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A Greek Tragedy: the Growing Complexity of Alzheimer Amyloid Precursor Protein Proteolysis

Robert J. Andrew^{1*}, Katherine A. B. Kellett², Gopal Thinakaran¹ & Nigel M. Hooper^{2*}

¹Departments of Neurobiology, Neurology, and Pathology, The University of Chicago, Chicago, IL 60637, USA

²Division of Neuroscience and Experimental Psychology, Faculty of Biology, Medicine and Health, University of Manchester, Manchester M13 9PT, UK

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*To whom correspondence should be addressed: rjandrew@uchicago.edu tel. +1 773 834 3771 or nigel.hooper@manchester.ac.uk tel. +44 161 306 5765.

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Abbreviations: A β , amyloid- β ; AD, Alzheimer disease; ADAM, a disintegrin and metalloprotease; AEP, asparagine endopeptidase; AICD, APP intracellular domain; APP, amyloid precursor protein; APLP, amyloid precursor-like protein; BACE1, β -site APP cleaving enzyme 1; CSF, cerebrospinal fluid; CTF, C-terminal fragment; PS, presenilin; sAPP, soluble amyloid precursor protein.

Abstract

Proteolysis of the amyloid precursor protein (APP) liberates various fragments including the proposed initiator of Alzheimer disease associated dysfunctions, amyloid- β . However, recent evidence suggests the accepted view of APP proteolysis by the canonical α -, β - and γ -secretases is simplistic, with the discovery of a number of novel APP secretases (including δ - and η -secretases, alternative β -secretases) and additional metabolites, some of which may also cause synaptic dysfunction. Furthermore, various proteins have been identified that interact with APP and modulate its cleavage by the secretases. Here, we give an overview of the increasingly complex picture of APP proteolysis.

Currently over 46 million people worldwide are living with dementia (www.alz.co.uk) with Alzheimer disease (AD) representing the most common form of dementia. In AD, the amyloid cascade hypothesis posits that amyloid- β (A β), produced through the sequential proteolytic cleavage of the amyloid precursor protein (APP) by the β - and γ -secretases, is a key molecule in initiating and propagating disease pathology including neurofibrillary tangle formation, neuronal cell loss, aberrant synaptic activity, and brain atrophy that lead to the clinically recognised symptoms of dementia (1). However,

identification of the A β peptide 25 years ago has not yet led to the advent of a viable therapeutic strategy which can slow or halt the progression of AD. Recent studies have revealed new complexities in the proteolytic processing of APP, including the identification of novel secretases which generate APP metabolites that accumulate in the brains of AD patients and may contribute to the synaptic dysfunction observed in the disease. In addition, numerous proteins are being identified that interact with APP, modulating its proteolysis and A β production. These new APP secretases and metabolites, along with the APP interactors, may present novel therapeutic targets, that are independent of direct modulation of the canonical secretases, and which will need to be considered when evaluating the results from current A β -directed therapies. In this minireview, we summarise the recent developments in APP proteolysis focusing on the novel secretases, APP interactors and APP metabolites that are impacting on our understanding of both APP biology and the neurodegenerative disease process.

The canonical α -, β - and γ -secretases and APP fragments

The generally accepted model of APP proteolysis is that APP is processed by one of two distinct proteolytic pathways (Fig. 1A). In the amyloidogenic pathway, β -secretase, the β -

site APP cleaving enzyme 1 (BACE1), cleaves APP within the ectodomain and liberates a soluble proteolytic fragment, termed soluble APP β (sAPP β), primarily in the endosomal system from the transmembrane APP holoprotein (2). The remaining C-terminal membrane-bound APP fragment, CTF β , is subsequently cleaved by the presenilin (PS)-containing γ -secretase multi-subunit complex to liberate the A β peptide and the APP intracellular domain (AICD) (Fig. 1A). γ -secretase cleaves CTF β at several sites in the transmembrane domain, 'trimming' the A β peptide from the initial ϵ -cleavage sites to produce shorter, and relatively benign, A β species (Fig. 2) (3). However, inefficient trimming of the A β peptide at its C-terminus results in the release of longer aggregation-prone A β species such as A β 42, which are central to the production of the neurotoxic oligomeric A β assemblies (4,5). In the non-amyloidogenic pathway, α -secretase, members of the "a disintegrin and metalloprotease" (ADAM) family, mainly ADAM10, cleaves APP at the cell surface within the A β domain liberating soluble APP α (sAPP α) and leaving an alternative membrane-bound C-terminal fragment, CTF α . CTF α can also be subsequently proteolytically processed by γ -secretase to liberate an N-terminally truncated version of the A β peptide referred to as p3 and the AICD (Fig. 1A). The AICD has a role as a nuclear transcription factor regulating the expression of various genes, including that of the A β -degrading neprilysin (6-8). Although the AICD produced via either the amyloidogenic or non-amyloidogenic pathways have the same peptide sequence, they appear to be functionally distinct. The AICD produced following β -secretase cleavage is transported to the nucleus and binds to the neprilysin gene promoter, whereas that produced following α -secretase cleavage is rapidly degraded in the cytosol by insulin-degrading enzyme (6).

