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## Cathepsin D: A Candidate Link between Amyloid $\beta$ -protein and Tauopathy in Alzheimer Disease

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### Abstract

Alzheimer disease (AD) is a debilitating neurodegenerative disorder characterized by extracellular deposition of the amyloid  $\beta$ -protein (A $\beta$ ) and intraneuronal accumulation of the microtubule-associated protein, tau. Despite a wealth of experimental and genetic evidence implicating both A $\beta$  and tau in the pathogenesis of AD, the precise molecular links between these two pathological hallmarks have remained surprisingly elusive. Here, we review emerging evidence for a critical nexus among A $\beta$ , tau, and the lysosomal protease cathepsin D (CatD) that we hypothesize may play a pivotal role in the etiology of AD. CatD degrades both A $\beta$  and tau *in vitro*, but the *in vivo* relevance of this lysosomal protease to these principally extracellular and cytosolic proteins, respectively, had remained undefined for many decades. Recently, however, our group found that genetic deletion of CatD in mice results in dramatic accumulation of A $\beta$  in lysosomes, revealing that A $\beta$  is normally trafficked to lysosomes in substantial quantities. Moreover, emerging evidence suggests that tau is also trafficked to the lysosome via chaperone-mediated autophagy and other trafficking pathways. Thus, A $\beta$ , tau and CatD are colocalized in the lysosome, an organelle that shows dysfunction early in AD pathogenesis, where they can potentially interact. Notably, we discovered that A $\beta$ 42—the A $\beta$  species most strongly linked to AD pathogenesis—is a highly potent, low-nanomolar, competitive inhibitor of CatD. Taking these observations together, we hypothesize that A $\beta$ 42 may trigger tauopathy by competitive inhibition of CatD-mediated degradation of tau—pathogenic forms of tau, in particular. Herein, we review the evidence supporting this hypothesis and explore the implications for the molecular pathogenesis of AD. Future research into these novel mechanistic links among A $\beta$ , tau and CatD promises to expand our understanding of the etiology of AD and could potentially lead to novel therapeutic approaches for combatting this devastating disease of brain and mind.

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Conflict of Interest Statement

The authors declare no conflict of interest.

## Keywords

Alzheimer disease; Amyloid  $\beta$ -protein; Cathepsin D; Lysosome; Tau

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## A $\beta$ and Tau in Alzheimer Disease

Alzheimer disease (AD) is an increasingly common age-related neurodegenerative disorder, currently affecting ~44 million people worldwide [1]. Histopathologically, the disease is characterized by progressive accumulation of extracellular deposits of the amyloid  $\beta$ -protein (A $\beta$ ), known as plaques, together with intraneuronal aggregates of hyperphosphorylated forms of the microtubule-associated protein, tau, known as neurofibrillary tangles (NFTs) [2]. Despite decades of intensive research within academia and private industry, disease-modifying treatments have not yet emerged. Indeed, several fundamental questions about the molecular pathogenesis of AD remain unresolved.

Among the most fundamental of all unresolved questions within the AD field is precisely how A $\beta$  accumulation triggers NFT formation [3]. A wealth of experimental evidence strongly implicates A $\beta$  mismetabolism in the pathogenesis of AD [4]. For instance, human molecular genetic research has identified hundreds of mutations in 3 separate genes—*amyloid precursor protein (App)* and *presenilin-1* and *-2 (Psen1* and *Psen2)*—that cause familial forms of AD with 100% penetrance [5]. Significantly, all of these mutations affect the production of A $\beta$  in one way or another. *App* mutations, on the one hand, increase the production of all forms of A $\beta$ . *Presenilin* mutations, on the other hand, specifically increase the A $\beta$ 42/40 ratio—i.e., the ratio of longer, more aggregation-prone A $\beta$  species, such as A $\beta$ 42, and shorter, less amyloidogenic species, such as A $\beta$ 40 [5,6]. The presenilins proteins make up the active site of  $\gamma$ -secretase, a proteolytic complex responsible for defining the C-terminus of A $\beta$  during its cleavage from the amyloid precursor protein (APP) [7–9]. The presenilin/ $\gamma$ -secretase complex can cleave APP at any of several sites, resulting in A $\beta$  peptides ranging in length from 37 to 43 amino acids [10]. AD-linked *presenilin* mutations specifically increase the A $\beta$ 42/40 ratio by perturbing the function of  $\gamma$ -secretase and, therefore, are believed to be the sole determinant of this critical parameter [11].

NFTs are another invariant feature of AD, emerging somewhat later than A $\beta$  deposits [3]. NFTs are comprised of aggregates of hyperphosphorylated tau that form within the cytosol of neurons [12]. Of note, NFTs are present in several other neurodegenerative diseases [13], in some cases due to genetic mutations in the gene for tau, *Mapt* [14]. These observations suggest that NFT formation is the necessary and most proximal cause of the neuronal cell death common to all these neurodegenerative diseases [13].

