

Mitochondrion-Derived Reactive Oxygen Species Lead to Enhanced Amyloid Beta Formation

Kristina Leuner,^{1,2} Tanja Schütt,¹ Christopher Kurz,¹ Schamim H. Eckert,¹ Carola Schiller,¹ Angelo Occhipinti,^{3,4} Sören Mai,⁵ Marina Jendrach,⁵ Gunter P. Eckert,¹ Shane E. Kruse,⁶ Richard D. Palmiter,⁶ Ulrich Brandt,⁷ Stephan Dröse,⁷ Ilka Wittig,⁷ Michael Willem,^{8,9} Christian Haass,^{8,9} Andreas S. Reichert,^{3,4} and Walter E. Müller¹

Abstract

Aims: Intracellular amyloid beta ($A\beta$) oligomers and extracellular $A\beta$ plaques are key players in the progression of sporadic Alzheimer's disease (AD). Still, the molecular signals triggering $A\beta$ production are largely unclear. We asked whether mitochondrion-derived reactive oxygen species (ROS) are sufficient to increase $A\beta$ generation and thereby initiate a vicious cycle further impairing mitochondrial function. **Results:** Complex I and III dysfunction was induced in a cell model using the respiratory inhibitors rotenone and antimycin, resulting in mitochondrial dysfunction and enhanced ROS levels. Both treatments lead to elevated levels of $A\beta$. Presence of an antioxidant rescued mitochondrial function and reduced formation of $A\beta$, demonstrating that the observed effects depended on ROS. Conversely, cells overproducing $A\beta$ showed impairment of mitochondrial function such as comprised mitochondrial respiration, strongly altered morphology, and reduced intracellular mobility of mitochondria. Again, the capability of these cells to generate $A\beta$ was partly reduced by an antioxidant, indicating that $A\beta$ formation was also ROS dependent. Moreover, mice with a genetic defect in complex I, or AD mice treated with a complex I inhibitor, showed enhanced $A\beta$ levels *in vivo*. **Innovation:** We show for the first time that mitochondrion-derived ROS are sufficient to trigger $A\beta$ production *in vitro* and *in vivo*. **Conclusion:** Several lines of evidence show that mitochondrion-derived ROS result in enhanced amyloidogenic amyloid precursor protein processing, and that $A\beta$ itself leads to mitochondrial dysfunction and increased ROS levels. We propose that starting from mitochondrial dysfunction a vicious cycle is triggered that contributes to the pathogenesis of sporadic AD. *Antioxid. Redox Signal.* 16, 1421–1433.

Introduction

SPORADIC ALZHEIMER'S DISEASE (AD), the most common age-related neurodegenerative disease, is characterized by initial memory impairment progressing toward total loss of mental and physical abilities (17, 39, 46). The key histopathological features are amyloid-beta ($A\beta$) containing plaques and microtubule-associated tau-bearing neurofibrillary tangles. In contrast to familial AD caused by a mutation in the amyloid precursor protein (APP), or the presenilin genes 1

and 2 leading to increased $A\beta$ load, the main risk factor for sporadic AD is aging itself (34, 38). Aging is associated with long-time exposure of our brain to oxidative stress, leading to accumulation of oxidized proteins, lipids, and nucleic acids. The mitochondrion, the major hub of cellular energy conversion, is a main source of reactive oxygen species (ROS) (35, 37). The majority of ROS derive from complexes I and III of the respiratory chain in the form of superoxide anion radicals (2, 27). Importantly, complex I activity declines substantially during normal brain aging, whereas complex III activity is

¹Department of Pharmacology, ZAFES, Biocenter, University of Frankfurt, Frankfurt/Main, Germany.

²Molecular and Clinical Pharmacy, FAU Erlangen/Nürnberg, Erlangen, Germany.

³Mitochondrial Biology, Frankfurt Institute for Molecular Life Sciences, Frankfurt/Main, Germany.

⁴Mitochondrial Biology, Medical School, Goethe University, Frankfurt/Main, Germany.

⁵Kinematische Zellforschung, Biocenter, University of Frankfurt, Frankfurt/Main, Germany.

⁶Department of Biochemistry, Howard Hughes Medical Institute, University of Washington, Seattle, Washington.

⁷Molecular Bioenergetics Group, Cluster of Excellence Frankfurt "Macromolecular Complexes," Medical School, Johann Wolfgang Goethe-Universität, Frankfurt/Main, Germany.

⁸DZNE—German Center for Neurodegenerative Diseases, Munich, Germany.

⁹Biochemistry, Adolf-Butenandt-Institute, Ludwig-Maximilians-University, Munich, Germany.

Innovation

We show that mitochondrion-derived reactive oxygen species (ROS) trigger amyloid beta ($A\beta$) production. This may set off a vicious cycle of enhanced $A\beta$ production in the progression of sporadic Alzheimer's disease (AD), since $A\beta$ itself accelerates mitochondrial dysfunction and its own production *via* enhanced β -site APP cleaving enzyme 1 activity due to increased ROS levels (Fig. 8). This mechanism may help to explain why aging, which is strongly associated with mitochondrial dysfunction, is the major risk factor to develop sporadic AD.

nearly unchanged (2, 27, 32), suggesting complex I as the major player of the brain aging scenario. Not only in familial AD but also in sporadic AD, a gradual increase of $A\beta$ levels over years or even decades is considered to play an important role in pathogenesis. Enhanced amyloidogenic processing of APP by the β -site APP cleaving enzyme (BACE) and the γ -secretase complex leads to increased intracellular levels of soluble oligomeric $A\beta$, resulting in pronounced synaptic failure and eventually in memory decline (17, 46). However, the mechanism by which APP processing is triggered in sporadic AD patients is still not known and probably represents one of the most important missing links in the understanding of this devastating disease.

Several recent findings show that mitochondrial dysfunction is one of the earliest pathogenic alterations in AD (11, 18, 44, 49). In post-mortem brain tissue of sporadic AD patients, a deficiency in cytochrome c oxidase (complex IV) activity is consistently reported (54). In several AD animal models, mitochondrial dysfunction resulting in decreased mitochondrial membrane potential (MMP), reduced ATP levels, declined complex IV activity, and enhanced oxidative stress was detected (18, 49). Furthermore, mitochondrial dynamics (fusion and fission) and morphology are altered in AD (47, 48, 52, 59). The aforementioned pathological changes are already observed when only oligomeric $A\beta$ could be detected and fibrillar plaques were not yet present (18, 49, 61), stressing the early contribution of mitochondrial dysfunction to the progression of the disease. Here, we asked whether mitochondrial dysfunction, especially complex I dysfunction associated with enhanced ROS production, might be the initial trigger for altered APP processing, which in turn might result in a vicious cycle further impairing mitochondrial dysfunction, leading to apoptosis, synaptic dysfunction, and memory decline.

Results

Complex I dysfunction induced by rotenone leads to $A\beta$ generation

As a simple experimental cell model for complex I dysfunction, we used the effects of the complex I inhibitor rotenone on mitochondrial function in HEK293 cells. Treatment with rotenone led to a significant reduction of MMP and ATP levels (Fig. 1A), and to a substantial increase in superoxide anion radicals and cytosolic ROS levels (Fig. 1B). MMP and ATP level constantly declined over 24 h (Supplementary Fig. S1A, B; Supplementary Data are available online at www.liebertonline.com/ars), whereas both superoxide anion radicals and cytosolic ROS levels reached a peak after 2 h

(Supplementary Fig. S1C, D). Furthermore, rotenone treatment induced pronounced mitochondrial fragmentation (Fig. 1C, D). These experiments confirm earlier studies (4, 22, 57) that rotenone as applied here induced mitochondrial dysfunction and increased mitochondrion-derived ROS formation. Next we asked whether complex I dysfunction is sufficient to induce enhanced $A\beta$ generation. $A\beta_{1-40}$ levels were determined after 2 h when ROS levels were maximally elevated and after 24 h when MMP, ATP, and mitochondrial morphology were significantly impaired. As early as 2 h after the insult with rotenone, $A\beta_{1-40}$ levels were modestly increased (Fig. 2A). After 24 h this effect was much more pronounced and $A\beta_{1-40}$ levels were significantly increased by 75% compared to unstressed control cells (Fig. 2A). The levels of $A\beta_{1-42}$ production at the scale of these experiments were too low for a reliable detection even after inhibiting complex I.

