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# NEW INSIGHTS INTO THE ROLES OF METALLOPROTEINASES IN NEURODEGENERATION AND NEUROPROTECTION

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Proteolytic enzymes constitute around 2% of the human genome and are involved in many stages of cell development from fertilization to death (apoptosis). The identification of many novel proteases from genome-sequencing programs has suggested them as potential new therapeutic targets. In addition, several well-characterized metalloproteinases were recently shown to possess new biological roles in neuroinflammation and neurodegeneration. As a result of these studies, metabolism of the neurotoxic and inflammatory amyloid peptide ( $A\beta$ ) is considered as a physiologically relevant process with several metalloproteinases being suggested for the role of amyloid-degrading enzymes. These include the neprilysin (NEP) family of metalloproteinases (including its homologue endothelin-converting enzyme), insulin-degrading enzyme, angiotensin-converting enzyme, plasmin, and, possibly, some other enzymes. NEP also has a role in metabolism of sensory and inflammatory neuropeptides such as tachykinins and neurokinins. The existence of natural enzymatic mechanisms for removal of amyloid peptides has extended the therapeutic avenues in Alzheimer's disease (AD) and neurodegeneration. The proteolytic events underlying AD are highly compartmentalized in the cell and formation of amyloid peptide from its precursor molecule APP (amyloid precursor protein) takes place both within intracellular compartments and in the plasma membrane, especially in lipid raft domains. Degradation of amyloid peptide by metalloproteinases can also be both intra- and extracellular

depending on the activity of membrane-bound enzymes and their soluble partners. Soluble forms of proteases can be secreted or released from the cell surface through the activity of “shedases”—another group of proteolytic enzymes involved in key cellular regulatory functions. The activity of proteases involved in amyloid metabolism depends on numerous factors (e.g., genetic, environmental, age), and some conditions (e.g., hypoxia and ischemia) shift the balance of amyloid metabolism toward accumulation of higher concentrations of A $\beta$ . In this regard, regulation of the activity of amyloid-degrading enzymes should be considered as a viable strategy in neuroprotection.

### I. Introduction

Proteolysis represents one of the key processes underlying biological events from fertilization through development to death. In the human genome there are more than 500 proteases and homologues (almost 2% of the genome), many of whose physiological roles are yet to be identified and which may provide potential therapeutic targets in the treatment of human disease. At present there are 70 known human hereditary diseases caused by mutations in protease-coding genes (<http://www.uniovi.es/degradome/>). Abnormal functioning of these genes are implicated in such pathologies as inflammatory diseases, cancer, cardiovascular diseases, and neurodegeneration. Understanding of the role of these enzymes and their evolutionary conservation is important for design of appropriate drugs and therapeutic strategies. Other eukaryotic species whose genomes have been deciphered to date also possess a very high number of protease and protease-like genes which in the case of *Drosophila melanogaster* and mouse are even higher than in human (Rawlings *et al.*, 2006). The number of species in which proteases have now been identified is approaching 3000 (<http://merops.sanger.ac.uk/>). Cysteine-, serine-, and metallopeptidases represent the major classes of peptidases; among these three classes, the metallopeptidase class is more consistently represented with the number of genes varying from 183 in *Drosophila* to 198 in mice (in human, 186). Two other classes have much higher diversity with the range in the number of genes for cysteine proteases from 76 in *Drosophila* to 153 in mice (Puente *et al.*, 2003). For the serine peptidases this range is even more pronounced: from 100 in *Caenorhabditis elegans* to 309 in *Drosophila*. There are a smaller number of aspartic proteinases, although some are of key therapeutic importance. This more conservative representation of metallopeptidases in the genomes of various species may reflect roles of these enzymes in more generic cellular functions and their unique catalytic properties which required water and metal ions for activation of the proteolytic (hydrolytic) process, which were carefully preserved in the course of evolution.

The metallopeptidases can be divided into 12 clans according to the type and number of metal ions required for their activity (Rawlings and Barrett, 2004). This chapter will focus on two distinct zinc metallopeptidase families belonging to one of these clans, namely MA, whose representatives require zinc for their activity and contain one or two histidine residues in the zinc binding motif. The first of these metallopeptidase families is the M13 family represented by neprilysin [or neutral endopeptidase (NEP)] and the second is the M2 family represented by angiotensin-converting enzyme [or peptidyl dipeptidase (ACE)]. Members of each of these families have served as important drug targets, particularly in cardiovascular disease and, more recently, have provided insight into mechanisms involved in neurodegeneration and neuroinflammation, especially from the point of view of processing of the amyloid precursor protein (APP) and its products in Alzheimer's disease (AD).

The discovery of ACE2 in our laboratory (Tipnis *et al.*, 2000), as a result of genomics approaches to the identification of zinc metalloproteinases, together with its critical role in cardiac and lung development and function (Crackower *et al.*, 2002; Donoghue *et al.*, 2000) and as the cell surface receptor for the severe-acute respiratory syndrome (SARS) *Coronavirus* (Li *et al.*, 2003), emphasizes the validity of this strategy for identification of novel therapeutic targets. ACE2 was also suggested to play an important role in the brain renin-angiotensin system being widely expressed in various brain areas but restricted mostly to neuronal cells (Doobay *et al.*, 2007).

