



COMMENTARY

ROLE OF NEUROTRANSMISSION IN THE REGULATION OF AMYLOID β -PROTEIN PRECURSOR PROCESSING

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Because of the central place of amyloid in the histopathology of Alzheimer's disease (AD‡), current research seeks to determine the proteolytic mechanisms involved in the processing of the amyloid β -protein precursor (APP). Cellular APP processing yields several cleavage products some of which appear to be neurotrophic or even neuroprotective, whereas others are potentially amyloidogenic and, in some experimental systems, neurotoxic. Understanding the biochemical mechanisms that regulate cellular APP processing is a requisite for developing treatments that affect APP metabolism and that might slow the rate of amyloid deposition in the brain of AD patients. Recent evidence from cell culture experiments suggests that APP processing pathways are regulated by a variety of first messengers coupled to activation of protein kinase C. These first messengers include the muscarinic acetylcholine receptor m1 and m3 subtypes that increase the secretion of N-terminal APP derivatives lacking the C-terminus (non-amyloidogenic APP^s), and that concomitantly decrease secretion of the potentially amyloidogenic $A\beta$ peptide. Brain tissue slice experiments indicate that similar APP processing mechanisms occur in mammalian brain tissue as in cell culture, and that APP processing in the brain may be a function of neuronal activity. This article reviews recent data on the regulation of APP processing by neurotransmitters, and prompts speculation that activating specific neuronal cell surface receptors will prove a novel pharmacological way to modify APP processing in the intact brain.

ALZHEIMER'S DISEASE AMYLOID

Amyloid deposits in brains of AD patients, Down syndrome subjects and aged individuals consist primarily of aggregates of 39–43 residue peptides,

variously termed amyloid β -protein, β -peptide, β -amyloid, A4, $\beta A4$, $\beta_{1-39/43}$, or simply $A\beta$. These peptides are derived, by proteolytic cleavage, from transmembrane glycoproteins known as APP. Aggregates of the 39 residue variant account for the congophilic angiopathy of cerebral blood vessels [1], and the 42/43 amino acid $A\beta$ appears to be the predominant form of extracellular amyloid in senile plaques [2, 3], which are often associated with a neuritic reaction. At high concentrations, $A\beta$ molecules tend to self-aggregate *in vitro* to form insoluble amyloid fibrils [4, 5] that are reminiscent of those deposited in the AD brain, but such additional amyloidotropic factors as apolipoprotein E [6, 7] or free oxygen radicals [8] may enhance the aggregation of $A\beta$ into amyloid *in vivo*. The biochemical mechanisms that regulate the synthesis of APP, the proteolytic APP degradation pathways that yield $A\beta$ -comprising derivatives, and the factors that promote aggregation of $A\beta$ -containing polypeptides into amyloid are central for understanding brain amyloid formation in health and disease.

STRUCTURE AND POSSIBLE BIOLOGICAL FUNCTIONS OF APP

APP is one of the most abundant proteins in the brain (for recent reviews, see Refs. 9 and 10). Nine APP gene transcripts derived from alternative splicing have been identified to date, encoding corresponding proteins that range from 365 to 770 amino acid residues [11–20]. Some of these (APP695, APP751, APP770) are expressed at high levels in the brain. APP molecules are membrane glycoproteins with a long extracytoplasmic N-terminal domain followed by a single transmembrane segment and a short cytoplasmic C-terminal tail (see Fig. 1). $A\beta$, the principal amyloidogenic component of AD-type brain amyloid begins 28 residues from the membrane, in the extracytoplasmic region, and extends 11 to 15 amino acids into the transmembrane portion. One set of transcripts that lacks exon 15 was initially identified in white blood cells, and named LAPP [19, 20]. These variants are predominantly expressed by immunocompetent cells and by microglial cells in the brain [19, 20]. Two APP isoforms APP770 and LAPP752, contain,

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‡ Abbreviations: AD, Alzheimer's disease; APP, amyloid β -protein precursor(s); APP^s, secreted forms of APP; KPI, Kunitz serine protease inhibitors; PNII, protease nexin II; FAD, familial AD; mAChR, muscarinic acetylcholine receptor(s); IL-1, interleukin 1; DAG, diacylglycerol; and PKC, protein kinase C.

