

Review

Is Alzheimer's Disease a Disorder of Mitochondria-Associated Membranes?

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Abstract. The subcellular localization of presenilin-1 (PS1) and presenilin-2 (PS2), two proteins that, when mutated, cause familial Alzheimer's disease (AD), is controversial. We have discovered that mitochondria-associated membranes (MAM) – a specialized subcompartment of the endoplasmic reticulum (ER) involved in lipid metabolism and calcium homeostasis that physically connects ER to mitochondria – is the predominant subcellular location for PS1 and PS2, and for γ -secretase activity. We hypothesize that presenilins play a role in maintaining MAM function, and that not only altered amyloid- β levels and hyperphosphorylated tau, but also many other features of AD (e.g., altered phospholipid and cholesterol metabolism, aberrant calcium homeostasis, and abnormal mitochondrial dynamics) result from compromised MAM function. The localization of presenilins and γ -secretase in MAM may help reconcile disparate ideas regarding the pathogenesis of AD, under a unifying hypothesis that could explain many features of both sporadic and familial AD, thereby taking AD research in a new and fruitful direction.

Keywords: Alzheimer's disease, calcium, cholesterol, endoplasmic reticulum (ER), mitochondria, mitochondria-associated membranes (MAM), phospholipids

ALZHEIMER'S DISEASE

Alzheimer's disease (AD), the most common late onset neurodegenerative dementing disorder, is characterized by progressive neuronal loss, especially in the hippocampus and cortex [1]. The two main histopathological hallmarks of AD are the accumulation of extracellular neuritic plaques, containing amyloid- β ($A\beta$), and of neurofibrillary tangles, consisting mainly of hyperphosphorylated forms of the microtubule-associated protein tau [1]. Most AD patients are sporadic (SAD), but three genes have been associated with the familial form (FAD): amyloid- β protein precursor ($A\beta$ PP), presenilin-1 (PS1), and presenilin-2 (PS2). Clinically, FAD is similar to SAD but has earlier onset.

Presenilins are components of the γ -secretase complex (also containing APH1, nicastrin, and PEN2) that, together with β -secretase, processes $A\beta$ PP to produce $A\beta$ [1]. In the mainstream view, both SAD and FAD arise when $A\beta$ PP is processed to $A\beta$, which accumulates in extracellular plaques. $A\beta$ is toxic to cells and the resulting stress promotes tau hyperphosphorylation, leading to the tangles. The overall process has been called the "amyloid cascade" hypothesis [2,3]. This hypothesis reconciles findings from different approaches to the disease and has served as the basis for many key experiments *in vivo* and *in vitro*. However, certain questions that are central to understanding the pathogenesis of AD and the processing of $A\beta$ remain unsolved.

The first question concerns features of AD that are not obviously linked to plaque or tangle formation. While plaques and tangles are hallmarks of the disease, other apparently unrelated laboratory abnormali-

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ties are routinely detected in patients, including elevated cholesterol [4], altered fatty acid [5,6], glucose [7, 8], and phospholipid [9] metabolism, aberrant calcium homeostasis [10], and mitochondrial dysfunction [11]. These features of AD have received far less attention because of the lack of direct links to the amyloid cascade, and have engendered numerous competing hypotheses to explain the pathogenesis of AD. These include tau hyperphosphorylation [12], altered lipid [13], cholesterol [14], and glucose metabolism [15,16], aberrant calcium homeostasis [17], glutamate excitotoxicity [18], inflammation [18,19], ER stress and the unfolded protein response (UPR) [20–23], and mitochondrial dysfunction and oxidative stress [24]. It remains to be determined to what degree these phenomena are causally interlinked, and whether they may be direct outcomes of defects in A β PP processing.

The second issue is commonly referred to as the “spatial paradox” [25]: whereas PS1 is believed to be located mainly in the ER [26] and Golgi [26,27] as a component of an intracellular γ -secretase [28], processing of A β PP to release extracellular A β is believed to occur at or near the plasma membrane (PM) [29]. Thus, there is an apparent physical disconnect between the intracellular location of presenilins and γ -secretase activity on the one hand and the presumed site of A β synthesis on the other.

