



Revisiting APP secretases: an overview on the holistic effects of retinoic acid receptor stimulation in APP processing

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Abstract

Alzheimer's disease (AD) is the leading cause of dementia worldwide and is characterized by the accumulation of the β -amyloid peptide ($A\beta$) in the brain, along with profound alterations in phosphorylation-related events and regulatory pathways. The production of the neurotoxic $A\beta$ peptide via amyloid precursor protein (APP) proteolysis is a crucial step in AD development. APP is highly expressed in the brain and is complexly metabolized by a series of sequential secretases, commonly denoted the α -, β -, and γ -cleavages. The toxicity of resulting fragments is a direct consequence of the first cleaving event. β -secretase (BACE1) induces amyloidogenic cleavages, while α -secretases (ADAM10 and ADAM17) result in less pathological peptides. Hence this first cleavage event is a prime therapeutic target for preventing or reverting initial biochemical events involved in AD. The subsequent cleavage by γ -secretase has a reduced impact on $A\beta$ formation but affects the peptides' aggregating capacity. An array of therapeutic strategies are being explored, among them targeting Retinoic Acid (RA) signalling, which has long been associated with neuronal health. Additionally, several studies have described altered RA levels in AD patients, reinforcing RA Receptor (RAR) signalling as a promising therapeutic strategy. In this review we provide a holistic approach focussing on the effects of isoform-specific RAR modulation with respect to APP secretases and discuss its advantages and drawbacks in subcellular AD related events.

Keywords APP-secretases · APP · RAR stimulation · Neuroregeneration · Alzheimer's disease

Introduction

Alzheimer's disease (AD) is a progressive neurodegenerative disease and the main cause of dementia in the elderly population [1], affecting around 6% of individuals over the age of 65 [2]. Although there are families with higher AD incidence (Familial AD, FAD), caused by autosomal dominant mutations in genes coding for the amyloid precursor protein (APP) and Presenilins (PSEN1 and PSEN2) [3], the main mechanisms causing AD are still, to some extent, unclear, with most cases occurring spontaneously.

Biochemically, AD is characterised by abnormal intracellular deposition of hyperphosphorylated Tau and extracellular accumulation of the amyloid beta ($A\beta$) peptide and the mechanisms of $A\beta$ processing and prevention are a current

topic of extensive research. The shedding of the APP ectodomain can be catalysed by two alternative proteases, α - and β -, which compete for the first APP cleavage [4], resulting in the APP secreted fragment (sAPP). The β -secretase pathway is the major contributor to the consequential $A\beta$ production, while cleavage by α -secretase prevents its accumulation [3]. Subsequently, γ -secretase cleavage generates the p3 (α -secretase pathway) or $A\beta$ (β -secretase pathway) peptides.

Although ubiquitously expressed in all tissues, the APP695 isoform is enriched in the brain. This is a single-pass transmembrane protein with a large extracellular N-terminus and a short cytosolic C-terminus [5]; following protein synthesis in the endoplasmic reticulum (ER)-associated polysomes, APP is *N*-glycosylated in the ER and transported to the Golgi apparatus where it undergoes *O*- and *N*-glycosylation, phosphorylation and sulphonation [6, 7].

APP is part of the type-I transmembrane mammal protein family, which includes the similarly processed APP-like protein 1 (APLP1) and 2 (APLP2). The human APP gene is located on chromosome 21 and contains 18 exons, spanning 290 kilobases [8], with three major isoforms resulting

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from alternative splicing as follows: APP695, APP751 and APP770 [9]. The two larger isoforms contain a 56-amino acid Kunitz Protease Inhibitor (KPI) extracellular domain and are expressed in most tissues [10], while APP695 lacks the KPI domain and is principally expressed in neurons [11]. The KPI domain is primarily a serine protease inhibitor [12] reported to play a role in APP dimerization, regulating its sub-cellular location, secretory pathway, and consequent processing of KPI-containing APP isoforms [13]. Protein and mRNA levels of KPI-containing APP isoforms are elevated in AD brains and correlate with increased A β deposition [14, 15]. In neurons, prolonged activation of extra-synaptic NMDA receptor can shift APP expression from APP695 to KPI-containing APP isoforms, accompanied by increased production of A β [16]. APP695 associates with NMDA receptors, in a manner implying regulation of intracellular trafficking [17], strengthening the theory that dysregulated splicing of APP RNA [15] and favouring APP isoforms facilitating access to the γ -secretase complex [16] contributes to AD pathogenesis.

