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## Mitochondria in Alzheimer's Disease and Their Potential Role in Alzheimer's Proteostasis

Ian W. Weidling, Russell H. Swerdlow\*

University of Kansas Alzheimer's Disease Center, University of Kansas Medical Center, Kansas City, KS, USA

### Abstract

Alzheimer's disease (AD) is a progressive brain disorder characterized by memory loss and the accumulation of two insoluble protein aggregates, tau neurofibrillary tangles and beta-amyloid plaques. Widespread mitochondrial dysfunction also occurs and mitochondria from AD patients display changes in number, ultrastructure, and enzyme activities. Mitochondrial dysfunction in AD presumably links in some way to its other disease characteristics, either as a cause or consequence. This review characterizes AD-associated mitochondrial perturbations and considers their position in its pathologic hierarchy. It focuses on the crosstalk that occurs between mitochondria, nuclear gene expression, and cytosolic signaling pathways that serves to maintain cell homeostasis. To this point, recent evidence indicates mitochondria trigger retrograde responses that influence cell proteostasis in general and AD proteostasis specifically. Potentially pertinent retrograde responses include the mitochondrial unfolded protein response (mtUPR), integrated stress response (ISR), autophagy/mitophagy, and proteasome function. A fuller perspective of mitochondrial dysfunction in AD, and its relation to protein aggregation, could enhance our overall understanding of this disease.

### Keywords

Alzheimer's disease; aggregation; metabolism; mitochondria; proteostasis; mitophagy; mitochondrial DNA

## 1. Introduction

Alzheimer's disease (AD) accounts for ~80% of all cases of dementia, making AD the most common form of dementia (Thies and Bleiler, 2011). Clinically, AD is defined by cognitive impairment pervasive enough to interfere with a person's ability to work or complete daily activities. The main histologic characteristics include amyloid plaques that largely contain

\*Correspondence: Russell Swerdlow, MD, University of Kansas Alzheimer's Disease Center, 4350 Shawnee Mission Parkway, Fairway, KS 66205, rswerdlow@kumc.edu.

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Conflicts of interest

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amyloid beta (A $\beta$ ) protein and neurofibrillary tangles (NFTs) that consist of hyperphosphorylated tau protein. There is often concomitant brain atrophy in the temporal lobe and medial parietal cortex, and decreased glucose utilization that at least early on predominates in posterior brain regions (McKhann et al., 2011). Current AD treatments confer a slight benefit but ultimately do not prevent progression (Grossberg et al., 2019).

Different AD variants are recognized. Most cases are genetically influenced but not considered genetically determined, at least not in a Mendelian sense (Swerdlow, 2007). Advancing age is particularly relevant in these cases, and prevalence and incidence increase in older populations. There are also Mendelian forms, which typically manifest in middle age within an autosomal dominant context. Autosomal dominant AD is caused by mutations in the amyloid precursor protein (APP) gene that carries within it the A $\beta$  amino acid sequence, the presenilin 1 (PS1) gene which encodes a subunit of the gamma secretase that cleaves APP, and the presenilin 2 (PS2) gene that is homologous to PS1 (Goate et al., 1991; Kelleher and Shen, 2017; Murrell et al., 1991).

Synapse loss and brain atrophy correlate well with cognitive decline, and brain volume measurements can predict disease progression and differentiate AD subtypes (DeKosky and Scheff, 1990; Risacher et al., 2017). Brain glucose utilization, measured using (18F)-2-fluoro-deoxy-D-glucose positron emission tomography (FDG-PET), also correlates with cognitive decline (Hoffman et al., 2000; Nestor et al., 2003; Silverman et al., 2001). Evidence suggests brain hypometabolism may be useful in early AD detection and diagnosis, as well as differential dementia diagnosis (Mosconi et al., 2008a; Mosconi et al., 2008b). Brain hypometabolism certainly occurs early in AD and worsens as the disease progresses. It is possible that brain hypometabolism may occur in the absence of discernable A $\beta$  or tau pathology (Minoshima et al., 1997; Mosconi et al., 2007; Reiman et al., 1996).

## 2. Metabolism-pertinent associations and alterations

Metabolism-related health parameters including diabetes, hypertension, and hypercholesterolemia associate with AD (Rosendorff et al., 2007; Schrijvers et al., 2010). Obesity during middle age increases AD risk three times, while overweight status increases AD risk two-fold (Whitmer et al., 2007).

Insulin receptor levels increase in the AD brain compared to age-matched controls (Frolich et al., 1998), but AD brains also display reduced glucose transporter levels, even after correcting for neuronal loss (Simpson et al., 1994). Brain derived neurotrophic factor (BDNF), an important regulator of neuronal development, survival, and metabolism is altered in the AD brain (Phillips et al., 1991).

Metabolomic studies provide more specific information regarding AD metabolic deficiencies (An et al., 2018). Studies utilizing nuclear magnetic resonance spectroscopy to assay metabolites consistently associate reduced *N*-acetylaspartate (NAA) with neurodegeneration (Barba et al., 2008). NAA's biological function in the brain is not well described, although it is worth noting neuron mitochondria synthesize NAA (Baslow, 2003). NAA may contribute to lipid conversion to myelin, aspartate storage, or osmoregulation,

although these roles remain speculative (Choi et al., 2007). NAA levels decrease in the AD brain, although NAA reduction does not differentiate AD from other neurodegenerative diseases. AD brains also display increased *myo*-inositol (mI). Little is known about the biological importance of mI changes (Kantarci et al., 2007; Martinez-Bisbal et al., 2004).