One potential solution to the spatial paradox would be to revise our current opinion on the subcellular distributions of presenilins. Indeed, although many believe that presenilins are located in the ER and/or Golgi, in truth, the subcellular localization of PS1 and PS2 has been the subject of controversy, with localizations reported in other compartments, including the nuclear envelope [30], endosomes [31], lysosomes [32], mitochondria [33], and the plasma membrane [28], where it is especially enriched at intercellular contacts known as adherens junctions [34].

Our understanding of the pathogenesis of AD, and by extension, our efforts to develop therapies for this devastating disorder, is highly dependent on a precise localization of this key proteolytic event and potential therapeutic target.

MITOCHONDRIA-ASSOCIATED MEMBRANES

Mitochondria-associated ER membranes (MAM) is a specialized subcompartment of the ER that connects this organelle to mitochondria, both biochemically and

physically [35–38]. It plays a critical role in calcium homeostasis, as well as in various housekeeping functions, such as phospholipid, glucose, sphingolipid, ganglioside, cholesterol, and fatty acid metabolism [38], as well as in calcium homeostasis and signaling [38] and in apoptosis [39]. This physical connection has been proposed to be mediated by phosphofurin acidic cluster sorting protein 2 (PACS2) [39] and mitofusin 2 (MFN2) [40].

MAM is distinct from “bulk” ER in its composition and behavior. For example, MAM is enriched in neutral lipids and cholesterol [41,42], which, upon subcellular fractionation, allows it to be separated from bulk ER as a low-density fraction [43]. In fact, MAM has been described as a detergent-resistant microdomain of the ER having the properties of intracellular lipid rafts [42, 44].

A POTENTIAL ROLE FOR MAM IN THE PATHOGENESIS OF AD

We recently reported a novel subcellular localization for presenilins in MAM [45], and discuss here a mechanism that could link this localization to the known metabolic changes in AD. Furthermore, based on several lines of evidence, we propose that defects in MAM function play a key role in the pathogenesis of both the sporadic and familial forms of AD.

PS1 and PS2 are enriched in the MAM

As alluded to above, PS1 has been localized to almost every membranous compartment of the cell, including ER [26,30,46–48], the Golgi apparatus [26,27,46,49], endosomes [31,50], lysosomes [32], the nuclear envelope [30], mitochondria [33,51], and the plasma membrane [28,52–55], including adherens junctions [34, 56].

Using a combination of biochemical, immunocytochemical, and functional assays, we have shown that, apart from its presence in the plasma membrane, PS1 and PS2 are actually highly enriched in only one other compartment of the cell, namely MAM [45]. Moreover, besides identifying MAM as the main subcellular compartment for the presenilins, we also found that γ -secretase activity associated with A β PP processing is essentially confined to the MAM [45]. Thus, our identification of A β PP together with high levels of both presenilins and γ -secretase activity in the same subcel-

lular compartment (i.e., MAM) could help resolve the spatial paradox.

Our results were somewhat surprising, because in the 15 years since mutations in PS1 [57] and PS2 [58, 59] were identified, many laboratories, using both morphological and biochemical approaches, localized the presenilins to numerous subcellular compartments, but never specifically to MAM.

As we noted in our initial report [45], we believe that the discrepancy between our results and those of others was due mainly to the use of appropriate markers that could identify MAM unambiguously. Furthermore, given the lipid raft-like nature of MAM, it is not surprising that standard techniques used to isolate membranous organelles would unavoidably result in co-purification of MAM along with bulk ER, Golgi, endosomes, and mitochondria [49,60–63]. We also note that both A β PP [64] and A β [65,66] have been detected in mitochondria, but because of the contamination of most mitochondrial preparations with MAM, these polypeptides could also be MAM-associated proteins that were inadvertently assigned to mitochondria [67].

Moreover, the fact that MAM is a detergent-resistant membrane (DRM) microdomain [44] means that immunocytochemical techniques that rely on the use of detergents for permeabilization will only reveal epitopes that are not embedded in DRMs, as exemplified by the difficulty in identifying plasma membrane lipid raft proteins [68,69], where the use of detergents as permeabilization agents is limited [70–73].

