

Perturbed mitochondrial Ca²⁺ signals as causes or consequences of mitophagy induction

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Abbreviations: ATP2A, ATPase Ca²⁺ transporting cardiac muscle; ATP2B, ATPase, Ca²⁺ transporting plasma membrane; BCL2, B-cell CLL/lymphoma 2; BECN1, Beclin 1, autophagy related; DNML1, dynamin 1-like; ER, endoplasmic reticulum; FIS1, fission 1 (mitochondrial outer membrane) homolog (*S. cerevisiae*); HSPA9, heat shock 70 kDa protein 9 (mortalin); ITPR, inositol 1,4,5-trisphosphate receptor; MCU, mitochondrial calcium uniporter; MFF, mitochondrial fission factor; MPT, mitochondrial permeability transition; mPTP, mitochondrial permeability transition pore; OMM, outer mitochondrial membrane; PINK1, PTEN-induced putative kinase 1; RHOT1, ras homolog family member T1/mitochondrial Rho GTPase 1; ROS, reactive oxygen species; Ψ_m , mitochondrial potential; SLC8A, Na⁺/Ca²⁺ exchanger; VDAC1, voltage-dependent anion channel 1

Mitophagy is an essential process that maintains mitochondrial quality and number, thus limiting cellular degeneration. Along with apoptosis, mitophagy participates in cellular fate decisions by eliminating damaged mitochondria. A variety of mitochondrial parameters, such as structure, membrane potential, and reactive oxygen species, are key determinants in triggering the mitophagic machinery. These parameters are also important regulators of the mitochondrial capacity for calcium (Ca²⁺) uptake. Rapid Ca²⁺ accumulation in the mitochondrial matrix allows for prompt stimulation of the organelle. This process requires a close morphofunctional coupling between mitochondria and the main intracellular Ca²⁺ stores. In mitophagy, the role of Ca²⁺ remains obscure. What role does mitochondrial Ca²⁺ play in metabolic sensing or in mitochondrial remodeling? Is endoplasmic reticulum (ER)-Ca²⁺ crosstalk involved? These are some of the questions that we address in this review.

Introduction

Mitochondria are pivotal organelles within complex endomembrane systems that are capable of transducing a Ca²⁺ signal into the cell. Currently, it is thought that any mitochondrial dysfunction will inevitably lead to disease. In fact, many pathological conditions are associated with mitochondrial failure, including neurodegenerative diseases, motor neuron disorders, autosomal dominant optic atrophy, ischemia-reperfusion injury, diabetes, aging, and cancer.¹ A large body of experimental evidence has

unambiguously shown that in addition to their well-established function of producing most cellular ATP, mitochondria trigger cell death, thereby influencing cell fate.² Mitochondria also have the important role of activating apoptosis by releasing specific mitochondrial pro-apoptotic proteins into the cytoplasm; these proteins activate caspases and lead to apoptotic cell death.³ A variety of extracellular stimuli ranging from the binding of hormones, neurotransmitters, and growth factors to phenomena such as cell–cell interactions, induce a rise in cytosolic Ca²⁺ concentration ([Ca²⁺]_i) through diverse mechanisms with defined timing, amplitude, and kinetics^{4,5} that have an impact on mitochondrial activities including ATP production or cell death. Ca²⁺ plays a key role in the regulation of structural and functional mitochondrial alterations.³ Mitochondrial Ca²⁺ overload promotes apoptosis by inducing mitochondrial membrane permeabilization, which is characterized by mitochondrial swelling, perturbation of the outer membrane and release of pro-apoptotic factors.² The execution of this process is connected/accompanied with/by specific mitochondrial dysfunction, including the loss of mitochondrial membrane potential, increased reactive oxygen species (ROS) production and decreased ATP production with the alteration of mitochondrial Ca²⁺ homeostasis.²

The number of mitochondria, and mitochondrial health, are regulated by mitophagy, a process by which excessive or damaged mitochondria are removed. Mitophagy has a cardinal role in cellular adaptation to stress by acting as a mitochondrial quality control mechanism.⁶ The maintenance of a healthy mitochondrial population is essential for sustaining cell metabolism in various physiological states. Thus, efficient mitophagic recognition and elimination of dysfunctional mitochondria sets the threshold for mitochondrial viability, thus making the cell able to counteract unwanted degeneration and prevent inflammation and apoptosis.⁷