Complex I-induced $A\beta$ increase is mediated by enhanced ROS level

To elucidate the mechanism responsible for complex I-induced increased $A\beta$ generation, we investigated whether elevated ROS levels are the trigger for altered APP processing. To test this hypothesis the antioxidant vitamin C was used to scavenge ROS. To determine the active antioxidant concentration, first the effects of different vitamin C concentrations (1–1000 μ M) on the levels of superoxide anion were tested. HEK293 cells were preincubated with vitamin C for 4 h, rotenone 25 μ M was added, and dihydroethidium (DHE) fluorescence was measured after 2 h when maximal superoxide anion radical levels were detected after rotenone insult. Vitamin C at a concentration of 1000 μ M reduced superoxide anion radicals by about 25% after rotenone treatment (Fig. 2B). Next we investigated whether vitamin C was sufficient to reduce rotenone-induced $A\beta$ formation. Indeed, vitamin C at the concentration that reduced ROS levels by about 25% was sufficient to reduce $A\beta_{1-40}$ levels by about 20% (Fig. 2C). This effect was accompanied by a protection against mitochondrial fragmentation (Fig. 2D, E). Taken together, these experiments demonstrate that triggering the formation of $A\beta$ can be suppressed by scavenging complex I-derived ROS.

Complex III-derived ROS also results in increased $A\beta$ production

To define whether these findings are an effect specifically mediated *via* complex I-derived ROS or whether ROS generation by complex III, the second key player generating mitochondrial ROS, might also trigger $A\beta$ production, the complex III inhibitor antimycin was administered and the effects on superoxide anion radical levels and soluble $A\beta_{1-40}$ were examined (Fig. 3). DHE fluorescence in HEK293 cells increased significantly over a period of 120 min (Fig. 3A). Similarly to rotenone, antimycin also increased the levels of soluble $A\beta_{1-40}$ modestly after 2 h and significantly after 24 h (Fig. 3B). We conclude that both complex I- and complex III-derived ROS trigger formation of $A\beta$.

$A\beta$ overproduction impairs mitochondrial function and mitochondrial dynamics

To simulate increased $A\beta$ levels during the progression of sporadic AD, HEK293 control cells that stably overexpress

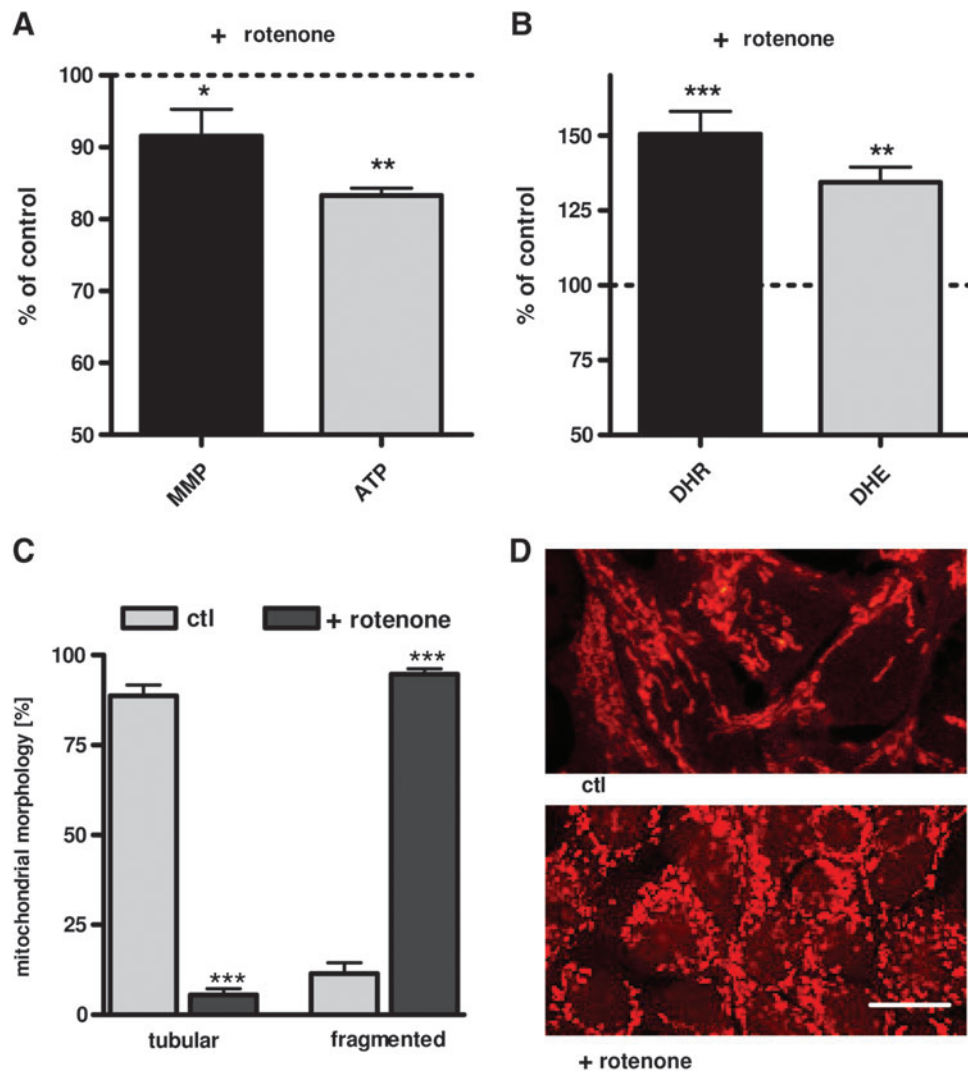


FIG. 1. Complex I inhibitor rotenone leads to mitochondrial dysfunction, fragmentation, and enhanced reactive oxygen species (ROS) production. (A) Mitochondrial membrane potential (MMP; R123 mean fluorescence intensity [MFI] normalized on% of untreated control) and ATP levels were significantly reduced after 24-h treatment with rotenone (25 μ M). (B) Levels of superoxide anion radicals (dihydroethidium [DHE] fluorescence normalized on% of untreated controls), and cytosolic ROS (dihydrorhodamin [DHR] fluorescence protein normalized on% of untreated controls) were increased after 2 h treatment with rotenone (25 μ M). (C) Histogram of quantitative analysis of mitochondrial morphology (MitoTracker CMXRos) after 24 h rotenone insult (100 mitochondria/*n*). (D) Representative confocal images that revealed changes in the mitochondrial morphology of human embryonic kidney (HEK) cells treated with rotenone (25 μ M, 24 h; bars represent 10 μ m) compared to untreated controls after mitochondrial staining with MitoTracker CMXRos (red). (A–C) $n = 6 \pm$ standard error of the mean (SEM); unpaired *t*-test; * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. (To see this illustration in color the reader is referred to the web version of this article at www.liebertonline.com/ars).

either wild-type APP (APPwt) or the Swedish mutation (APPsw) were used to elucidate the effects of enhanced A β levels on mitochondrial function and ROS production. The cells were characterized by different A β_{1-40} loads increasing from control cells (untransfected human embryonic kidney cells [HEKut]), to APPwt to APPsw cells (Fig. 4A). Using APPwt or APPsw cell lines allowed us to study the dose-dependent effects of A β , both representing a model of chronic A β stress characterized by A β_{1-42} /A β_{1-40} ratios of 1/100 in APPwt and 1/1000 in APPsw cells. Superoxide anion radicals were increased to a similar extent in APPwt and APPsw cells (Fig. 4B) although A β_{1-40} levels were 100-fold higher in APPsw cells than in APPwt cells (Fig. 4B). Comparing A β_{1-40} , ATP levels (Fig. 4C), MMP (Fig. 4E), and

cell viability (Fig. 4D) were significantly impaired in both cell types compared with control cells. To assess the capacity of the entire oxidative phosphorylation system (Fig. 4F), the respiratory control ratio (RCR) was determined by dividing basal respiration by respiration in the presence of the complex V inhibitor oligomycin as an indicator of the state of coupling (21). A significant reduction in RCR was detected in APPwt and APPsw cells, which was consistent with reduced ATP levels in APPwt and APPsw cells (Fig. 4F).