Lipid homeostasis is increasingly implicated in AD. Consistent correlations between sphingolipids and AD progression and severity are recognized (Varma et al., 2018). Ceramide accumulates in AD brains, which is of interest because ceramide can stimulate apoptosis (He et al., 2010). Lipid changes in AD blood or CSF may have the potential to serve as disease biomarkers (Wong et al., 2017).

### 3. Susceptibility to mitochondrial dysfunction and the AD COX defect

Mitochondria contribute to diverse cellular processes including apoptosis, cell growth and division, calcium storage, and lipid metabolism (Galluzzi et al., 2012). Deficient mitochondrial function is associated with numerous diseases (Wallace, 2005) and a driving role for mitochondrial dysfunction is recognized in multiple diseases (Niyazov et al., 2016). Primary mitochondrial disorders preferentially affect the brain and heart, organs known for their high energy demands. Based on these observations, the brain and heart are thought to have a lower threshold for tolerating mitochondrial dysfunction relative to other tissues (Wallace and Chalkia, 2013).

Changes in mitochondrial enzyme activity occur in AD (Swerdlow, 2012). Reduced cytochrome oxidase (COX) activity has consistently been observed across numerous tissues. Initial studies describe decreased COX activity in AD patient brains and platelets. The discovery of COX deficiency in non-degenerating tissues such as platelets suggests mitochondrial dysfunction occurs independently of neurodegenerative processes (Parker et al., 1990). Purified COX from AD brains showed anomalous kinetic behavior (Parker and Parks, 1995). COX activity reductions are easier to detect than complex I and II-III activity reductions (Mutisya et al., 1994).

Mitochondrial DNA (mtDNA) could contribute to reduced AD COX activity, and this possibility was addressed in studies utilizing cytoplasmic hybrids (cybrids). Generating cybrids involves repopulating mtDNA depleted cells ( $\rho 0$  cells) with exogenous mtDNA from human subject-derived platelets. Cybrid cell lines containing mitochondria transferred from AD patients, called AD cybrids, effectively model AD mitochondrial function on a stable nuclear background. This includes reduced COX activity and decreased mitochondrial oxygen consumption. AD cybrids also have decreased NAD<sup>+</sup>/NADH and increased ADP/ATP ratios (Silva et al., 2013). The collective cybrid evidence argues mtDNA contributes to AD mitochondrial dysfunction (Ghosh et al., 1999; Swerdlow et al., 1997).

Post-mortem analysis of AD brain tissue reveals decreases in COX subunits with disease progression (Kish et al., 1999). Elderly control subjects show decreased COX protein relative to young control subjects (Ojaimi et al., 1999). These findings suggest COX levels decline with age, and can surpass a threshold that associates with and possibly contributes to AD

AD hippocampi show increased numbers of COX deficient neurons. In one relevant study, the investigators performed an immunohistochemistry survey using antibodies to COX and complex II subunits. Neurons lacking COX staining in the presence of preserved complex II staining were designated COX deficient. This result suggests it is possible to selectively reduce COX subunits without proportionally eliminating other mitochondrial constituents (Cottrell et al., 2001). A subsequent study looked for correlations between COX deficiency and AD pathology, and found tangle-containing neurons are consistently COX-positive (Cottrell et al., 2002). The reasons for this are unclear but the non-randomness of the observation is consistent with the possibility of an NFT-mitochondria relationship.

#### 4. Other AD mitochondrial defects

AD mitochondria show numerous changes (Swerdlow, 2012). Mitochondrial surface area decreases, while cristae structure is altered and increased variability in mitochondrial shape occurs (Baloyannis, 2006). Changes in the mitochondrial fission and fusion machinery are early AD features that may precipitate these changes. There are changes in fusion and fission proteins that appear to affect mitochondrial localization in AD neurons (Manczak et al., 2011; Wang et al., 2008). Indeed, neuronal cultures with AD-relevant fission/fusion protein alterations recapitulate AD-like changes in mitochondrial distribution (Wang et al., 2009).

Three-dimensional electron microscopy (3D EM) studies of AD brains revealed a novel mitochondrial morphology called “mitochondria on a string” (MOAS) (Zhang et al., 2016). The investigators who described this proposed MOAS formation occurs in response to AD bioenergetic stress. MOAS formation may inhibit mitophagy, thereby preserving a low level of mitochondrial function under extreme stress. Related findings suggested MOAS arises due to arrested mitochondrial fission.

Lysosomal alterations are potentially tied to AD mitochondrial defects. AD neurons attempt to increase lysosomal proteins early in disease progression, specifically upregulating cathepsin D mRNA and protein levels with concomitant increases in lysosomal structures (Cataldo et al., 1995). Dystrophic AD neurons experience disrupted axonal and dendritic autophagy, with an accompanying accumulation of partially digested cellular components (Nixon and Yang, 2011). Along these lines, AD neurons from one study reported increased COX protein and mtDNA levels despite morphometric analyses showing reduced mitochondrial mass (Hirai et al., 2001). Rather than signaling an increase in functional mitochondria, observed increases in COX and mtDNA in that study potentially reflected deficient mitochondrial degradation. In AD neurons containing increased mitochondrial components, those components tended to colocalize with lysosomal structures (Hirai et al., 2001).

