgins, 1992; Walsh et al., 2002; Hardy, 2009). $A\beta$ is produced by the sequential proteolytic cleavage of the membrane-bound amyloid precursor protein (APP) by an aspartic protease, β -secretase (BACE1), followed by the presenilin-dependent γ -secretase (for details see **Figure 1**). Under normal physiological conditions it has important neuronal functions including transcriptional regulation (Koudinov and Berezov, 2004; Barucker et al., 2014). However, in some individuals mutations in the APP gene, or in the

presenilin genes (PS1 and PS2), cause an increase in relative abundance of $A\beta_{42}$ and development of AD pathology at a relatively early age. Our understanding of the molecular mechanisms of AD pathology to date derive from studies of the families manifesting early-onset AD and from studying transgenic animals expressing human genes bearing these pathological mutations (Guerreiro et al., 2012; LaFerla and Green, 2012). However, all attempts to create an effective drug against AD pathology based exclusively on the amyloid cascade hypothesis have not been fruitful. This can be explained by the fact that the majority of AD cases are of the late-onset, sporadic form not linked to mutations of the major AD-related genes but caused by some other pathological changes in normal brain physiology which predispose to overproduction and accumulation of $A\beta$ in the brain over the years. Among them are neuroinflammation, poor diet, toxic environment, brain trauma, hypoxia, stroke and mutations in a number of other neuronal genes which not only shift the whole neuronal metabolism towards accumulation of $A\beta$ (Karch et al., 2012) but also affect its intrinsic clearance both via transport and perfusion mechanisms or proteolytic cleavage.

Abbreviations: $A\beta$, amyloid β -peptide; AD, Alzheimer's disease; AICD, APP intracellular domain; APLP, APP-like protein; APP, amyloid precursor protein; ECE, endothelin-converting enzyme; IDE, insulin-degrading enzyme; HDAC, histone deacetylase; NEP, nepriylisin; PKC, protein kinase C; TTR, transthyretin; VA, valproic acid.



It is now becoming more evident that A β levels in the brain are manipulable due to a dynamic equilibrium between its production from APP and removal by a cohort of amyloid clearance proteins which can be either of enzymic nature (proteases) or non-enzymic (binding/transport proteins) (Figure 1). The number of enzymes capable of proteolytic degradation of A β discovered to date is rapidly growing and currently the family of amyloid-degrading enzymes (ADEs) embrace more than 20 members both membrane-bound and soluble, and of differing cellular and subcellular locations (for review see Marr and Spencer, 2010; Nalivaeva et al., 2012a,c; Grimm et al., 2013; Pacheco-Quinto et al., 2013). Intriguingly several of the main ADEs are members of the M13 peptidase family (neprilysin (NEP), NEP2 and endothelin converting enzymes (ECE-1 and ECE-2)). Another metallopeptidase from the M16 family, insulin-degrading enzyme (IDE), also plays a significant role in A β degradation in the brain (Leissring et al., 2003; Qiu and Folstein, 2006). All these enzymes have been mostly studied in recent years

with regard to their role in AD pathology or as therapeutic targets. This review will focus on the mechanisms regulating expression of their genes *in vivo* and *in vitro*.

The amyloid binding/transport proteins which interact with A β and modulate its solubility, transport, clearance, degradation, and fibril formation are now widely studied. The serum amyloid P component (SAP), as well as apolipoprotein J (clusterin), have been described as the main A β -binding proteins while various apolipoproteins (apoA-IV, apoE, and apoA-I), as well as albumin (HSA) and fibulin were identified as minor contributors (Calero et al., 2012; Yu and Tan, 2012). Despite being a minor contributor to A β -binding in the plasma, apoE (especially the apoE4) is considered as one of the major contributors to A β clearance in the brain and is the major genetic risk factor for development of late-onset AD (for review see Hauser and Ryan, 2013). It has been suggested the ApoE/LRP1-mediated clearance of A β across the blood brain barrier (BBB) is the key event in the regulation of A β transport from brain to periphery which

suggests that direct targeting of this process at the BBB could have potential in the treatment of late-onset AD (Martiskainen et al., 2013).