We further characterized mitochondrial function in these cells by analyzing mitochondrial morphology and dynamics (Fig. 5A–C). Cells overexpressing APP demonstrate a significantly increased fraction of fragmented mitochondria (Fig. 5A, B). Further, live-cell imaging of MitoTracker Deep

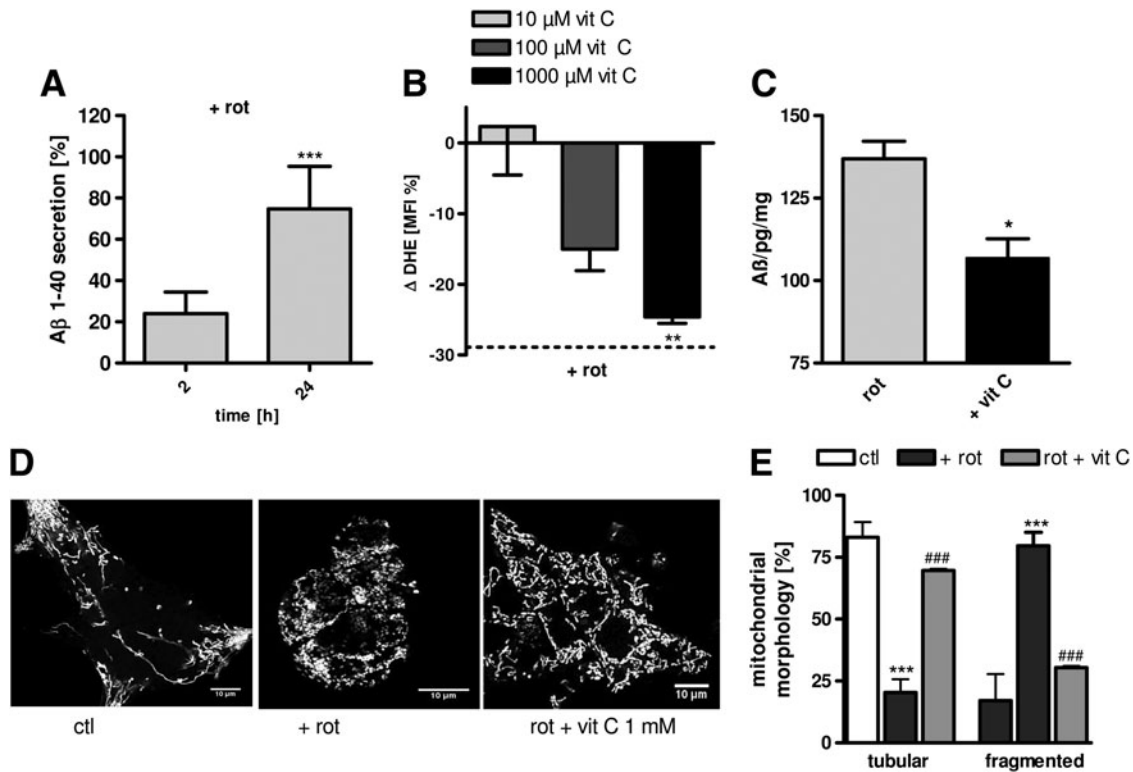


FIG. 2. Complex I dysfunction leads to ROS-dependent A β generation. (A) Soluble A β_{1-40} levels in HEK cells are significantly increased after 24-h insult with rotenone (rot; 25 μ M) compared to control cells (ctl). (B) 4-h preincubation with vitamin C (1000 μ M) leads to a significant reduction of superoxide anion radicals (Δ DHE MFI, normalized on % of untreated controls) after rotenone insult (25 μ M, 2 h). (C) ROS scavenging using vitamin C (1000 μ M) results in significantly reduced A β_{1-40} levels after 24 h insult with rotenone (25 μ M). (D) Representative images reveal changes in mitochondrial morphology when cells are pretreated with vitamin C (1000 μ M) and afterward stressed with rotenone (25 μ M) compared to untreated controls. Mitochondria were stained with MitoTracker CMXRos (bars represent 10 μ m). (E) Histogram of quantitative analysis of mitochondrial morphology in the presence and absence of vitamin C (1000 μ M, preincubation 4 h) after 24-h rotenone insult (100 mitochondria/ n). (A–C) $n = 6 \pm$ SEM; unpaired t -test; * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. (E) $n = 6 \pm$ SEM; unpaired t -test, *** $p < 0.001$ ctl compared to rotenone treated cells, ### $p < 0.001$ rotenone treated cells against vit C + rotenone-treated cells.

Red-stained mitochondria was performed for 2 min and the mobility of mitochondria as revealed by the average change in mitochondrial localization was determined. The APPwt and APPsw cells exhibited a slight but significant reduction of mitochondrial mobility compared to control cells (Fig. 5C).

Taken together, mitochondrial function and the extent of ROS formation is affected to a similar extent in APPwt and APPsw cells when compared to control cells. These results indicate that deterioration of mitochondrial functionality might already be promoted at moderately elevated A β levels and does not further increase with higher A β levels such as those present in APPsw cells. This might be a relevant finding for disease progression in sporadic AD, since it suggests that moderate elevation of A β can be sufficient to impair mitochondrial function already at early stages of AD.

Involvement of ROS in A β -mediated mitochondrial dysfunction

BACE1, together with a disintegrin and metalloprotease domain (ADAM) and γ -secretase, regulates APP processing (17). To test whether elevated A β levels are only due to the overexpression of APPwt or APPsw, or if other mechanisms such as mitochondrial dysfunction and elevated ROS are also involved, APPwt and APPsw cells were treated with vitamin

C, and ROS levels, A β_{1-40} , and BACE1 activity were investigated. We focused on BACE1 activity because BACE1 activity was earlier shown to increase upon applying external oxidative stress using H₂O₂ (55). BACE1 activity was two- to threefold increased in both APPwt and APPsw cells compared to control cells (Fig. 6A). To investigate the possible role of increased ROS levels, vitamin C was used and its effects on superoxide anion radicals, BACE1 activity, and A β levels were tested. APPwt and APPsw cells were incubated for 24 h with vitamin C (1000 μ M) (Fig. 6). Superoxide anion radicals were significantly reduced in both cell types (Fig. 6B) and BACE1 activity was significantly diminished (Fig. 6C). In addition, A β levels were moderately reduced in APPwt cells and significantly reduced in APPsw cells (Fig. 6D). We conclude that altered APP processing promoting A β formation is at least in part linked to ROS-dependent BACE1 activity.

Mitochondrial dysfunction leads to increased A β production in vivo

After demonstrating that complex I dysfunction leads *via* enhanced ROS production to elevated A β levels and that A β itself further impairs mitochondrial function, we asked whether these findings could be confirmed in a neuronal cell line and two mouse models. In SH-SY5Y cells, a dose-dependent

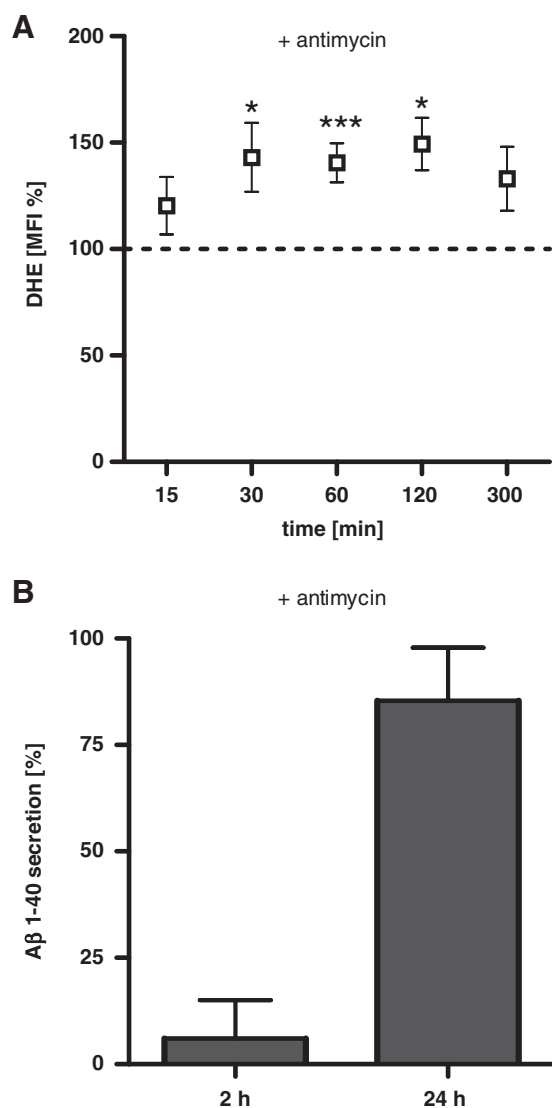


FIG. 3. Complex III dysfunction also leads to enhanced ROS and A β levels. (A) Levels of superoxide anion radicals (DHE MFI normalized on untreated controls) were significantly increased after the treatment with antimycin ($100 \mu\text{M}$) for 30, 60, and 120 min. (B) Soluble A β_{1-40} levels in HEK cells are significantly increased after 24-h insult with antimycin ($100 \mu\text{M}$) compared to cells without antimycin. (A, B) $n = 6 \pm \text{SEM}$; unpaired t -test; * $p < 0.05$, *** $p < 0.001$.