Even though the inherent biological role of APP is of understandable interest for Alzheimer's research, its physiological function remains puzzlingly elusive. Its most validated role is in synaptic formation and repair, with APP expression being upregulated during neuronal differentiation and following neural injury [18]. Roles in cell signalling, long-term potentiation, cell adhesion, and transport, have been proposed, but are supported by, as-yet, limited research [19, 20]. Similarities in post-translational processing have warranted comparisons with the signalling role of the surface receptor protein Notch, a shared substrate of several APP secretases [21].

Literature suggests additional functions for APP as a cell surface receptor-like protein and ligand, mediating several physiological or pathological effects, either from the cell surface or via the released proteolytic fragments [7]. Moreover, APP presence is described in spermatozoa [22], marking it as a sentinel protein for male reproduction [23], suggesting a wide range of yet unravelled functions.

The importance of phosphorylation in AD is well established [24], with research correlating α -secretase phosphorylation with increased cleavage activity (and consequent amyloid protection) [25]. Moreover, APP phosphorylation is particularly significant, as its trafficking is regulated by the phosphorylation state of the cytoplasmic domain [26]. Phosphorylation at serine 655 determines the fate of APP with respect to Golgi or lysosomal targeting [27, 28]. But most relevant to the work here discussed is that threonine 668 (Thr668) phosphorylation by MAPK8 promotes β -cleavage, by facilitating secretase-APP interaction [29, 30] (Fig. 1). However, this theory remains unconfirmed, as the same Thr668 phosphorylation also decreases extracellular A β and γ -secretase activity [31].

As it is evident, proteolytic processing of the transmembrane region of APP is a crucial step in the progression of AD and, as such, has been the subject of extensive research, revealing novel secretases and cleavages, beyond the classic α -, β -, and γ -cleavages. The C-terminus is generated by sequential cleavages by the γ -secretase complex (ϵ -cleavage [32] followed by ζ - [33] and γ -cleavages) resulting in release of either p3 or A β , depending on the original cleavage (α -, β -, respectively) [34].

APP secretases

α -Secretases

α -secretase is mainly localised in the plasma membrane, where it cleaves full-length APP, but can also be found in the Golgi apparatus [35–37]. APP α -cleavage occurs between Lys-16 and Leu-17 within the A β peptide, believed to be determined by an α -helical conformation and membrane distance from the hydrolysed bond. The action of α -secretase on APP results in a membrane-anchored carboxyterminal fragment (C83) and the extracellular release of the large soluble fragment sAPP α [38–40].

The soluble APP N-terminal fragment derived from α -cleavage, sAPP α , is proposed to be associated with neurotrophic and neuroprotective functions, further supporting the therapeutic value of increasing APP α -secretase cleavage [41]. sAPP α has been shown to be constitutively secreted from cells and stimulation of protein kinase C (PKC) by phorbol esters increases sAPP α release, demonstrating that APP cleavage by α -secretase can either be constitutive or regulated by phosphorylation, potentially suggesting the existence of different α -secretase proteases [42–44].

The anti-amyloidogenic α -secretase A Disintegrin And Metalloproteinase (ADAM) domain-containing protein 10 (ADAM10) is a relevant α -secretase with constitutive activity that directly competes for APP at the cell surface [45]. The ADAM protein family is characterised by conserved amino-acid domains, which include an N-terminal signal sequence (required for directing the proteins to the secretory pathway), a pro-domain (responsible for proper protein folding), a metalloproteinase domain, a disintegrin domain, a cysteine-rich region, an EGF-like domain (with the exception of ADAM10 and ADAM17), a transmembrane domain, and a cytoplasmic domain [46, 47].

The diversity of the ADAM protein family is increased by alternative splicing, with 21 described human isoforms. ADAMs are divided in two groups as follows: the catalytically inactive group, which includes proteases lacking a functional Zn-binding active site, acting via other mechanisms such as protein folding or protein interaction, and the catalytically active group (where ADAM10 and ADAM17