Another group of transport proteins, namely the ATP-binding cassette (ABC) transporters, which are localized on the surface of brain endothelial cells of the BBB and brain parenchyma, also contribute to A β clearance. Among these transporters the most important role in A β binding and transport is ascribed to ABCB1 (P-glycoprotein, P-gp), ABCG2 (breast cancer resistant protein, BCRP), ABCC1 (multidrug resistance protein 1, MRP1), and the cholesterol transporter ABCA (Abuznait and Kaddoumi, 2012). Recently special attention has been paid to transthyretin (TTR, formerly known as thyroxine binding prealbumin) which can suppress the AD phenotype in transgenic animal models and reduce cerebral A β deposition (Li et al., 2013). Although being amyloidogenic itself in peripheral tissues, in the brain it was shown to have an anti-A β -amyloidogenic effect and is considered to have potential therapeutic value (Buxbaum and Reixach, 2009). In the brain this protein is mainly expressed by the cells of choroid plexus (Sousa et al., 2007) but can also be detected and regulated in neuronal cells (Kerridge et al., 2014) and apart from the transport function it can contribute to regulation of important neuronal proteins e.g., 14-3-3 ζ protein and neuropeptide Y (Nunes et al., 2006; Vieira and Saraiva, 2013) and brain functions, including memory (Brouillette and Quirion, 2008; Vieira and Saraiva, 2014). TTR has been one of the proteins of interest in our recent research and the mechanisms of its epigenetic regulation were shown to be similar to those of an amyloid-degrading peptidase, NEP (Kerridge et al., 2014). Recent data also suggest that TTR expression in neuronal cells is regulated by heat shock factor 1 (HSF1) which is the major regulator of cellular stress responses (Wang et al., 2014a).

Within neuronal cells abnormal accumulation of A β might also result from the impairment of the two major protein quality control systems providing clearance of misfolded, aggregated or long-lived proteins and represented by autophagy-lysosome and ubiquitin-proteasome systems (for review see Lee et al., 2013). One of the lysosomal peptidases, namely cathepsin B, was shown to degrade A β and its insufficient expression or inactivation caused by its endogenous inhibitor cystatin C (CysC) could lead to A β accumulation (Wang et al., 2012). Deficit of another lysosomal enzyme, sialidase NEU1, also leads to accumulation and amyloidogenic processing of an oversialylated APP in lysosomes, and extracellular release of A β peptides by excessive lysosomal exocytosis (Annunziata et al., 2014). Reduced proteasome activity was demonstrated to increase levels of intracellular and secreted A β while accumulation of improperly degraded A β products in the lysosomes causes lysosomal disruption and cell death (Agholme et al., 2012). In turn, accumulation of A β oligomers in cells causes proteasome inhibition leading to cell death (Tseng et al., 2008). The oligomeric A β can be transmitted from one neuron to another causing neurotoxicity and as such the drugs which stop the spread of intracellular toxic A β aggregates may also be useful for early prevention of developing AD pathology (Agholme and Hallbeck, 2014). Both proteasomal and lysosomal degradation systems can be impaired during life by a

variety of pathological factors resulting in accumulation of A β and predisposing to late-onset AD (Cuanalo-Contreras et al., 2013).

Understanding the clearance mechanisms in the brain and their regulation will help us to design therapies allowing the brain to fight against undesirable accumulation of toxic protein aggregates and to prolong its normal functioning. Deciphering the mechanisms of regulation of the major ADEs, in particular of NEP, lead us to a conclusion that there are some common targets which can be treated simultaneously by the same compounds modulating expression of several proteins involved in amyloid clearance (for example NEP and TTR), and this can result in design of a therapeutic strategy towards improved amyloid clearance.

NEPRILYSIN (NEP) AND RELATED PEPTIDASES (NEP2, ECE-1, ECE-2)

One of the first ADEs in the brain to be identified was a cell-surface, zinc metallopeptidase now known as NEP although this enzyme was originally identified in the brush border membrane of the kidney, where it is very abundant playing a role in degrading circulating biologically active peptides (Kerr and Kenny, 1974). It has subsequently been rediscovered in several guises in the body, for example in B lymphocytes where it is known as the common acute lymphoblastic leukaemia antigen (CALLA, CD10) (Letarte et al., 1988), and in the brain where it was initially identified as the peptidase turning off neuropeptide (enkephalins, substance P) signaling (Roques et al., 1980; Matsas et al., 1983). NEP is also the primary enzyme hydrolysing members of the atrial natriuretic peptide family in the periphery.

NEP preferentially cleaves small peptides (up to about 50 amino acids) on the N-terminal side of hydrophobic residues and hence the A β peptide is efficiently hydrolysed as was first shown *in vitro* by Howell et al. (1995). Subsequently, the enzyme was shown to be a major activity degrading both A β 40 and A β 42 in the brain by examining A β degradation in NEP-deficient mice and through the use of potent NEP inhibitors such as thiorphan (Iwata et al., 2001; Shirotani et al., 2001). Viral gene delivery of NEP to the brain of AD transgenic mice also was shown to reduce amyloid pathology (Marr et al., 2003) and subsequent studies, including the application of a recombinant, brain-targeted NEP (Spencer et al., 2014), have confirmed and extended these observations on the critical nature of NEP to amyloid clearance (Leissring et al., 2003). However, some caution is needed in over-expressing human NEP as a therapeutic strategy since, in a *Drosophila* model, while reducing transgenic A β 42 levels this was accompanied by axonal loss and a reduction in lifespan (Iijima-Ando et al., 2008). Over-expression of a *Drosophila* homologue of NEP also resulted in significant behavioral deficits (Bland et al., 2009). These changes probably are a consequence of the substrate promiscuity of NEP resulting in altered levels of neuropeptides. A strategy to overcome this problem has involved identifying critical catalytic residues and hence engineering the specificity of human NEP to selectively enhance its A β -degrading capacity (Pope et al., 2014; Webster et al., 2014). Functional profiling of several ADEs in elderly and AD patients' brains has provided additional support for NEP as the major protease involved in A β degradation (Wang et al., 2010).