effect of rotenone was observed on MMP and ATP levels as well as on A β_{1-40} levels (Fig. 7A, B). Already at a concentration of $2.5 \mu\text{M}$ rotenone, a significant decrease of ATP and MMP was detected, which correlated with enhanced soluble A β_{1-40} levels. A maximal effect was measured at a concentration of $25 \mu\text{M}$ rotenone, which was in agreement with the effect of rotenone in HEK cells. Our data are consistent with the findings reported in fibroblasts, where rotenone leads to maximally increased ROS levels and a reduction of complex I activity only at concentrations in the micromolar range (57).

Moreover, we used a mouse model with complex I deficiency due to inactivation of the *Ndufs4* gene (complex I subunit) first described by Kruse *et al.* (2008). We determined soluble A β_{1-40} levels in whole brain homogenates of 5-week-old homozygous knockout (KO) *Ndufs4* KO mice compared to

age-matched heterozygous and wild-type *Ndufs4* mice. The KO mice have reduced complex I activity. Until week 5 they appear healthy, then ataxia progresses until death at week 7 (8, 26). Mice heterozygous for *Ndufs4* are indistinguishable in behavior compared to wild-type mice. In this genetic model of complex I dysfunction, soluble A β_{1-40} levels in brain homogenates were significantly enhanced in KO mice compared to heterozygous (het) and wild-type (wt) mice (Fig. 7C).

To further corroborate our results, we decided to treat mice representing a well-established mouse model for AD with the complex I inhibitor rotenone. C57BL/6 mice bearing the human Swedish (S:KM595/596NL) and London (L:V717I) mutations in the 751 amino acid form of human APP (tgAPP) under the control of a murine Thy-1 promoter at an age of 13 months. Age-matched nontransgenic littermate animals were treated for 3 days with rotenone i.p. ($10 \text{ mg/kg/body weight [BW]}$) and soluble A β levels in brain homogenates were investigated. Again, A β_{1-40} levels were increased in animals treated with rotenone compared to animals only receiving the vehicle (Fig. 7D). These results strongly support our hypothesis that mitochondrial dysfunction associated with elevated ROS, in particular complex I dysfunction, induces enhanced amyloidogenic APP processing resulting in elevated A β levels.

Discussion

Our study provides several lines of evidence that mitochondrion-derived ROS are a sufficient trigger for inducing formation of A β . This may have major implications as it suggests that mitochondrial dysfunction is involved early in the pathogenesis of sporadic AD (Fig. 8). This view fits to the fact that mitochondrial dysfunction associated with enhanced mitochondrial ROS production is considered to be intimately involved in the aging process (5). Mitochondria are a major source and target of ROS produced by the respiratory chain that attack mitochondrial constituents, including proteins, lipids, and mtDNA (37). The two major sites of oxidative stress generation are complex I and complex III (40, 41, 45). Mainly, complex I is specifically susceptible to the aging process because 7 of 13 mt-DNA encoded polypeptides acting as subunits of respiratory chain complexes are found in complex I (43). A progressive alteration of mitochondrial gene expression was observed in rats and humans, including the NDUFV1 subunit of complex I, which is involved in electron transfer (6, 30).

On the basis of the following arguments, we hypothesize that complex I dysfunction associated with increased ROS production is a starting point and driving force of the amyloid cascade in AD. First, complex I dysfunction was induced in HEK293 cells with the complex I inhibitor rotenone leading to severe mitochondrial dysfunction, increased ROS, a fragmentation of mitochondria, and significantly increased soluble A β_{1-40} levels. This increase could be attenuated by scavenging of ROS with vitamin C, which also improved mitochondrial morphology showing that mitochondrion-derived ROS contribute to amyloidogenic APP processing. The group of Palmiter recently published an effect of rotenone on microtubule depolymerization that was independent of complex I (8). However, we primarily consider rotenone-induced ROS formation as relevant for our findings since increasing ROS levels by complex III inhibition with antimycin A also leads to significantly increased A β levels. Our findings that ROS are involved in enhanced APP processing are

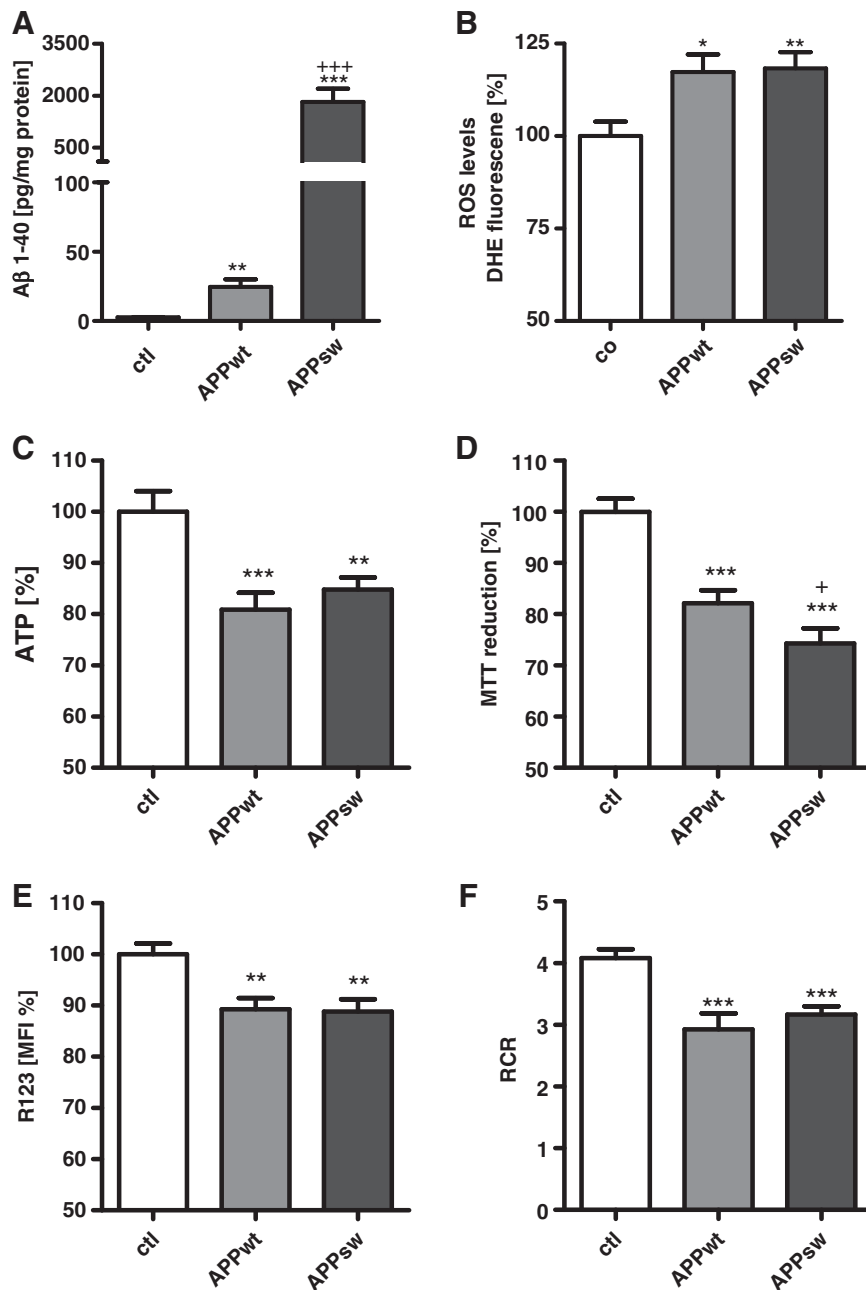


FIG. 4. Mitochondrial function is greatly impaired in wild-type amyloid precursor protein (APPwt) and APP containing the Swedish mutation (APPsw) cells. (A) $A\beta_{1-40}$ levels in transfected HEK cells are significantly increased in APPwt and APPsw cells. (B) Superoxide anion radicals (DHE fluorescence units/mg protein normalized on control cells) are significantly enhanced in APPwt and APPsw cells. (C) ATP levels and cell viability (D) are reduced in both APPwt and APPsw. (E) MMP (R123 units/mg protein expressed as MFI normalized to control cells) is significantly impaired in APPwt and APPsw cells. (F) Using a high-resolution respiratory system, respiratory control ratio (RCR; basal respiration/respiration under the treatment with oligomycin) representing the mitochondrial coupling state is significantly reduced again in APPwt and APPsw cells (A–E) $n=6 \pm \text{SEM}$; unpaired *t*-test; ctl against APPwt or APPsw * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. + $p < 0.05$ APPwt against APPsw, +++ $p < 0.001$ APPwt against APPsw.