Mitophagy impairment also occurs in the AD brain. A recent study found reductions in numerous elements of the mitophagy program in AD hippocampus, in induced pluripotent stem cell-derived human AD neurons, and in AD animal models. The authors concluded impaired mitophagy may contribute to AD and enhancing mitochondrial clearance may prove therapeutically useful (Fang et al., 2019).

The root cause for AD mitochondrial dysfunction remains controversial. Initially, researchers assumed mitochondrial defects were a consequence of neuronal degeneration, but considerable evidence argues this is unlikely to represent the sole cause. A $\beta$  or tau pathology may also trigger mitochondrial defects (Caspersen et al., 2005; Devi et al., 2006), but cannot account for its entirety. If neurodegeneration, A $\beta$ , or tau pathology do not entirely account for AD mitochondrial dysfunction, then what other possibilities warrant consideration?

## 5. Potential role of mtDNA

MtDNA inheritance and an accumulation of somatic mtDNA mutations influence mitochondrial function. These effects play out against the nuclear genome, certainly on a fundamental level and perhaps also in AD (Andrews et al., 2019). Studies implicate somatic mtDNA mutations in aging and AD progression (Corral-Debrinski et al., 1992; Corral-Debrinski et al., 1994; Cottrell et al., 2001).

Deletions represent one type of somatic mtDNA mutation that may contribute to neurodegeneration (Corral-Debrinski et al., 1992). The 4,997 base pair “common deletion” increases in the brain during normal aging. Brain areas with the highest metabolic activity display the greatest common deletion burden. One study that focused on AD COX-deficient neurons found an association between COX deficiency and increased aging-related mtDNA deletions (Krishnan et al., 2012), which suggests mtDNA deletions may contribute to AD bioenergetic defects. Early AD brains display increased common deletion burden compared to age-matched controls. Around age 75, though, the frequency of common deletion detection actually declines in the AD brain. This is in contrast to age-matched control brains, which accumulate the common deletion to a greater extent beyond age 75 (Corral-Debrinski et al., 1994; Hamblet and Castora, 1997).

Oxidative damage often associates with mitochondrial dysfunction and may contribute to mtDNA damage (Lovell and Markesbery, 2007). Levels of oxidative damage increase in the AD brain, especially in the parietal lobe (Nunomura et al., 2001; Nunomura et al., 1999; Perry et al., 2002). One study found a three-fold increase in the amount of an oxidized nucleoside related to AD brain mtDNA, while AD nuclear DNA displayed only a small increase in oxidative damage (Mecocci et al., 1994). This established that mtDNA experiences increased oxidative damage in AD and suggests mtDNA is more prone to damage by this mechanism than nuclear DNA. It is interesting to note that the region displaying the most mtDNA oxidative damage, the parietal lobe, also exhibits early reductions in glucose consumption during AD (Silverman et al., 2001), suggesting a possible link between mitochondrial dysfunction and brain hypometabolism.

Another study reported mtDNA control region point mutations accumulate to a greater extent in the AD brain (Coskun et al., 2004). Mutations in this mtDNA segment correlate with disrupted mtDNA transcription and replication. The AD brains in this study showed an approximate 50% reduction in their mtDNA/nuclear DNA ratio. Control region mutations, therefore, may also contribute to AD mitochondrial dysfunction.

More recent studies utilizing chip-based or next generation sequencing reveal increased mtDNA substitution variants in AD patients (Casoli et al., 2014; Casoli et al., 2015). In one study that assessed mtDNA integrity in early stage AD patient hippocampi, there was an observed dramatic increase in mtDNA mutations. Based on further analysis, the authors speculated this increase more likely reflected an enhanced accumulation of replication errors than a direct consequence of oxidative damage (Hoekstra et al., 2016).

MtDNA inheritance may also influence AD risk. Some studies suggest AD shows a maternal inheritance predominance (Edland et al., 1996), which is consistent with an mtDNA effect because mtDNA is maternally inherited. It is possible, though, that excess maternal inheritance reflects an artifact of enhanced female longevity or perhaps an inherently increased female AD risk (Heggeli et al., 2012). Other studies show a maternal AD history also associates with brain hypometabolism and lower COX activity in cognitively normal, middle aged adults (Mosconi et al., 2007; Mosconi et al., 2011). Furthermore, individuals with a maternal AD history experience progressive brain hypometabolism in the same brain regions as AD patients (Mosconi et al., 2009). Epidemiology and endophenotype studies, therefore, are consistent with the possibility that mtDNA contributes to both AD risk and biomarker endpoints.

The AD cybrid data also suggest mtDNA contributes to AD pathogenesis (Swerdlow et al., 2017). As mentioned earlier, AD cybrids display reduced COX activity, while maintaining activity of other respiratory chain complexes (Ghosh et al., 1999). Beyond COX deficiency, AD cybrids produce more reactive oxygen species (ROS), have swollen mitochondria with reduced membrane potential, and recapitulate AD-like pathology features (Khan et al., 2000; Swerdlow et al., 1997; Trimmer et al., 2000). AD cybrids have elevated intracellular A $\beta$  and secrete A $\beta$  into the media at a greater rate (Khan et al., 2000; Onyango et al., 2010). Concomitantly, AD cybrids increase caspase-3 activity and cytochrome c release. These apoptotic responses may facilitate A $\beta$  accumulation in AD cybrids (Khan et al., 2000). A $\beta$  treatment in AD cybrids leads to an accentuated apoptotic response compared to age-matched control cybrids (Cardoso et al., 2004).