In the case of the presenilins, we have found that the use of detergents, such as Triton X-100 (TX100), to permeabilize cells prior to the application of antibodies against PS1 or PS2 yields a dramatically different result as compared to that obtained following the use of organic solvents, such as methanol (MeOH), for cell permeabilization (Fig. 1). If TX100 is used for permeabilization, the anti-PS1 signal is spread diffusely among essentially all membranous compartments of the cell (Fig. 1A). However, when MeOH is used, the signal co-localizes predominantly with the MitoTracker Red signal, especially in the perinuclear region, where most of the ER resides (Fig. 1B). We confirmed these results by performing a triple staining in human fibroblasts permeabilized with MeOH, labeling mitochondria with MitoTracker Red (red) and immunostaining with anti-PS1 (green) and with anti-KDEL (blue) as an ER marker (Fig. 1C).

Our finding that presenilins and γ -secretase activity are enriched in MAM [45] is consistent with reports that PS1 and other γ -secretase components [31,74], as well as γ -secretase activity itself [75–80], are present in DRMs and/or lipid rafts.

Altered MAM function in AD

The presence of presenilins, γ -secretase activity, and A β PP in MAM is consistent with the amyloid cascade hypothesis. Nevertheless, we believe that the accumulation of plaques and tangles in AD, which are clearly detrimental, are merely features of the disease (and probably exacerbate its course and progression), but are not its underlying cause. Rather, we propose that the fundamental pathogenetic cause of AD is the alteration of MAM function, which could explain many of the disparate features of the disease noted above, including, but not limited to, the formation of plaques and tangles. Three aspects of MAM function are particularly noteworthy (Fig. 2A).

The role of MAM in lipid metabolism

More than fifteen proteins involved in fatty acid, phospholipid, glycolipid, and triglyceride metabolism are enriched in the MAM [38,45]. The role of MAM as a compartment connecting ER with mitochondria is illustrated very nicely by a major cellular pathway for the synthesis of phosphatidylethanolamine (PtdEtn). PtdEtn can be synthesized *de novo* in the ER from free ethanolamine via the Kennedy pathway [81], but most PtdEtn is made in a collaborative effort between MAM and mitochondria (see Fig. 2A): phosphatidylserine (PtdSer) is synthesized in the MAM via the serine-exchange enzyme phosphatidylserine synthase 2 (PTDSS2); PtdSer is then translocated to the mitochondria [82], where it is decarboxylated to PtdEtn by phosphatidylserine decarboxylase (PISD); finally PtdEtn is transferred back to the MAM, where it is methylated by phosphatidylethanolamine methyltransferase (PEMT) to generate phosphatidylcholine (PtdCho) [83].

The kinetics of trafficking of PtdSer from MAM to mitochondria is a recognized measure of MAM function [84]. Using such an approach, we recently detected a significant difference in PtdSer and PtdEtn synthesis in PS-mutant versus control cells (data not shown). This result is consistent with the reported aberrations in phospholipid profiles in AD patients [9,85]. Intriguingly, significant changes in PtdEtn and PtdCho levels have also been found in the brains of SAD patients [86], implying that a defect in this known MAM function could play a role not only in the familial, but also in the sporadic, form of the disease.

Remarkably, phospholipids, and especially PtdEtn, play a role in tau phosphorylation [87]. Thus, it is