supported by earlier findings demonstrating that H_2O_2 also induced elevated $A\beta$ levels (16, 55). Furthermore, hypoxia and energy deprivation that are also associated with enhanced ROS levels as well lead to increased $A\beta$ levels in cell and mouse models (42, 53).

To explore if $A\beta$ itself can cause mitochondrial dysfunction and oxidative stress and thereby may start a vicious cycle accelerating amyloidogenic APP processing, HEK293 cells overexpressing human APPwt, and the APPsw mutation were used. APPwt cells reflect the physiological situation during aging with moderately elevated $A\beta$ levels and APPsw, the scenario occurring in the familial AD with high $A\beta$ levels. Mitochondrial function was broadly disturbed in both cell types as reflected by reduced MMP, decreased ATP levels, declined RCR, increased ROS levels, and altered mitochondrial morphology and mobility. Our findings are in line with

recent studies in animal and cell models of AD (18, 25, 49, 61), which also showed a decrease in MMP and ATP levels. Complex IV activity is specifically attenuated by $A\beta$. In addition, others and we showed that complex I activity is synergistically downregulated by $A\beta$ and tau to the already impaired complex I activity during aging (9, 18, 49). In both cases, expression of different subunits of complexes I and IV is deregulated (49). Decreased expression levels may be further result from the interaction of $A\beta$ with the translocase of the outer mitochondrial membrane (TOM) (10) as $A\beta$ has been proposed to block TOM and thereby the import of nuclear encoded proteins important for the respiratory chain (1). Furthermore, we observed mitochondrial fragmentation, and reduced mitochondrial mobility in APPwt and APPsw cells pointing to an imbalance in mitochondrial fission and fusion processes. These findings are in line with experiments

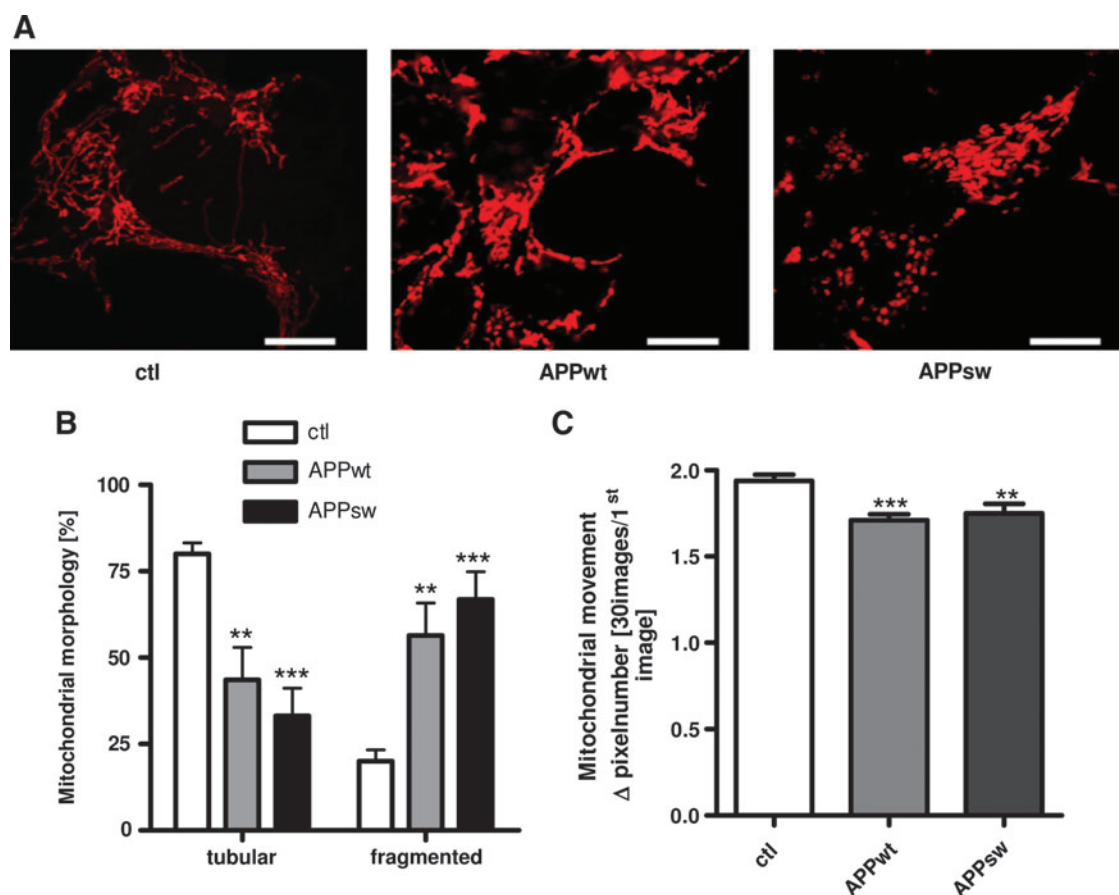


FIG. 5. Mitochondrial morphology is strongly altered in APPwt and APPsw cells. (A) Representative example of confocal microscopic images revealing mitochondrial morphology changes in APPwt and APPsw cells. Mitochondrial staining was done using MitoTracker CMXRos (red, bars represent 10 μ m). (B) Histogram of mitochondrial morphology quantification (100 mitochondria/ n were analyzed). (C) Live cell imaging of mitochondria stained with MitoTracker Deep Red. Images were recorded over 2 min (one picture every 1.5 s) to study mitochondrial dynamics. Histogram depicting quantitative changes in mitochondrial dynamics in APPwt and APPsw cells. (B, C) $n=6 \pm$ SEM; unpaired t -test; ** $p < 0.01$, *** $p < 0.001$ ctl against APPwt or ctl against APPsw, respectively. (To see this illustration in color the reader is referred to the web version of this article at www.liebertonline.com/ars).

showing that oligomeric A β leads to mitochondrial fragmentation and increased fission associated by an increased expression of fission factors such as DRP-1 (51, 52, 58, 59).

Importantly, in our cell model moderately elevated A β levels are sufficient to induce mitochondrial dysfunction. There seems to be a maximal effect on mitochondrial function already observed in APPwt cells, which have much lower A β levels than APPsw cells. These findings could explain why moderately enhanced A β levels due to mitochondrial dysfunction during aging are sufficient to initiate the pathological cascade of sporadic AD.

In addition, we found that ROS levels and BACE1 activity were significantly increased in APPwt and APPsw cells. The connection between elevated oxidative stress and increased A β production in HEK control cells, APPwt, and APPsw cells was further supported by elevated A β_{1-40} levels after the treatment with H₂O₂ (Supplementary Fig. S2). Importantly, ROS scavenging leads to reduced A β levels and BACE1 activity. The enhanced oxidative stress in this AD cell model is presumably caused by two different mechanisms: (1) impairment of complex I activity directly by A β (18, 49) and (2) the induction of oxidative stress by A β aggregation itself

(33, 46). Transition metals such as Cu²⁺, Zn²⁺, or Fe³⁺ enhance A β neurotoxicity by producing H₂O₂. These findings are supported by several groups using different AD models (3, 18, 25, 36, 46, 49). Furthermore, our findings are consistent with earlier reports in which H₂O₂, energy deprivation, or ischemia, stressors that are known to cause elevated ROS levels, increase the activity and the expression levels of BACE1 (55, 56). Importantly, elevated BACE1 activity after ischemia was reversed by the antioxidant trolox or superoxide dismutase overexpression (16). At the signal transduction level, the c-jun N-terminal kinase/c-jun pathway is discussed to be key player to regulate BACE1 expression after oxidative stress (55).