The established view is that these sequential cleavages of APP occur through separate enzyme-substrate interactions which are temporally and spatially separated. However, recent evidence indicates that ADAM10 and γ -secretase physically interact and work in partnership to sequentially cleave APP (9). ADAM10 and γ -secretase co-immunoprecipitated from cells and mouse brain, and were shown to interact by

superresolution microscopy. The complex between the two secretases was stabilised by members of the tetraspanin family of scaffold proteins (namely tetraspanin 12 and 17). Limited data also indicated a physical interaction between BACE1 and γ -secretase, albeit in a complex distinct from the ADAM10- γ -secretase complex (9). This comprehensive biochemical study suggests that cells possess large multiprotease complexes capable of sequentially and efficiently processing transmembrane substrates such as APP through a spatially coordinated regulated proteolytic mechanism (9). This raises the interesting question as to whether these multiprotease complexes could be targeted to modulate selectively APP processing in the amyloidogenic pathway.

Whether there is a reciprocal relationship between the amyloidogenic and non-amyloidogenic APP processing pathways has remained a contentious issue, possibly as a result of differences in the model systems being examined (10). In monkeys, BACE1 inhibition decreased sAPP β and A β in cerebrospinal fluid (CSF) and increased sAPP α as measured by ELISA but there was no change in labelled sAPP α kinetics, suggesting BACE1 inhibition may not boost α -secretase processing of APP to the same degree (11). In human induced pluripotent stem cell-derived neurons inhibition of BACE1 reduced sAPP β and A β and reciprocally increased sAPP α (12), while inhibition of γ -secretase resulted in an increase in sAPP α and a decrease in sAPP β (9). This latter result suggests a level of feedback within the ADAM10- γ -secretase complex (9). Activating α -secretase has been suggested as a potential therapeutic approach for reducing A β production although the evidence for this from *in vivo* studies is somewhat mixed (13,14). For example, moderate neuronal overexpression of ADAM10 in APP_{V717I} transgenic mice increased the secretion of sAPP α , reduced the formation of A β peptides, and prevented their deposition in plaques (15). While in APP/PS-1 transgenic mice the intracerebral injection of the vitamin A analogue acitretin, which stimulates ADAM10 promoter activity, led to a reduction of A β 40 and A β 42 (16). However, although a recent clinical trial reported increased CSF sAPP α levels in patients with AD treated with acitretin, there was only a trend to decline in sAPP β that did not reach

significance and no change in the levels of A β 40 or A β 42 (17). Moreover, ADAM10 is implicated in the ectodomain shedding of several substrates such as Notch and ErbB2, which promote cancer progression and inflammatory diseases. Thus, further work with more selective α -secretase activators in human neurons and *in vivo* models is required to clarify whether α -secretase activation is a viable therapeutic approach for AD either by reducing the neurotoxic A β and/or increasing sAPP α which is reported to have neuroprotective functions (Table 1).

The exact function of several of the APP metabolites (Table 1), including sAPP α , much like the function of the holo-APP molecule, is unclear, in part due to the focus of most APP research being on A β . The significantly different, and even opposing, properties of the various APP metabolites adds further to the complexity of the biological functions of APP, and on what the impact will be of inhibiting or activating any particular secretase on the balance of neuroprotective versus neurotoxic outputs.

Although the contribution of the canonical α -, β - and γ -secretases to APP proteolysis has been studied in depth, the proteolytic cleavage of APP, like many proteins, is more complex than originally envisaged. An increasing number of additional secretases have been identified that also proteolytically process APP *in vivo*. Here we review each of these new secretases and, where known, the properties of the APP metabolites produced by their action. A summary of these new secretase cleavage sites within APP is provided in Fig. 1 and the functions and/or characteristics of the metabolites produced through these cleavage events are summarised in Table 1. Although APP can also be cleaved in its intracellular domain (recently reviewed (18) this review will focus on cleavages within the APP ectodomain.

δ -secretase

Aparagine endopeptidase (AEP), previously linked to AD through its capacity to cleave tau, which forms the neurofibrillary tangles (19), was recently shown to cleave APP at two separate sites in the ectodomain (Fig. 1B) (20). AEP is a pH-controlled soluble lysosomal cysteine protease that cleaves after asparagine residues. In an elegant series of experiments, Zhang et al. (20) showed that