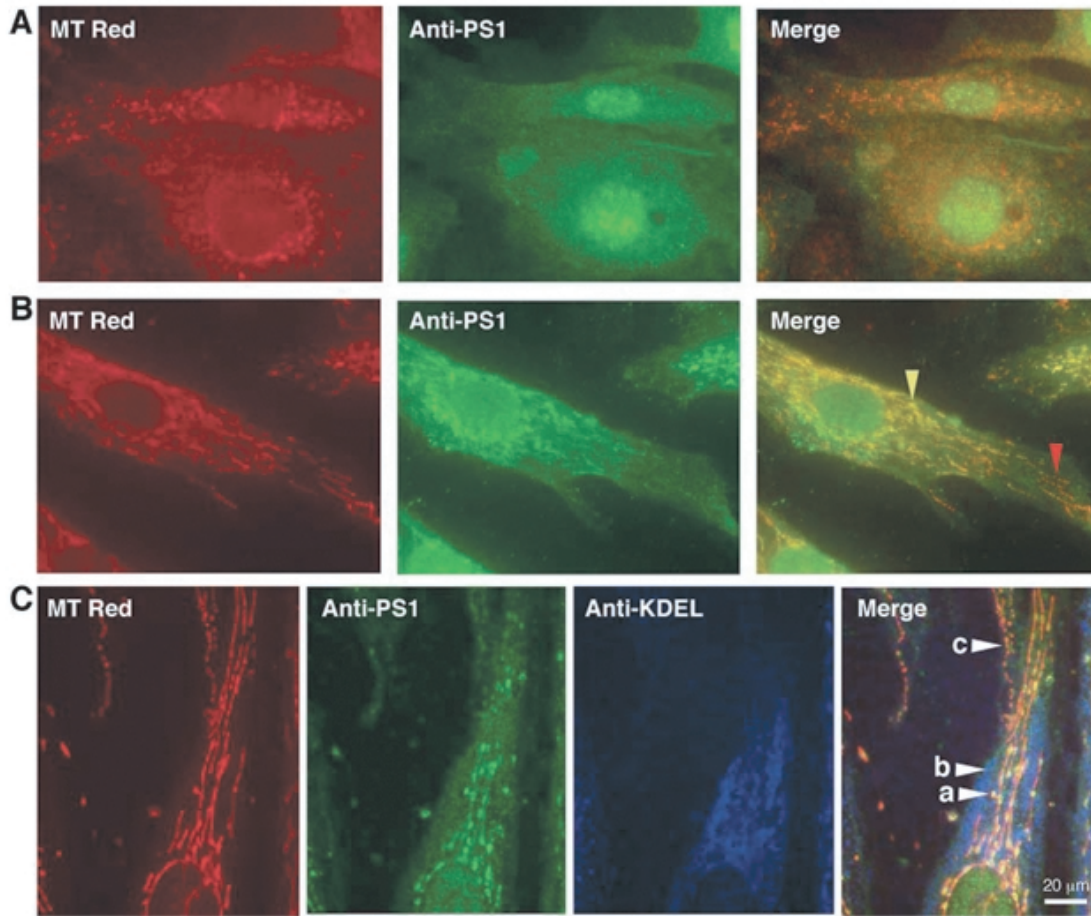


Fig. 1. Immunolocalization of PS1 in human fibroblasts. A) Fixation with paraformaldehyde (PF) and permeabilization with TX100. Note poor co-localization of the two signals (the orange staining in the merge panel is the non-specific overlap of the MitoTracker Red [MT Red] stain with the diffuse anti-PS1 stain). B) Fixation with PF and permeabilization with MeOH. Note the co-localization of PS1 and MT Red in the perinuclear region (yellow arrowhead) but not in more distal regions (red arrowhead). Images captured by confocal microscopy (100x). C) Co-localization of MT Red, anti-PS1, and anti-KDEL, following MeOH fixation. Note that PS1 and MT Red “co-localize” (i.e., yellow signal), but only in regions where both ER and mitochondria are present (arrowhead marked “a”), whereas yellow signals are barely detectable in regions that contain ER but no mitochondria (arrowhead marked “b”) or mitochondria but no ER (arrowhead marked “c”). This result confirms that the yellow areas do not represent a true co-localization of ER and mitochondria, but rather a region below the level of confocal resolution where the two organelles are in apposition and make contact (i.e., MAM) (see also Fig. 3 in [45]).

possible that altered MAM function in AD patient cells could help explain the accumulation of tangles containing hyperphosphorylated forms of tau [88].

The role of MAM in cholesterol metabolism

MAM is not only a lipid raft-like domain rich in cholesterol, but it also contains a key enzyme of cholesterol metabolism, namely, acyl-CoA:cholesterol acyltransferase (ACAT) [89], which catalyzes the conversion of free cholesterol to cholesteryl esters [90]. There are two ACAT isoforms in mammals – ACAT1 (gene *SOAT1*) and ACAT2 (gene *SOAT2*) – but ACAT1 is the

predominant isoform in humans (and is the main functioning isoform in mouse brain [91]), whereas ACAT2 is expressed mainly in the intestine [90]. ACAT1 affects cholesterol homeostasis by controlling the dynamic equilibrium between membrane-bound free cholesterol and cholesteryl esters stored in cytoplasmic lipid droplets [14].