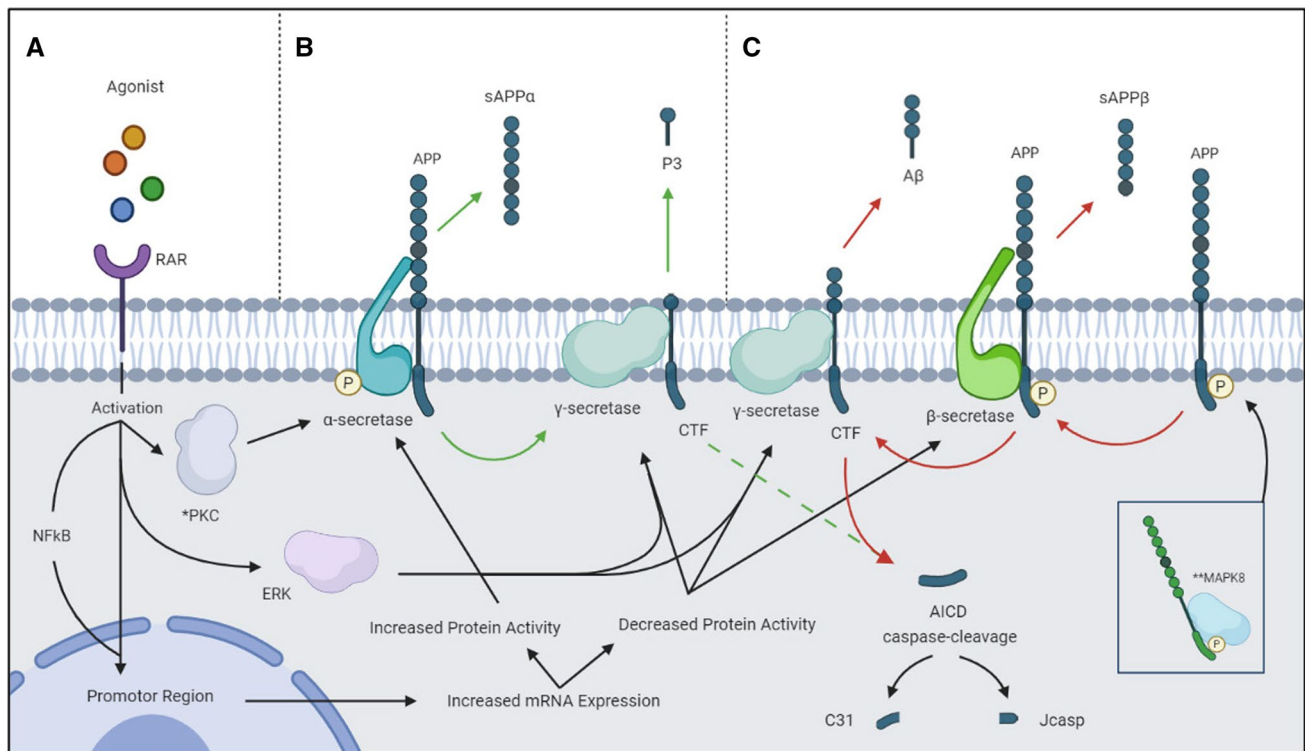


Fig. 1 Retinoid signalling and the integrated impact on APP processing and consequent fragment production. Treatment with atRA alters the gene promotor region for each of secretase. This stimulus can be either direct [120] or mediated by NFκB [87]. Activation of several kinases by the RA receptors (represented by PKC) can have a direct impact on α-secretase activation, contributing to augmented non-amyloidogenic APP processing. ERK pathway activation by RAR stimulus also results in loss of γ-secretase activity, even though its mRNA levels are increased; the same observations are described for the β-secretase BACE1. AICD resulting from β-cleavage is more transcriptionally active (represented by the solid arrow, while the dashed arrow corresponds to the less transcriptionally active). APP's

3 main structural elements are represented accordingly: circles representing the extracellular domain; linear representing the transmembrane domain; continuous representing the intracellular domain. Red arrows correspond to the amyloidogenic pathway while green arrows correspond to the anti-amyloidogenic pathway. **A**—RAR activation. **B**—Anti-amyloid pathway. **C**—Amyloid cascade. *PKC is represented since it is the most relevant kinase activated by RAR, but other kinases are described to take part in RAR-induced activation of α-secretase. **MAPK8 is represented to phosphorylate APP in Thr668 since it is the kinase most frequently described to produce this effect, but several other kinases are shown to produce the same modification

are included), containing proteases with a Zn-binding active site [37, 46]. α-secretase cleavage was classically described as a sequence independent process, determined by an α-helical conformation and a 12–13 residue interval between the membrane cleavage site [37], but a cleavage preference for ADAM10 was eventually described [48]. Initially reported to be responsible for the proteolytic activation of the membrane precursor of TNFα [1], ADAM17, like ADAM10, was found to target a range of substrates implicated in several physiological mechanisms [49]. Notch receptors, ligands, cadherins, IL-6 receptor, EGF receptor ligands, and other type-I transmembrane proteins are also cleaved by α-secretases, resulting in the release of their respective extracellular domains [50].