## II. The NEP Family

NEP, or neprilysin as it is now known, is a cell surface membrane-bound glycoprotein and zinc peptidase also known as CD10 or common acute lymphoblastic leukemia antigen (CALLA). It was originally identified as a major antigen of renal membranes over 30 years ago and, at that time, was implicated in the metabolism of insulin. However, as found later, NEP degrades only the insulin B chain *in vitro* and not the intact insulin dimer, which suggests that NEP does not have any physiological role in degradation of insulin. Moreover, another zinc metallopeptidase, insulin-degrading enzyme (IDE; insulysin), was subsequently discovered which appeared to fulfill the physiologically relevant function of insulin degradation. Whereas the highest concentrations of NEP are in the renal microvillar membrane, the first clues to its physiological roles came from studies on the metabolism of neuropeptides [especially the enkephalins and substance P (SP)] in the central nervous system where NEP is several orders of magnitude less abundant (Malfroy *et al.*, 1978; Matsas *et al.*, 1984; Relton *et al.*, 1983). It is now accepted that NEP functions to turn off neuropeptide signals

at the synapse in an analogous fashion to the hydrolysis of acetylcholine by acetylcholinesterase at cholinergic synapses (see [Turner and Tanzawa, 1997](#) for review). Evidence *in vitro* has clearly demonstrated that synaptic membranes efficiently degrade enkephalins and SP and that NEP was the primary enzyme responsible for these events ([Matsas et al., 1983](#)). Combined with the data obtained *in vivo* in rodents using potent and selective NEP inhibitors, such as phosphoramidon and thiorphan ([Roques et al., 1980](#)), key roles were established for NEP in the central nervous system. Subsequently, renal NEP was shown to be the principal enzyme inactivating the vasodilator, atrial natriuretic peptide ([Kenny and Stephenson, 1988](#)), which has led to much investment in the development of NEP inhibitors, either alone or in combination with ACE inhibitors (vasopeptidase inhibitors), as drugs in the treatment of hypertension, congestive heart failure, and renal disease ([Bralet and Schwartz, 2001](#)), although concerns over their safety have been raised ([Quaschnig, 2005](#)).

NEP also plays important roles in other peripheral tissues such as in chemoreception and in potentiation of the response of the carotid body to hypoxia via degradation of its preferred substrate, SP ([Kumar et al., 1990, 2000](#)). NEP was also detected in the liver, lungs, muscles, fat deposits, bones, the vertebrae, articular cartilages, and synoviae ([Sales et al., 1991](#)). In the bones, NEP plays a role in regulation of osteoblast and osteoclast metabolism mediated by both hormones and local bone peptide factors ([Howell et al., 1993](#); [Ruchon et al., 2000](#)). In the skeletal muscles, NEP participates in regeneration of muscle fibers and there are data on its role associated with hereditary muscle disorders ([Broccolini et al., 2006](#)).

The cloning of NEP also revealed its identity with the CALLA or CD10 and has implicated NEP in cancer mechanisms ([Letarte et al., 1988](#); [Tran-Paterson et al., 1989](#)). For example, in human prostate cancer, NEP is dramatically downregulated ([Papandreou et al., 1998](#)) allowing mitogenic peptides such as bombesin and endothelin to drive androgen-independent cell division in the prostate. The survey of the expression of NEP and the NEP homologue, endothelin-converting enzyme 1 (ECE-1), in a range of prostate cancers demonstrated that there is a certain balance between the levels of expression of NEP and ECE-1 which determines the level of malignancy of the cells and that upregulation of ECE-1 expression in metastatic cells may be indicative of its role in metastatic progression ([Usmani et al., 2002](#)). Later it was shown that NEP and ECE-1 act as mediators of prostate cancer invasion via a stromal-epithelial interaction ([Dawson et al., 2004](#)). This and related observations have led to suggestions that the dysregulation of the balance of NEP and ECE can lead to the disease and selective reexpression of NEP in prostate cells may provide a novel approach to the treatment of prostate cancer. This is an excellent example where two homologous peptidases counterbalance each other's actions in physiology and pathology.

NEP cleaves a wide range of substrates including SP and other tachykinin peptides, in particular neurokinin B ([Fig. 1](#)), which makes it an important player

**Proinflammatory peptides cleaved by metalloproteinases**

- Substance P (NEP, ACE)
- Bradykinin (NEP, ACE, ECE)
- CGRP (NEP)
- Neurokinins (NEP, ACE)
- Endothelin (NEP)
- Angiotensin II (ACE2)
- Interleukin-1 $\beta$  (NEP)
- Insulin (IDE)
- Insulin B chain (NEP)
- A $\beta$  (NEP, ECE, ACE, IDE)

Fig. 1. List of proinflammatory peptides cleaved by metalloproteinases.

in the arena of inflammation (Hooper and Turner, 1985). SP is released from sensory nerves inducing neurogenic inflammation and NEP, via SP degradation, limits its effects and those of other proinflammatory peptides. There are several studies reporting the role of NEP in peripheral inflammation, for example in the skin (Scholzen and Luger, 2004; Scholzen *et al.*, 2001). Moreover, NEP but not ACE was shown to be the most important for CGRP degradation in human skin, and NEP inhibitors facilitated neurogenic inflammation in the skin (Kramer *et al.*, 2005). NEP levels were also found to be significantly decreased in the plasma and monocytes of patients with juvenile idiopathic arthritis (Simonini *et al.*, 2005). In the mouse model of intestinal inflammation caused by nematode infection NEP was demonstrated to downregulate the early onset of inflammation (Barbara *et al.*, 2003). Inhibition of NEP was found to exacerbate both experimental pancreatitis and the associated lung injury (Day *et al.*, 2005), and pretreatment with recombinant human NEP ameliorated this injury in NEP<sup>-/-</sup> transgenic mice (Lightner *et al.*, 2002). In this connection, upregulation of NEP is considered as a potential therapeutic approach for pancreatitis-associated lung injury, which can also be true in the case of other inflammatory diseases.