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As accumulating evidence has indicated, both the induction of autophagy and apoptosis are partially regulated by the same proteins. For example, the anti-apoptotic protein BCL2 regulates autophagy and apoptosis by binding to the pro-autophagic protein BECN1, and the pro-apoptotic protein BAX.⁸ It is clear that the health of mitochondria and their Ca²⁺-sensing capacity could determine the difference in cellular outcome between mitophagy and apoptosis. We therefore propose that Ca²⁺ signaling might be a key regulator of mitophagy and that it maintains a responsive mitochondrial network in the cell. Moreover, several studies in mammalian cells and in yeast models of autophagy have demonstrated a potential role for mitochondrial parameters regulated by Ca²⁺ signals [mitochondrial ROS production, membrane potential (Ψ_m) variations and fusion/fission dynamics] in modulating and/or triggering mitophagy.⁹⁻¹⁵

In this review, we summarize our current knowledge of the mechanisms of mitophagy, focusing our attention on mitochondrial morphology, Ψ_m and ROS. We also speculate on the possible pathophysiological roles of Ca²⁺ signaling and associated factors in mitophagy for the maintenance of mitochondrial homeostasis.

Intracellular Ca²⁺ Circuit

The technological advancements in probe design and detecting systems, allowed the accurate measurement of Ca²⁺ concentration ([Ca²⁺]) and distribution in intracellular compartments, and revealed a marked asynchronicity in cell response and a high spatio-temporal complexity of the intracellular Ca²⁺ signal. We now know that Ca²⁺ signals can be conveyed as repetitive [Ca²⁺]_c spikes (commonly referred to as Ca²⁺ oscillations)¹⁶ as well as localized [Ca²⁺]_c increases that may either be confined or gradually propagated to the rest of the cell (“Ca²⁺ waves”).^{17,18}

Cell Ca²⁺ entry is driven by the presence of a large electrochemical gradient across the plasma membrane. Various entry channels are involved with widely different properties: the voltage-operated channels, receptor-operated channels, second-messenger-operated channels, and store-operated channels or G protein-operated-calcium channels. The interior of the cell is the more negative, yet the [Ca²⁺]_c is less than 10,000th of that in the extracellular milieu. There are also intracellular organelles, such as the ER, the Golgi apparatus, and secretory granules, that contain 1 to 10,000-fold greater [Ca²⁺] than the cytoplasm. During the “on reaction,” stimuli induce both the entry of external Ca²⁺ and the formation of second messengers that release internal Ca²⁺ that is stored within the ER or Golgi apparatus. Ca²⁺ release from internal store is controlled by Ca²⁺ itself, or by an expanding group of messengers, such as inositol 1,4,5-triphosphate (IP₃), cyclic ADP ribose, nicotinic acid adenine dinucleotide phosphate, and sphingosine-1-phosphate, which either stimulate or modulate the release channels on the internal stores. Most of this Ca²⁺ is bound to buffers, whereas a small proportion binds to the effectors that activate various cellular processes. During the course of a typical Ca²⁺ transient wave, the generation of Ca²⁺ signaling is counteracted by the “off reaction” systems, when various pumps and exchangers remove Ca²⁺ from the cytoplasm. The pumping mechanisms have important homeostatic functions in which

they maintain the resting level of Ca²⁺ and ensure that internal stores are kept loaded. Four different pumping mechanisms are responsible for the “off reaction”: ATP2B (ATPase, Ca²⁺ transporting, plasma membrane), SLC8A (Na⁺/Ca²⁺ exchanger), ATP2A (ATPase, Ca²⁺ transporting, cardiac muscle), and MCU (mitochondrial calcium uniporter).^{4,19,20} SLC8A and ATP2B extrude Ca²⁺ to the outside, whereas ATP2A pumps Ca²⁺ back into the ER. Mitochondria also have an active function during the recovery process in which they sequester Ca²⁺ rapidly through the MCU, and release it more slowly back into the cytosol to be dealt with by ATP2A and ATP2B. Both pumps have lower transport rates but high affinities, which means that they can respond to modest elevations in Ca²⁺ levels and set basal Ca²⁺ levels. The SLC8A and MCU have much greater transport rates, and can limit transient Ca²⁺ changes over a wider dynamic range.^{21,22}

Mitochondrial Morphology and Mitochondrial ER Contact Sites

The mitochondrial morphology of living cells is heterogeneous and is the result of the balance between fusion and fission events. A growing body of evidence indicates that mitochondrial morphology is critical for cell physiology. Changes in mitochondrial shape have been associated with many different processes, such as development, neurodegeneration, Ca²⁺ signaling, ROS production, cell division, and apoptotic cell death.