AEP, or δ -secretase, cleaves APP between N373-E374 and N585-I586 (note APP695 numbering used henceforth) *in vitro* and *in vivo* potentially generating three soluble APP fragments and CTFs (Fig. 1B). Cleavage of APP before T584 was described previously and referred to as δ -cleavage, although the protease responsible was not identified (21). The AEP cleavage of APP could be blocked *in vitro* using buffers in which the pH (pH 7.4) inhibited the catalytic activity of AEP, by mutation of critical residues (C189 and N323) within the catalytic domain of AEP, by mutation of the δ -secretase cleavage sites within APP or through antibody or peptide inhibition of the enzyme (20). The shorter N-terminal APP fragment, sAPP₁₋₃₇₃, produced by AEP cleavage, but not the sAPP₁₋₅₈₅ or sAPP₃₇₄₋₅₈₅ fragments (Fig. 1B), was toxic to primary cultured neurons (Table 1), suggesting AEP could be a key player in the generation of toxic metabolites within the brain (20). In addition, recombinant APP protein corresponding to the AEP-derived CTF was a better substrate for BACE1 proteolysis in comparison to full-length APP when assayed *in vitro*, although it is unknown if this is true for membrane-bound APP in intact cells. Nevertheless, significantly less A β was detected in the conditioned medium of AEP knock-out neurons (20). Upregulation and increased activity of AEP was observed in aged mice, along with increased AEP activity and AEP produced APP fragments using antibodies specific to the N- and C-termini of these fragments within the brains of AD patients (20). Furthermore, knockout of AEP in the 5xFAD mouse model reduced A β deposition, synapse and dendritic spine loss and behavioural deficits (20). AEP gene knockout similarly protected against memory deficits in another AD mouse model, APP/PS1 mice (20). Thus, these two studies (19,20) provide compelling evidence for a role of AEP in AD-like neurodegeneration. However, further work is required to confirm these observations and to clarify the contribution of δ -secretase cleavage of APP to disease pathogenesis and whether inhibition of AEP may be a therapeutic approach in AD.

η -secretase

Recent work from two groups revealed that η -secretase contributes to the production of A β , while also producing proteolytic

fragments with the capacity to induce synaptic dysfunction (22,23). Both groups identified the matrix metalloproteinase MT5-MMP as contributing to the η -secretase cleavage of APP. Both soluble and membrane-bound matrix metalloproteinases have been of interest to the AD field for some time due to their capacity to proteolytically cleave APP and A β *in vitro* and *in vivo* (24,25). In the recent work, η -secretase was shown to cleave APP between N504-M505, resulting in the shedding of a ~80-95 kDa soluble fragment, leaving the novel membrane-bound CTF, CTF η (Fig. 1C) (22,23). Using a suite of antibodies and extensive mass spectrometry analyses, further processing of CTF η by both α - and β -secretases to produce fragments termed A η - α and A η - β was elucidated (Fig. 1C) (23). Both A η - α and A η - β were detectable in mouse brain homogenates and also in human CSF, where levels were estimated to be five-fold higher than A β (23). Interestingly, A η - α but not A η - β inhibited long term potentiation in hippocampal brain slices from mice and suppressed neuronal activity in hippocampal neurons (Table 1) (23). In support of the data obtained in human CSF, η -secretase cleavage of APP exceeded β -secretase cleavage by almost 10-fold in human neurons, and accumulation of η CTFs was also observed in dystrophic neurites surrounding amyloid plaques in the brains of AD patients (23). In a separate study, and despite MT5-MMP not possessing β -secretase like activity, MT5-MMP knockout in 5xFAD mice significantly reduced both A β plaque deposition, soluble A β and APP CTFs within the brain (22). In addition, a concomitant reduction in markers of gliosis, increases in neuronal integrity as evidenced by increased MAP2 and synaptophysin staining, preserved hippocampal LTP and improved performance in spatial memory tasks were all observed in the MT5-MMP knockout mice (22). MT5-MMP expression in HEK cells expressing APP_{SWE} increased A β and CTF production as well as the liberation of the 95 kDa soluble APP N-terminal fragment (sAPP95), presumably that identified by Willem et al. (23) as sAPP η . In the 5xFAD/MT5-MMP knockout mice, this soluble fragment was significantly reduced in brain homogenates (22). Of concern, both genetic and pharmacological inhibition of BACE1 activity resulted in the accumulation of CTF η and A η -

α (23), highlighting that therapeutic inhibition of BACE1 as currently underway in multiple clinical trials needs to be carefully monitored to ensure that accumulation of alternative neurotoxic APP fragments such as A η - α do not occur under such therapeutic intervention.

Meprin β

Meprin β is a zinc metalloprotease that has also been proposed as a candidate β -secretase. Meprin β proteolytically cleaves peptide substrates spanning the β -secretase cleavage site in APP at the β -site M596-D597, as well as at the adjacent D597-A598 and A598-E599 sites (Fig. 1D) (26). Furthermore, cells expressing meprin β produced significant amounts of A β 2-X even in the presence of a BACE1 inhibitor, while meprin β inhibition significantly reduced its production (26). Further work has suggested that unlike BACE1, meprin β cleaves APP at the cell surface and may directly compete with ADAM10 *in vivo*, as indicated by increased sAPP α in the soluble fractions derived from meprin β knockout mice brains (27). Meprin β knockout also increased sAPP β in the soluble brain fraction as detected with a neoepitope-specific antibody, while conditioned medium from cells expressing APP_{SWE}, which is a better substrate for BACE1 than wild type APP (12), significantly altered the ratio of A β 2-40:A β 1-40 production indicating direct competition between meprin β and BACE1 for APP (27). Importantly in the context of AD, A β 2-40 also showed increased aggregation propensity compared to A β 1-40 implicating this species in the preferential production of oligomeric assemblies of A β (27). Still, in the brain A β 2-X peptides are several fold lower in abundance relative to A β 42 species. Thus, the potential contribution of meprin β to AD pathogenesis remains to be established.