within the extracytoplasmic N-terminus, a 57-residue domain homologous to the family of Kunitz serine protease inhibitors (KPI) along with a 19-residue segment homologous to the thymocyte OX2 antigen. The APP751 and LAPP733 variants also contain the KPI but not the OX2 segment. Extracytoplasmic portions of mature APP are N- and O-glycosylated and sulfated [21]. Secreted KPI-containing N-terminal APP derivatives are homologous to protease nexin II (PNII) [22, 23], a member of a larger family of transmembrane proteins that bind to, internalize, and inhibit extracellular proteases. This protease inhibitory function of C-terminally truncated, secreted APP/PNII may be involved in the regulation of proteases that control the blood coagulation cascade [22–26]. The membrane-associated forms of APP contain a G protein binding domain that resembles a family of cell surface transmembrane receptors [27], suggesting a possible, yet unidentified, role in cellular signalling. Recently, a metalloprotease inhibitor domain has been described within the extracellular glycosylated portion of APP [28]. This domain reportedly inhibits collagenase type IV, an enzyme involved in the degradation of extracellular matrix proteins. The extracellular N-terminal portion of APP contains segments that specifically bind to collagen, laminin and heparin [29], suggesting a possible biological function in cell adhesion and in cell growth. APP also exists in a chondroitin sulfate proteoglycan form [30], underscoring the possibility of interactions with the extracellular matrix. There is accumulating evidence that the C-terminally truncated, secreted forms of APP (APP^s) protect cultured primary neurons from damage induced by glutamate excitotoxicity and glucose deprivation by limiting the increase in intracellular free Ca²⁺ levels [31]. These observations suggest that APP^s may protect neurons against such toxic insults as excitotoxicity, hypoglycemia and Ca²⁺-mediated cellular damage. Furthermore, APP and some of its derivatives have trophic effects on a variety of cells in culture by stimulating neurite outgrowth and neurite branching [32] in PC-12 cells, and by enhancing the rate of survival of primary hippocampal neurons in culture [33]. These data on neurotrophic and neuroprotective biological functions of APP imply that its mistreatment could have two distinct important consequences: the disruption of biologic processes normally influenced by APP and its metabolites, as well as the generation of amyloidogenic derivatives leading to amyloid plaque formation.

APP maps to human chromosome 21 [11, 12]. Additional genes encoding for the APP-like proteins APLP1 and APLP2 with homologous N-terminals but lacking A β segments, have identified recently and mapped to human chromosomes 19 and 11, respectively [34, 35]. APLP1 and APLP2 are non-amyloidogenic proteins, but, because of their structural similarity to APP, may interfere with APP processing pathways, and thus may indirectly affect APP function and amyloid formation.

APP PROCESSING PATHWAYS

The full-length, mature forms of APP have a very

short half-life (20–30 min in cell culture) as they are degraded proteolytically by at least four alternative processing pathways. Some of these pathways generate derivatives that contain intact (potentially amyloidogenic) A β segments, whereas other, non-amyloidogenic, pathways prevent the formation of such fragments by cleaving APP within the A β domain (Fig. 1). The specific proteases mediating APP catabolism have not yet been identified and much of the data generated thus far is based upon analyses of APP fragments. The APP processing pathways known to date are referred to as α - and β -secretase cleavage, secretase-II cleavage and endosomal-lysosomal processing (Fig. 1).