The question of how A $\beta$  accumulation leads to NFT formation has constituted an enduring enigma within the AD field. On the one hand, plaques are extracellular, so A $\beta$  has been widely regarded as a secreted protein [15]; indeed, the proteases responsible for the production of A $\beta$  from APP are referred to as “secretases” to reflect this understanding [16]. On the other hand, tau has been regarded as primarily a cytosolic protein [12]. How—and where—then, can extracellular A $\beta$  and intracellular tau interact?

## Lysosomal A $\beta$ and Tau—A Paradigm Shift

In the light of emerging evidence, the long-standing view of A $\beta$  as an exclusively secreted protein, and of tau as an exclusively cytosolic one, has proved to be incorrect. Instead, it has become clear that at least a subset of both proteins co-exist within the lysosome. With respect to A $\beta$ , several observations are relevant. First, within neurons, extracellular A $\beta$  is trafficked via the endolysosomal pathway to lysosomes, where it is degraded by lysosomal proteases [17,18]. Of note, this trafficking is mediated by apolipoprotein E (ApoE), the strongest genetic risk factor for late-onset AD [18,19]. Second, recent findings by our group have demonstrated that a significant portion of newly synthesized A $\beta$  is normally trafficked to the lysosome [20]. Specifically, we found that genetic deletion of cathepsin D (CatD), a lysosomal aspartyl protease discovered more than 40 years ago [21], results in dramatic, ~3 to ~4-fold increases in cerebral A $\beta$  by just 3 weeks of age [20]. Notably, the magnitude of these increases exceeds those obtained following genetic deletion of all previously described A $\beta$ -degrading proteases (A $\beta$ DPs), including the “major” A $\beta$ DPs neprilysin or insulin-degrading enzyme — or even both simultaneously [20]. Given that CatD is an aspartyl protease, and thus operative only at an acidic pH, it would be predicted that the increases in cerebral A $\beta$  are occurring exclusively within the acidic environment of the lysosome [22]. Confirming this, CatD-null mice exhibit robust deposition of intralysosomal A $\beta$ —endogenous murine A $\beta$ —by just ~26 days of age [20], something not seen in any other A $\beta$ DP-null animal [23]. Taken together, these findings strongly imply that a substantial fraction of A $\beta$  is trafficked to lysosomes, where it is normally degraded by CatD and other lysosomal A $\beta$ DPs such as cathepsin B [24]. Given that the  $\beta$ - and  $\gamma$ -secretases responsible for A $\beta$  production are both aspartyl proteases, too [16], this conclusion is perhaps not too surprising, but there had been little direct evidence prior to the analysis of CatD-null mice.

With respect to tau, emerging evidence has also challenged the idea that it is an exclusively cytosolic protein. Tau has long been known to be present in cerebrospinal fluid, and its levels correlate with AD severity, but mechanistically this was initially attributed to non-specific release from dying neurons [25]. Over the past decade, however, a substantial body of research has shown that tau is secreted via multiple vesicular and non-vesicular pathways, not all associated with disease [26] (Figure 1). Because the extracellular space is topologically contiguous with the lumen of the lysosome, these secretion mechanisms render tau capable of eventual interaction with A $\beta$  and CatD. Among several identified trafficking mechanisms, endogenous tau has been shown to be secreted via unconventional protein secretion pathways from primary neurons [26–31]. Once secreted, extracellular tau can enter neurons and other cell types via fluid-phase endocytosis and micropinocytosis [29], whereupon it can be trafficked to the lysosome via conventional mechanisms. Tau can also enter the lysosome directly from the cytosol via both nonselective and selective mechanisms (Figure 1). In the nonselective pathway, lysosomes degrade cytosolic contents in bulk via macroautophagy, wherein cytosolic contents are first enveloped in a membrane that subsequently fuses with the lysosomal membrane to release its contents [32]. The selective pathway, on the other hand, is known as chaperone-mediated autophagy (CMA), wherein substrate proteins directly cross from the cytosol into the lysosome, one at a time [33]. CMA is mediated by a specific targeting motif (KFERQ-like), present within tau, that

binds to the cytosolic chaperone, HSC70, which then brings the substrate to the lysosomal surface for internalization [34].

Collectively, these observations overturn conventional thinking about the subcellular localization of A $\beta$  and tau, showing that a significant fraction of both proteins is trafficked to the lysosome.