The human genome contains seven NEP-like genes, several of which have now also been implicated in A β degradation. The closest homologue to NEP, NEP2 (also known as membrane metalloendopeptidase-like protein (MMELP)), can also degrade A β 40 and A β 42 *in vitro* and *in vivo* and is recognized as an important ADE and hence possible therapeutic target (Hafez et al., 2011). However, there are significant substrate and inhibitor specificity differences between rodent and human NEP2 so some caution is needed in extrapolating data between species (Whyteside and Turner, 2008). Unlike NEP, NEP2 exists in alternatively spliced forms with differing subcellular distributions but little is known of factors affecting NEP2 location or expression levels. Both NEP and NEP2 expression are altered in mild cognitive impairment (MCI) subjects relative to non-impaired subjects in AD-susceptible regions (Huang et al., 2012). NEP2 enzymic activity was decreased in both MCI and AD and was positively associated with cognitive functions which suggested that NEP2 may serve as a preclinical biomarker for AD (Huang et al., 2012).

Two other NEP-like gene products that act as ADEs are the endothelin converting enzymes (ECE-1 and ECE-2). ECE-1 is mainly located in vascular endothelial cells where its principal role is to act as a biosynthetic enzyme in the formation of the vasoconstrictor peptide endothelin-1 from its precursor proendothelin-1. ECE-1 may also metabolize some other circulating peptides, e.g., bradykinin (Hoang and Turner, 1997). However, significant levels of ECE-1 are present in the CNS (Barnes and Turner, 1997) being involved in brain endothelin synthesis. It also plays a role in endosomal neuropeptide metabolism regulating peptide receptor recycling (Cottrell et al., 2009). Like NEP, ECE-1 can degrade A β *in vitro*, and *in vivo* transgenic studies have implicated the enzyme in physiological A β metabolism (Eckman and Eckman, 2005). The much less studied homologue ECE-2, originally identified by Emoto and Yanagisawa (1995) is also an excellent candidate ADE being mainly brain located. ECE-2 levels are reported to be increased in AD and it is up-regulated by A β itself (Palmer et al., 2009). ECE-2, which has an acidic pH optimum, is localized in secretory compartments and appears to be involved in protein processing events (Mzhavia et al., 2003), including some opioid peptides and thereby regulating opioid receptor activity (Gupta et al., 2014). Increased concentrations of both A β 1-40 and A β 1-42 are found in the brains of ECE-2 knockout mice (Eckman et al., 2006). Recently using SH-SY5Y cells overexpressing wild-type APP and pharmacological inhibition of endogenous ECE activity it was shown that ECE-1 and ECE-2 participate in the degradation of distinct pools of A β , one destined for secretion and the other being produced and degraded within the endosomal-autophagic-lysosomal pathways (Pacheco-Quinto and Eckman, 2013). Although ECE-1 regulates both pools of A β , ECE-2 regulates mainly the intracellular pool of the peptide, in particular in the autophagic vesicles, suggesting that therapeutic targeting of these enzymes might have different outcomes since it will affect different pools of A β (Leissring and Turner, 2013; Pacheco-Quinto and Eckman, 2013).

Consistent with the observations that AD patients have reduced cerebral blood flow preceding onset of dementia, Palmer and colleagues have been able to link these changes with

A β -induced cerebral vasoconstriction increasing ECE-1 levels and hence ET-1 in a free radical-mediated process (Palmer et al., 2009, 2012, 2013). Modulating ECE-1 levels therefore could have opposing neuroprotective and neurotoxic effects through effects on both A β and ET-1 levels.

INSULIN-DEGRADING ENZYME (INSULYSIN, IDE)

Another principal ADE, and the first to be identified (Kurochkin and Goto, 1994), is the IDE (insulysin). This is a zinc peptidase but structurally and mechanistically distinct from the NEP family and also showing distinct cellular and subcellular localization. A very diverse range of studies, from *in vitro* and cell-based studies through to animal models now support an involvement of IDE in amyloid clearance mechanisms (for review see Fernández-Gamba et al., 2009; Nalivaeva et al., 2012a). Amyloid peptides associated with British and Danish familial dementia were found among the specific IDE substrates (Morelli et al., 2005). As its name suggests, IDE was originally described as an enzyme implicated in insulin metabolism and therefore of potential significance in diabetes mellitus providing one of a number of links between diabetes and AD (Yang and Song, 2013; Haque and Nazir, 2014). Recently it was shown that IDE inhibitors might represent a new therapeutic strategy to treat type-2 diabetes (Maiani et al., 2014).