The relationship of MAM-localized ACAT1 to AD is intriguing, for at least three reasons. First, ACAT1 affects A β PP processing [91–93] and is required for the generation of A β [14,94,95]. Second, there may be a positive feedback loop between MAM content and ACAT1 activity, because elevated cholesterol stimu-

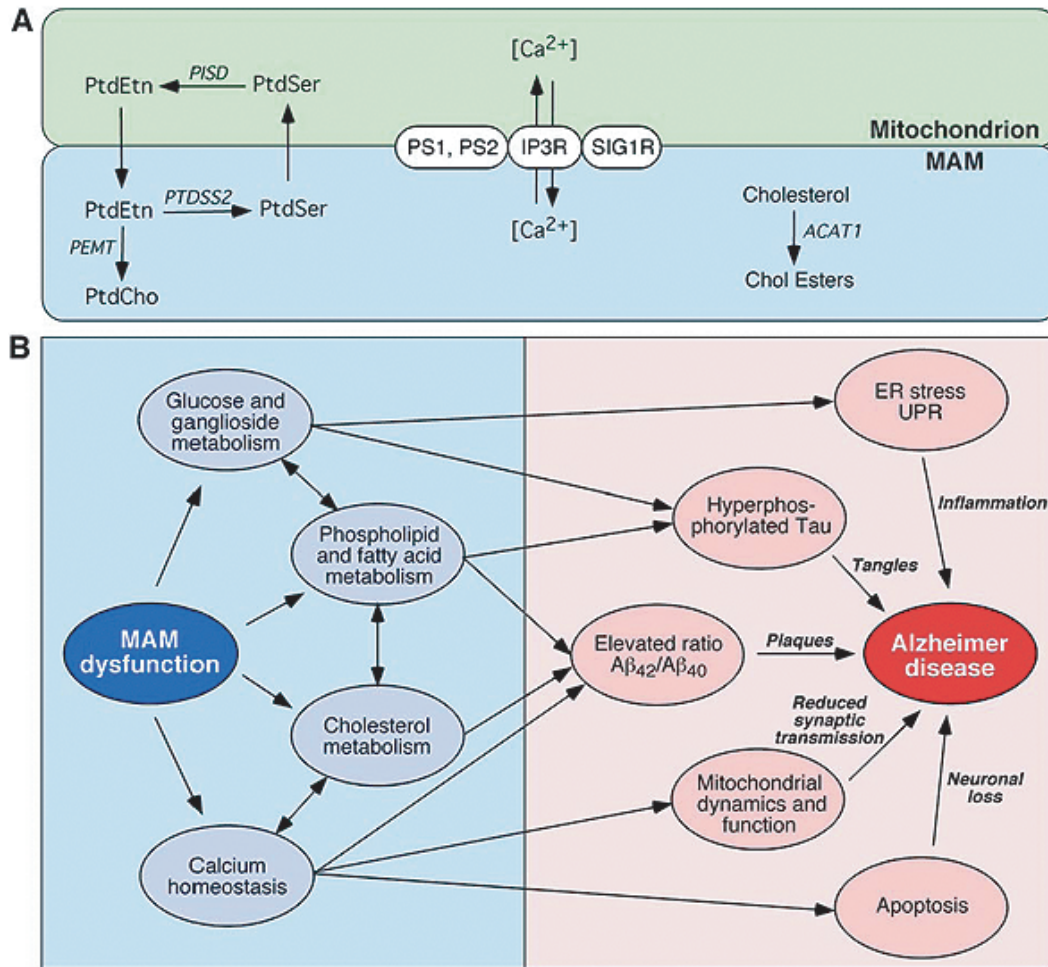


Fig. 2. Working model for the pathogenesis of AD due to abnormalities in MAM function. A) Illustrated are the three MAM functions discussed in the text: phospholipid transport and biosynthesis (pathway at left); calcium homeostasis (center); and cholesterol metabolism (right). Note that presenilins have been associated with IP3 receptors (IP3R), which in turn associate with the sigma-1 receptor (SIG1R); both are involved in Ca²⁺ signaling. B) Altered MAM function (resulting, for example, from mutations in PS1) affect the indicated pathway (light blue ovals), each of which can have one or more effects (pink ovals) that result in the features of AD (bold). The model as shown is somewhat simplified, as the various MAM functions can actually affect each other (double-headed arrows). UPR, unfolded protein response.