The secretory pathways

Soluble APP derivatives that contain a large (110–125 kDa) extracytoplasmic N-terminal portion but not the cytoplasmic C-terminus of APP (APP^s) are secreted by a great variety of cultured cells [21, 37], are also found in superfusates of brain slice preparations [38], in human brain and cerebrospinal fluid [21, 39], as well as in human serum [40]. Human serum APP^s may be largely derived from platelets, which release APP^s in response to activation with heparin [41, 42]. The cellular mechanisms leading to APP^s secretion involve a proteolytic cleavage event that leaves behind a small cell-associated C-terminal fragment [37]. Secretory APP cleavage events of this type are referred to as *secretase* processing pathways (Fig. 1). Three distinct secretase-type cleavage events have been suggested to date. The first is α -secretase cleavage which occurs at position Lys16-Leu17 (referring to A β 1–43) within the A β domain and thus generates two non-amyloidogenic metabolites [43–46]. The efficiency of this cleavage event is highest at the precise distance of 12 amino acid residues extracytoplasmic from the membrane surface, i.e. between residues 16 and 17 of A β , but appears to be remarkably independent from the specific amino acids flanking the cleavage site [47]. β -Secretase cleavage generates a secreted N-terminal derivative that is 16 residues shorter than the α -secretase product and ends at the N-terminus of the A β domain [48]. If, indeed, cellular full-length APP is a substrate for this cleavage event (as opposed to the secreted α -secretase product), the remaining cell-associated C-terminus is potentially amyloidogenic and may be a possible progenitor of secreted soluble A β [36]. It is, however, also possible that the secreted N-terminal β -secretase product does not reflect a single enzymatic cleavage event but is derived from multi-processing events (e.g. extracellular nibbling) at the C-terminus of the secreted α -secretase cleavage product. A third secretase cleavage reportedly occurs at a yet unidentified site near the C-terminus of A β and was named *secretase II* [49] (Fig. 1).

Secretion of soluble A β

Soluble 4 kDa A β was identified in conditioned cell culture media from transfected and primary cells [50–52] as well as in human cerebrospinal fluid [53] (Fig. 1). Like any A β -containing polypeptide, these peptides are potentially amyloidogenic and could theoretically contribute to amyloid formation. On

APP PROCESSING PATHWAYS

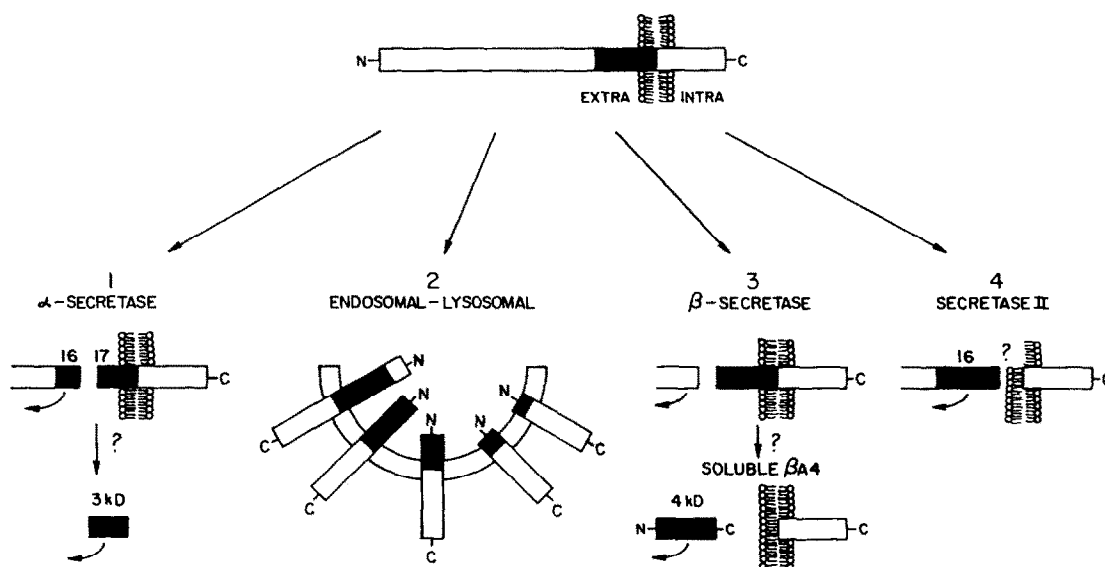


Fig. 1. APP processing pathways (1) α -Secretase cleavage within the $A\beta$ domain prevents the formation of amyloidogenic derivatives and generates secreted APP^s that carries some of the neurotrophic and neuroprotective functions of the molecule. A 3 kDa fragment, which is also secreted, may derive from the remaining C-terminus generated by α -secretase cleavage [36]. (2) Endosomal-lysosomal APP processing generates multiple C-terminal derivatives, some of which contain intact $A\beta$ sequences and, thus, are potentially amyloidogenic. (3) β -Secretase cleavage occurs at the N-terminus of the $A\beta$ domain and generates a large secreted N-terminal derivative. The remaining C-terminus is potentially amyloidogenic and may serve as the progenitor molecule for secreted $A\beta$. (4) Secretase II cleavage occurs at a yet unidentified site close to the C-terminus of $A\beta$.