Mitochondrial fusion facilitates the exchange of materials between organelles and aids in the repair of defective mitochondria. Mitochondrial fission allows for proper mitochondrial segregation, enhancing distribution along the cytoskeleton or isolation of dysfunctional mitochondria. Impaired mitochondrial fusion results in reduced cell growth, decreased Ψ_m and defective respiration.²³ A similar phenotype is observed when fission is deficient, with additional loss of mitochondrial DNA (mtDNA) and reduced ATP production.²⁴

Studies on the mammalian mitochondrial fusion machinery have shown that MFN1/mitofusin 1 and MFN2/mitofusin 2 are located on the outer mitochondrial membrane (OMM),²⁵ whereas OPA1/optic atrophy 1 (autosomal dominant) is located on the inner mitochondrial membrane.²⁶ Additionally, mitochondrial division is regulated by DNM1L/dynamin 1-like,²⁷ FIS1/fission 1 (mitochondrial outer membrane) homolog (*S. cerevisiae*)²⁸ and MFF/mitochondrial fission factor.²⁹ DNM1L is a cytosolic GTPase, when its expression is inhibited or down-regulated, a highly interconnected mitochondrial network forms.²⁷ The same phenotype results from the downregulation of FIS1 and MFF, two proteins proposed to act as a mitochondrial receptor for DNM1L.²⁸ FIS1 and MFF have been detected by blue native electrophoresis in complexes with different molecular weights, suggesting that at least two different macromolecular complexes participate in mitochondrial fission events. Furthermore, a conditional *Fis* knockout (KO) had indicated that FIS1 is dispensable for DNM1L-mediated fission, whereas MFF is not (Fig. 1).³⁰

The organization of the mitochondrial network is fundamental for the regulation of Ca²⁺ homeostasis. In fact, it has been

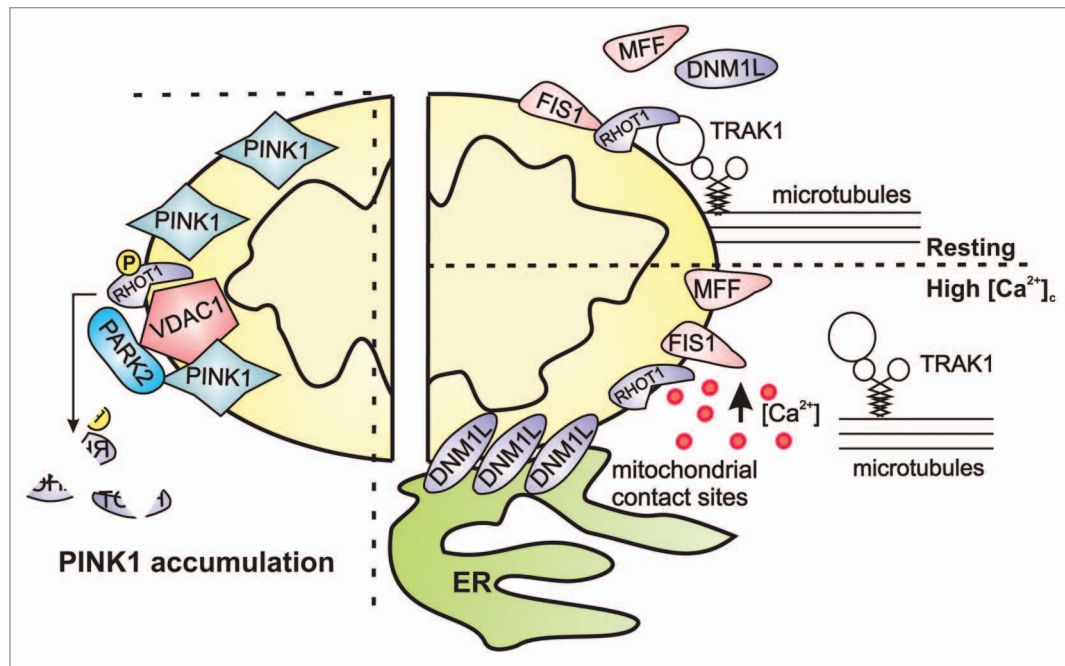


Figure 1. Mitochondrial integrity is a key factor involved in mitophagy, which is regulated by specific fission proteins, including DNM1L, FIS1, and MFF, which are recruited by mitophagy-related inducers. The figure shows the involvement of the mitochondrial Ca^{2+} -sensing protein RHOT1, an OMM protein that under resting conditions interacts with the cytoplasmic adaptor protein TRAK2, mediating mitochondrial sliding along the cytoskeleton. Sustained $[\text{Ca}^{2+}]_i$ elevations induce the RHOT1-dependent motility block, allowing DNM1L-induced fragmentation. Contact sites have been recently shown to be required for the DNM1L polymerization process that generates a constriction around mitochondria, a process that is necessary for mitochondrial fission. In depolarized neurons, PINK accumulation favors RHOT1 phosphorylation, inducing PINK-RHOT1-PARK2 aggregation. This complex promotes RHOT1 degradation, preventing mitochondrial movement and quarantining the damaged mitochondria.