Several ADAM proteases have α-secretase activity [51]: selective interference of individual ADAM10, ADAM17, and ADAM19 genes, in cell and animal models, had no noticeable impact on non-amyloid APP processing [52, 53].

ADAM10 was shown to have the most relevant α-secretase activity in neurons [45]. We have described that even though several ADAMs act on APP, only ADAM10 and ADAM17 interact directly with it, with other proteins playing a supporting role such as escorting or bridging α-secretase activators through post-transduction modifications (most commonly phosphorylation) (da Cruz e Silva et al., submitted). Additionally, the secretase ADAMTS4 (A disintegrin and metalloproteinase with thrombospondin motifs 4) was shown to interact with APP in in vitro models [54].

Retinoic Acid (RA) metabolism and signalling are essential for neuronal health, and several studies have described its impairment in AD patients, where RA precursor levels are decreased [55, 56]. Considering the promising results of promoting α-secretase expression in AD, functional studies described two potential RA responsive elements in the ADAM10 promotor region, 203 and 302 bp upstream from gene translation start site [57]. Promotor reporter assays in

neuroblastoma cells treated with all-trans RA (atRA) demonstrated significant increase in ADAM10 transcriptional activity, mRNA, and protein levels and, consequently, sAPP α secretion [58–60]. RA receptor (RAR) activation (discussed below in “[modulation of retinoic acid receptors](#)”) as a means to increase α -secretase regulatory activity is well established, as is the case for ADAM10 [61]. Moreover, RA activates several kinase proteins (including PKC) [60, 62] with anti-amyloid effects, both by interacting with target promoters [63] and through direct activation of α -secretase activity via phosphorylation [64] (Fig. 1).

Even though α -secretases are complex therapeutical targets, due to their large substrate number and the range of signalling pathways in which they are involved, they are, nonetheless, prime candidates to prevent A β deposition. However, most studies regarding AD, A β formation, and APP proteolytic processing, focus on β and γ -secretases, and their influence on APP cleavage events, lacking a holistic approach encompassing α -secretases and their supporting interactors [65].

β -Secretases

BACE1 (beta-site APP cleaving enzyme 1) is the principal protein with β -secretase activity [66]. This secretase plays a central role in A β generation, being considered by some as the initial (and rate-limiting) stage of APP amyloid processing [67]. These observations result from repeated and well-validated experiments whereby knocking out BACE1, A β formation completely ceases [68–70].

BACE1 is a membrane-bound aspartyl protease, structurally similar to the pepsin family [71], containing two active site motifs in the luminal domain (amino acids 93–96 and 289–292) [72]. Each motif contains a highly conserved signature sequence of aspartic proteases, D^T_S G^T_S, in which the aspartic acid residue is essential for catalytic activity. BACE1 also has four putative N-linked glycosylation sites and six luminal cysteines, which allow for the formation of up to three intramolecular disulphide bonds.

β -secretase activity is highest in the secretory pathway compartments, namely the Golgi apparatus, trans-Golgi network (TGN), secretory vesicles, and endosomes [73]. Like APP, it is highly expressed in the brain, but is nonetheless ubiquitously present in most tissues, with the pancreas being a close second. Pancreatic presence is marked by high levels of an mRNA splice variant, lacking exon 3, resulting in a different isoform with low activity, but its relevance is not yet clear [74, 75].

The therapeutical value of β -secretase has been widely investigated, with progress being made in regards to an inhibitor [76, 77], that although promising, fails to specifically inhibit the cleavage of APP alone, interfering with other BACE1 substrates. Specific inhibition proved

particularly challenging, due to the fact that there are approximately 70 putative substrates cleaved by β -secretase, mostly other type I transmembrane proteins [78–80].

It is apparently contradictory that BACE1 knockout mice are viable, fertile, and lack morphological or developmental alterations [68–70]. However, these animals show subtle behavioural phenotypes, with mild memory impairment and spontaneous activity changes [81, 82], reiterating the complexity of BACE1 selective inhibition.

The phenotypes observed in animal models can be explained by the role of BACE1 in the myelination process [83] as follows: very highly expressed during post-natal stages, BACE1 acts on the NRG1 (Neuregulin-1) signalling pathway, believed to promote myelination [84]. Consistently, all BACE1 knockout animal models present hypomyelination [83, 85]. The association between BACE1 and myelination, however, remains controversial, with as yet-limited research. BACE1 has also been described to regulate voltage-dependent sodium channels [86], although with a probably diminished impact on behavioural changes.