IDE has important substrates other than insulin and A β . In particular, IDE is involved in elimination of oxidized proteins in peroxisomes (Morita et al., 2000). It is also the principal proteinase degrading cytosolic APP intracellular domain (AICD) (Edbauer et al., 2002). Another physiological substrate for IDE is somatostatin, a neuropeptide that declines in aging and AD, which is also able to bind to and enhance IDE activity towards A β through an allosteric action (Ciaccio et al., 2009) and to upregulate NEP expression (Saito et al., 2005). Although it is primarily located in the cytosol, IDE is found in lesser amounts in mitochondria where A β can also be found (Leissring et al., 2004). Surprisingly, given that it lacks any known secretory signal, a small but significant proportion of IDE is secreted from cells through an unconventional protein secretion pathway (Zhao et al., 2009). This secreted IDE is functional in extracellular A β degradation and it appears to be routed via detergent-resistant membrane complexes into exosomes for secretion, along with A β (Bullock et al., 2010).

The recent development of novel IDE activators and inhibitors (Cabrol et al., 2009; Leissring et al., 2010; Abdul-Hay et al., 2013; Maiani et al., 2014) combined with detailed structural studies of the enzyme (Im et al., 2007) should aid in unraveling the importance of IDE in amyloid metabolism and pathology, and as a therapeutic target.

OTHER ADEs

A wide and diverse variety of other proteases of all main catalytic classes have been suggested as potential ADEs and their involvement in these processes has been reviewed elsewhere (e.g., Nalivaeva et al., 2012a) and will not be covered in detail here. These include some metallopeptidases (matrix metalloproteinases, glutamate carboxypeptidase II), serine proteases (plasmin, acylpeptide hydrolase), cysteine proteases (cathepsin B)

and the aspartic protease, BACE-2. The latter enzyme was a particularly efficient ADE and able to degrade intracellular A β (Abdul-Hay et al., 2012). Although angiotensin-converting enzyme (ACE) was shown to be capable of A β cleavage (Hemming and Selkoe, 2005) mostly acting as a carboxypeptidase and converting the more hydrophobic and toxic A β ₄₂ to A β ₄₀ (Zou et al., 2007), its role in AD pathology is still not clear. A recent study employing ACE overexpression in myelomonocytes of APP(SWE)/PS1(Δ E9) mice has convincingly demonstrated the protective effect of ACE against cognitive decline but this effect was most likely linked to an enhanced immune response, coupled with increased myelomonocytic expression of catalytically active ACE (Bernstein et al., 2014). The ACE homologue, ACE2, is a metallo-carboxypeptidase that converts A β ₄₃ to A β ₄₂ which can then be converted to A β ₄₀ by ACE (Liu et al., 2014). Hence, maintaining brain ACE2 and ACE activities might be important for preventing accumulation of more toxic A β species.

DEFICIT OF ADEs UNDER PATHOLOGICAL CONDITIONS AND AGEING

Ageing is considered as one of the major risk factors of late-onset AD. Although literature data demonstrate a link between AD pathology and the level of activity and expression of ADEs in the brain there are some contradictions in the reported results which might be caused by the source of the brain material used, its maintenance before the analysis and also by the techniques applied. Reduced NEP mRNA levels were reported in the hippocampus and temporal gyrus of AD patients suggesting a relationship between NEP activity and deficient degradation of A β peptide leading to high number of senile plaques in these brain areas (Yasojima et al., 2001). Similarly, reduced IDE levels were reported in the hippocampus of AD patients bearing the APOE ϵ 4 allele (Cook et al., 2003). It was also shown that NEP and IDE decline with age in human cortex and hippocampus and IDE is more oxidized in the hippocampus of AD patients compared to the cerebellum (Caccamo et al., 2005). Reduced activity of NEP was also observed in the cerebrospinal fluid (CSF) of demented patients with Lewy body pathology (Maetzler et al., 2010). On the contrary there were no differences reported in NEP mRNA levels in the temporal lobe of AD patients compared to age-matched controls although the authors observed some changes in the somatostatin system suggesting that this might impair NEP regulation and cause a deficit of its activity leading to A β accumulation (Gahete et al., 2010). Moreover, postmortem analysis of NEP activity by immunocapture-based fluorogenic assays revealed an increase in NEP and IDE activity in the frontal cortex from subjects of different ages and with different pathological stages of AD progression (Miners et al., 2009). Based on these observations the authors suggested that reduction in NEP and IDE activity is not the primary cause of A β accumulation in AD, but rather a late-stage phenomenon secondary to neurodegeneration. Our own data on rat brain demonstrate that NEP mRNA and protein levels in the cortex and hippocampus significantly decline with age being the highest in the first month of animal life when development of the nervous system and its neuronal networks is the most active. On the contrary, in the striatum, NEP

expression remained at a relatively high level during advanced age (Nalivaeva et al., 2004, 2012c). Regarding the human brain there are no systematic data showing the dynamics of NEP or other ADEs expression in various brain structures with aging and in the cases of development of MCI and AD which would significantly contribute to our understanding of the role of these enzymes in normal human brain development, functioning and pathogenesis. The recently developed McGill-Thyl-APP transgenic mouse model of AD demonstrates significant down-regulation of IDE at the preclinical early stage of AD pathology which could make it a valuable model for exploring mechanisms to restore enzyme activity (Ferretti et al., 2011).