BACE1 regulates, together with ADAM and γ -secretase, APP processing. Increased BACE1 activity was proposed to be linked to AD (20, 28, 60). Overexpression of the enzyme was demonstrated to dramatically increase A β production, while a knock-down of BACE1 is associated with reduced A β generation (7, 31). Furthermore, BACE1 protein was found to be increased in frontal cortex of AD patients compared to controls (19). In addition, an increase of γ -secretase was found in temporal cortex of AD patients (15). Taken together, we propose

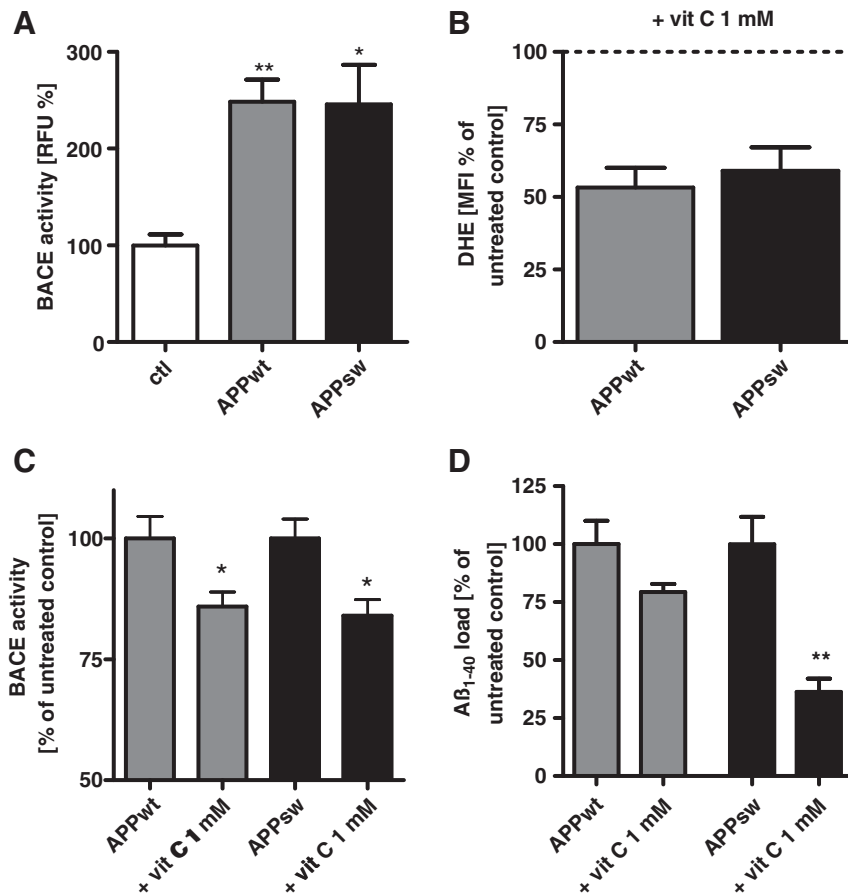


FIG. 6. ROS are also involved in amyloidogenic APP processing in APPwt and APPsw cells. (A) Basal β -site APP cleaving enzyme 1 (BACE1) activity is increased in APPwt and APPsw cells. **(B)** Effectivity of ROS scavenging in APPwt and APPsw cells by vitamin C on DHE MFI (1000 μ M; 4 h incubation). **(C)** BACE1 activity is reduced in APPwt and APPsw cells by 4-h incubation of vitamin C (1000 μ M). **(D)** Reduction of $A\beta$ levels in APPwt and APPsw cells by vitamin C (1000 μ M, 4 h incubation). **(A–D)** $n=6 \pm$ SEM; unpaired t -test; * $p < 0.05$, ** $p < 0.01$. **(A)** ctl against APPwt or ctl against APPsw. **(C, D)** APPwt or APPsw against APPwt + vit C or APPsw against APPsw + vit C.

that one possible mechanism explaining enhanced $A\beta$ formation is linked to the ROS-dependent activation of BACE1.

To further test our hypothesis that mitochondrial dysfunction and especially complex I dysfunction is the starting point of the amyloid cascade in sporadic AD, we used SH-SY5Y cells as a neuronal cell model and two mouse models of complex I dysfunction. In SH-SY5Y cells, we found similar effects of rotenone on $A\beta$ levels and mitochondrial function. In our first mouse model, which was deficient in complex I due to inactivation of the *Ndufs4* gene (22), $A\beta$ levels were increased even before there was notable pathology or behavioral effects. Interestingly, in an AD animal model crossed with a complex IV KO model, $A\beta$ levels were not increased, but, on the contrary, amyloid plaques were even reduced (14). This reduction is accompanied by a reduction in BACE1 activity, and ROS levels. These findings strongly suggest that not dysfunction of mitochondrial complexes *per se* is sufficient to induce $A\beta$ elevation but that the mitochondrion-derived ROS mediate this deleterious effect.

In the second mouse model we used, Thy-1 APP mice treated with rotenone for 3 days, $A\beta_{1-40}$ levels were increased. These results are in line with recently published findings showing that in APP transgenic mice (Tg2576) the pesticide paraquat, which enhances ROS levels, also increases $A\beta$ levels.

Not only in sporadic AD but also in sporadic Parkinson disease (PD), aging is the most prominent risk factor. We suggest that in both pathologies, complex I dysfunction that is tightly associated with aging plays an important role in the pathogenesis of these disorders. Several patients suffer

from mixed forms of PD and AD associated with not only α -synuclein but also $A\beta$ plaques. This could be explained by the mechanism proposed here. Disease-specific pathological features such as the APOE4 status in AD or the high sensitivity of substantia nigra neurons in PD might then trigger further progression of the respective neurodegenerative disease.

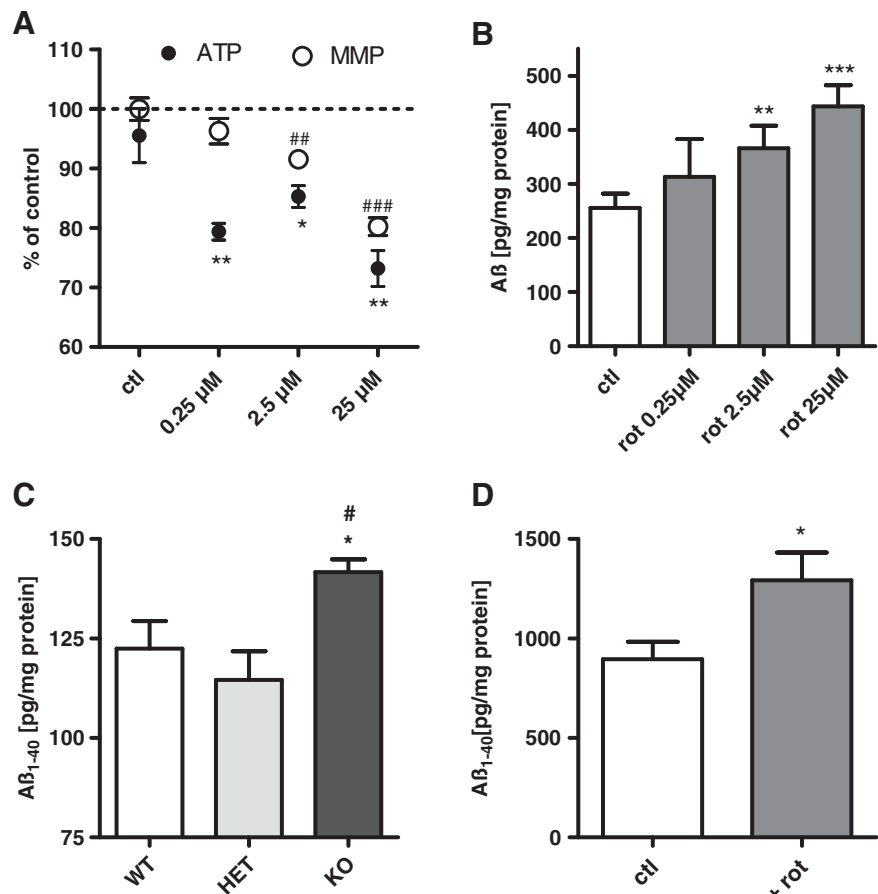
An important question that arises from our data is whether patients suffering from mitochondrial disorders such as mitochondrial encephalopathy, lactacidosis, stroke-like episodes (MELAS), myoclonic epilepsy with ragged red fibers, or Kearns Sayre syndrome show cognitive decline and dementia (mitochondrial dementia). Indeed, cognitive impairment and dementia are frequent findings in mitochondrial disorders. Several clinical, morphological, functional, and chemical manifestations were detected in these patients (13). Recently, a sporadic case of progressive cognitive and behavioral decline was identified in patient with a rare m.3291T > C MELAS mutation (50). Interestingly, AD-like $A\beta$ plaques were found in a female MELAS patient, who was only 54 years old at the time of testing, even though no evidence for familial AD resulting from APP mutations was found (24).