Like α -secretases, BACE1 activity also correlates with RA. Treatment with atRA was shown to alter both BACE1 expression and activity in a human neuroblastoma IMR-32 cell line, while its homologue BACE2 remained unaltered [60]. Interestingly, BACE1 mRNA levels are significantly increased, but have no impact in overall protein quantity [60]. In a different study, using rat primary cultures of cortical neurons, BACE1 expression levels were reduced by atRA treatment [87]. The same authors described that this alteration to BACE1 expression was mediated through NF κ B (Fig. 1); disruption of NF κ B led to increased transcription of BACE1 and reversed the effects of atRA treatment [87].

Although BACE2 is homologous to BACE1, its involvement in APP processing has not been fully described. BACE2 was initially considered a β -secretase [88–90], cleaving APP at the β -site [90]. Later studies showed BACE2 to cleave within the A β region [91], similar to α -secretase, suggesting a protective role [92–94], as BACE2 overexpression prevents production of A β [91, 95–98]. Given that BACE2 expression is lower in the brain [99], its impact on AD may be minor. However, its β -secretase activity has recently been reiterated, particularly when facilitated by AD-associated conformational changes in APP [100]. The correlation of BACE2 with AD pathophysiology is corroborated by its increased activity in pre-clinical AD [101]. These findings further strengthen the need for a holistic approach to AD, revealing novel pathways in which the amyloid process can be decreased/inhibited.

γ -Secretases

γ -secretase is a multiprotein complex consisting of presenilin (PSEN1 and 2), nicastrin, Aph-1, and Pen-2, with

PSEN proteases containing the two catalytic aspartates that mediate peptide bond scission [102], and cleaving APP within the transmembrane domain (TMD) [103]. The cleavage occurs by the two critical aspartyl residues within TMDs 6 and 7 of PSEN1/2 [104]. Although the specific function of each component of this complex has been subject to intense scrutiny over the last decade, consensus has not been achieved [6, 105–108].

PSEN1 and PSEN2 are involved in the processing of type-1 transmembrane proteins, including APP [6, 109]. Their closely related genes were discovered as mutated loci in a large proportion of human pedigrees with inherited early AD onset; these two genes encode components of γ -secretase complexes that cleave transmembrane proteins within lipid bilayers, including APP, the Notch receptor, E-cadherin, Nectin1, and others [110, 111].

Importantly, γ -secretase intramembrane processing of APP is not restricted to a single site; this complex is widely accepted to cleave at several sites within the TMD of their targets, and in the case of APP with three cleavage points separated by approximately three amino acids each [112–115]. Under physiological conditions, the last cleavage is variable, occurring between positions 37–43 of the A β peptide. This variation is highly relevant for AD pathology, directly and proportionally linked to A β aggregation, deposition, and toxicity [116]. These multiple cleavages are thought to be due to a stepwise cleavage mechanism, and research suggests that this may be a general characteristic of all γ -like-secretases [117–119]. The distinction between the three cleavages is of great importance to AD and may hold the key to therapeutic strategies [76], being that the longer peptides exhibit a greater tendency to aggregate.

RAR signalling might not just be restricted to α and β -secretases, but may also impact the γ -secretase complex. Its activity is largely reduced with RA treatment, leading to a threefold increase of γ -secretase substrate, C99 [120]. This is an important objection against the therapeutic effects of RA, since the cellular accumulation of C99 is toxic [121]. The same study showed that isolated inhibition of γ -cleavage reduces A β secretion and that RA-mediated γ -secretase inhibition requires ERK activation [120]. RA regulates various signalling pathways, including kinases, and the ERK-pathway is a negative regulator of γ -secretase [122]. A more targeted analysis of the impact of atRA treatment on PSEN1 and 2 revealed increased mRNA levels of PSEN1, but, mirroring the situation with BACE secretases, unaltered for PSEN2 [60]. In addition, although PSEN1 mRNA levels are increased, protein levels remain largely unchanged, and activity is actually decreased (Fig. 1).

Alternative APP-cleaving secretases

Besides the above-described proteases, other APP cleaving enzymes have recently been described.

Membrane-Type Matrix Metalloproteinases (MT-MMP) were shown to be involved in the regulation of APP processing, cleaving, and shedding of ectodomain fragments, generating CTFs, specifically MT1-MMP, MT3-MMP, and MT5-MMP [123, 124]. Mouse AD models suggest pro-amyloidogenic roles for MT1-MMP. [125], while the absence of MT5-MMP (MT5-MMP^{-/-}) increased cognitive function in a FAD mouse model, without altering α -, β - and γ -secretases' activities, but altering sAPP secretion [126]. Additionally, MT5-MMP also promotes AD pathogenesis in the same model [127]. The same study found the impact of MT5-MMP expression in APP processing to reside on its ability to affect cellular APP trafficking [127].