In addition to cleavage near the β -secretase site, three further meprin β cleavage sites within APP have been identified (Fig. 1D) (28). Degradomics analysis identified meprin β cleavage sites within APP between A124-D125, E380-T381 and G383-D384, while subsequent *in vitro* analysis identified an N-terminal proteolytic fragment with a molecular mass of 11kDa, resulting from cleavage at A124-D125, which directly corresponded to a fragment previously identified in human CSF (28,29). The site in APP at which meprin β cleaves may depend on its subcellular location,

with membrane-bound meprin β cleaving APP at the β -site while soluble meprin β produces the N-terminal APP fragments (30). Other short N-terminal APP fragments have been reported (31-33), though whether they correspond to the same fragments as produced by meprin β or through proteolytic cleavage by alternative proteases remains unknown.

Cathepsin B

The lysosomal cysteine protease cathepsin B has also been proposed as a putative β -secretase (Fig. 1A) (34). The role of cathepsin B as a β -secretase remains controversial, with conflicting evidence indicating genetic deletion or inhibition of cathepsin B in APP transgenic mice can either enhance (35) or reduce (36) A β pathology. Moreover, unlike BACE1 (37), cathepsin B does not accumulate with close spatial proximity to amyloid plaques (38). Cathepsin B cleavage of APP may enhance the production of N-terminally truncated pyro-glutamated forms of A β (pGlu-A β) in which the N-terminal glutamate in A β 3-X or A β 11-X is cyclised by glutaminyl cyclase (34). pGlu-A β exhibits increased aggregation propensity, increased cellular toxicity and disrupts long term potentiation to a greater extent than A β 1-X species (39-41). In addition, recent work has proposed pGlu-A β as the predominant A β species within the brains of AD patients (42) and efforts to design therapeutics specifically targeting this A β species have proved successful in mouse models (43). However, evidence for direct proteolysis of APP between A673-E674 by cathepsin B remains to be provided. An alternative scenario for the production of N-terminally truncated A β species is the truncation of the A β 1-X peptide by aminopeptidases following BACE1 cleavage.

Mystery proteases

The recent identification of novel APP secretases indicates our understanding of APP proteolysis and its contribution to AD is far from complete. Indeed, a series of studies on human CSF has identified numerous APP N-terminal fragments (29) and N-terminally extended A β species which may have (patho)physiological functions (44,45). Evidence also exists for the N-terminal truncation of the A β peptide at every one of its first 11 amino acids, though again, the biological relevance of the majority of these

species remains uncertain (46). At least one N-terminally truncated species of A β (A β 5-X) has been shown to increase in the CSF of patients treated with a BACE1 inhibitor, suggesting it is liberated in a BACE1-independent manner and the protease responsible for its liberation acts in direct competition with BACE1 (47). In addition to the typically monitored fragments (sAPP α , sAPP β , A β , C99 and C83 CTFs and AICD), a plethora of additional N-terminal and C-terminal APP fragments are likely present in the brain though it is currently unclear which of these are biologically relevant or functional, how they are regulated and how the proteolytic pathways interrelate. Until the proteases involved in these novel APP proteolytic pathways are identified, the interrelationship between these distinct pathways is reconciled and the biological functions of the resulting APP metabolites fully elucidated, we are a long way from understanding how APP metabolism impacts on normal cellular biology, let alone in AD.

Modulation of APP proteolysis by interacting proteins

A major issue undermining secretases as therapeutic targets in AD is the indiscriminate nature with which their direct inhibition blocks proteolysis of their multiple substrates. Both BACE1 and γ -secretase cleave numerous substrates, producing metabolites which are key in an array of biological roles (48,49). This has led to a search for alternative mechanisms through which APP proteolysis can be selectively disrupted. Protein-protein interactions have been widely shown to influence APP trafficking and processing, highlighting the APP interactome as a novel source of potential therapeutic targets for the selective disruption of APP proteolysis. A summary of proteins which directly interact with APP and modulate its proteolysis are shown in Table 2. There are likely multiple mechanisms by which interactors modulate APP proteolysis, for example through acting as a physical blockade (e.g. BRI2) to prevent the access of the proteases to APP (50), or by altering APP trafficking (e.g. sortilin related receptor (SORLA) (51), and thus either enhancing or reducing the likelihood of APP encountering the secretases.