Materials and Methods

Materials

Rhodamine 123 (R123), DHE, dihydrorhodamin (DHR), Mitotracker CMX ROS, Mitotracker Deep Red, and MTT were purchased from Invitrogen. Rotenone, antimycin, and ascorbic acid were obtained from Sigma. The Vialight Plus assay

FIG. 7. Enhanced A β levels in a neuronal cell model and two animal models of complex I dysfunction. (A) SH-SY5Y cells were treated with rotenone (0.25, 2.5, and 25 μ M) for 24 h and ATP and MMP as well as soluble A β_{1-40} levels **(B)** were determined $n=6 \pm$ SEM, unpaired t -test, **(A)** * $p < 0.05$, ** $p < 0.01$, ATP ctl against rot, ## $p < 0.01$, ### $p < 0.001$ MMP against rot. **(B)** ** $p < 0.01$ ctl against rot 2.5 μ M, *** $p < 0.001$ ctl against rot 25 μ M. **(C)** APP transgenic animals received rotenone *via* i.p. application (10 mg/kg/body weight) or vehicle for 3 days and soluble A β_{1-40} levels in brain homogenates were measured. $n=6 \pm$ SEM per treatment group unpaired t -test * $p < 0.05$. **(D)** In homozygous knockout (KO) *Ndufs4* mice, A β_{1-40} levels are significantly increased compared to wild-type (wt) and heterozygous (HET) mice. *Ndufs4* mice wt $n=5 \pm$ SEM, HET $n=5 \pm$ SEM, KO $n=12 \pm$ SEM; unpaired t -test; * $p < 0.05$ wt against KO, # $p < 0.05$ HET against KO.



was purchased from Lonza. Mouse A β_{1-40} , human A β_{1-40} , and A β_{1-42} enzyme-linked immunosorbent assay (ELISA) were obtained from Invitrogen. The BACE activity assay was purchased from Calbiochem.

Cell culture

HEK cells were transfected with DNA constructs harboring the human mutant APP (APP^{sw}, K640/n671L) gene, and the APP^{wt} gene, inserted downstream of a cytomegalovirus promoter using the FUGENE 6 technology (Roche Diagnostics) (12, 25). The stably expressing APP^{wt} and APP^{sw} HEK 293 cells were cultured in Dulbecco's modified Eagle's medium supplemented with 10% heat-inactivated fetal calf serum, 50 units/ml penicillin and 50 μ g/ml streptomycin, and 400 μ g/ml G418 at 37°C in a humidified incubator containing 5% CO₂. HEKut cells were grown in Dulbecco's modified Eagle's medium supplemented with 10% heat-inactivated fetal calf serum, 50 units/ml penicillin, and 50 μ g/ml streptomycin at 37°C in a humidified incubator containing 5% CO₂.

SH-SY5Y cells were grown in Dulbecco's modified Eagle's medium supplemented with 10% heat-inactivated fetal calf serum, 5% heat-inactivated horse serum, 50 units/ml penicillin, and 50 μ g/ml streptomycin at 37°C in a humidified incubator containing 5% CO₂.

Fluorescence-activated cell sorting measurement

HEK cells were seeded at a density of 10⁵ cells/well the day before the experiment in 48-well plates. They were

incubated for 0.5, 1, 2, 5, or 24 h with rotenone (25 μ M) at 37°C in culture medium at pH 7.4 and 37°C. Superoxide anion radical concentration was investigated after incubation with 5 μ M DHE for 30 min. Other ROS species were detected after 15-min incubation with 10 μ M DHR. After incubation with the fluorescence dyes, cells were washed with Hanks' balanced salt solution (HBSS) containing 138 mM NaCl, 6 mM KCl, 1 mM MgCl₂, 2 mM CaCl₂, 5.5 mM glucose, and 10 mM HEPES (pH 7.4, 37°C). Afterward, cells were resuspended in HBSS and immediately analyzed by flow cytometry (FACS Calibur; BD Bioscience) using Cell Quest pro software (BD Biosciences).

ATP assay

HEKut, HEK APP^{wt}, HEK APP^{sw}, and SH-SY5Y cells were plated the day before at a density of 2 \times 10⁴ cells/well in a white 96-well plate. HEKut cells were incubated with rotenone (25 μ M) for 0.5, 1, 2, 5, or 24 h at 37°C in culture medium at pH 7.4 and 37°C. SH-SY5Y cells were incubated for 24 h with rotenone (0.25, 2.5, and 25 μ M). Afterward, cells were washed twice with HBSS and the reagents were added according to the ViaLight Plus protocol. The bioluminescent method (ViaLight Plus Kit; Lonza) utilizes an enzyme, luciferase, which catalyzes the formation of light from ATP and luciferin. The emitted light is linearly related to the ATP concentration and is measured using a luminometer (Victor² multiplate reader; PerkinElmer Life Sciences).

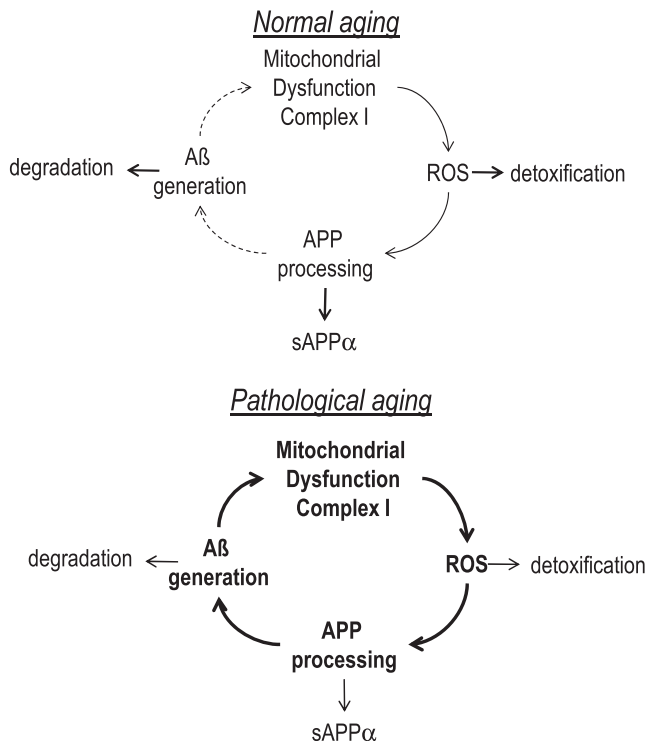


FIG. 8. Schematic illustration of mitochondrial dysfunction in healthy brain aging and pathological brain aging. In normal brain aging there is an equilibrium between mitochondrion-derived ROS, APP processing, and $A\beta$ generation on the one hand and detoxification and degradation mechanisms on the other hand. During the disease process this balance is shifted toward the toxic mechanism with preponderance for mitochondrion-derived ROS, APP processing associated with increase BACE activity, and $A\beta$ generation.

Determination of MMP

HEKut, HEK APPwt, HEK APPsw cells, and SH-SY5Y cells were plated the day before at a density of 2×10^5 cells per well in a 24-well plate. HEK ut cells were incubated for 0.5, 1, 2, 5, or 24 h at 37°C in culture medium at pH 7.4 and 37°C. SH-SY5Y cells were incubated for 24 h with rotenone (0.25, 2.5, and 25 μ M). The MMP of HEK cells and SH-SY5Y cells was measured using the fluorescence dye R123. The experimental conditions used have been shown previously to detect even small changes (16, 21). Transmembrane distribution of the dye depends on the MMP. The dye was added to the cell culture medium in a concentration of 0.4 μ M for 15 min (21). The cells were washed twice with HBSS and the fluorescence was determined with a fluorescence reader (Victor[®] multilabel counter; Perkin-Elmer) at 490/535 nm.