Among the factors which predispose to the development of late-onset AD are hypoxia, ischaemia, stroke, stress, diabetes, trauma and neuroinflammation. All of them were shown to affect amyloid metabolism and to some extent the levels of expression and activity of ADEs. The analysis of ischaemically damaged brains of patients demonstrated that ischaemic episodes trigger dysregulation of expression of a number of AD-related genes (Pluta et al., 2013). Monitoring plaque formation in real time in a mouse model has revealed that stroke can trigger accelerated amyloid deposition, most likely through interference with amyloid clearance pathways along interstitial fluid drainage routes (Garcia-Alloza et al., 2011). Our studies have demonstrated that experimental four-vessel occlusion ischaemia in rats resulted in down-regulation of NEP and ECE-1 as well as up-regulation of APP and BACE both in the cortex and hippocampus (Nalivaeva et al., 2004, 2005). On the contrary, levels of IDE were up-regulated after ischaemia both at the mRNA and protein levels (unpublished data). These findings strongly correlate with the changes in NEP and IDE expression patterns observed in rat thalamus after focal cerebral ischaemia (Hiltunen et al., 2009). Up-regulation of IDE mRNA was also observed in a permanent two-vessel occlusion ischaemia model in rats which was attenuated by administration of a natural product (Choto-san) widely used in Japan for treatment of vascular dementia (Hayashi et al., 2005). The apparent anti-dementia effects of this medicine have been shown to be due to its anti-hypertensive, free radical scavenging, and anti-excitotoxic effects (Watanabe et al., 2003). However, these authors used whole brain mRNA extracts which diminishes the value of their results in relation to the brain areas affected by AD. A different pattern of IDE regulation under ischaemic conditions was also observed in wild-type mice and mice with a deficient Toll-receptor system suggesting that the Toll/interleukin-1 receptor domain-containing adaptor inducing interferon- β (TRIF) pathway regulates IDE expression (Famakin et al., 2014).

Cerebrovascular pathology and ischaemia are the major factors leading to insufficient oxygen supply to the brain causing metabolic changes in neuronal cells predisposing to neurodegeneration and AD (Bazan et al., 2002). Previously we have demonstrated that hypoxia in neuroblastoma NB7 cells and rat primary cortical neurones lead to down-regulation of mRNA and protein levels of NEP as well as its enzyme activity (Fisk et al., 2007). We have also observed around 30% decrease in expression of ECE-1 under hypoxic conditions at the protein level, although at the level of ECE-1 mRNA there were no statistically

significant changes (Fisk et al., 2006). These data correlate with reduced NEP activity in the cortex and hippocampus of rats subjected to prenatal hypoxia (Nalivaeva et al., 2012b; Wang et al., 2014b).

In the AD brain decreased levels of NEP expression were also observed along the vasculature suggesting its role in the development of cerebral amyloid angiopathy (CAA) in AD patients (Carpentier et al., 2002; Miners et al., 2006). Assessing the protective role of NEP in the vasculature it was shown that NEP can rescue cerebrovascular smooth muscle cells against A β -induced cell death and prevent complications of CAA (Miners et al., 2011). Along with the age-related decrease of NEP expression observed in neuronal cells, Apelt and colleagues have reported up-regulation of this enzyme in reactive astrocytes surrounding amyloid plaques in AD transgenic mice (Apelt et al., 2003) which is considered to be a compensatory reaction of a specific set of brain cells possessing a protective function. These observations stimulated a cascade of studies on possible mechanisms of NEP up-regulation as a strategy for AD treatment through stimulating clearance of A β peptides and/or their various aggregated forms.