Although the role of NEP in peripheral inflammation is well characterized, there are much less data on the role of NEP in inflammatory processes in the brain. However, the data on the localization and properties of NEP in the nervous system of insects provide evidence for an evolutionarily conserved role for NEP in the inactivation of tachykinin-related peptides in the brain (Isaac and Nassel, 2003; Isaac *et al.*, 2002).

It was demonstrated that NEP might play an important role in the pathogenesis of AD due to its capacity to cleave the neurotoxic and inflammatory amyloid- $\beta$  (A $\beta$ ) peptide (Iwata *et al.*, 2000) that is a primary trigger for the

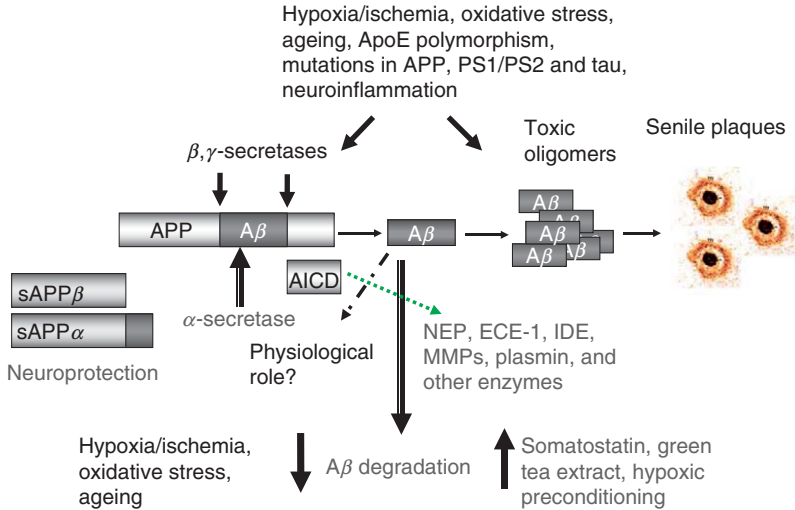


FIG. 2. Amyloidogenic processing of APP and formation of amyloid (A $\beta$ ) peptide, fibrils, and plaques. Main avenues in neurodegeneration and neuroprotection. APP, amyloid precursor protein; sAPP $\alpha$ , soluble product of  $\alpha$ -secretase cleavage; sAPP $\beta$ , soluble product of  $\beta$ -secretase cleavage; AICD, C-terminal fragment of APP, product of  $\gamma$ -secretase cleavage.

development of this disease (Hardy and Higgins, 1992). It is now well documented that A $\beta$  is formed from a large precursor molecule called APP via two consecutive cleavages (Fig. 2). The first of these cleavages occurs in the extracellular or luminal domain and is mediated by a membrane-bound aspartic protease termed  $\beta$ -secretase (BACE) (Vassar and Citron, 2000). It releases a large soluble fragment of sAPP $\beta$  and the residual membrane-bound fragment. The latter is cleaved by a  $\gamma$ -secretase protease complex, at residues 40–42 (termed  $\gamma$ -site) or at residues 48–52 (termed  $\epsilon$ -site) within the transmembrane domain. The presenilin-dependent  $\gamma$ -secretase and  $\gamma$ -site proteolytic activities are dependent on a multimeric complex of at least four different membrane proteins, including presenilin-1 (PS1) or presenilin-2 (PS2), nicastrin, Aph-1, and Pen-2 (Francis *et al.*, 2002; Yu *et al.*, 2000). In these complexes, the presenilins have been proposed as a novel type of transmembrane aspartic protease bearing the catalytic core of the  $\gamma$ -secretase (Wolfe *et al.*, 1999). Whereas the cleavage at the  $\gamma$ -site generates A $\beta$ , the subsequent cleavage at the  $\epsilon$ -site generates a cytosolic fragment referred to as ICD (Passer *et al.*, 2000) or AICD ( $\beta$ APP IntraCellular Domain). The exact role of AICD remains unclear but it has been suggested to act as a functional transcriptional regulator (Cao and Sudhof, 2001) in combination with the regulatory proteins Fe65 and the chromatin-associated histone acetyltransferase, Tip60. There were reports that AICD and nicastrin regulate expression of NEP but this is controversial and still has to be

proved experimentally in animal models (Hass and Yankner, 2005; Hebert *et al.*, 2006; Pardossi-Piquard *et al.*, 2005, 2006). An additional component of the  $\gamma$ -secretase complex, termed TMP21, which is a member of the p24 cargo protein family, appears to differentially regulate  $\gamma$ -secretase cleavage without affecting  $\varepsilon$ -secretase activity (Chen *et al.*, 2006). The proteolytic events involved in processing of APP are highly compartmentalized in the cell taking place both within intracellular compartments and in the plasma membrane. The rate limiting reaction of APP cleavage by  $\beta$ -secretase (BACE) was shown to take place especially in lipid raft domains enriched with cholesterol and glycosphingolipids and targeting BACE to lipid rafts increased production of A $\beta$  (Cordy *et al.*, 2003). Depletion of cell cholesterol by lovastatin resulted in a decrease in both of sAPP $\beta$  and A $\beta$  levels in the cell culture model. This explains the positive effect of statins on the development of AD pathology observed in patients with statin treatment (Sparks *et al.*, 2006).