Consistently, inhibition of the lysosomal aspartic endoprotease cathepsin D was also beneficial in reducing A β load and improving memory, in a transgenic mouse model [128]. Early studies correlated cathepsin D with AD [129, 130], without affecting A β formation in a cathepsin D knockout model [131]. Cathepsin D gained more significance when animal studies described a specificity for the APP β -cleavage site [132], which also highlighted that selective inhibition of the lysosomal cysteine protease cathepsin B significantly decreased A β (40/42) production, independent of β -secretase activity.

Other proteins involved in APP processing should be mentioned, among them meprin B, which can act as a sheddase for APP [133], cleaving within the N-terminal region without toxic fragment production [134, 135]. Also noteworthy, overexpression of ADAMTS4 in cell models increased A β secretion, verified in in vivo AD model, where ADAMTS4^{-/-} knockout resulted in decreased A β [136]. The study further presented oligodendrocytes as a source of amyloid peptides, shedding new light on the peptide's origin.

Except for some tenuous associations (namely with MT5-MMP), the impact of RA in alternative APP cleaving secretases remains elusive [137]. This adds another layer for the potential therapeutic exploitation, should the alterations induced by RA prove beneficial in the AD context.

Modulation of retinoic acid receptors

RA exerts a profound effect on homeostatic properties and signalling pathways [138], ranging from physiological functions to pathology [139, 140], and the nervous system is importantly regulated by this pathway. Unravelling the modulation of RAR in AD is of paramount importance, as regulation of APP cleaving secretases is a strong candidate for translational research for a therapy [141]. Most

studies on RA-induced alteration to secretase activity are based exclusively on atRA [60]. However, the influence of isoform specific RAR signalling in neuronal function and homeostasis is currently well defined [142, 143] and its overall significance in the context of AD has received recent interest, with some retinoid drugs currently undergoing clinical trials (Table 1). RAR activation as a therapeutic candidate is being explored in AD models [144, 145], as it reduces neuroinflammation and contributes to neuroregeneration [146], adding possible paths to promote neuronal health and rehabilitation [147]. The A β peptide inhibits RA synthesis, aggravating AD symptoms and progression [145], which correlates with the observed decreased serum levels of retinoid metabolites in AD patients [55, 56]. The potential of systemic retinoid as therapy has long been established, although not completely without side-effects [148], and its use has been approved for several conditions (Table 1). However, systemic retinoid therapy requires careful patient monitoring, as information on long-term use and mechanism of potential adverse reactions is still lacking [149].

RA signalling is translated via two families of nuclear receptors as follows: RAR has three isoforms (α , β and γ) that can be activated by both atRA and 9-cis-RA enantiomer [150]. The retinoic X receptor (RXR) also has three isoforms and is activated by 9-cis-RA [151], playing a role in the RA-related negative feedback system, mediating anti-proliferative effects [152]. RXR increases DNA binding and transcriptional function, with a direct effect on their respective response elements [102]. Both families can form heterodimers as RAR/RXR [153].

Similar to other type II nuclear receptors, each RAR isoform produces several splice variants [154–156]. Agonist binding results in detachment of corepressor proteins, activating the receptor [153]; RAR signalling is highly dependent on recruiting coactivator proteins promoting downstream gene expression [157]. RAR gene expression is itself regulated by RAR activation via promoter methylation events [158]. While RAR α and RAR β have been extensively studied and explored, the isoform RAR γ

is less well described [159], although the physiological processes regulated by this receptor are not entirely clear [160], it appears to share some of the broad functions in embryogenesis and cell differentiation, common to other members of the RAR family [161].

RAR/RXR ligand binding and heterodimer crosstalk

Although RARs can also be activated by atRA, RXRs are only activated by the less lipophilic 9-cis [150, 162]. Previous research has demonstrated that retinoid effects are also mediated by heterodimers formed by different RAR and RXR isotypes, which can act as transcription repressors or activators [163].

RXR Arg316 is the only polar contact, where its ligands can form an ionic connection; binding shape and lipophilic contacts are the primary determinants of ligand recognition, as most RXR ligands have the classic fatty acid design [164]. New classes of agonists with a better safety profile and less lipophilic properties are being developed [165, 166].