A wide range of approaches has been taken to identify APP-interacting proteins both *in*

vitro and *in vivo*. *In vitro*, yeast two-hybrid studies of the APP interactome have identified several proteins which interact with the intracellular domain of APP, including perhaps the best established APP interactor Fe65 (Table 2). Fe65 interacts with the cytoplasmic tail of APP (via the YENPTY motif) and influences APP internalisation. Despite its intensive study, the effect of Fe65 on APP proteolysis has remained controversial (see (52)). In a similar manner, proteins from the mint family have been shown to interact with the APP YENPTY motif, with conflicting results reported on their effect on APP proteolysis (53). Using a split-ubiquitin version of the yeast two-hybrid approach, several APP interactor proteins were identified, one of which, BRI2 was shown to influence the proteolysis of APP (50) and was also linked to familial forms of dementia in which increased APP proteolysis was observed (54). Gautam et al. (55) used various glutathione-S-transferase-tagged APP ectodomain constructs to isolate interacting proteins from the soluble fraction of mouse brains. Novel interactions between the APP ectodomain and three members of the synaptogamin family of proteins were identified by mass spectrometry, two of which were subsequently shown to influence APP proteolysis (55). Recently, the first study of the APP interactome in a cell culture context was reported using the commonly used, non-neuronal human embryonic kidney cell line, where tagged-APP was immunoprecipitated from stable isotope labelled amino acids in cell culture (SILAC) labelled cells and interactors were identified by liquid chromatography-tandem mass spectrometry (56). This study identified interactors for wild-type and Swedish mutant APP (and other neurodegeneration-linked proteins), focusing on the interaction between APP and the mitochondrial Leucine-rich PPR motif-containing protein (LRPPRC) (56). Though not shown to directly influence A β generation, the authors suggested this interaction (which was higher for the Swedish mutant APP) could lead to mitochondrial dysfunction as LRPPRC has a key role in mitochondrial gene regulation (56). We recently employed a similar approach, whereby the interactome of two APP isoforms was studied in the neuron-like SH-SY5Y cells (Andrew et al. unpublished data). Key differences in the interactomes of

the two APP isoforms, APP695 and APP751, that differ in their ability to be cleaved by β -secretase and to produce A β , were identified. We determined the proteins enriched in the interactome of each APP isoform and identified specific enrichment of proteins implicated in mitochondrial function and nuclear transport specifically in the APP695 interactome. Further interrogation of the APP interactome and subsequent experimental validation revealed Fe65 and ataxin-10 as specific modulators of APP695 proteolysis and GAP43 as a specific modulator of APP751 proteolysis, altering A β generation (Andrew et al. unpublished data). We observed differences in the interactomes of these isoforms, but also identified interactors which specifically altered APP proteolysis in an isoform-dependent manner. In this study we identified GAP43 as a modulator of APP proteolysis, converging on this protein alongside another recent study of the γ -secretase interactome (57), with similar results observed on the production of A β .

Various studies have investigated the *in vivo* interactome of APP. One such study investigated the *in vivo* APP interactome in wild-type mice, comparing the interactome with that of amyloid precursor-like protein (APLP)1 and APLP2 (58). Thirty-four APP interactors were identified, of which one, leucine-rich repeat and immunoglobulin-like domain-containing protein 1 (LINGO-1), was subsequently shown to influence A β generation in human embryonic kidney cells (58), though its effect was later contested (59). In a similar *in vivo* mouse study, Kohli et al. (60) generated a human APP mouse model with a tandem affinity purification tag inserted into the protein in the AICD region. Various proteins involved in synaptic vesicle trafficking were enriched in the APP interactome, along with members of the 14-3-3 family, leading the authors to propose an important role for APP in synaptic signalling (60). A human *in vivo* APP interactome study identified 21 proteins which interacted with human APP in AD and control brains, although none of the identified proteins interacted specifically with APP in either the AD or control brains (61).

Specifically targeting the interaction between the Vps29 and Vps35 subunit of the retromer complex pharmacologically (though in this case to stabilise, rather than disrupt their interaction) was recently shown to reduce

APP proteolysis through alterations in its trafficking (62) indicating targeted drug screening can identify compounds that modulate APP processing. Indeed, this approach is being taken to identify drugs which disrupt APP dimer formation which has been shown to increase A β production (63). As a protein-protein interaction is likely indicative of a functional relationship, a complete understanding of the implications of disrupting such interactions is required if targeting these interactions are to become viable and successful therapeutic options in AD.