PHARMACOLOGICAL AND EPIGENETIC REGULATION OF ADE GENES

Various strategies have been suggested to increase expression and activity of ADEs, in particular of NEP, in the brain areas vulnerable to accumulation of amyloid burden and neuronal cell death. Developing targeted gene delivery techniques several viral vectors have been utilized including Sindbis viral (Hama et al., 2001), lentiviral (Marr et al., 2003) or adenoviral (Iwata et al., 2013) delivery which proved to be effective in reducing amyloid burden in treated brain areas. The last approach, which allowed global neuronal gene expression throughout the brains, utilized peripheral intravascular administration of the gene-targeted vector. Refining the methods of NEP delivery from the periphery to the brain, intra-peritoneal injections of a lentiviral vector expressing NEP fused with the ApoB transport domain was found to be effective in reducing levels of A β and the number of plaques in the brain of AD transgenic mice (Spencer et al., 2011). The optimal timing of NEP over-expression has also been examined suggesting that earlier up-regulation of NEP was more beneficial in alleviating AD symptoms in a mouse model (El-Amouri et al., 2008). In line with the attempts at transgenic over-expression of NEP in neuronal cells it was also shown that increased IDE expression can lead to reduced brain A β and delay of AD pathology (Leissring et al., 2003).

Delivery of NEP to peripheral tissues has also proved effective in reducing the deposits of islet amyloid polypeptide (IAPP) which contribute to type 2 diabetes. Thus, adenoviral delivery of NEP to the pancreas reduced amyloid deposits and cell death in the islets (Zraika et al., 2010). However, in this case, NEP did not act via degradation of IAPP but appeared to act by inhibiting the amyloid fibril formation through protein-protein interactions involving the enzyme active site, rather than by hydrolysing the peptide.

Because brain and plasma A β are considered to be in an equilibrium through transport mechanisms (Deane et al.,

2004), Hersh and colleagues have investigated whether enhancing peripheral degradation of A β by NEP could reduce brain levels and associated pathology. Their reports suggest that in AD transgenic mice over-expression of NEP in erythrocytes or leukocytes leads to a reduced A β burden in the brain (Liu et al., 2007; Guan et al., 2009). Similar results were observed when NEP was over-expressed in skeletal muscle (Liu et al., 2009). An alternative strategy of expressing a secreted, soluble form of NEP in plasma through an adenovirus construct was also effective in clearing brain A β yet did not affect plasma levels of other peptide substrates of NEP such as bradykinin or substance P (Liu et al., 2010). Expressing NEP in plasma might provide a simple system allowing the monitoring of its long-term activity, and this approach has recently been re-examined by using albumin-fused NEP with extended half-life (Henderson et al., 2014). This study demonstrated that although NEP highly effectively degraded A β in the periphery it did not alter brain or CSF A β levels, suggesting that the peripheral sink hypothesis might not be valid and supporting earlier observations of Walker et al. (2013). However, the experiments in both studies have been performed in transgenic mice and non-human primates and the validity of these conclusions for human pathology still needs to be assessed.

Apart from gene-targeted manipulations of the expression of ADEs, a number of studies have aimed at pharmacological up-regulation of these enzymes and one of the earlier works reported that retinoic acid which induces cell differentiation was able to increase IDE expression and activity (Melino et al., 1996). Aiming at NEP regulation, Saido et al. have put forward a hypothesis that elevated levels of neuropeptide substrates of NEP could themselves up-regulate NEP via a feedback control mechanism. They hence screened a wide range of NEP substrates demonstrating that, of those tested, only somatostatin was capable of up-regulating NEP expression in primary neuronal cells in a mechanism possibly mediated through somatostatin receptor sub-types 2 or 4 (Saito et al., 2005). Utilization of somatostatin agonists as a possible therapeutic strategy for prevention of AD was recently reinforced by Saido (2013). An alternative strategy for pharmacological up-regulation of NEP was reported in a study analyzing the effects of a selective peroxisome proliferator activated receptor- δ (PPAR δ) agonist, GW742, which activated the NEP promoter driving luciferase expression in transfected HEK293 cells (Kalinin et al., 2009). This treatment reduced plaque burden in 5xFAD mice which harbor 3 mutations in APP and 2 mutations in PS1 not only by NEP activation but also by increased expression of IDE. IDE expression was also shown to be up-regulated by norepinephrine via the β_2 adrenergic receptor resulting in activation of A β uptake and degradation by microglia (Kong et al., 2010). Another brain metabolite, namely kynurenic acid, was reported to regulate NEP mRNA and protein levels in SH-SY5Y cells and mouse cortical neurones and to have a protective effect on cell survival which was thiorphan-dependent (Klein et al., 2013).

Although reports on the effect of the protein kinase C inhibitor and anticancer drug Gleevec on NEP up-regulation were to some extent contradictory (Eisele et al., 2007; Vázquez et al., 2009), our recent data confirmed that Gleevec can increase NEP

expression in cell models (Kerridge et al., 2014). On the other hand, selective activation of protein kinase C ϵ (e.g., with bryostatin) was also shown to reduce A β levels through enhancing NEP expression and cell-surface activity (Lim and Alkon, 2014).