the other hand, the 4 kDa $A\beta$ identified in cell culture media fails to form aggregates as indicated by the absence of $A\beta$ immunoreactivity in high-speed centrifugation pellets of cell culture supernatants. This absence of aggregation could reflect low peptide concentrations (0.3 ng/mL/hr, estimated from [50]), or the absence of residues 41–43 which promote aggregation [5]; or the presence of a cell-derived factor that prevents aggregation; or the lack of amyloidotrophic factors necessary for aggregation [6, 8]. An additional 3 kDa C-terminal fragment of $A\beta$ (p3) is also secreted into cell culture media and cerebrospinal fluid. This fragment could be generated by cleavage of the remaining cell-associated C-terminal APP stump derived from α -secretase cleavage [36]. An initial argument supporting the hypothesis that secreted $A\beta$ may contribute to brain amyloidosis and the development of AD comes from a Swedish familial AD (FAD) kindred that carries a double mutation in the APP gene causing a substitution of two residues close to the N-terminus of the $A\beta$ domain [54]. Overexpression of this mutant in cell culture is associated with a 5- to 6-fold higher $A\beta$ release as compared with normal APP [55, 56].

The endosomal-lysosomal pathways

Alternatively to the secretory pathways, APP holoprotein can be internalized from the plasma

membrane and targeted to endosomal-lysosomal compartments [57], possibly via clathrin-coated pit internalization mediated by an Asn-Pro-Thr-Tyr consensus sequence in the C-terminus of APP [58]. In addition to this re-internalization pathway, APP holoprotein may be targeted directly from the post-Golgi to the endosomal-lysosomal compartment. Full-length APP is detectable in endosomal-lysosomal preparations and degraded within this compartment, yielding multiple C-terminal APP fragments [59, 60] (Fig. 1). Some of these endosomal-lysosomal C-terminal APP derivatives appear to contain intact $A\beta$ sequences and thus are potentially amyloidogenic.

CELL SURFACE RECEPTOR REGULATION OF APP PROCESSING

Increase of APP^s secretion by activation of cell surface receptors

The relative activities of individual proteolytic APP processing pathways can be regulated by first messengers via stimulation of neurotransmitter and neuromodulator receptors. Initial evidence for this novel role of cell surface receptors came from stimulation experiments of human embryonic kidney cells transfected with cDNA encoding for human muscarinic acetylcholine receptor (mAChR) subtypes. These experiments demonstrated that

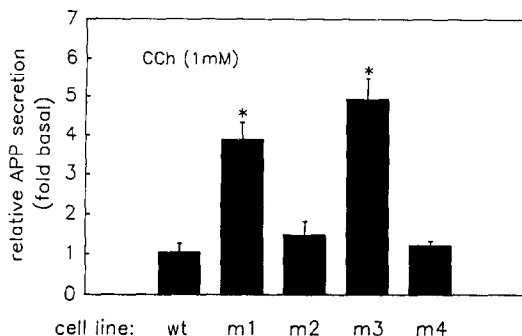


Fig. 2. Increase in APP^s secretion by cell surface receptors. Activation of muscarinic acetylcholine receptor subtypes m1 and m3 with carbachol (CCh) increases the release of APP^s from HEK 293 cells stably transfected with the cDNA encoding for the human receptor subtypes. Wild type HEK cells (wt), as well as cells expressing the cDNA for the m2 and m4 receptor subtypes, did not respond to carbachol with increased APP^s secretion, indicating that APP^s secretion, indicating that APP^s secretion is specifically increased by the m1 and m3 receptor subtypes. Values are means \pm SEM, N = 5–7 experiments per group. Key: (*) P < 0.01 versus unstimulated control condition in each cell line. Reprinted with permission from Nitsch *et al.*, *Science* 258: 304–307, 1992. Copyright (1992) AAAS. [Ref. 61].