widely demonstrated that mitochondria can uptake Ca^{2+} due to their close apposition with the ER.³¹ At these sites, ITPR/inositol 1,4,5-trisphosphate receptor on the ER side is juxtaposed with VDAC1/voltage-dependent anion channel 1 on the OMM via the chaperone activity of HSPA9/heat shock 70 kDa protein 9 (mortalin).³² In this scenario, Ca^{2+} released through the ITPR generates microdomains at high Ca^{2+} concentrations, and mitochondria can rapidly uptake Ca^{2+} through the MCU. Once within the mitochondrial matrix, Ca^{2+} rapidly diffuses through the whole network and is extruded through the mitochondrial $\text{Na}^+/\text{Ca}^{2+}$ exchanger or the $\text{Ca}^{2+}/\text{H}^+$ antiporter.³³ Alterations in mitochondrial morphology can clearly impair Ca^{2+} uptake and its flow through the network. It has been demonstrated that *Mfn* KO cells, in which the amount of contact with ER is reduced, display impaired Ca^{2+} uptake.³⁴ Similarly, DNM1L-overexpressing cells, in which mitochondria have normal contacts with the ER but are fragmented, show a consequent loss of matrix connectivity and reduced Ca^{2+} uptake.

The relationship between mitochondrial shaping and Ca^{2+} is bidirectional due to Ca^{2+} -dependent regulation of mitochondrial morphology. At least two interconnected mechanisms have to be considered. First, the mitochondrial Rho-GTPase (RHOT1) is an OMM protein with two EF hands for Ca^{2+} binding that interacts with TRAK1, a cytoplasmic adaptor able to bind the kinesin 1 heavy chain on microtubules. Under resting conditions, RHOT1 mediates mitochondrial sliding along the cytoskeleton, thus favoring mitochondrial fusion by impeding DNM1L

activity. Elevation of the $[\text{Ca}^{2+}]_i$ induces the RHOT1-dependent block in motility and allows DNM1L-induced fragmentation (Fig. 1).³⁵

Second, Scorrano and colleagues showed that elevation of $[\text{Ca}^{2+}]_i$ induces calcineurin activation and subsequent dephosphorylation at serine 637 of DNM1L that then accumulates in mitochondria.³⁶ Interestingly, another group found that Ca^{2+} influx through VDACs induces DNM1L phosphorylation at serine 600 via activation of CAMK1/calcium/calmodulin-dependent protein kinase I with the consequent induction of mitochondrial fragmentation.³⁷ These data suggest that different Ca^{2+} sources can lead to the same result through different pathways.

Mitophagy is also involved in the wide range of physiological pathways that regulate fusion/fission events. Incorporation of mitochondria within an autophagosome, which has a maximum diameter of approximately 1 μm , is sterically impossible if it is not preceded by a fission event. Accordingly, mitochondrial fragmentation has been detected before mitophagy during mitochondrial stress.³⁸ Moreover, OPA1 overexpression decreases mitophagy, whereas blocking mitochondrial fission induces autophagy without mitophagy, and dysfunctional mitochondria accumulate.^{24,39} It appears clear that fission is relevant for the success of mitophagy; however, this process is not sufficient to induce mitophagy as shown in FIS1-overexpressing cells that display only a weak increase in mitophagy.⁴⁰ In yeast cells, which are used to model important aspects of autophagy in eukaryotes, the