Analyzing the effects of such common drugs as statins on the status of ADEs in the brain Tamboli et al. (2010) demonstrated a potential positive effect of lovastatin and itraconazole on A β degradation and clearance via increased exosome-associated secretion of IDE by microglia. Lovastatin injections also stimulated release of IDE in the circulation of mice. However, in another study using a transgenic mouse model the authors failed to observe any effects of simvastatin on NEP activity (Papadopoulos et al., 2014). Among lipid species, docosahexaenoic acid (DHA) was also shown to up-regulate IDE while palmitic acid had an opposite effect (Du et al., 2010).

A variety of other strategies to enhance activity levels of NEP have also been examined including epigenetic approaches (see below), as well as natural products that can upregulate the enzyme (green tea catechins, curcumin, flavones, etc.) (Melzig and Janka, 2003; Ayoub and Melzig, 2006; Kiss et al., 2006; Deng et al., 2014; Fujiwara et al., 2014). Green tea catechins were shown to be preventive in AD animal models via up-regulation of NEP (Lim et al., 2013). Human adipose tissue-derived mesenchymal stem cells have been shown to secrete exosomes carrying functionally active NEP (Katsuda et al., 2013) and neuronally differentiated human umbilical cord mesenchymal stem cells transplanted into APP transgenic mice reduced A β levels and enhanced both NEP and IDE levels, as well as cognitive function, raising the prospect of future cell therapy for AD (Yang et al., 2013). Recently a non-invasive physiologically relevant way to up-regulate NEP expression was examined in an animal model demonstrating that enriched environment has a protective effect against A β accumulation and age-related cognitive decline (Mainardi et al., 2014) supporting earlier observations that brain NEP is upregulated under such conditions (Lazarov et al., 2005).

ROLE OF APP IN REGULATION OF ADE GENES

Apart from A β and N-terminal products released from APP during its proteolytic processing via γ -secretase cleavage (see **Figure 1**) there are several C-terminal fragments or AICDs. Their formation is similar to the cleavage of the Notch protein, which liberates an intracellular domain (NICD) capable of translocating to the nucleus and regulating gene transcription (Schroeter et al., 1998). AICD was also proposed to act as a transcriptional regulator (Passer et al., 2000) and by using luciferase reporter-based assays, it was shown that AICD can form a transcriptionally active complex with the nuclear adaptor (and AICD stabilizing protein) Fe65 and the histone acetyltransferase Tip60 (Cao and Südhof, 2001).

Since that first report of the transcriptional activity of the C-terminal fragment released from APP cleavage by γ -secretase, the transcriptional activity of AICD has been intensively studied (for review, see Beckett et al., 2012; Konietzko, 2012; Pardossi-Piquard and Checler, 2012) and the number of genes suggested to be regulated by AICD is steadily increasing. However, to date, only

the NEP gene has unequivocally been shown to be functionally regulated by AICD (Pardossi-Piquard et al., 2005; Belyaev et al., 2009). Moreover, it has been established that only the AICD derived from the neuronal APP₆₉₅ but not from APP₇₅₁ or APP₇₇₀ in a β -secretase-dependent pathway is accumulated in the nucleus and up-regulates NEP expression (Belyaev et al., 2010). Mechanistically at the transcriptional level up-regulation of NEP expression by AICD involves the binding of AICD to the MED12 unit of the Mediator RNA polymerase II complex (Xu et al., 2011). This finding provides a missing functional link between nuclear AICD binding and its transcriptional activity (Turner et al., 2011) and allowed the validation of additional AICD-dependent genes such as aquaporin-1, MICAL2 and Fibronectin-1 (Xu et al., 2011).

Using two neuroblastoma cell lines, SH-SY5Y characterized by very low levels of NEP expression, and NB7 which produce a significant amount of NEP we have demonstrated that in the case of low NEP-expressing cells the *NEP* promoter is occupied by the histone-deacetylase HDAC1 while in NB7 cells by AICD. Treating SH-SY5Y cells with HDAC inhibitors trichostatin A or valproic acid (VA) we were able to up-regulate levels of NEP expression (Belyaev et al., 2009). VA is chiefly known as a highly successful and widely used antiepileptic drug but its efficacy in neurodegenerative disease has been much less studied (Nalivaeva et al., 2009), although there are several recent reports of its beneficial effects in reducing amyloid accumulation and improving cognitive function in AD mice (Qing et al., 2008), and amyloid clearance via microglial phagocytosis (Smith et al., 2010). VA also up-regulates NEP in the cortex and hippocampus and restores memory deficit caused by hypoxia in rats (Nalivaeva et al., 2012b) and in transgenic mice subjected to prenatal hypoxia (Wang et al., 2014b). The potential of VA and other HDAC inhibitors in the treatment of neurodegeneration has been further strengthened by the recent report that inhibitors of class 1 HDACs reverse contextual memory deficits in an AD mouse model (Kilgore et al., 2010), a process termed “epigenetic memory rescue”. Others have also supported the potential value of VA in AD as a mechanism to “untie tangles” coupled with its ability to induce neurogenesis of neural progenitor/stem cells both *in vitro* and *in vivo* via multiple signaling pathways including up-regulation of the nerve growth factor gene (Nalivaeva et al., 2009; Tariot and Aisen, 2009; Noh and Seo, 2014). There is clearly scope for more robust clinical trials on selective HDAC inhibitors in AD, particularly at earlier stages in disease progression. Given the prolonged and successful use of VA clinically in the treatment of epilepsy, there are grounds for more detailed retrospective epidemiological surveys in relation to AD incidence in valproate-users and control patients.