## 6. An AD mitochondrial cascade hypothesis

A mitochondrial cascade hypothesis argues AD neuropathology arises secondary to mitochondrial dysfunction (Swerdlow, 2018; Swerdlow et al., 2010, 2014; Swerdlow and Khan, 2004; Swerdlow and Khan, 2009). This view of AD does not attempt to discount the potential detrimental effects of aggregating proteins and tries to provide a rationale for why protein aggregation occurs in this disease.

The mitochondrial cascade hypothesis proposes an individual's mtDNA and nuclear DNA inheritance determine their baseline mitochondrial function and durability. As the individual ages, their mitochondrial dysfunction declines; this decline may represent a consequence of, or occur independent of, somatic mtDNA mutation. Initially, compensatory responses can maintain adequate mitochondrial function in the face of diminished efficiency. At some point, though, the extent of mitochondrial function exceeds the limits of compensation and disease ensues (Figure 1). Insoluble protein aggregates may appear in response to changing

mitochondrial function, either during the initial compensation phase or the subsequent uncompensated phase (Swerdlow et al., 2010).

Threshold effects are pertinent to the mitochondrial cascade hypothesis. Each organ likely possesses its own threshold for tolerating mitochondrial dysfunction, beyond which normal function becomes impossible. Neurons are highly dependent on mitochondria for a variety of functions, rendering them particularly susceptible to mitochondrial dysfunction (Tomasi et al., 2013; Wallace and Chalkia, 2013). This could explain why AD presents primarily as a brain disease, albeit one that associates with subtle systemic phenotypes.

## 7. Connections between mitochondria and protein aggregation

Many studies report the effects of amyloid and tau species on mitochondrial function. Exposing cultured cells to A $\beta$  peptides perturbs multiple mitochondrial endpoints, including mitochondrial membrane potential, respiratory chain activities, and oxygen consumption (Pereira et al., 1998). Isolated mitochondria, when incubated with A $\beta$ , show decreased COX, alpha-ketoglutarate, and pyruvate dehydrogenase activities, which recapitulates observed reductions of these enzyme activities in tissues from AD subjects (Casley et al., 2002; Gibson et al., 1998). APP accumulates in mitochondrial translocases, where it appears to disrupt mitochondrial function (Anandatheerthavarada et al., 2003; Anandatheerthavarada and Devi, 2007; Devi et al., 2006). A $\beta$  is found within mitochondria, where it interacts with a mitochondrial matrix alcohol dehydrogenase alternatively referred to as the A $\beta$ -binding alcohol dehydrogenase (ABAD) enzyme. ABAD contributes to proper mitochondrial function and A $\beta$  binding inhibits ABAD activity (Lustbader et al., 2004). Other studies interrogating the co-localization of mutant APP/A $\beta$  with mitochondria show a physical interaction with cyclophilin D (Du et al., 2008), as well as accentuated mitochondrial free radical production and oxidative DNA damage (Manczak et al., 2006).

Studies of AD brain suggest mitochondrial transport throughout the cell is disturbed in AD neurons (Panchal and Tiwari, 2019). AD neurons contain reduced numbers of synapse mitochondria (Pickett et al., 2018). The reasons for this are not entirely clear, but one hypothesized cause is tau aberration. Tau contributes to microtubule stability, and dysfunctional tau may preclude the physiologic transport of mitochondria along microtubules.

Direct interactions between tau and mitochondria are also reported. Low-capacity runner (LCR) rats display metabolic defects along with hippocampal neurodegeneration. These rats accumulate hyperphosphorylated tau within their mitochondria. In this model, co-localization of tau with mitochondria is not an artifact of forced overexpression. The authors of this study speculated mitochondrial dysfunction in LCR rats altered tau physiology and contributed to neurodegeneration (Choi et al., 2014).

Additional studies reveal mitochondria-localized tau protein. In AD brains, hyperphosphorylated tau accumulates in voltage dependent anion channel 1 (VDAC1) structures present on the mitochondrial outer membrane (Manczak and Reddy, 2012).

Phosphorylated tau also interacts with VDAC1 in APP, APP/PS1, and triple transgenic AD mice, where it appears to inhibit VDAC1 function (Manczak and Reddy, 2012).

Truncated tau species with the ability to impede mitochondrial function collect in AD neurons. Tau cleaved at aspartate 421 (Asp-421) increases in AD brains, and A $\beta$  can promote this processing (Gamblin et al., 2003). Overexpressing this tau fragment in neuronal cell culture causes oxidative stress and mitochondrial fragmentation (Quintanilla et al., 2009). Overexpressing a different tau fragment, NH2-26-44, causes primary neuron death. N-terminal tau fragments cause mitochondrial dysfunction by disrupting adenine nucleotide transporter (ANT) function (Atlante et al., 2008).