activation of both the m1 and the m3 AChR with the muscarinic receptor agonist carbachol (a stable acetylcholine analog) significantly increases the release of soluble large N-terminal APP derivatives lacking the C-terminus (APP^s) [61] (Fig. 2). These initial findings were subsequently confirmed in a rat pheochromocytoma PC-12 cell line transfected with the muscarinic m1 receptor gene, and extended by the observation that stimulation of interleukin 1 (IL-1) receptors also increases the release of N-terminal APP derivatives [62].

The increased release of APP derivatives in response to receptor activation is unaffected by the translation inhibitor cycloheximide in the initial 30-min period after stimulation, indicating that preexisting APP molecules are cleaved and released in response to receptor activation. Concomitantly, levels of cell-associated full-length APP decrease to 20–40% of control levels as a result of a 30-min receptor stimulation period. These observations indicate that first messengers can activate, via receptor stimulation, a proteolytic APP processing pathway that cleaves preexisting APP holoprotein, resulting in the secretion of APP^s into the extracellular medium.

Decrease of A β secretion by activation of cell surface receptors

Recent evidence from experiments in cell lines overexpressing both human APP and human mAChR indicates that activation of these receptors significantly decreases the release of soluble A β by more than 50% as compared with the unstimulated control condition [63]. Concomitantly, the secretion of p3, a 3 kDa fragment of A β lacking its N-terminus (see Fig. 1), was increased along with the increase

in APP^s secretion, suggesting that the cleavage mechanisms generating p3 and APP^s are stoichiometrically coupled.

Taken together, these data indicate that mAChR affect APP processing in a complex way by enhancing the secretion of both APP^s and p3, and by simultaneously blocking A β secretion. Based upon the assumption that APP^s and p3 are derived from proteolytic pathways involving α -secretase cleavage and that A β is a product of β -secretase cleavage [36], we propose that receptor activation enhances α -secretase cleavage while decreasing β -secretase processing (Fig. 3). As a consequence, amyloidogenic APP processing may be decreased by receptor activation, while non-amyloidogenic processing may be enhanced.

Previous findings suggest that the double mutation in the APP gene associated with the Swedish FAD kindred [54] causes a 5- to 6-fold increase in A β secretion when overexpressed in cell culture [55, 56]. To determine the effect of cell surface receptors on this pathologically high A β production, we coexpressed both APP with the Swedish double mutation and m1 AChR in the same cell line and found that increased A β secretion was blocked by m1 AChR activation with carbachol [63]. These data suggest that not only normal A β secretion but also pathologically high A β secretion caused by an APP mutation can be diminished by cell surface receptor activity. This conclusion provides a novel theoretical strategy for the pharmacological modification of A β secretion, even in inherited genetic conditions associated with abnormally high rates of A β formation.

Receptor subtype specifically

The increase in APP^s release mediated by mAChR is specific to the m1 and m3 receptor subtypes as activation of the m2 and m4 subtypes does not change APP^s release [61]. Because activation of bradykinin [64,*] and IL-1 [62] receptors causes a similar stimulation of the secretory APP processing pathway, it is likely that the second messenger systems coupled to the receptors account for the specificity of the response. Bradykinin, m1 and m3 mAChR, and IL-1 receptors are all coupled to diacylglycerol (DAG) formation via phospholipase activation [65], whereas m2 and m4 receptors are primarily coupled to the cAMP signal transduction pathway. These findings led to the hypothesis that such cell surface receptor types that generate DAG as part of their signal transduction may stimulate APP^s secretion and inhibit A β formation.

SIGNAL TRANSDUCTION PATHWAYS IN THE REGULATION OF APP PROCESSING

Mediation of receptor-coupled APP^s secretion by protein phosphorylation

DAG is a central molecule for the regulation of cellular events controlled by protein kinase C (PKC), as DAG is the physiological activator of PKC. DAG is formed by phospholipid hydrolysis as a result of first messenger-induced stimulation of cell surface

* Nitsch *et al.*, unpublished observations.