## A $\beta$ 42 Potently Inhibits CatD

Knowing that A $\beta$  and tau can be colocalized in the lysosome, how might they interact? One intriguing possibility is via competition for degradation by CatD. While characterizing A $\beta$  degradation by CatD, our group made the surprising discovery that CatD degrades A $\beta$ 42 and A $\beta$ 40 with remarkably different kinetics [20]. Most A $\beta$ DPs hydrolyze A $\beta$ 40 and A $\beta$ 42 similarly, with Michaelis-Menten constant ( $K_M$ ) values in the low- to mid-micromolar range. CatD hydrolyzes A $\beta$ 40 with a low-micromolar  $K_M$ , but—in marked contrast—it degrades A $\beta$ 42 with a  $K_M$  value more than two orders of magnitude lower, in the low-nanomolar range, corresponding to a significantly stronger affinity of A $\beta$ 42 for CatD [20]. In terms of the turnover number,  $k_{cat}$ , which corresponds to the number of substrate molecules hydrolyzed per unit time by each protease molecule, the difference between A $\beta$ 42 and A $\beta$ 40 is similarly striking: the  $k_{cat}$  of A $\beta$ 42 degradation by CatD is ~200-fold slower than that for A $\beta$ 40 [20]. In absolute terms, the  $k_{cat}$  of A $\beta$ 42 degradation determined by multiple independent assays was approximately  $0.23 \text{ min}^{-1}$ , *meaning that it takes >4 minutes for each molecule of A $\beta$ 42 to be processed by each molecule of CatD* [20].

Taken together, the low  $K_M$  and  $k_{cat}$  values of A $\beta$ 42 degradation by CatD render A $\beta$ 42 a highly potent competitive inhibitor. For example, in competition experiments using a fluorogenic peptide substrate to monitor CatD activity, the  $IC_{50}$  of A $\beta$ 40 was ~3  $\mu\text{M}$ , whereas that for A $\beta$ 42 was a phenomenally low 0.00097  $\mu\text{M}$ , *meaning that A $\beta$ 42 competitively inhibits CatD with subnanomolar potency* [20]. Perhaps more intriguingly, we discovered that the marked differences between A $\beta$ 40 and A $\beta$ 42 extend to the corresponding  $\alpha$ -secretase-derived P3 fragments ending at positions 40 and 42 (e.g., A $\beta_{17-40}$  and A $\beta_{17-42}$  or P3<sub>40</sub> and P3<sub>42</sub>) [20]. This finding highlights the fact that these differential kinetics occur independently of A $\beta$  aggregation. Moreover, it is notable that P3 fragments are produced in ~10-fold higher quantities than A $\beta$  [35], substantially increasing the likelihood that these fragments could inhibit CatD at near-physiological levels.

## A New Take on the A $\beta$ 42/40 Ratio

As mentioned above, it had long been implicitly assumed that the A $\beta$ 42/40 ratio is determined exclusively by the action of the presenilin/ $\gamma$ -secretase complex during the production of A $\beta$  from APP. In CatD-null mice, however, cerebral A $\beta$ 42/40 ratios were found to be consistently increased, independent of any effect on APP processing [20]. Our finding that A $\beta$ 42 and A $\beta$ 40 are processed so differently suggests that, at least in the case of CatD, A42/40 ratios can also be regulated after A $\beta$  production, via differential degradation. Whereas elevated A $\beta$ 42/40 ratios are known to be the root cause of familial forms of AD due to *presenilin* mutations [11], this finding suggests that perturbed A $\beta$  catabolism might

also affect this key parameter, possibly playing a role in the etiology of late-onset forms of AD.

In terms of the molecular pathogenesis of AD, the ability of A $\beta$ <sub>42</sub> and P3<sub>42</sub> to so potently inhibit CatD suggests another tantalizing, albeit speculative, possibility. Specifically, we hypothesize that the mechanism by which elevated A $\beta$ <sub>42/40</sub> (and P3<sub>42/40</sub>) ratios trigger downstream pathological sequelae may, in part, involve competitive inhibition of CatD [20]. In humans and other animals, loss-of-function mutations in CatD lead to multiple forms of neurodegenerative disease [36–38]. Genetic variations in CatD, moreover, have been linked to late-onset AD specifically [39]. In the light of these observations, it seems plausible that dysregulation of CatD by A $\beta$ <sub>42</sub> could represent one mechanism linking A $\beta$  accumulation to downstream pathological sequelae.

### Inhibition of Tau Processing by A $\beta$ <sub>42</sub>

As one of the principal lysosomal proteases, it is no surprise that CatD can degrade tau once it reaches the lysosome [40]. It follows that the accumulation of A42 and P3<sub>42</sub> could potentially lead to increases in total levels of tau via competitive inhibition of CatD [20]. The situation is actually more complex, however, since CatD can also process tau proteolytically in several pathologically relevant ways, in some cases producing tau species that are more aggregation-prone and/or directly toxic and in other cases clearing the pathogenic tau species [41–43]. One finding is clear, however: inhibition of CatD and/or dysregulation of lysosomal function increases the levels of multiple neurotoxic tau fragments. In a *drosophila* model expressing human tau, for example, genetic deletion of CatD significantly exacerbated tauopathy [44]. This effect was mediated not by an increase in overall tau levels, but instead by a selective increase in a neurotoxic, caspase-cleaved form of tau [44]. Given that most tau remains cytosolic, the lack of effect on total tau is unsurprising. Nevertheless, this study supports the idea that CatD is involved in the regulation of pathological forms of tau. Regardless of the underlying complexity, the hypothesis that A $\beta$ <sub>42</sub> might trigger tauopathy via its ability to potently inhibit CatD seems well substantiated by the existing literature and worthy of further research.