lates an increase in low density ER vesicles (presumably MAM) containing ACAT1 [96]. Finally, MAM is also enriched in microsomal triacylglycerol transfer protein large subunit (MTTP) [89] that, together with protein disulfide isomerase (PDI) [97], catalyzes the transport of cholesteryl esters, phospholipids, and triglycerides between phospholipid surfaces, and which is required for the secretion of plasma lipoproteins [97].

Importantly, patients with AD have elevated circulating cholesterol [4,98], and ACAT1 is elevated in the blood [99] and in fibroblasts [100] from AD patients, but the reason for these observations is currently unclear. We suggest that altered communication between the MAM and mitochondria in AD results in increased

ACAT1 activity, thereby affecting circulating cholesterol levels and Aβ production.

The role of MAM in calcium signaling

Given that the ER is the cell's main source, and that the mitochondrion is the cell's main sink, of calcium [101], it is perhaps not surprising that MAM, the compartment connecting these two organelles, plays a key role in calcium trafficking [38]. Proteins involved in Ca²⁺ trafficking have been shown to be enriched in the MAM, including inositol-1,4,5-trisphosphate (IP3) receptors [102,103], ryanodine receptors [104,105], the sigma-1 opioid receptor [106], and perhaps even

calnexin [107], emphasizing the intimate relationship between ER and mitochondria in regulating calcium homeostasis [108]. Conversely, Ca^{2+} regulates the apposition of ER and mitochondria via autocrine motility factor receptor (AMFR) [109], an apparently MAM-enriched protein [110,111].

A defect in calcium signaling due to altered MAM function could explain the well-known disturbances in calcium homeostasis in AD [17,112,113], including enhanced IP₃-mediated release of Ca^{2+} in fibroblasts from patients with SAD [114] and with FAD due to mutations in PS1 and PS2 [114–117], as well as in PS-mutant mouse cells [118].

Since MAM plays a role in calcium buffering [37], mutations in PS1 that alter MAM function could cause the defects in calcium homeostasis observed in AD patients. Consistent with this, presenilins are required for Ca^{2+} influx into cells through “store-operated” Ca^{2+} (SOC) channels located in the plasma membrane (“capacitative calcium entry” [CCE]), which require microdomains containing both an active sarcoplasmic/endoplasmic reticulum calcium ATPase (SERCA) – a protein associated with PS1 [119,120] – and neighboring mitochondria [121]. In cells with FAD-linked mutations, ER [Ca^{2+}] was increased [117,122] and CCE was inhibited [122–124], with downstream effects on A β PP processing and A β production [123–125].

Perhaps the most compelling evidence for a role of MAM in calcium dysregulation in AD is the finding that both PS1 and PS2 interact directly with IP₃ receptors (IP₃R), and that FAD-linked mutations in both proteins not only enhance IP₃R gating dramatically to increase intracellular Ca^{2+} but also stimulate A β production [126,127].

Among calcium’s many functions is its role as a key regulator of mitochondrial movement along microtubules in response to changes in the local Ca^{2+} gradient [128]. Mitochondria with normal membrane potential tend to move towards the periphery, whereas loss of membrane potential and of ATP synthesis result in increased retrograde transport towards the cell body [129]. Two cargo adaptor proteins, Miro and Milton, are implicated in the specific linkage of mitochondria to microtubules (via kinesin-1) [130]. Disruption of both Miro [131] and Milton [132] function causes redistribution of mitochondria from terminals to the cell body. Importantly, Miro binds Ca^{2+} and, when mutated, causes aggregation of mitochondria in the perinuclear region [131]. Thus, Miro has the potential to be an important regulator of mitochondrial motility, in

essence operating as a sensor of local concentrations of Ca^{2+} and ATP: in the Ca^{2+} -unbound state, Miro binds Milton and mitochondria are attached to microtubules, whereas in the Ca^{2+} -bound state, Miro cannot bind Milton and mitochondria are uncoupled from microtubules [128,133,134]. Remarkably, only Ca^{2+} mobilized via the IP₃ receptors (or, in muscle, the ryanodine receptors) could effect this result [128].