Concluding remarks

The recent identification that APP can be proteolytically processed by secretases other than the canonical α -, β -, and γ -secretases adds considerable complexity to the biology of APP and raises important questions. What is the contribution of the recently identified δ - and η -secretases to AD? Why have no mutations around the δ - and η -secretase cleavage sites in APP that give rise to familial AD been identified to date? As noted above both of these new secretases can increase A β production by initially cleaving the full-length APP molecule, making it a better substrate for BACE1 cleavage by reducing the steric hindrance of the large N-terminal ectodomain, as well as generating additional neurotoxic fragments (20,22). What is the role of APP metabolites other than A β in AD and in normal

biology? What is the contribution of other proteases, including meprin β and cathepsin B, to APP processing in AD? Given that several other APP metabolites have been identified in the human brain, how many other proteases remain to be identified that influence APP processing? Careful and detailed studies analysing multiple processing pathways and APP metabolites under appropriate conditions will be required to determine the relative amount of APP processed by each secretase under normal and disease situations. Will inhibition of either the δ - and/or η -secretases be viable alternative therapeutic approaches to alleviate some or all of the symptoms of AD? Will targeting these new secretases be required in addition to targeting β - and or γ -secretase or A β immunotherapy to negate the neurotoxicity of other APP metabolites? What is the role of the recently described APP interactors in regulating the production of A β or other biologically active APP fragments? Will any of these interactors offer novel targets for therapeutic intervention in AD or in other diseases associated with mis-metabolism of APP such as Fragile X Syndrome (64). These recent reports of novel APP secretases and interactors open up the field and underline that further research is needed before we fully understand the complexities of APP proteolytic processing and the roles of its various metabolites in health and disease.

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Conflict of interest

The authors declare that they have no conflicts of interest with the contents of this article.

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APP Fragment	Function/Characteristics
sAPP β	-Induces neural differentiation of stem cells (65). -100-fold less effective than sAPP α at protecting mouse hippocampal neurons from excitotoxic stress (66). -Cleaved to produce an N-terminal fragment which induced axonal pruning (33) but may be independent of β -secretase activity (32).
CTF β	-Evidence for early pathological accumulation in AD mouse models (67). -Disruption of LTP (68). -Linked to learning and memory deficits in AD mouse models (69). -Reduction of spine density and induction of synaptotoxicity (70).
A β	-The major APP metabolic fragment involved in the initiation and propagation of AD. For recent reviews see (1,5).
sAPP α	-Induction of Akt cell survival pathway (71). -Protection against neuronal damage caused by traumatic brain injury (72). -Protection against synaptic dysfunction (73) and roles in synaptic plasticity (74).
CTF α	-Reduction of spine density and induction of synaptotoxicity (70). -Possible role as a γ -secretase inhibitor (75).
p3	-Accumulates in amyloid plaques (76) but less aggregation prone than A β (77). -Forms calcium permeable ion channels resulting in neuronal toxicity (78).
AICD	-Transcriptional regulator regulating several proteins linked to AD (8,79). -Contradictory evidence for a pathological role for AICD in AD (80,81).
sAPP η /sAPP95	-No specific function described but identified in APP transgenic mouse brain lysates with some discrepancy in molecular weight (22,23).
A η - α	-Inhibited LTP in hippocampal brain slices from mice and suppressed activity in hippocampal neurons (23).
A η - β	-Has none of the effects reported for A η - α (23).
CTF η	-Indirect evidence that CTF η is a better substrate for BACE1 and γ -secretase cleavage (22). -Accumulated in dystrophic neurites surrounding amyloid plaques in transgenic mouse and human AD patient brains (23).
CTF δ	-The shorter of the two CTF δ forms accumulated in brain lysates from AD patients (20).
sAPP δ (1-448, 1-660, 449-660)	-sAPP ₁₋₄₄₈ neurotoxic to neurons -No neurotoxicity was observed for other soluble fragments (20).
N-APP fragments	-Increased production of 11kDa fragment during neuronal differentiation (31). -N-APP fragment ₁₈₋₂₈₆ bound neurons with higher affinity than sAPP α via an undetermined receptor and increased phosphatidylinositol phosphate lipid levels (82).

Table 1: Properties of the proteolytic fragments generated from APP.