### Conclusion

In conclusion, we hypothesize that A $\beta$ <sub>42</sub>—the A $\beta$  species most strongly linked to AD pathogenesis—can trigger tauopathy by competitively inhibiting the clearance of neurotoxic tau species by CatD within the lysosome. As reviewed above, accruing evidence supports the idea that significant quantities of both tau and A $\beta$  are normally trafficked to the lysosome and degraded by CatD. The recent finding that A $\beta$ <sub>42</sub> and P3<sub>42</sub> potently inhibit CatD [20] suggests a discrete molecular mechanism linking A $\beta$ <sub>42</sub> accumulation to the accumulation of neurotoxic tau species. Since lysosomes become dysfunctional and leaky in aging generally [45], and in response to A $\beta$ <sub>42</sub> specifically [46], accumulated neurotoxic tau fragments could reach the cytosol, where they might seed the formation of NFTs and, via this mechanism and others, contribute to cell death (Figure 1). In addition to being well supported by a range of evidence, reviewed herein, this hypothesis has the advantage of being specific and readily

testable. Given the enormous economic and societal burden exacted by AD, future research into this hypothetical pathogenic mechanism seems highly warranted.

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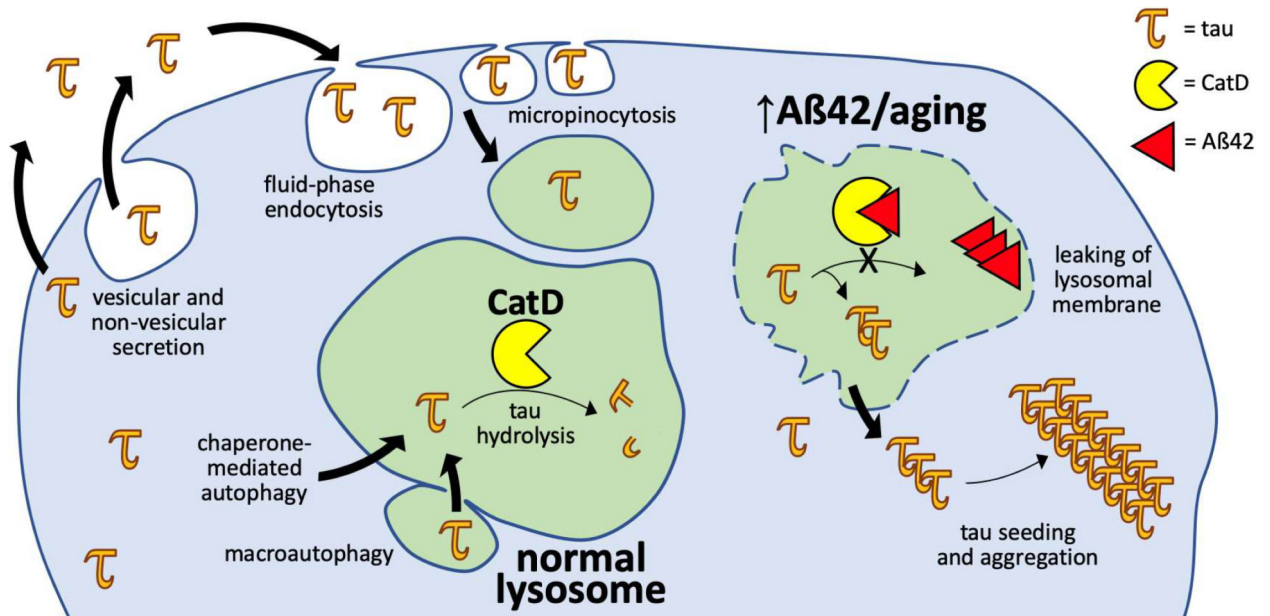
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**Figure 1: Cellular trafficking pathways linking tau, Aβ42 and CatD.**

Cartoon illustrating the several pathways by which tau can be trafficked to lysosomes. Within normal lysosomes (*left*) tau is hydrolyzed efficiently by CatD, but in the presence of elevated Aβ42 levels (*right*) CatD is inhibited, preventing tau hydrolysis, and thereby promoting accumulation of tau species. During aging and in AD, the lysosomal membranes become leaky, permitting the efflux of aggregated tau into the cytosol, which can seed the formation of NFTs.