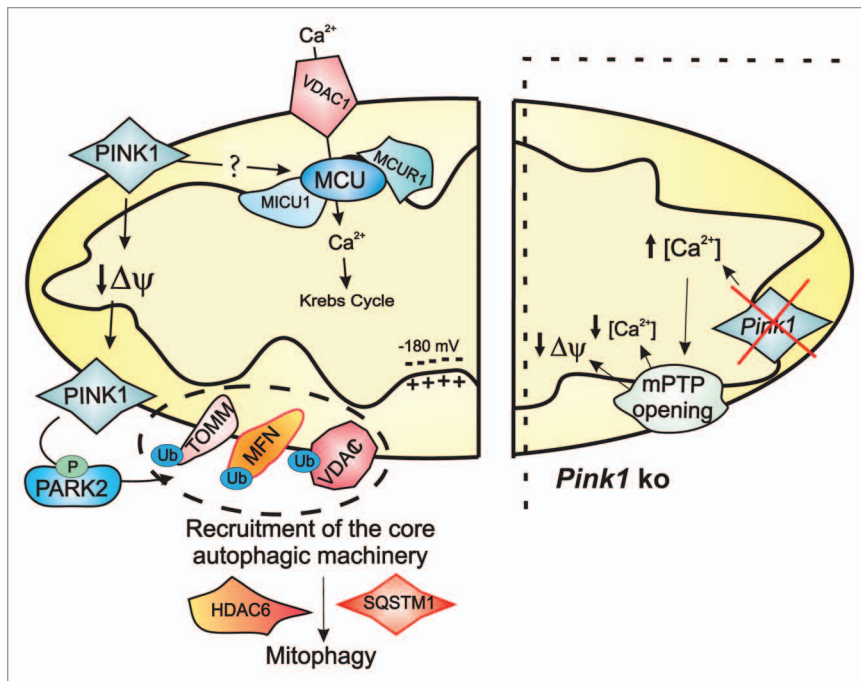


Figure 2. The ubiquitination of a subset of OMM proteins including VDAC1, TOMM, and MFNs by the ubiquitin ligase PARK2 promotes the dissipation of Ψ_m , inducing the recruitment of a series of adaptor proteins (such as SQSTM1) that promote mitochondrial sequestering. Ψ_m represents a huge driving force for Ca^{2+} -entry into the organelle through the recently identified mitochondrial calcium uniporter MCU. The activity of the channel is regulated by the mitochondrial proteins MICU1/mitochondrial calcium uptake 1 and MCUR1/mitochondrial calcium uniporter regulator 1. The loss of Ψ_m impairs Ca^{2+} uptake and mitochondrial Ca^{2+} -buffering causing PINK1 accumulation and stabilization on the OMM. In the inset, *Pink1* KO cells show reduced Ψ_m via the increased mitochondrial Ca^{2+} uptake and mPTP (mitochondrial permeability transition pore) opening.

role of mitochondrial fission in promoting autophagy is debated. Genetic screening revealed that deletion of the profission *DNM1* gene, the ortholog of mammalian *DNM1L*, is associated with reduced mitophagy.⁴¹ In contrast, in a different study, the KO of fission factor genes, such as *DNM1*, *MDVI*, and *CAF4*, did not alter mitophagy,⁴² suggesting that *Dnm1*-dependent fission is not essential for mitophagy in yeast. However, it cannot be excluded that mitochondrial fission may precede mitophagy in yeast through unknown mechanisms and/or upon different types of stimulation. These observations suggest that a fission event is necessary for mitochondrial segregation, but another event, such as Ψ_m or ROS, is required for mitochondrial engulfment, and will be discussed later.

The work from Wang in 2011 is noteworthy because it describes the first molecular link between mitochondrial morphology and mitochondrial quality control. PINK1 (PTEN-induced putative kinase 1) and the ubiquitin ligase PARK2/Parkin, are two molecular players involved in the recognition of “damaged” mitochondria and their delivery to the autophagosome.⁴³ Wang observed that in mouse and *Drosophila* depolarized neurons, RHOT1 exists in a molecular complex with PINK1 and PARK2. This interaction induces RHOT1 phosphorylation and degradation that precedes blockage of mitochondrial motility (Fig. 1).⁴⁴ Unfortunately, the readout of both mitophagy and the Ca^{2+} -dependent activity of RHOT1 after its phosphorylation is not detected in such conditions.

RHOT1 was initially characterized in yeast as a participant in the ER-mitochondria encounter structure (ERMES) that tethers the ER to mitochondria, and this localization was later confirmed in mammalian cells.⁴⁵ Contact sites have been recently shown to be required for the DNML polymerization process that generates a constriction around mitochondria, a process that is necessary for mitochondrial fission.⁴⁶ In addition, contact sites have just been demonstrated to play a role in autophagosome

generation.⁴⁷ It could thus be speculated that Ca^{2+} signals at contact sites induce a RHOT1-dependent block in mitochondrial sliding (possibly in front of specific ER subdomains) and DNML-dependent fission.

The Mitochondrial Membrane Potential

As mentioned above, mitochondria are the main sites of ATP production. The enzymatic systems involved in this process are the tricarboxylic acid cycle and the mitochondrial electron transport chain complex. The products from glycolysis and fatty acid metabolism are converted to acetyl-CoA and enter the tricarboxylic acid cycle, which generates NADH and FADH₂, triggering the electron transport chain. The electrons move along the respiratory chain, and the energy is stored as an electrochemical H⁺ gradient across the inner membrane, creating the negative mitochondrial membrane potential, which is estimated to be around -180 mV (Fig. 2). This membrane potential provides a huge driving force for Ca^{2+} entry into the organelle.