Protein	Interaction details	Effect on proteolysis	Ref.
AP-4 complex	Identified by yeast 2-hybrid. μ 4 subunit interacts with the YKFFE motif in APP cytoplasmic tail. Induces export of APP from the TGN.	siRNA knockdown of μ 4 subunit \uparrow A β , \downarrow CTFs.	(83)
BRI2	Identified by yeast 2-hybrid screen. Masks the recognition site for α -secretase and BACE1.	siRNA knockdown \uparrow sAPP β , \uparrow A β 40, \uparrow A β 42.	(50)
BRI3	Identified by a yeast 2-hybrid screen. Specifically interacts with full length APP but not CTFs.	siRNA knockdown \uparrow sAPP β , \uparrow A β 40, \uparrow A β 42. Over-expression \downarrow sAPP α/β , \downarrow A β 40, \downarrow A β 42.	(84)
CD74	Identified by yeast 2-hybrid screen. Binds the ectodomain of APP.	Over-expression \downarrow A β 40, \downarrow A β 42.	(85)
Dab2	Binds the NPxY motif in the cytoplasmic tail of APP. Identified due to ability to bind a similar motif in LDLR. Mediates endocytosis of APP to endosomes.	Over-expression of full length protein \uparrow A β 40, \uparrow A β 42.	(86)
GRP78	Binds APP and slows its maturation and secretion.	Over-expression \downarrow A β 40, \downarrow A β 42.	(87)
LRP-1	Identified due to similar ability to bind KPI domain containing tissue factor pathway inhibitor. Induces endocytosis of APP.	Over-expression \uparrow A β , \downarrow sAPP α . LRP1 antagonist RAP \downarrow A β .	(88,89)
LRP1B	Investigated due to similarities to LRP1. Binds full length APP. Increases cell surface levels of APP.	Over-expression \uparrow sAPP α , \downarrow A β 40, \downarrow A β 42, \downarrow CTF β .	(90)
LRP10	Investigated due to homology to LDLR family members. Interacts with the ectodomain of APP causing retention within the Golgi.	Overexpression \downarrow A β 40, \downarrow sAPP α/β .	(91)
Lingo-1	Extracellular ligand for APP identified through a brain interactome study.	siRNA knockdown \uparrow CTF α , \downarrow CTF β . Over-expression \downarrow sAPP α , \downarrow sAPP β .	(58,59)
Nogo receptors (NgR)	Investigated due to localisation to amyloid plaques in AD brains. Interact with APP ectodomain in human brain and cells.	Overexpression of NgR1 \downarrow A β . Overexpression of NgR2 and NgR3 \uparrow A β 40 \uparrow A β 42.	(92,93)

PAT1a	Investigated due to prior studies showing APP and PAT interacted directly.	siRNA knockdown ↓Aβ, ↓CTFs.	(94)
Pin1	Identified due to capacity of Pin1 to bind pThr-Pro motifs. Binds APP and alters the cis/trans isomerisation of the P668/T669 bond.	Overexpression ↑Aβ40, ↑Aβ42. Alternatively, <i>in vivo</i> knockout ↓sAPPα, ↑sAPPβ, ↑Aβ42.	(95,96)
Reelin	Extracellular ligand for APP identified by brain interactome study.	Overexpression ↓sAPPα, ↓sAPPβ, ↓CTFs, ↓Aβ40, ↓Aβ42.	(59)
SNX17	Binds the NPxY motif in the cytoplasmic tail of APP. Identified due to ability to bind a similar motif in LRP1. Proposed to increase APP recycling to cell surface.	Dominant negative mutant and siRNA knockdown ↑Aβ40, ↑Aβ42.	(86)
SORCS1	Investigated due to homology to SORLA. Binds full length APP. Genetic link to AD.	Over-expression ↓Aβ40, ↓Aβ42. siRNA knockdown ↑Aβ40.	(97)
SORLA	Investigated due to reduced expression in AD brain. Binds to the GFLD and carbohydrate domains of APP. Causes retrograde transport of APP to the trans-Golgi network.	Over-expression ↓sAPPα, ↓sAPPβ, ↓Aβ40.	(51,98)
Spondin-1	Identified through a brain interactome study. Binds extracellular domain of APP.	Overexpression ↓CTFs. Independent study showed overexpression had no effect.	(59,99)
Syt-1 and Syt-9	Identified in an ex vivo APP ectodomain interactome study. Interact with the APP ectodomain between the E1 and KPI domains.	Syt-1 and Syt-9 overexpression ↑sAPPβ, ↑Aβ40, ↑Aβ42. Syt-1 siRNA knockdown ↓sAPPβ, ↓Aβ40, ↓Aβ42.	(55)
TRPC6	Investigated due to previously identified link between presenilin2 and TRPC6 activity. Binds directly to APP CTFβ.	siRNA knockdown ↑Aβ40, ↑Aβ42. Overexpression ↓Aβ40, ↑Aβ42.	(100)

Table 2: Protein interactors of APP and their effect on APP proteolysis.

(GFLD, growth factor-like domain; KPI, Kunitz protease inhibitor; LDLR, low-density lipoprotein receptor; LRP, low-density lipoprotein receptor-related protein; Rap, receptor associated protein).

Figure legends

Figure 1. The proteolytic processing of APP

(A) The traditional model of APP proteolysis involves APP processing in either the non-amyloidogenic pathway, where sequential cleavage by α -secretase (ADAM10; pink) and the γ -secretase multisubunit complex (here shown for simplicity as a single entity; blue) liberates sAPP α and p3, or in the amyloidogenic pathway, where sequential cleavage by β -secretase (BACE1 or possibly cathepsin B; green) and γ -secretase liberates sAPP β and A β . Both pathways produce AICD which can be proteolytically degraded or translocated to the nucleus where it has roles in transcriptional regulation. (B) APP processing by the δ -secretase (AEP; yellow) causes the release of three soluble fragments of APP (sAPP₁₋₅₈₅, sAPP₁₋₃₇₃ and sAPP₃₇₄₋₅₈₅). The remaining CTF δ is then further processed by β - and γ -secretases to release A β and AICD. (C) η -secretase (suggested to be MT5-MMP; orange) releases the soluble sAPP η fragment and leaves the membrane bound CTF η . CTF η can be further processed by α - or β -secretase to release A η - α or A η - β , respectively. Following α - or β - cleavage, the remaining CTF can be cleaved by γ -secretase to release p3 and AICD, or A β and AICD, respectively. (D) Meprin β (purple) acts as a β -secretase producing a fragment similar to sAPP β as well as two shorter, soluble fragments (sAPP_{1-380/3} and sAPP₁₋₁₂₄). The remaining CTF can then be processed by γ -secretase to release A β _{2-X} and AICD. See text for further details.