Another AD related protein, apolipoprotein E (apoE), is pertinent to mitochondria. The APOE e4 (APOE4) allele is the strongest known sporadic AD genetic risk factor. The apoE4 protein builds up in endosomal compartments and poorly stimulates cholesterol efflux relative to the apoE2 and apoE3 isoforms (Heeren et al., 2004). The apoE4 isoform appears particularly susceptible to c-terminal protease cleavage. Neuronal cells transfected with truncated apoE4 display increased NFT formation, suggesting apoE4 fragments can induce NFT formation (Huang et al., 2001). Subsequent studies revealed physical associations between apoE fragments and mitochondrial proteins. ApoE4 binds to mitochondrial complex III and IV subunits, and apoE4 fragments bind more strongly than full length apoE4. Expressing truncated apoE4 in Neuro-2a cells reduced complex III and IV activity compared to cells expressing full length apoE4. This line of research suggests apoE4-derived peptide fragments promote neurodegeneration by inhibiting mitochondrial function (Chang et al., 2005; Chen et al., 2011; Nakamura et al., 2009).

While proteins such as A $\beta$ , APP, tau, and apoE can influence mitochondria, a reciprocal relationship in which mitochondria influence these proteins is also recognized (Figure 2). Fibroblasts treated with a mitochondrial uncoupler display increased tau phosphorylation at AD-relevant sites (Blass et al., 1990). This suggests the uncoupling of oxidative phosphorylation reported in the AD brain (Sims et al., 1987) may contribute to tau abnormalities. Studies with complex I inhibitors also demonstrate a relationship between mitochondrial function and tau. Two complex I inhibitors, annonacin and 1-methyl-4-phenylpyridinium (MPP+), alter tau splicing in human neurons, which leads to a predominance of 4R tau (Bruch et al., 2014). In rats, chronic rotenone treatment increases brain tau hyperphosphorylation and aggregation, as well as alpha-synuclein deposits (Hoglinger et al., 2005).

## 8. Protein stress responses, mitochondria, and cell proteostasis

Unfolded protein responses (UPRs) help maintain cell proteostasis. Well described mechanisms for responding to unfolded proteins exist for the endoplasmic reticulum (ER) and the cytosol. The UPR in the ER (erUPR) utilizes numerous strategies to maintain cell proteostasis in the face of diverse stressors. One involves increasing ER chaperone protein expression to restore proper protein folding and prevent aggregation. Simultaneously, ER stress may initiate eukaryotic initiation factor 2 $\alpha$  (eIF2 $\alpha$ ) phosphorylation, which inhibits general protein translation to reduce the cell protein load. The erUPR also includes a process



called ER-associated degradation (ERAD). ERAD components degrade misfolded and accumulated proteins (Bravo et al., 2013). Together, these programs identify and rectify protein misfolding and aggregation in the ER to maintain homeostasis. Prolonged erUPR activation, however, promotes inflammatory responses and apoptosis (Fribley et al., 2009; Grootjans et al., 2016).

The cytosol also senses and responds to misfolded and aggregating proteins. Exposed hydrophobic residues act as markers of peptide misfolding. Cytosolic chaperones, including heat shock protein 70 (Hsp70) and heat shock protein 90 (Hsp90) family members, sense misfolding and refold proteins. The ubiquitin-proteasome system (UPS) degrades unsalvageable damaged or unfolded proteins. Members of the E3 ubiquitin ligase family tag misfolded proteins and designate them for destruction by the proteasome. ATP-independent small heat shock proteins (sHsps) help solubilize and prevent protein aggregates through direct binding (Buchberger et al., 2010).

Aggresomes additionally mediate cytosolic proteostasis. Aggresomes form when misfolded proteins accumulate into large inclusion bodies, which serve as misfolded protein repositories. Proteasomal components and chaperones move to aggresomes and attempt to degrade them (Kawaguchi et al., 2003). Autophagy-lysosome machinery also contributes to aggresome removal (Zaarur et al., 2014). Aggresome formation typically follows proteasome failure (Johnston et al., 1998).

Increasing evidence reveals an important role for mitochondria in proteostasis. Mitochondria possess intrinsic chaperones and proteases that handle internally misfolded proteins and aggregation. The presence of unfolded protein within mitochondria triggers a mitochondrial unfolded protein response (mtUPR), which upregulates the mitochondria's resident chaperones and proteases (Jovaisaite et al., 2014). Most evidence for the mtUPR comes from studies in *Caenorhabditis elegans* (*C. elegans*). Diverse mitochondrial insults stimulate the mtUPR in *C. elegans*, including decreases in mitochondrial ribosomes, mtDNA depletion, and impaired mitochondrial translation. Respiratory chain inhibition and knockdown of mitochondrial chaperones and proteases also initiate the mtUPR. The mtUPR activates and operates independent of cytosolic heat shock and erUPR stress responses (Yoneda et al., 2004).

In *C. elegans*, activating transcription factor associated with stress-1 (ATFS1) mediates the mtUPR. Under non-stress conditions, mitochondria import ATFS-1 where it undergoes degradation. Mitochondrial impairment or stress impairs ATFS-1 import, which redirects it to the nucleus. Nuclear ATFS-1 upregulates the expression of mitochondrial chaperones and proteases (Nargund et al., 2012). In mammalian cells, activating transcription factor 5 (ATF5) plays a similar role to ATFS-1, mediating the mtUPR under select conditions. However, on some parameters the mammalian and *C. elegans* mtUPRs diverge, as disrupting mitochondrial translation, respiration, protein import, and membrane potential fail to activate the mammalian mtUPR (Fiorese et al., 2016).

Although these mitochondrial insults fail to engage the mammalian mtUPR, they do activate other proteostasis mechanisms, including the integrated stress response (ISR) (Figure 3).