Several intracellular signals can induce irreversible mitochondrial damage, destabilizing mitochondrial integrity and favoring the loss of Ψ_m . This alteration represents an activating factor for the induction of apoptotic cell death⁴⁸ and probably for the recruitment of the mitophagic machinery.

It has been demonstrated that the mitochondrial permeability transition (MPT) is an important event for inducing the autophagic process.⁴⁹ The MPT is a critical event involved in controlling cell fate and results from the opening of the so-called mitochondrial permeability transition pore (mPTP), an aggregate multicomponent protein localized in the mitochondrial compartments that includes factors in the inner and outer mitochondrial membrane.⁵⁰ Opening of the mPTP can lead to loss of Ψ_m with subsequent swelling of the mitochondrial matrix and a transient, but strong, release of ROS and Ca^{2+} ions.

Damaged and depolarized mitochondria are sequestered into autophagic vacuoles identified with the autophagosome marker microtubule-associated protein 1 light chain 3 (MAP1LC3). In particular, the level of mitophagy increases when a subset of mitochondria are experimentally depolarized with ionophores including carbonyl cyanide *m*-chlorophenylhydrazone (CCCP) or valinomycin that simulate mitochondrial damage.^{51,52} For these reasons, it appears that Ψ_m is a critical point for the removal of impaired, aged, and dysfunctional mitochondria.

In aging and degenerative processes, PARK2 selectively translocates to depolarized and disturbed mitochondria and, in turn, promotes their autophagic removal.⁵¹ It has been demonstrated that the recruitment of PARK2 to impaired mitochondria is modulated by PINK1 expression and activity.^{43,53} Loss-of-function mutations in PINK1 have been linked to familial Parkinson disease (PD), where it has been reported that loss of the protein impairs mitochondrial respiratory activity in mouse brains.⁵⁴ In *Pink1* KO cells, the enzymatic activities of the mitochondrial electron transport chain complex are normal, but the Ψ_m is reduced through increased mitochondrial Ca^{2+} uptake and mPTP opening (Fig. 2).⁵⁴

PINK1 contains an N-terminal mitochondrial targeting motif and a highly conserved kinase domain that shows strong homology to the Ca^{2+} /calmodulin-dependent serine/threonine kinase family.⁵⁵ The kinase domain of PINK1 is oriented toward the cytosol, and it can physically interact with PARK2 and modulate its mitochondrial localization via direct phosphorylation.⁵⁶ Under normal conditions, PINK1 is localized in the OMM as a 64-kDa full-length protein, which is processed in a cleaved form of 52-kDa and imported into the IMM. This cleaved form of PINK1 is rapidly degraded by a protease; therefore, the endogenous amount of PINK1 is low, and the mitophagy of healthy mitochondria is blocked. When a subset of mitochondria suffer a loss of Ψ_m (prompted by strong stressors or uncoupling agents), the full-length PINK1 accumulates and stabilizes on the OMM of damaged mitochondria where it recruits PARK2.⁵⁷ In the mitochondrial compartment, PARK2 ubiquitinates a subset of OMM proteins, such as VDAC1 and MFN.⁵⁸ This incremental ubiquitination on the mitochondria induces the recruitment of a series of adaptor proteins (such as SQSTM1), which connect the autophagic process to ubiquitinated proteins (Fig. 2). As a result, the damaged mitochondria are recruited by MAP1LC3 and autophagosomal membranes that finally fuse with the lysosome.⁵⁹ In yeast, selective mitochondrial degradation via micro- and macroautophagy is associated with impairment of Ψ_m and mitochondrial biogenesis in cells lacking *Fmc1*, a mitochondrial protein required under heat stress conditions for the proper assembly of the ATP synthase complex.⁶⁰ Additionally, reduced Ψ_m , mitochondrial swelling and fragmentation have been described in yeast cells when the mitochondrial K^+/H^+ exchanger, *Mdm38*, is depleted, thus leading to increased mitophagy and growth defects on nonfermentable carbon sources.⁶¹ However, the reduction in Ψ_m appears to be insufficient for the induction of mitophagy in yeast. Yeast mutants lacking *Cox4* show a similar reduction in Ψ_m as *mdm38* Δ cells, but they do not undergo mitophagy.⁶¹ In addition, in contrast to mammalian cells, the chemical depolarization

of yeast mitochondria via CCCP does not induce mitophagy.⁶² These lines of evidence suggest that damaged mitochondria are degraded by mitophagy in yeast and a change in the Ψ_m may only influence, but not trigger, this process. Therefore, yeast and mammalian cells may have different cell parameters and stimuli for inducing and/or regulating mitophagy, although the selective removal of the organelles may be completed through similar mechanisms.