Under normal conditions, A $\beta$  occurs as a soluble fragment, the concentration of which is normally tightly controlled below the threshold for its self-aggregation into  $\beta$  sheet fibrils (Burdick *et al.*, 1992). Until recently, production of A $\beta$  in the brain and other tissues was thought to be an irreversible process, leading in the case of their disruption, to amyloidogenic diseases. However, in the last few years, neprilysin and several other proteases (IDE, ECE-1 and ECE-2, plasmin) have been found to be capable of degrading A $\beta$  *in vitro* and *in vivo* (for review see Carson and Turner, 2002; Turner *et al.*, 2004). The sites of A $\beta$  cleaved by known proteinases are shown in Fig. 3. Pathological downregulation of these enzymes and, in particular of NEP, could predispose to accumulation of A $\beta$  and the development of AD (Apelt *et al.*, 2003; Nalivaeva *et al.*, 2004). In particular, in mice deficient in NEP or ECE-1, amyloid deposits are seen to deposit at significant levels in the brain (Eckman *et al.*, 2003; Hersh *et al.*, 2002). Furthermore, injection of amyloid- $\beta$  peptide into the brains of rodents significantly enhances the concentrations of NEP mRNA and protein, suggesting the operation of a regulatory feedback mechanism to protect neurons from toxic damage (Mohajeri *et al.*, 2002). NEP levels appear to be reduced in high-plaque-bearing areas of human brain in AD and in cerebral amyloid angiopathy (Carpentier *et al.*, 2002; Yasojima *et al.*, 2001) but no association has been detected to date between polymorphisms in the NEP gene and AD (Lilius *et al.*, 2003). Clinical data suggest that ischemia and stroke predispose to development of AD (Snowdon *et al.*, 1997), and it was shown that hypoxia and ischemia lead to a decrease of NEP and ECE expression (Fisk *et al.*, 2006; Nalivaeva *et al.*, 2004). Thus, a possible therapeutic approach for treatment of AD might be a chronic upregulation of these proteinases (Fig. 4), either pharmacologically or through a gene therapy approach (Marr *et al.*, 2003; Saito *et al.*, 2005; Turner *et al.*, 2004).

Maintenance of cellular concentrations of NEP, which is rather widely distributed in the body, is critical to peptide homeostasis and its up- or down-regulation can lead to a range of pathological conditions including those of



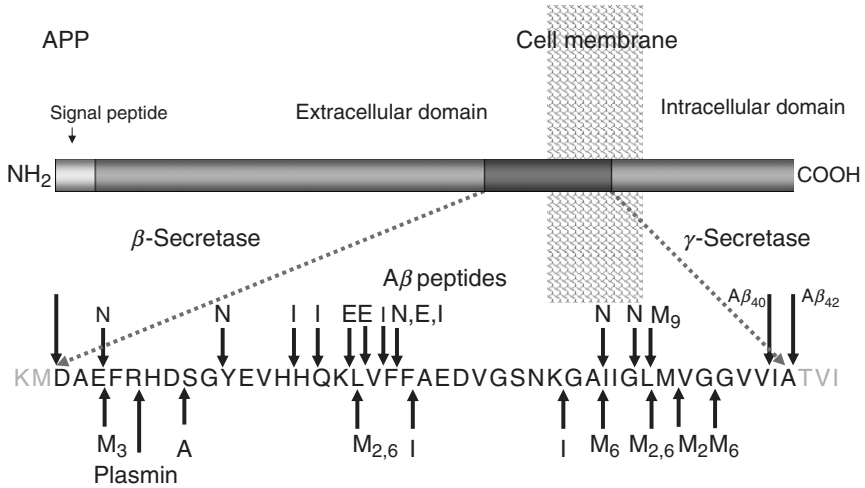


FIG. 3. Cleavage sites of  $A\beta$ -degrading enzymes. A, angiotensin-converting enzyme; E, ECE-1; I, IDE; N, NEP; M, matrix metalloproteinases (MMPs: M3, MMP-3; M2 and M6, MMP-2 and MMP-6; M9, MMP-9).

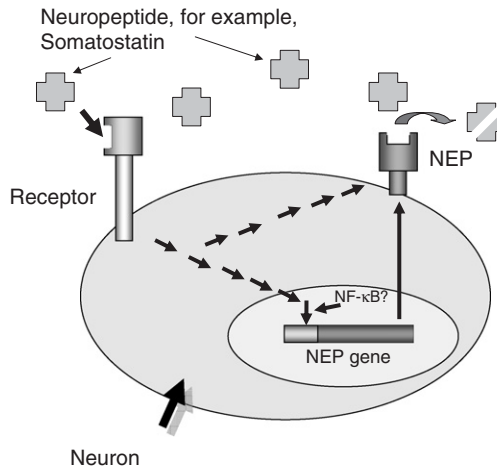


FIG. 4. Scheme of upregulation of NEP gene and its possible involvement in neuroprotection [adapted from Saito *et al.* (2003)].

cardiovascular, neurodegenerative, and tumorigenic origins. NEP was, for quite some years, a lone mammalian zinc peptidase apparently mechanistically similar to the bacterial enzyme, thermolysin, both enzymes being potently inhibited by phosphoramidon. The structural solution of the catalytic domain of human NEP

complexed with phosphoramidon (Oefner *et al.*, 2000) reveals both similarities and differences with thermolysin, and the restricted access to the active site highlights why the enzyme acts exclusively as an oligopeptidase rather than a proteinase, unlike thermolysin.