Mitochondrial stress inhibits cytosolic translation by increasing eIF2 $\alpha$  phosphorylation. While eIF2 $\alpha$  phosphorylation represses general cell translation, the translation of certain stress response factors, including activating transcription factor 4 (ATF4), increases. ATF4 knockdown impedes cell proliferation and slows recovery following ethidium bromide-induced mtDNA depletion (Quirós et al., 2017). Another study found respiration inhibitors induce an ATF4-dependent stress response (Garaeva et al., 2016).

Studies performed in yeast, *C. elegans*, and mammalian cells reveal a relationship between the electron transport chain (ETC) and proteasome activity, in which ETC impairment associates with reduced proteasome function. Reactive oxygen species (ROS), which favor proteasome disassembly, may mediate this relationship as antioxidant treatment reverses proteasome disassembly. ATP levels and proteasome function also correlate, which implies bioenergetic status may also link mitochondrial function to the UPS (D'Amico et al., 2017).

Very specific types of mitochondrial stress can alternatively activate the proteasome. Defective mitochondrial protein import causes mitochondrial protein precursors to accumulate in the cytosol, which the cell responds to by increasing proteasome activity and decreasing protein translation. This response to the cytosolic accumulation of mitochondrial proteins is called the UPR activated by mistargeting of proteins (UPRam) (Wrobel et al., 2015).

In *C. elegans* there is also a mitochondrial stress response pathway that depends on lipid biosynthesis. Knockdown of a mitochondrial chaperone, mtHSP70, triggers cytosolic lipid accumulation which activates transcription factors that increase the expression of lipid metabolism and cytosolic chaperone genes (Kim et al., 2016). Further studies need to determine the relevancy of these pathways in mammalian cells.

## 9. Mitochondrial protein clearance pathways

Studies in yeast suggest mitochondria actively degrade aggregation prone-proteins. Disrupting this process by interfering with mitochondrial protein import and protease function promotes the formation of cytosolic protein aggregates (Ruan et al., 2017). As part of a related phenomenon, defective cytosolic chaperone function causes protein aggregates to accumulate within mitochondria. While aggregating proteins move into the mitochondria most robustly under heat shock stress conditions, under basal conditions a limited stream of aggregation-prone proteins continue to access the mitochondria, where they undergo degradation. Human cells appear to display a similar mechanism (Ruan et al., 2017).

In addition to the protease-mediated removal of mitochondria-internalized peptides, the lysosomal elimination of mitochondria through mitophagy also supports proteostasis. In APP transgenic mice, PTEN-induced putative kinase 1 (PINK1) knock-down impairs mitophagy and increases plaque deposition, while PINK1 overexpression enhances mitophagy and reduces plaque deposition. PINK1 overexpression also reduces synaptic loss and preserves memory task performance in these mice (Du et al., 2017).

Mitochondria can relegate protein aggregates to discrete regions. The contaminated sections specifically recruit parkin and undergo fission-mediated removal from the rest of the

organelle. Under conditions of fission inhibition, parkin tagging of mitochondria transforms from a focal to diffuse pattern, which leads to a generalized mitophagy response. Fission, therefore, regulates a balance between selective degradation of mitochondrial protein aggregates and their less specific removal through mitophagy (Burman et al., 2017).

## 10. Concluding remarks

Mitochondrial function is altered in AD. Multiple factors may contribute to this, including genetics, protein stress, and stress responses. Accumulating evidence argues mitochondria play an important role in AD and may even contribute directly to its classic plaque and tangle histology. A growing body of experimental data firmly link mitochondrial dysfunction to A $\beta$  and tau homeostasis. Some studies focus on the ability of A $\beta$  and tau to alter mitochondrial function. Others show mitochondria influence A $\beta$  and tau homeostasis, as well as their aggregation. The connections between mitochondria and cell proteostasis are extensive and reflect fundamental cell biology. Mitochondria modify protein translation and degradation infrastructure, and in the case of protein degradation serve as part of that infrastructure. Targeting mitochondria to mitigate protein aggregation in AD, and ideally to provide clinical relief, seems reasonable.

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## Abbreviations:

<b>A<math>\beta</math></b>	beta amyloid
<b>ABAD</b>	A $\beta$ -binding alcohol dehydrogenase
<b>AD</b>	Alzheimer's disease
<b>ANT</b>	adenine nucleotide transporter
<b>ApoE</b>	apolipoprotein E
<b>APP</b>	amyloid precursor protein
<b>ATF</b>	activating transcription factor
<b>ATFS1</b>	ATF associated with stress-1
<b>BDNF</b>	brain derived neurotrophic factor
<b>COX</b>	cytochrome oxidase
<b>Cybrid</b>	cytoplasmic hybrid
<b>eIF2<math>\alpha</math></b>	eukaryotic initiation factor 2 $\alpha$
<b>ER</b>	endoplasmic reticulum

<b>ERAD</b>	ER-associated degradation
<b>ETC</b>	electron transport chain
<b>FDG-PET</b>	(18F)-2-fluoro-deoxy-D-glucose positron emission tomography
<b>Hsp</b>	heat shock protein
<b>ISR</b>	integrated stress response
<b>LCR</b>	low capacity runner
<b>MOAS</b>	mitochondria on a string; mI, myo-inositol
<b>MPP+</b>	1-methyl-4-phenylpyridinium
<b>mtDNA</b>	mitochondrial DNA
<b>NAA</b>	N-acetylaspartate
<b>NFTs</b>	neurofibrillary tangles
<b>PINK1</b>	PTEN-induced putative kinase 1
<b>PS</b>	presenilin
<b>ROS</b>	reactive oxygen species
<b>UPR</b>	unfolded protein response
<b>UPRam</b>	UPR activated by mistargeting of proteins
<b>UPS</b>	ubiquitin-proteasome system
<b>VDAC</b>	voltage dependent anion channel