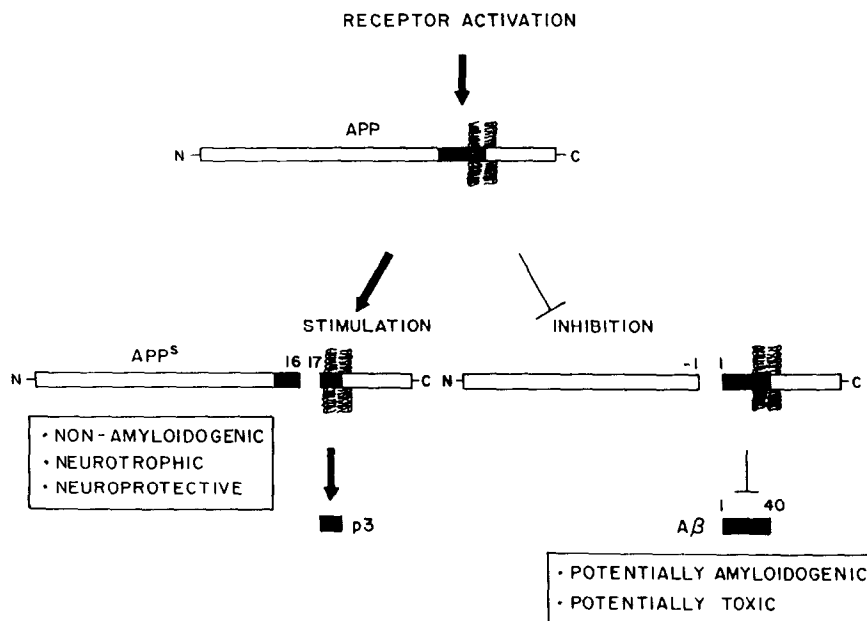


Fig. 3. Regulation of AAP processing by cell surface receptors. Receptor activation increases APP processing into non-amyloidogenic derivatives and prevents processing into amyloidogenic derivatives. Activation of muscarinic m1 and m3 receptors increases secretion of both APP^s and p3, and concomitantly depresses Aβ secretion. Thus, activation of cell surface receptors may promote the formation of neurotrophic and neuroprotective APP derivatives and slow the formation of potentially toxic products.

receptors that are coupled, via G protein, to phospholipase C activation (see Ref. 66 for review). In our experiments, receptor-activated APP^s secretion was blocked by many protein kinase inhibitors including calphostin C, chelerythrine chloride, and staurosporine, indicating that a protein kinase is involved in the signal transduction cascade that links receptor activation to APP processing. Experiments with fibroblasts transfected with the cDNA encoding for the PKCα isoenzyme clearly indicate that this PKC subtype can stimulate APP^s secretion [67]. PKC activation with phorbol esters also increases the secretion of APP^s from cells in culture [67, 68], and raises cellular levels of remaining C-terminal APP cleavage products [69]. Activation of PKC with phorbol esters also decreases the amount of secreted Aβ, thus mimicking the effect of receptor stimulation (see above, [63]). Together, these findings imply a central role for PKC in the signal transduction cascade coupling cell surface receptor activation to both increased APP^s secretion and decreased Aβ formation.

The downstream phosphorylation target of PKC activity with respect to the mechanism of APP^s secretion is yet unclear. The possibility that receptor-activated phosphorylation of the APP molecule itself [70, 71] is necessary for increased secretion is unlikely because mutants lacking the phosphorylation sites are still cleaved and secreted in response to PKC activation [72]. However, it is possible that substrates other than APP, e.g. proteases involved in APP cleavage, are phosphorylated in response to receptor activation.