Since AICD is rapidly degraded within the cytoplasm, in particular by IDE (Cupers et al., 2001; Edbauer et al., 2002) treatment of cells with IDE inhibitors or an alkalinising agent such as NH₄Cl (Vingtdeux et al., 2007) was proved to be able to stabilize AICD and its nuclear pool resulting in increased NEP expression and activity and reduced A β levels in the cell medium (Kerridge et al., 2014). Apart from degradation, A β -sequestration by clearance proteins also precludes A β oligomerization and plaque formation. A major A β -binding protein in the brain is TTR (Du et al., 2012), which suppresses A β aggregation, facilitates its clearance and

prevents A β -induced cytotoxicity (Tsuzuki et al., 2000; Brouillette et al., 2012; Li et al., 2013). Increased levels of TTR have been observed in transgenic mice over-expressing mutant APP (Stein and Johnson, 2002) but whether this effect was mediated by AICD and is APP isoform-dependent has not been investigated. Recently we have reported that TTR is regulated by AICD and HDAC similarly to NEP (Kerridge et al., 2014).

Among therapeutic strategies to improve A β clearance in the brain special attention has been paid to a recently reported effect of a retinoid X receptors (RXR) agonist bexarotene also used as an anti-cancer drug in patients with cutaneous T-cell lymphoma (Cramer et al., 2012). Oral administration of this drug to mice with AD pathology caused a rapid enhanced clearance of soluble A β which resulted within a few days in a reduced amyloid plaque area and in rapid reversal of cognitive, social, and olfactory deficits. Such fast clearance of A β in the brain had an ApoE-dependent character although there might be other mechanisms involved and more studies are needed to evaluate the clinical value of this drug in AD (LaFerla, 2012; Strittmatter, 2012). Bexarotene also blocks calcium-permeable ion channels formed by A β peptides by competing with a cholesterol-binding domain in A β (Fantini et al., 2014).

FUTURE PERSPECTIVES

As suggested above, epigenetic regulation of AD-related genes is now considered a plausible strategy for designing new therapies against late-onset AD. For example, simultaneous up-regulation of NEP and TTR gene expression by Gleevec might provide a platform for designing a strategy towards enhancement of amyloid clearance in the ageing brain via different mechanisms. Epigenetic regulation of the clusterin gene expression can also play an important role in AD pathogenesis via inhibition of A β aggregation (Li et al., 2014).

Although several compounds have been discarded on the grounds of limited clinical efficacy, all major clearance-related approaches still hold promise. Among some drug candidates advanced to Phase III trials are anti-A β antibodies, metal complexing agents, ginseng extracts, and intravenous immunoglobulins (Kurz and Perneckzy, 2011). Recent data, including our own reports, strongly support the possibility that clearance-related strategies have the potential for protecting neuronal cells and cognitive functions via reducing the levels of soluble and particularly toxic A β species in the brain.

With all the advances in our knowledge of amyloid metabolism and the increase in number of ADEs that have been identified in multiple cell types and brain regions acting co-ordinately to regulate A β levels, it is still very surprising that relatively little is known about the precise physiological role of this peptide. Considering that in the cells there is a very well defined and tuned mechanism of A β production and removal one can expect that this peptide might have an important role which, when disturbed, can lead to the disease. New functions of A β continue to emerge, for example, even as a regulator of gene transcription (Maloney and Lahiri, 2011; Barucker et al., 2014). Recent strategies in drug design could be more successful if more effort had been put into the study of normal physiology of this peptide and its precursor protein APP (Nalivaeva and Turner, 2013).

Taking into account that AD pathology develops over many years, early manipulation of ADEs might be essential to prevent amyloid deposition and disease progression. However, the efficacy of any preventive treatment will be strongly driven by the development of early diagnosis and pre-clinical markers of AD. Recent systematic studies of blood protein biomarkers have shown potential in prediction and monitoring the progression of AD (Kiddle et al., 2014; Sattlecker et al., 2014). Levels of expression and activity of ADEs, e.g., in blood serum, might be of some importance but more systematic analysis is required to prove any correlation between these enzymes and disease progression. Since AD is a multifactorial disease a single focus for diagnostics or treatment is unlikely to be productive so a combination therapy targeting various links in the chain of pathological events leading to AD is likely to be optimal. Combining the efforts in gaining new knowledge about various protective mechanisms and the ways of their enhancement is the key to success.

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