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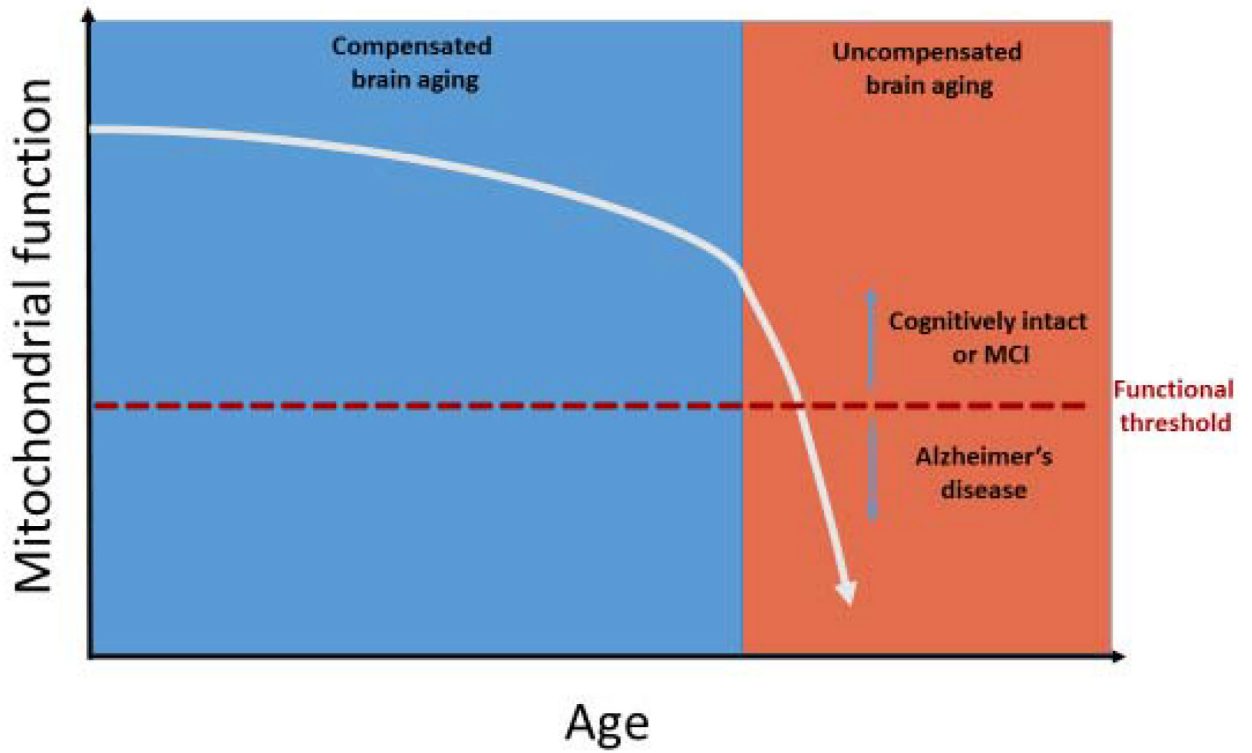
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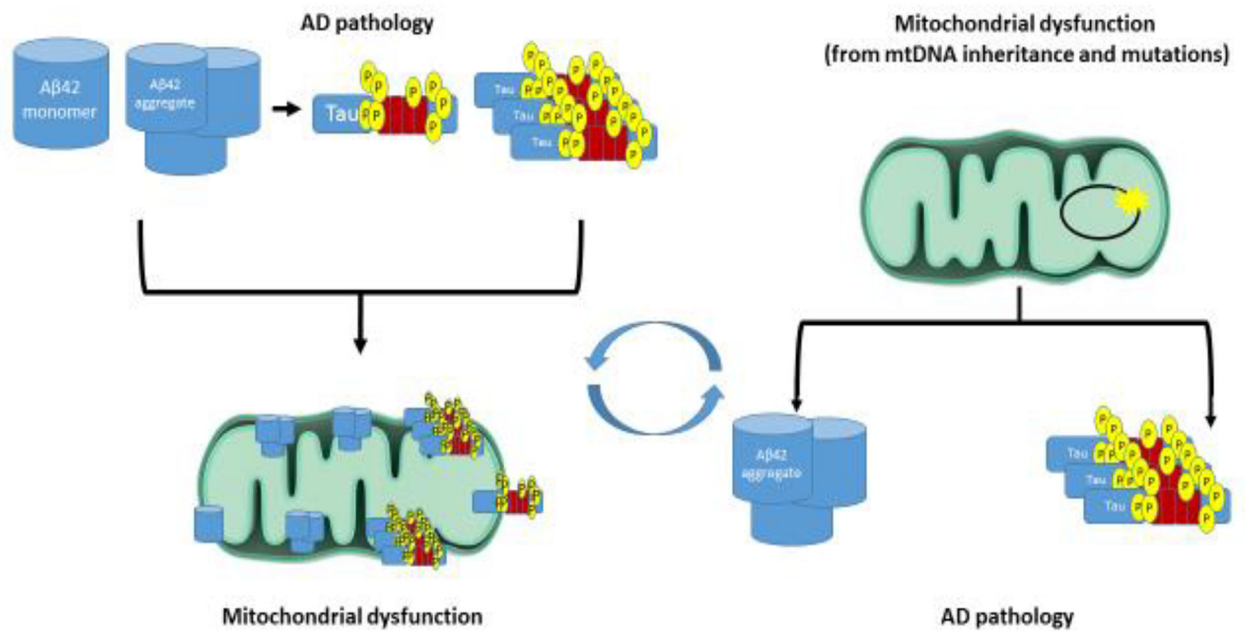
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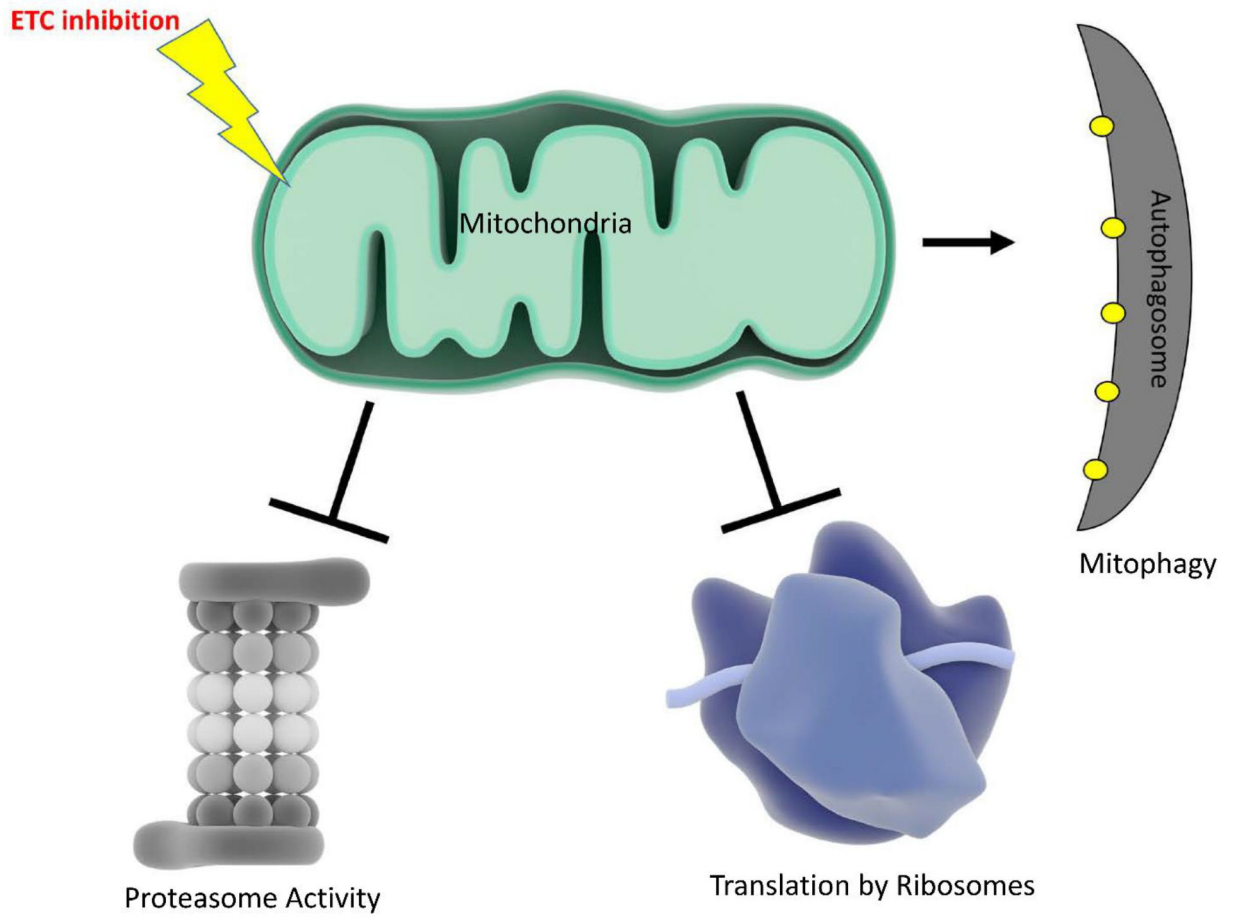
**Figure 1. Compensated versus uncompensated brain aging as predicted by the mitochondrial cascade hypothesis.**

The sporadic AD mitochondrial cascade hypothesis proposes mitochondrial dysfunction progressively declines with advancing age, which initially prompts compensation (compensated brain aging). At some point, this decline reaches a point at which adequate compensation is no longer possible, and the brain transitions from compensated to uncompensated brain aging. Clinical symptoms and signs are most evident during the stage of uncompensated brain aging.



**Figure 2. Mitochondria and AD-relevant proteins influence each other.**

Amyloid and tau pathology could drive AD mitochondrial dysfunction. Alternatively, AD mitochondrial dysfunction could exist independent of these proteins, and may in fact set the stage for amyloid plaque and NFT formation.



**Figure 3. Mitochondrial stress impacts cellular proteostasis.** ETC inhibition decreases proteasome activity, inhibits protein translation, and increases mitophagy.