Possible role of DAG, phospholipases and Ca²⁺

Activation of PKC in response to stimulation of cell surface receptors can be achieved by at least three independent pathways via receptor-coupled activation of the phospholipases C, D, and A₂, as well as by a combination of any of these. All three enzymes are activated via GTP-binding (G) protein in response to agonist-induced stimulation of the receptor molecules. The large class of receptors coupled to phospholipase activation include the mAChR subtypes m1 and m3, metabotropic glutamate receptor subtypes, serotonin receptors, and neuropeptide receptors [66, 73–76]. Phospholipase C subtypes hydrolyze inositol phospholipids as well as choline phospholipids to yield DAG and inositol triphosphate (IP₃). Membrane-associated (lipophilic) DAG activates PKC by translocating the cytosolic forms to the plasma membrane. Phospholipase D, activated by both m1 and m3 receptor stimulation [75], yields phosphatidic acid which is readily dephosphorylated to form DAG, resulting in PKC activation, as described above. Receptor-mediated activation of phospholipase A₂ yields free fatty acids, in particular arachidonic acid, which can activate PKC directly. The corresponding lysophospholipid, in particular lysophosphatidylcholine, potentiates many effects of DAG, and thus contributes to sustained PKC activation (for a detailed review, see (Ref. 66)). In addition to lipase activation, stimulation of m1 and m3 AChR transiently increases levels of intracellular free Ca²⁺ derived from two independent sources.

IP₃, generated by phosphatidylinositol-specific phospholipase C, binds to IP₃ receptors at the endoplasmic reticulum (ER), thereby opening Ca²⁺ channels that release Ca²⁺ from the ER into the cytoplasm. Additionally, m1 and m3 AChR also open receptor-operated calcium channels at the plasma membrane, resulting in influx of extracellular free Ca²⁺ [77]. Receptor stimulation in the absence of extracellular free Ca²⁺, produced a smaller APP^s secretory response than stimulation in the presence of Ca²⁺. This observation suggests that the signal transduction cascade that links receptor activation to APP^s secretion is co-activated by DAG and elevation of free intracellular Ca²⁺. This concept is compatible with the finding that some PKC subtypes are co-activated by DAG and Ca²⁺ [66]. Taken together, these findings suggest that protein kinase isoforms, activated by DAG and Ca²⁺, are central enzymes in the signal transduction cascade that couples receptor activation to APP^s secretion. Evaluation of the effects on APP processing of the more than ten identified individual PKC isoforms will be necessary to determine potential differences among various isoforms expressed by individual cell types.

REGULATION OF APP PROCESSING BY NEURONAL ACTIVITY

The regulation of biochemical pathways in the intact brain is, in many ways, much more complex than that in cell culture model systems. For example, biochemical reactions in brain cells *in situ* can be affected simultaneously by many neurotransmitters and neuromodulators. This situation is very different from the cell culture condition in which one first messenger is tested at a time. Experiments designed to determine the significance of receptor activation for APP processing in the intact brain are just beginning, and only some initial data are available to date. Our first approach to investigating APP processing in mammalian brain tissue was to develop a hippocampal slice superfusion system for the measurement of APP^s release in response to neuronal depolarization. Electrical stimulation of brain tissue slices in this system depolarizes excitable cells in the preparation and the resultant action potentials trigger influx of sodium and calcium ions into the synaptic terminals, resulting in exocytosis of neurotransmitter-containing vesicles. We found that electrical depolarization of superfused hippocampal slices increased the release of endogenous neurotransmitters including acetylcholine and glutamate 3- to 5-fold. Concomitantly, electrical depolarization enhances APP^s release from the slices 2-fold within 50 min of stimulation [38]. Increased APP^s release correlated with increasing stimulation frequencies in the range of 8 to 18 Hz, which matches the physiological firing frequency of hippocampal pyramidal cells. These data suggest that APP^s release from hippocampal slices *in vitro* may be a function of neuronal activation. Pharmacological blockade of action potential formation with tetrodotoxin (a sodium channel blocker) inhibits depolarization-induced APP^s release. These findings demonstrate that action potentials can regulate APP processing in brain tissue. It is now important to determine the

specific neurotransmitter systems involved in APP processing in brain tissue, to determine the cellular signalling mechanisms, and to investigate whether APP processing is modified by neurotransmission in the intact human brain.

POSSIBLE RELEVANCE FOR AD

Are neurotransmission deficits related to amyloid formation in AD?