Figure 2. Formation of A β by γ -secretase cleavage of APP CTF β

Cleavage of APP CTF β by γ -secretase follows a 'nibbling' pattern in the direction indicated by the black arrows, where the initial (ϵ) cleavage dictates the final (γ) cleavage. The initial cleavage dictates the C-terminal length of A β and thus its amyloidogenic potential. N, N-terminus; C, C-terminus.

Fig. 1

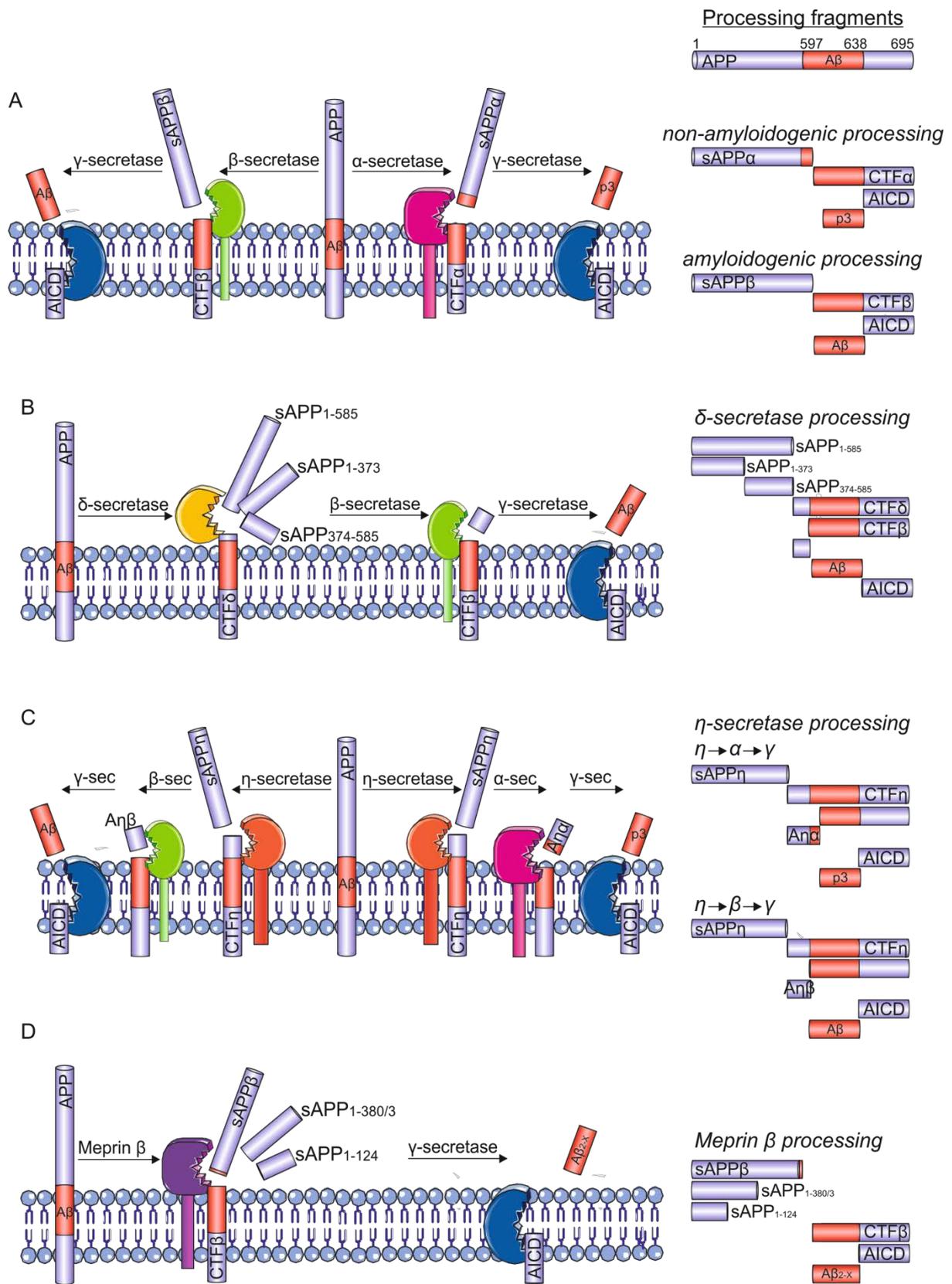


Fig. 2