A homologue of NEP, namely neprilysin 2 (NEP2), was discovered and in the brain shown to be restricted mainly to developing and differentiated fields of the CNS. Unlike NEP and ECE-1, which are broadly expressed in the CNS and periphery, NEP2 was found to be almost exclusively expressed only in selected populations of neurons and in the spinal cord. The only peripheral areas where expression of NEP2 was detected were the pituitary and choroid plexuses. NEP2 was also found capable of degrading  $A\beta$  and its distinct localization from NEP suggests that, together with ECE-1, it may be better poised to catabolize  $A\beta$  as it is more abundantly expressed in the areas relevant to AD pathology (Facchinetti *et al.*, 2003; Thomas *et al.*, 2005).

The human genome is now known to contain at least seven NEP-related enzymes (summarized in Turner *et al.*, 2001), of which the best characterized is ECE-1, which catalyzes the final step in the biosynthesis of the potent vasoconstrictor peptide, endothelin-1 (ET-1; Matsumura *et al.*, 1990; Xu *et al.*, 1994). Several of the NEP-like enzymes are, as yet, orphan peptidases with no recognized peptide substrates. Novel strategies are urgently needed to allow the identification of physiologically relevant substrates for such newly identified proteases.

### III. The NEP Homologue ECE-1

ECE-1 was first purified from rat lung (Takahashi *et al.*, 1993) but then was also found in a variety of tissues. It is most abundant in endothelial cells but is also expressed by exocrine cells, smooth muscle cells, neurons, and glia in the brain (Barnes and Turner, 1999; Barnes *et al.*, 1997; Takahashi *et al.*, 1995). To date, four isoforms of human ECE-1 differing only in a part of their N-terminal cytoplasmic region but which cleave big ETs with similar efficiencies have been characterized: named ECE-1a, ECE-1b, ECE-1c, and ECE-1d (Schweizer *et al.*, 1997; Valdenaire *et al.*, 1999). Although the relative levels of the isoform mRNA species vary between human tissues, ECE-1c mRNA is generally the predominant isoform message. There are distinct subcellular localizations for the four isoforms: whereas ECE-1a, ECE-1c, and ECE-1d proteins are localized mainly at the cell surface, ECE-1b was found to be intracellular and showed significant colocalization with a marker protein for the *trans*-Golgi network (Schweizer *et al.*, 1997). There are no significant differences in the catalytic properties between them, so it has been suggested that intracellular ECE-1 localized in Golgi and vesicles might be involved in processing of big ET whereas cell surface ECE-1 may metabolize other regulatory peptides (Turner *et al.*, 1998).

ECE-1 and its product ET-1 have been shown to be involved in such inflammatory conditions as asthma (Zhang *et al.*, 2004), chronic rhinitis with its expression in the nasal epithelium and mucosa being much higher in the case of rhinitis than in controls (Furukawa *et al.*, 1996), and idiopathic pulmonary fibrosis (Saleh *et al.*, 1997). In the latter case, an increased release of ET-1 was accompanied by increased levels of ECE-1 mRNA. Using normal bronchial epithelial cell culture, these authors have demonstrated that proinflammatory cytokines (IL-1 $\alpha$ , IL-1 $\beta$ ) induced a significant increase in ET-1 release and mRNA expression, while TNF- $\alpha$  stimulated expression of ECE-1 mRNA. In the model of acute gastric infection caused by administration of *Helicobacter pylori* lipopolysaccharide, it was also shown that the levels of ET-1 and expression of ECE-1 were significantly increased in the gastric mucosa of infected cells on day 4 but then significantly reduced (down to 60%) by day 10 following reduced gastric inflammation (Slomiany *et al.*, 2000). Developing this work further, the authors have discovered that ET-1 has also an effect on leptin production in the gastric mucosa as a consequence of ET(A) receptor activation (Slomiany and Slomiany, 2005).

Together with ET-1, ECE-1 is abundantly present in human arteries and is involved in chronic inflammation in human atherosclerosis. Upregulation of the ECE-1–ET-1 system was shown to be closely linked to the presence of chronic inflammation at the very early stages of plaque evolution and, thus, has been suggested as a target in atherosclerosis therapy (Ihling *et al.*, 2001, 2004). Plasma levels of ECE-1 were also shown to reflect the severity of ischemic complications after subarachnoid hemorrhage. The higher levels of plasma ECE-1 resulted in reduced big ET-1 and increased ET-1/big ET-1 ratio in patients who experienced symptomatic delayed cerebral ischemia, compared with other patients (Juvela, 2002). However, the levels of ECE-1 expression in rat brain cortex hemispheres and hippocampus was found to be decreased after 15-min global ischemia and restored to control levels after reperfusion (Nalivaeva *et al.*, 2004), which might reflect an adaptive reaction of the brain to increased blood supply to the affected areas.