RXR regulates lipid, carbohydrate, and amino acid metabolism [167–169]. RXR activation affects lipid metabolism by increasing the expression of ApoE (apolipoprotein E) and ABCA1 (ATP-binding cassette transporter ABCA1), which leads to an increase in ApoE lipidation mediated by ABCA1 and HDL levels in the brain [170, 171]. This is particularly relevant because APP processing, beta amyloid generation, and plaque development in vivo are all affected by changes in intracellular lipid homeostasis [172], much of which is controlled by the ApoE lipoprotein transport system [173, 174]. The convergence of the amyloid cascade theory (which posits A β brain deposition as the fundamental step in AD) [175] and the ApoE/lipid recycling cascade concept [176] supports lipid homeostasis changes as a common denominator for ApoE and A β dysfunctions in AD. Furthermore, RXR activation by bexarotene has been reported to cause A β phagocytosis in brain myeloid cells, linked to an increase in the expression of the phagocytic receptors [177].

Table 1 Retinoids undergoing pre-clinical or clinical trials for AD

Drug	Effect	Other conditions	Status in AD
9-cis retinoic acid	Pan agonist, RXR preference	Kaposi's sarcoma and chronic hand eczema—approved	Explored [226]
Tamibarotene (AM-80)	RAR α / β agonist	Acute Promyelocytic Leukaemia—approved (Japan), under development (US, EU, China)	Explored in AD, no outcomes [227]
Isotretinoin	Possible precursor to RAR/RXR agonists [228]	Acne Vulgaris—approved	Explored [146, 229]
Acitretin	Possible RAR/RXR agonist	Psoriasis—approved	Explored [230]
Bexarotene	RXR Agonist	Cutaneous T cell lymphoma—approved	Explored in clinical trials: negative outcome [231]
Tazarotene	RAR- γ and RAR- β agonist	Psoriasis; Acne Vulgaris -approved	Considered [146, 232]

RAR α

RAR α is also denominated nuclear receptor subfamily 1, group B, member 1 (NR1B1) [178]; its activation by the selective agonist AM580 is protective against the decreased RA synthesis in a neuroblastoma cell line [145], inhibits A β generation in vitro via increased ADAM10 expression [48, 100], and directly inhibits γ -secretase cleavage of APP in cellular models [120]. Of note, not only does RAR α signalling prevent A β synthesis, but it is also neuroprotective against A β [152].

RAR α activation plays a central role in cell growth [180], differentiation [181], and organ formation during embryonic development [182]. RAR α signalling has been linked to various pathways [183], especially in early embryonic development [184], inducing differentiation of Neuronal Progenitor Cells (NPC) into migrating fibroblasts and consequent maturation into neurons [185]. It plays a central role in regulating neural differentiation [186], via the expression of the pro-neural induction factor Neurogenin 2 [187, 188].

RAR β

RAR β is another cytoplasmic nuclear receptor [189], directed to subnuclear compartments following activation [190]. This receptor also mediates signalling in cell growth, differentiation, and embryonic events: it has been described to increase the proliferation of NPCs through the Sonic Hedgehog Pathway (Shh) [185] and to be a key player in the neurite growth through the signalling sequence for the Nerve Growth Factor (NGF) [191]. Curiously, it is theorized to limit the growth of many cell types by regulating gene expression, as it acts in embryonic development controlling numerous aspects of cell proliferation, differentiation, and inducing apoptosis of selected cell populations [182, 192–194].

A Genome-wide association study associates RAR β as a risk gene for several neurodegenerative pathologies, including Alzheimer's, Parkinson's, and Huntington's diseases [195]. Its activation in a neuropathic pain model restores mechanisms involved in cell adhesion [196], neuronal cone growth [197], gap junction [198], and pain-related pathways [199]. RAR β is central for retinoid-mediated neurite outgrowth [200], also acting in mature neurons [201] recruiting mitochondria to the neurite growth cone [147]. Moreover, RAR β neuroprotective roles additionally include the reduction of neuroinflammation and increase of neuroplasticity [202].

Activation of RAR in a neuronal setting

Modulating different RAR isoforms can induce significantly different physiological responses [203]. Targeting

RAR as a potential therapeutic target for neurodegenerative diseases has been a topic of extensive research [144, 146, 204], with several studies showing a clear difference between isoform-specific stimulation [205–209]. Specific RAR γ stimulus has been linked to apoptosis in a melanoma cell line and to increased cell differentiation [205]. Moreover, a study in embryonal carcinoma cells revealed that different RAR isoforms perform distinct roles in the differentiation of spiny neurons [207].