Synapse loss, along with dysfunction and death of neurons [78, 79], are the elemental lesions in AD that account for dementia. As a result of neuronal damage, levels of many neurotransmitters, including acetylcholine, serotonin, glutamate, somatostatin and norepinephrine, are decreased [80–83]. Furthermore, signal transduction pathways may be impaired as protein kinase alterations occur at an early stage of AD [84, 85]. These observations raise an important question: Does dysfunctional neurotransmission lead to changes in APP metabolism that comprise the normal biological function of APP and promote amyloid formation? Attempts to answer this question must take the following points into account. First, neurotransmission is impaired in many brain diseases including Parkinson's disease, Huntington's disease and the system atrophies (e.g. olivopontocerebellar atrophy), yet these diseases are not associated with accelerated amyloid deposition in the brain. Second, in AD, amyloid is deposited throughout the neuropil including brain areas that otherwise are relatively spared from neuronal damage and that presumably have preserved neurotransmission. Third, amyloid formation probably occurs independently from neurotransmitter deficits in specific subgroups of AD patients, e.g. Down syndrome which is associated with an increased APP gene dosage (triplicate chromosomes 21), or the Swedish FAD family with a double mutation in the APP gene that may cause altered APP processing. These points argue that abnormalities in neurotransmission may not be the primary cause of amyloid deposition in all AD cases. However, these arguments do not exclude the possibility that APP mismetabolism as a result of impaired neurotransmission may secondarily contribute to amyloidogenesis.

APP in the pathogenesis of AD

An additional central question regarding the molecular pathology of AD is yet unanswered: What is the etiologic significance of APP in AD? Specifically, do APP and its derivatives cause AD-type dementia because they are neurotoxic and initiate a series of events leading to neuronal death and synaptic failure? Or does amyloid deposition result from the response of the brain to an unknown primary damage causing synapse loss and dysfunctional neurotransmission, and therefore represents a misguided attempt at healing? The latter idea stresses the possibly important biological functions of APP rather than the potential toxicity ascribed to some of its derivatives. These two views both have merits and weaknesses. The strongest evidence for APP having a direct role in causing AD comes from the handful of FAD cases linked to APP

gene mutations [54, 86–89]. Although these mutations are rare and do not account for the vast majority of cases [90, 91], they provide an important lead into the cause of some FAD pedigrees. Second, amyloid deposition in the brain of Down syndrome subjects carrying an extra copy of the APP gene begins early in life, and all become demented by the 4th or 5th decade of life with AD-type histopathology [92]. The third point stems from the observation that A β can be neurotoxic in some experimental systems [93, 94]. However, attempts to replicate the initial reports on the toxicity of amyloid revealed the narrow confines in which they were reproducible, and detracted from the neurotoxic hypothesis in causing AD [95]. The fourth argument that initially supported a direct relation of APP expression and AD histopathology came from transgenic mouse experiments which showed that animals carrying the transgene for human APP express increased amounts of human APP, but those papers that reported resultant increased amyloid deposits in brain have been retracted.

In opposition to these arguments, two major observations are poised against a primary role of amyloid in AD etiology: amyloid plaques are found in brains of neurologically normal individuals and, in AD, amyloid plaques do not correlate with clinical estimates of dementia severity, number of neurofibrillary tangles, or with duration of illness [96]. These reservations, however, do not exclude the possibility that amyloid is involved in an early stage of neuronal degeneration that is remote from the final clinical and neuropathologic hallmarks of AD.

An alternative view of the role of amyloid in AD was presented in the section on the biological functions of APP. This line of reasoning is based upon observations that APP derivatives such as APP^s and even A β fragments have protective and trophic biological functions [31–33], which may be disrupted by APP mist metabolism, regardless of the additional formation of amyloid.

The concept that neurotransmitters can regulate APP processing pathways does not attempt to discriminate between the neurotrophic and the neurotoxic hypotheses and is relevant to AD regardless of which view will prevail. If A β accumulation is toxic and leads to neuronal degeneration, pharmacological activation of neurotransmitter receptors that inhibit A β formation may reduce the rate of amyloid deposition, and possibly slow the progression of AD. Alternatively, if APP or some of its non-amyloidogenic fragments are neurotrophic or neuroprotective, stimulation of specific cell surface receptors to increase secretion of such APP derivatives may promote the biological function of APP and thus help restore neuronal function.

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