Although ECE-1 has been regarded as a highly specific endopeptidase, it was demonstrated to be able to hydrolyze, apart from big ET-1, a number of other biologically active peptides, such as bradykinin, SP, neurotensin, angiotensin I, and insulin B chain; it is not yet clear whether any of these, or other peptides, are physiological substrates of ECE-1 (Hoang and Turner, 1997; Johnson *et al.*, 1999). It was demonstrated that ECE-1 can also degrade amyloid peptide A $\beta$ , which made it an important player in the arena of AD (Eckman *et al.*, 2001). Overexpression of ECE-1 in Chinese hamster ovary cells, lacking endogenous ECE activity, was found to reduce extracellular A $\beta$  concentration by up to 90% and this effect was completely abolished by treatment with a metalloproteinase inhibitor phosphoramidon. Recombinant soluble ECE-1 was shown to hydrolyze synthetic A $\beta$ <sub>40</sub> and A $\beta$ <sub>42</sub> *in vitro* at multiple sites. Comparing ECE heterozygous

and knockout mice, [Eckman \*et al.\* \(2003\)](#) showed that the concentration of A $\beta$  peptides in the brain of these animals was elevated in comparison with control littermates in a gene-dependent manner.

#### IV. The ACE Family

ACE was originally identified 50 years ago as a “hypertensin-converting enzyme” ([Skeggs \*et al.\*, 1956](#)) and its primary substrate was identified as angiotensin I, which it converts into the vasoconstrictor angiotensin II. In parallel, it inactivates the vasodilator and inflammatory peptide bradykinin. Hence, inhibition of ACE has a powerful effect in reduction of blood pressure and the enzyme has therefore been a major cardiovascular target for many years. The catalytic activity of ACE is primarily as a “peptidyl dipeptidase,” removing dipeptides from the C-terminus of a susceptible peptide substrate. In the hydrolysis of some peptides (e.g., SP, luliberin), ACE can act as an endopeptidase, although with much lower catalytic efficiency ([Turner and Hooper, 2002](#)). Mammalian ACE exists as two distinct forms, arising from the use of alternative promoters. The simplest form is germinal or testicular ACE, which is essential for male fertility and which carries a single zinc-binding and catalytic domain. Elsewhere in the body, the somatic form of ACE is duplicated and carries two active sites. The analysis of ACE X-ray structures has revealed that ACE most closely resembles a neurotensin-degrading zinc endopeptidase known as neurolysin rather than NEP, or carboxypeptidase A, on whose structure the design of ACE inhibitors was originally based ([Hooper and Turner, 2003](#)).

While seeking novel expressed sequence tags encoding zinc metallopeptidases, we identified and cloned the first human homologue of ACE (ACEH), which is now more commonly referred to as ACE2 ([Tipnis \*et al.\*, 2000](#)). ACE2 is also a type I integral membrane peptidase showing 40% identity and 61% similarity with ACE and conserving the critical active site residues. It contains a single catalytic domain like testicular ACE, and it is most abundantly expressed in kidney, heart, and lung ([Donoghue \*et al.\*, 2000](#); [Tipnis \*et al.\*, 2000](#)). Physiologically, the principal role of ACE2 is thought to be the conversion of angiotensin 2 to angiotensin (1–7), which opposes the actions of ACE. Hence ACE and ACE2 act as counterbalances in metabolism in the renin–angiotensin system. Clues to the roles of ACE2 have come from the development of mice deficient in the ACE2 gene ([Crackower \*et al.\*, 2002](#)). These mice have severe cardiac contractility defects, increased plasma angiotensin II levels, and an upregulation of cardiac hypoxia-related genes, implicating ACE2 as an essential regulator of heart function. Intriguingly, a double knockout in mice of both the ACE and ACE2 genes is able to rescue the cardiac defect seen with the ACE2-deficient mice ([Crackower \*et al.\*, 2002](#)). ACE2 mRNA and protein levels are

substantially reduced in the kidney in diabetic rats, suggesting that the enzyme may have a role in the development of diabetic complications (Tikellis *et al.*, 2004). It has been shown that ACE2 is widely distributed throughout the brain but is mainly localized to the cytoplasm of neuronal cells in the brain and not present in glia. Moreover, ACE2 levels appear to be highly regulated by the renin–angiotensin system, suggesting its involvement in this system in the brain. ACE2 expression in the brain structures involved in the control of cardiovascular function suggests that it may have a role in the central regulation of blood pressure and hypertension (Doobay *et al.*, 2007).

The most remarkable discovery in relation to ACE2 biology has been the demonstration that the enzyme functions as the receptor for the SARS virus (Li *et al.*, 2003) and numerous subsequent studies have confirmed and extended this observation. Thus, the structure of the SARS *Coronavirus* spike receptor-binding domain complexed with receptor has been determined (Li *et al.*, 2005) and compounds blocking spike protein and ACE2 interaction discovered, for example emodin (Ho *et al.*, 2007). ACE2 also appears to play a critical role in protection against acute lung injury from SARS infection, or other causes of acute respiratory distress syndrome (Imai *et al.*, 2005).