The combined modulation of RAR differs from the conjugated effects of isolated isoform stimulus [203]. Co-activation of RAR α and β is described to play an important signalling role in adult neurogenesis, modulating the Fibroblast Growth Factor (FGF) and Shh signalling pathways [185], while the sequential activation of RAR α and β , in vitro, results in neuronal differentiation of cultured spinal cord progenitor cells (SCPC) [210]. Although both receptors are expressed in adult neurons of the subventricular zone (SVZ) [211] their role in neurogenesis, especially co-modulation, remains somewhat elusive [185]. Interestingly, the disruption of both RAR and RXR families, independent of isoform, causes an impairment in hippocampal memory and synaptic plasticity in mice [212].

In addition to protective effects in neurodegenerative settings [202], pan-RAR activation promotes neuroplasticity and regeneration [185, 191, 213–217], and individual activation of all RAR isoforms promotes neurite outgrowth [218]. A study in a rat model of ageing found atRA to reduce neuroinflammation [219], while activation of RAR β was described to be involved in NG2-neuronal cross-communication, diminishing the formation of the glial scar [179, 188] and promoting regeneration [179] and remyelination [188], in a rodent model of spinal cord injury. RAR β activation can also revert inhibition of neurite growth via PKC-induced events [220].

ADAM10 overexpression reduced levels of brain A β and reversed Long-Term Potentiation (LTP) inhibition and spatial learning impairments in APP transgenic mice, providing a proof-of-concept therapeutic option for increasing α -secretase activity [221]. Furthermore, deprenyl, an AD anti-dementia medication, appears to increase APP cleavage mediated by α -secretase in AD patients [222].

Activation of nuclear receptors is a promising therapeutic approach for AD [204]. These receptors act as ligand-activated transcription factors, regulating gene expression with cell type-specific effects [223]. AD is associated with a variety of pathophysiological features beyond amyloid plaques, including inflammation, cell death and regeneration processes, altered neurotransmission, and age-related changes. RARs and retinoids are a potential therapeutic target, as they are involved in all of these [204, 223]. As such, considering the plethora of crucial pathways involved, the future possibilities of targeting RAR for

neurodegenerative disease therapy and regeneration cannot be overstated.

Towards a holistic and systems approach

A relevant approach of pivotal importance to AD is promoting APP α -secretase cleavage, which may be crucial to delaying disease onset, and understanding alterations to key proteins, induced through receptor modulation. Promoting α -cleavage of APP has long been a prime therapeutic target in AD and, as such, the holistic methodology is a relevant approach; this strategy investigates global and dynamic molecular changes, considering interactions under normal and pathological conditions, thus representing a promising approach for the study of AD and other complex pathologies [40, 224].

Applications of omics approaches is attracting growing interest due to its association with different diseases [224]. The study of protein interactions (interactomes) has shown promising results in distinguishing key chains of events and functions of important proteins, with central roles in various pathways, either physiological or associated with disease [23, 225], (da Cruz e Silva et al., submitted).

For pathologies involving many affected pathways and regulation systems, analysis and data integration from different omics technologies is crucial for a fuller understanding of the disease, supporting the development of personalized diagnostic and therapeutic tools. Several omics studies aim to determine novel pathways and networks, suggesting new pathologic mechanisms associated with disease states and cross-linked with other diseases. The limitation to the holistic approach is the challenge in distinguishing whether the alteration of molecule and marker networks are a cause or an effect of the disease. Nevertheless, it is helpful in identifying new targets or in validating previously identified ones.

Overall, the notion of APP secretases as therapeutic targets for AD grows stronger. As the three secretase classes cleave a significant pool of substrates (not restricted to APP) affecting several signalling and metabolic pathways, purposefully altering their activity is a complex procedure with possible adverse outcomes. Secretase selective inhibition establishes problems in maintaining the physiological pathways inherent to normal cell function, with the answer lying on targeted modulation of several pathways. Besides, substrate build-up can have unforeseen cytotoxic effects and thus be counterproductive for promoting homeostasis and preventing neurodegeneration.

RAR-induced secretase alterations have been, to some extent, described in a specific context, lacking a holistic approach to determine whether they are restricted to the studied protein complex, or actually have deeper effects in the AD interactome. This knowledge is of utmost

importance, as it allows determining whether these alterations are compatible with homeostasis and, consequently, a potential AD therapy.

In closing, the holistic and systems approach focuses on several molecular players and not only the underlying individual disease processes, with the unique advantage of identifying signalling cascades and crosstalk between different pathways, related to a specific molecular target, involving many fronts of the disease.

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