Since mitochondria need to be positioned strategically at sites where metabolic demand is high [135,136], a problem in calcium-mediated mitochondrial movement along axons in AD could have highly deleterious effects on neuronal function in general and on synaptic transmission in particular. We have observed aberrant mitochondrial dynamics in fibroblasts from FAD patients (data not shown), and altered mitochondrial dynamics has also been observed in cells from patients with SAD, including defects in mitochondrial distribution, transport, and morphology [11,137–139]. It remains to be seen whether these changes are related to altered MAM function.

A WORKING MODEL FOR MAM-MEDIATED PATHOGENESIS OF AD

We think that the enrichment of presenilins in MAM is important conceptually to our understanding of AD, for at least three reasons. First, MAM is a true subcompartment with specific functions, not merely a topological elaboration of the ER. Second, MAM is a known key control point for cholesterol, glucose, lipid, and calcium metabolism [83], all of which functions are deranged in AD; we think that this is more than mere coincidence. Third, MAM connects ER to mitochondria, implying that mitochondria may play a much more important role in AD than had previously been suspected, as dysfunctional MAM could explain the aberrant mitochondrial dynamics and function found in the disease.

Accordingly, we propose a working model in which altered MAM function plays a fundamental role in the pathogenesis of AD, and provides a unifying hypothesis that could explain many of the seemingly-unrelated features of the disease (Fig. 2B). Specifically, we propose that altered MAM function could explain the elevated ratio of A β_{42} /A β_{40} (via changes in the content of cholesterol), the hyperphosphorylation of tau (via changes in phospholipid metabolism), and the aberrant mitochondrial dynamics, with retention of large numbers of [fragmented] mitochondria in the perinuclear

region (via abnormal Ca^{2+} transport between ER and mitochondria).

Although we describe here a relatively simple one-to-one relationship between individual MAM functions and individual aspects of AD pathology, the reality is likely to be far more complicated, as various MAM components probably interact with, and affect, each other. For example, changes in $[\text{Ca}^{2+}]$ almost certainly affect the activity of other MAM (and mitochondrial) proteins that are calcium-sensitive (e.g., PTDSS2, which is both Ca^{2+} - and ATP-sensitive [67,140]), with downstream effects not only on mitochondrial dynamics, but also on $\text{A}\beta$ production and apoptosis [141]. Similarly, altered cholesterol metabolism affects not only $\text{A}\beta$ production, but may also change the topology of the MAM membrane [142], a cholesterol-rich DRM, thereby affecting not just $\text{A}\beta$ PP cleavage (e.g., by influencing the orientation of $\text{A}\beta$ PP in the membrane and hence the position at which it is cleaved by the γ -secretase [142]), but also the amounts, activities, and interactions among other membrane-embedded MAM proteins.

Importantly, while aberrant MAM function can ultimately result in the deposition of $\text{A}\beta$ in plaques and of hyperphosphorylated tau in tangles [88], we believe that these “canonical” features of AD are not the primary cause of the disease [3,143]. Rather, we propose that they are consequences of pre-existing metabolic disturbances in MAM. Put another way, we believe that it is overall MAM dysfunction, and not plaques or tangles *per se*, that are important in triggering the onset of the disease.

Notably, all of the metabolic and morphological phenotypes noted above have been found in both FAD and SAD, including, most recently, perinuclear mitochondria in SAD [11]. Thus, the “MAM hypothesis” offers a potentially coherent and unified explanation of many of the features of both the familial and sporadic forms of the disease. It also opens the door to new ways of thinking about treatment that are complementary to approaches focused directly on plaques and tangles. In fact, a strategy designed to “fix” the MAM may prove to be a more tractable therapeutic approach. In addition, we believe that it may be possible to exploit aberrant MAM function as a useful marker for the development of a diagnostic tool for AD.

While the MAM hypothesis will require modification in some of its particulars, we believe that the finding that presenilins are physically and functionally associated with MAM, and that AD patients display a number of defects associated with MAM function, is sufficiently compelling to warrant further investigation.

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