One feature that both ACE (Hooper *et al.*, 1987) and ACE2 (Lambert *et al.*, 2005) share is the ability to be shed from the plasma membrane by cleavage within the juxtamembrane region releasing the bulk of the protein, including the intact catalytic domain, into the extracellular medium. This process is common to a growing number of membrane proteins of diverse characteristics (see Hooper *et al.*, 1997 for review), an event which is generally receptor-regulated and sensitive to inhibition by a group of hydroxamate metalloproteinase inhibitors such as batimastat. This has led to the identification of members of the ADAMs (a disintegrin and metalloproteinase) family of zinc proteinases, typified by tumor necrosis factor- $\alpha$  converting enzyme (“TACE”; ADAM17) as candidate shedding enzymes (Allinson *et al.*, 2004). Our data suggest that NEP might be also shed from the cell surface by a similar mechanism (Fisk, L., Nalivaeva, N. N., and Turner, A. J., unpublished data). However, the detailed molecular mechanism of this phenomenon has still to be elucidated.

ACE inhibitors have been shown to reduce development of diabetes, improve surrogate markers of inflammation, and reduce cardiovascular disease and renal disease (McFarlane *et al.*, 2003). Increasing evidence indicates that systemic inflammation and neuroinflammation are central features in cerebrovascular disease and that hypertension, through the vasoactive peptides angiotensin and ET-1, promotes and accelerates the atherosclerotic process via inflammatory mechanisms (Di Napoli and Papa, 2005). It was demonstrated that in humans the product of ACE activity angiotensin II induces IL-6 production through a mineralocorticoid receptor-dependent mechanism (Luther *et al.*, 2007). This suggests that ACE inhibitors might also be considered as targets in neuroprotection.

An ACE polymorphism was demonstrated to be associated with AD in the Japanese population (Hu *et al.*, 1999), and later it was found that ACE can indeed hydrolyze A $\beta$  *in vitro* and reduce accumulation of A $\beta$  in cell cultures (Hu *et al.*, 2001; Oba *et al.*, 2005). However, Eckman *et al.* (2006) have demonstrated that *in vivo* ACE does not have a physiological role in clearing A $\beta$  and it is cleaved in the brain mostly by NEP and ECE-1 since ACE-deficient mice did not demonstrate accumulation of A $\beta$  while deficit of NEP or ECE-1 activity resulted in additive increases in brain A $\beta$  levels.

### V. Ischemia/Hypoxia and Ageing as Factors Affecting Metalloproteinases

It is becoming more obvious that neurodegeneration and development of AD can be promoted by cardiovascular lesions, ischemia and stroke (Hofman *et al.*, 1997; Kalaria, 2000). Indeed, the analysis of various autopsy series demonstrates that 60–90% of AD cases exhibit variable cerebrovascular pathology. Hypertension has also been suggested as a risk factor in development of AD (for review see Skoog and Gustafson, 2006). Taking into account that NEP and ECE-1 are involved in vascular functions and can contribute to amyloid metabolism, we have analyzed levels of expression of ECE-1 in the brain cortex of rats after 15-min global ischemia and found a significant decrease of NEP and ECE-1 protein levels in brain hemispheres and both hippocampi which returned to normal levels after 2-h reperfusion (Nalivaeva *et al.*, 2004). We have also demonstrated that NEP and ECE-1 levels were lower in the cortex and striatum of rats subjected to prenatal hypoxia (7% O<sub>2</sub>, 3 h, 13th day of gestation) (Nalivaeva *et al.*, 2003). Preconditioning to mild (15% O<sub>2</sub>) hypoxia before the episodes of acute hypoxia had a protective effect restoring the levels of NEP and ECE-1 in rat brain structures analyzed during the first month after birth. Using human neuroblastoma NB7 cells, we have also demonstrated that hypoxia (1.0–2.5% O<sub>2</sub>) resulted in a decrease in expression of ECE-1 (Fisk *et al.*, 2006) and also in expression of NEP both at the protein and mRNA levels at and NEP activity (Fisk *et al.*, 2007). Moreover, both hypoxia and ischemia resulted in an increased production of sAPP $\beta$  and reduced amount of sAPP $\alpha$ . These data allowed us to conclude that hypoxic and ischemic conditions in the brain might lead to a shift of amyloid metabolism toward formation of higher levels of A $\beta$  due to an increased rate of  $\beta$ -secretase reaction and reduced activity of such amyloid-degrading enzymes as NEP and ECE-1 (Fig. 4).

Analyzing the effect of chronic hypoxia (1%, 24 h) on expression of NEP estimated by the method of real-time PCR in rat primary cortical neurons and astrocytes, we have found that NEP mRNA levels were downregulated (by 20%) under hypoxia in neurons and upregulated in astrocytes (Fig. 5).

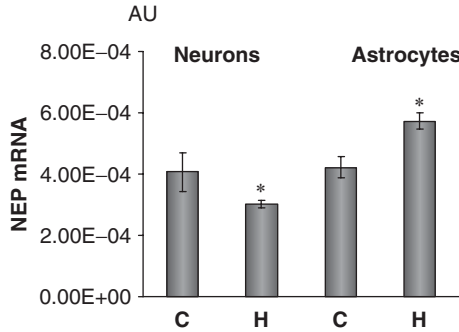


FIG. 5. Effect of hypoxia on the level of NEP mRNA expression in primary cortical neurons and astrocytes. NEP mRNA detected by real-time PCR (related to GAPDH mRNA). C, control; H, hypoxia (1% O<sub>2</sub>, 24 h,  $n = 12$ ). \* $p < 0.05$  compared to control.