MTT assay

HEK cells were plated the day before at a density of 2×10^4 cells/well in a 96-well culture plate. The assay is based on the cleavage of the yellow tetrazolium salt MTT into purple formazan by metabolically active cells. This cellular reduction involves the pyridine nucleotide cofactors NADH and NADPH. Twenty microliters (final concentration 1.0 mg/ml) of MTT reagent was added 2 h before the end of incubation. The formazan crystals were solubilized by adding 100 μ l of a

20% sodium dodecyl sulfate/50% *N,N*-dimethyl-formamide solution. The absorption of the solubilized formazan was measured at 570 nm using a microplate reader.

Mitochondrial respiration

HEK cells were harvested from culture plates, counted, adjusted to 3×10^6 cells per 2 ml in 37°C tempered cell medium, and transferred to the chamber of the Oxygraph2k from Oroboros Instruments. The cells were immediately measured parallel to control cells in the following setting: basal respiration, respiration after addition of oligomycin (2 μ g/ml final concentration), carbonyl cyanid p-(trifluoromethoxy)phenylhydrazone (1 μ M), rotenone (2 μ M), and finally KCN (2 mM). The quotient of basal respiration and respiration after oligomycin incubation was calculated and used as degree of the respiratory ratio.

Human $A\beta$ 1–40 ELISA and mouse $A\beta$ 1–40 ELISA

For the detection of secreted soluble mouse and human $A\beta$ 1–40 and $A\beta$ 1–42, a specific sandwich ELISA employing monoclonal antibodies was used. The ELISA was performed according to the instructions given in the Abeta-ELISA kit by Invitrogen. Briefly, to measure human basal soluble $A\beta$ _{1–40} and $A\beta$ _{1–42} levels, transfected HEK cells were allowed to grow until 80% confluence. Afterward, supernatants were collected and ELISA was conducted. Cell pellets were used for protein determination to normalize the samples. To detect $A\beta$ _{1–40} in HEKut cells, HEK cells were incubated with rotenone (25 μ M) or antimycin (100 μ M) for 2 or 24 h in the absence of presence of vitamin C (1000 μ M). Afterward, supernatants were collected and after a centrifugation step (400 g for 5 min) and the ELISA was conducted. Cell pellets were used for protein determination to normalize the samples.

Ndufs4-null mice (KO) were generated as described elsewhere (21). All animal experiments were approved by the Animal Care and Use Committee at the University of Washington. Mice were maintained with rodent diet (5053; Picolab) and water available ad libitum with 12-h light–dark cycle at 22°C. At an age of 5 weeks, mice were anesthetized with an overdose of pentobarbital and whole brains were frozen in isopentane/dry ice, and stored at -80°C until use. The cerebellum was removed and the tissue was homogenized in eightfold-volume ice-cold buffer (phosphate-buffered saline [PBS]/protease inhibitor [PI]) of the brain weight and homogenized using a glass homogenizer (10–15 strokes, 400 rpm) The resulting homogenate was centrifuged at 15,000 g for 30 min at 4°C and directly transferred to the $A\beta$ _{1–40} mouse ELISA measurements using a Victor² multiplate reader (PerkinElmer Life Sciences). The protein content was determined according to the method of Lowry (29) using bovine serum albumin as the standard (BIO-RAD).

Heterozygous C57BL/6J mice (from Charles River) bearing the human Swedish mutation (KM670/671NL) and London mutation (V717I) in the 751 amino acid form of tgAPP under the control of a murine Thy1.2 promoter were bred in our animal facilities and were used in these experiments at an age of 13 months. All animal care and experimental procedures were in concordance with the German law on animal care and handling of transgenic animals. At weaning, the animals were genotyped from tail biopsies by means of an appropriate digest and polymerase chain reaction (data not shown). The mice were treated with rotenone 10 mg/kg/BW solubilized in

mygliol/dimethyl sulfoxide (2%) i.p. for 3 days. Afterward, animals were sacrificed by decapitation, and the brain hemispheres were rapidly dissected and washed in ice-cold buffer (PBS/PI). After removing the cerebellum, the tissue was homogenized in eightfold-volume ice-cold buffer (PBS/PI) of the brain weight homogenized using a glass homogenizer (10–15 strokes, 400 rpm), and the resulting homogenate was centrifuged at 15,000 *g* for 30 min at 4°C. The supernatant was diluted 1:50 in standard diluent buffer provided by Invitrogen, and A β_{1-40} levels were determined using a specific human A β_{1-40} ELISA (Invitrogen) using a Victor² multiplate reader (PerkinElmer Life Sciences). The protein content was determined according to the method of Lowry (29) using bovine serum albumin as the standard (BIO-RAD).

Confocal laser scanning microscopy

HEK cells were seeded 3 days before measurement on cover slips, which were coated with 0.01% gelatin. For live cell imaging experiments, cells were incubated overnight with 25 nM Mitotracker Deep Red. Micrographs were taken with a Leica SP 5 confocal laser scanning microscope (Leica) fitted with the appropriate filters and a plan-apochromate 63 \times , 1.4 NA. Live cell experiments were performed at 37°C and 5% CO₂ in a humidified chamber. For mitochondrial mobility studies, a picture was taken every 1.5 s over 2 min and the increase in gray scales was calculated compared to the first picture (23).

For morphological analyses, cells were incubated overnight with 25 nM Mitotracker CMXRos and fixed with 4% formalin in PBS (pH 7.4, 37°C) for 20 min at room temperature, washed three times with PBS, lysed for 30 min with 0.2% Triton \times 100 solution, and washed three times with PBS. The samples were embedded in Mowiol and analyzed with the confocal laser scan microscope TCS SP5 (Leica). For analysis of mitochondrial dynamics, ImageJ 1.38 \times (National Institutes of Health) was used. For analyses of mitochondrial morphology, Imaris Version 6.2 (Bitplane) was used. AutoQuant X Version 2.1 from Media Cybernetics was used for deconvolution.

BACE1 activity

To determine basal BACE1 activity, HEK control, HEK APPwt, and APPsw cells were allowed to grow until 80% confluence. Cells were collected and resuspended in ice-cold extraction buffer. The resulting supernatant was used according to the instructions given in the β -Secretase Activity Assay Kit, Fluorogenic by Calbiochem. For normalization, protein levels of every probe were determined.

Statistical analysis

The data are given as the mean \pm SEM. For statistical comparison, Student's *t*-test and one-way analysis of variance followed by Tukey's *post hoc* test for multiple comparisons were used. *p*-Values < 0.05 were considered statistically significant.

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Author Disclosure Statement

No competing interests exist.

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Address correspondence to:

Prof. Kristina Leuner
Department of Pharmacology
ZAFES, Biocenter
University of Frankfurt, Frankfurt/Main
Max-von-Laue-Str.9
60438 Frankfurt
Germany

E-mail: leuner@em.uni-frankfurt.de

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Abbreviations Used

A β = amyloid beta
AD = Alzheimer's disease
ADAM = a disintegrin and metalloprotease domain
APP = amyloid precursor protein
APP^{sw} = APP containing the Swedish mutation
APP^{wt} = wild-type APP
BACE1 = β -site APP cleaving enzyme
BW = body weight
complex IV = cytochrome c oxidase
DHE = dihydroethidium
DHR = dihydrorhodamin
ELISA = enzyme-linked immunosorbent assay
HBSS = Hanks' balanced salt solution
HEKut = untransfected human embryonic kidney cells
MELAS = mitochondrial encephalopathy, lactacidosis, stroke-like episodes
MFI = mean fluorescence intensity
MMP = mitochondrial membrane potential
KO = knockout
PBS = phosphate-buffered saline
PD = Parkinson disease
PI = protease inhibitor
R123 = Rhodamine 123
RCR = respiratory control ratio
ROS = reactive oxygen species
rot = rotenone
SEM = standard error of the mean
tgAPP = human APP
TOM = translocase of the outer mitochondrial membrane