Mitochondrial ROS Production

Oxidative stress is inseparably associated with mitochondrial dysfunction, as mitochondria are both the generators of and targets for reactive oxygen species.⁶³ The mitochondria, especially in brain cells, are a major site of the generation and action of both ROS and reactive nitrogen species (RNS). Specific forms of ROS and RNS include hydrogen peroxide (H_2O_2), superoxide ($\text{O}_2^{\bullet-}$), nitric oxide (NO), and peroxynitrite (ONOO^-).⁶⁴ Both exogenously added H_2O_2 and mitochondrial ROS activate autophagy. Autophagy is essential for degrading ROS-producing organelles such as mitochondria and peroxisomes.⁶⁵ However, beyond activating autophagy, it is not clear whether ROS is also involved in the activation of mitophagy. Based on the above findings, very recent papers have proposed a role for ROS in initiating mitophagy. Using a mitochondrial-targeted photosensitizer, mitochondrial KillerRed, three different groups induced an increase in ROS levels in the mitochondrial matrix, resulting in the loss of membrane potential, fragmentation and the subsequent activation of PARK2-dependent mitophagy.⁶⁶⁻⁶⁸ In particular, $\text{O}_2^{\bullet-}$ was determined to be the specific ROS that damaged mitochondria because the overexpression of SOD2 (superoxide dismutase 2, mitochondrial) or an $\text{O}_2^{\bullet-}$ scavenger inhibit both mitochondrial fragmentation and the mitophagy induced by mitochondrial KillerRed activation.⁶⁷ In support of these observations, mammalian cells under mild oxidative stress generate moderate levels of ROS; additionally, a DNMI1-dependent type of mitophagy is triggered, but nonselective autophagy is not detected. These results suggest an earlier temporal role for mitophagy in response to mitochondrial damage that governs the selective removal of dysfunctional mitochondria.⁶⁹ In yeast, it has been proposed that the physiological role of mitophagy is to remove excess mitochondria that may generate a ROS surplus in cells.⁷⁰ Under nitrogen starvation, a condition that induces mitophagy, *atg32* Δ and *atg11* Δ yeast cells lacking genes essential for the selective recruitment of mitochondria to the autophagosomal machinery, show ROS overproduction associated with impaired mitochondrial function. In these mitophagy-deficient cells, ROS surplus causes mtDNA depletion that ultimately leads cells to a petite phenotype unable to grow on respiratory carbon sources.⁷¹ Based on this study, mitophagy appears to be responsible for mitochondrial quality control to sustain cell life when damaged organelles are generated. In the frataxin-deficient yeast cells, *yfh1* Δ , a model of Friedreich ataxia characterized by mitochondrial iron overload, there is an increase in ROS production and oxidative damage. When these cells are treated with rapamycin, which inhibits the TOR pathway, thus inducing autophagy