Previously, [Apelt \*et al.\* \(2003\)](#) reported NEP mRNA upregulation in amyloid plaque-surrounding reactive astrocytes in transgenic Tg2576 mice that produce human amyloid- $\beta$  peptides from birth and develop amyloid- $\beta$  plaques which may suggest a role of plaque-mediated astrogliosis in A $\beta$  degradation. In our experiments, mRNA levels were also upregulated in hypoxic astrocytes, which might be an adaptive reaction of astrocytes to pathological conditions ([Fisk \*et al.\*, 2007](#)).

It is important to note that expression of NEP with ageing was found to decrease in the cortex and hippocampus of rats, while its levels in the striatum (where amyloid deposits have not been reported in AD brains) were as high as at the end of the first month after birth ([Nalivaeva \*et al.\*, 2004](#)). Decreased levels of another A $\beta$ -degrading enzyme, IDE, have also been reported in the brain of aged mice ([Caccamo \*et al.\*, 2005](#)) and in rat brain structures ([Nalivaeva-Turner \*et al.\*, 2006](#)). Moreover, our experiments demonstrated that in the brain of rats with experimental type II diabetes IDE levels were lower than in control animals ([Kochkina \*et al.\*, 2006](#)). These data suggest that age-related deficit of amyloid-degrading enzymes might be one of the factors leading to the development of the sporadic form of AD and upregulation of NEP and other A $\beta$ -degrading enzymes become one of the possible therapeutic targets in neurodegeneration and AD.

Several physiological and pharmaceutical ways of upregulation of the neprilysin gene have been suggested. One of the approaches, suggested by [Saito \*et al.\* \(2003\)](#), involves NEP substrates as molecules activating expression of the NEP gene via a positive feedback mechanism and as yet unknown signaling pathways ([Fig. 4](#)). Analyzing various NEP substrates in this experimental paradigm, these authors ([Saito \*et al.\*, 2005](#)) were able to demonstrate that only somatostatin was capable to stimulate NEP activity in primary cortical neurons. Since somatostatin levels in the brain decrease with age these results indicate that age-related

downregulation of somatostatin expression could be one of the triggers for A $\beta$  accumulation leading to late-onset sporadic AD. In our experiments using human neuroblastoma cells expressing NEP and ECE-1, we were not able to detect somatostatin-dependent upregulation of NEP mRNA or activity while ECE-1 was significantly upregulated by this peptide in a dose-dependent manner (Fisk, L., Nalivaeva, N. N., and Turner, A. J., unpublished data).

Another physiological pathway of regulation of NEP gene has been suggested by Checler and colleagues who demonstrated that the C-terminal product of APP cleavage by  $\gamma$ -secretase (AICD) was able to transactivate the NEP gene promoter activating NEP expression and that presenilin molecules (PS1 and PS2) and the protein nicastrin in the  $\gamma$ -secretase complex were essential for this effect (Pardossi-Piquard *et al.*, 2005, 2006).

Among chemical compounds that can upregulate NEP expression, green tea extract (EFLA85942) has been demonstrated as effective in human neuroblastoma SK-N SH cells (Ayoub and Melzig, 2006; Melzig and Janka, 2003). According to our observations, the active compound of the green tea extract, namely, polyphenol (-)-epigallocatechin-3-gallate stimulates in a dose-dependent manner both NEP expression at protein level and its activity in human neuroblastoma NB7 cells (Fisk, L., Nalivaeva, N. N., and Turner, A. J., unpublished data).

## VI. Conclusions

In this chapter, several examples have demonstrated the role of metalloproteinases in neurodegeneration, neuroprotection, and neuroinflammation. This was mostly shown for NEP, ECE-1, and ACE; however, there are other enzymes whose targeting might be beneficial for prevention of neurological disorders. Among them are the enzymes of amyloidogenic processing of APP by  $\beta$ -secretase (and subsequently by  $\gamma$ -secretase) and nonamyloidogenic APP processing by  $\alpha$ -secretase (for review see Cordy *et al.*, 2006; Neve, 2003). Although both  $\alpha$ - and  $\beta$ -secretases produce neurotrophic fragments of APP (sAPP $\alpha$  and sAPP $\beta$ ) and are believed to play a role in normal functioning of neuronal cells (Thornton *et al.*, 2006; Turner *et al.*, 2003), the  $\alpha$ -secretase pathway prevents production of A $\beta$  and thus is regarded as neuroprotective. Downregulation of  $\alpha$ -secretase or upregulation of  $\beta$ -secretase activity will lead to changes in the balance of production of A $\beta$  toward its accumulation and there are emerging experimental data that this might be the case in ischemic or hypoxic brain (Nalivaeva *et al.*, 2004; Wen *et al.*, 2004). There are also some data that the same compounds can activate both  $\alpha$ -secretase and NEP activity, for example green tea extracts (Levites *et al.*, 2003; Melzig and Janka, 2003), suggesting that neuroprotective therapies might target several points in pathogenic processes. However, there also might be



situations when one compound upregulates one neuroprotective pathway and downregulates another. For example, the phorbol ester PMA was shown to activate the  $\alpha$ -secretase pathway (Zhu *et al.*, 2001) but inhibit expression of ECE-1 (Fisk *et al.*, 2006). This observation implies the necessity of differential analysis of the effects of potentially effective neuroprotective drugs on various enzymes participating in amyloid metabolism.

Metalloproteinases represent important therapeutic targets not only in neurodegeneration but also in cardiovascular diseases and prostate cancer, and understanding their intricate interrelationship is still one of the most fascinating areas of modern molecular and cell biology.

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