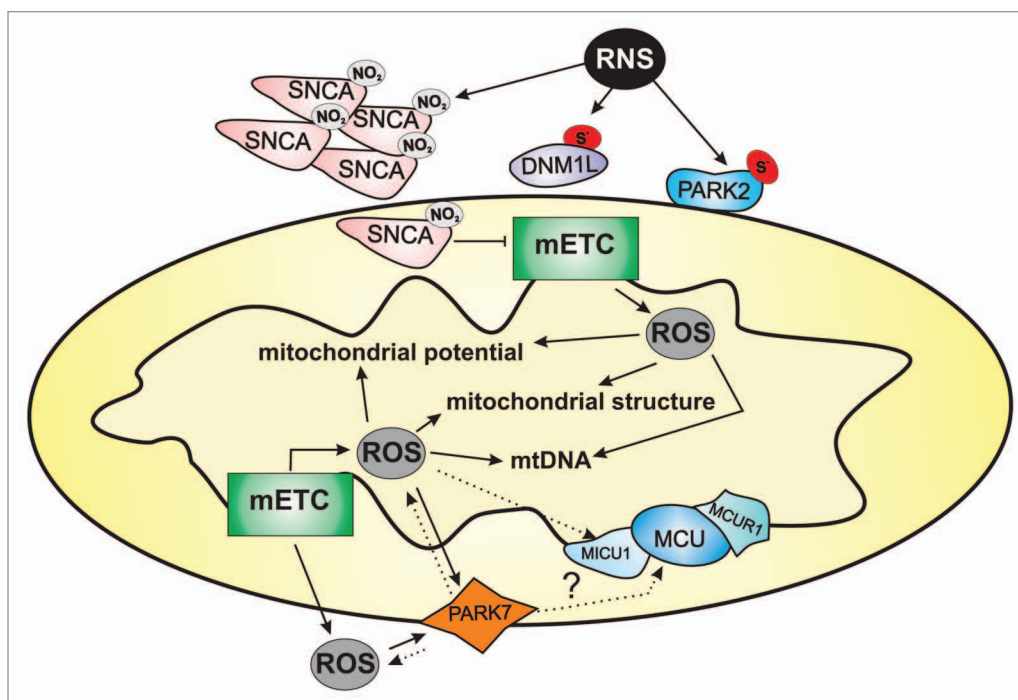


Figure 3. ROS and RNS are responsible for the decrease in mitochondrial potential, mitochondrial fission and mtDNA mutations. Indeed, ROS and RNS regulate several mitophagic molecular targets through protein modification. ROS, reactive oxygen species; RNS, reactive nitrogen species; mETC, mitochondrial electron transport chain complex.

in yeast and mammals,⁷² a reduction in both mitochondrial ROS and mass is observed, most likely because of the removal of damaged mitochondria.⁷³

Many proteins involved in mitophagy can be regulated by ROS. For example, SNCA/ α -synuclein and PARK2 are S-nitrosylated (the addition of NO to thiol groups). Nitrogen modification of SNCA makes the protein prone to aggregation,⁷⁴ and S-nitrosylation of PARK2 inactivates it (Fig. 3).⁷⁵

In this scenario, several mitochondrial signals, including impaired ATP production, activation of the MPT and loss of Ψ_m , appear able to trigger mitophagy, but enhanced ROS generation certainly plays a pivotal role. ROS cooperate with Ca^{2+} signaling in the control of ER-mitochondrial functions, and their levels are not only mutually regulated but also perfectly mirror the healthy state of a cell.⁷⁶ What is the role of Ca^{2+} in the context of oxidative stress-mediated mitophagy? Several observations in studies on PD support the influential activity of Ca^{2+} in oxidative stress-mediated disease. PD is characterized by mitochondrial dysfunction and oxidative stress as well as an imbalance in protein homeostasis due to an increase in protein misfolding and aggregation and the inability to remove misfolded proteins.⁷⁷ Among the different proteins implicated in PD, PARK7 plays an important role in the maintenance of mitochondrial integrity. Mutant PARK7 proteins that are associated with PD are stabilized by binding to PARK2, and this interaction is enhanced by oxidative stress. The predominant role of PARK7 is as an antioxidant, and PARK7 knockdown alters Ca^{2+} homeostasis in skeletal muscle.⁷⁸ Furthermore, PARK7-deficient dopaminergic neurons exhibit very low levels of mitochondrial uncoupling and correspondingly

higher levels of oxidative stress, suggesting that PARK7 might somehow regulate the mitochondrial response to oxidative stress (Fig. 3). Importantly, blocking the L-type Ca^{2+} channels, which are plasma membrane channels that allow Ca^{2+} entry into the cytosol, completely rescues the oxidative stress effect.⁷⁹ The loss of PARK7 function weakens the compensatory mechanisms in mitochondria, making the dopaminergic neuron much more vulnerable to oxidative stress in the substantia nigra. The key finding of this study is that the abolition of Ca^{2+} accumulation in mitochondria can reverse the intracellular dysregulation resulting from PARK7 mutation. Considering the interplay between PARK2 and PARK7 in mitochondrial quality control,^{80,81} it will be interesting to investigate the basal level of mitophagy in *Park7*-null dopaminergic neurons and to determine whether the use of L-type Ca^{2+} blockers, such as isradipine, might either increase or attenuate the mitophagic process. Interestingly, Ca^{2+} -influx through the channel increases mitochondrial superoxide, NADH production and metabolic activity in quiescent cardiac myocytes, reinforcing the concept that L-type channels could regulate mitochondrial functions.⁸²

As previously mentioned, the state of the mitochondrial network is a critical step in mitophagy because fragmented mitochondria are more readily taken up by autophagosomes due to their size. Mitochondrial fission is a deleterious effect of chronic oxidative stress, especially in neuronal cells,⁸³ and this process is accompanied by a robust decrease in mitochondrial Ca^{2+} levels. Thus, a mitochondrion that is ready to be engulfed is damaged by ROS, fragmented and, hypothetically, Ca^{2+} depleted. On the other hand, Ca^{2+} overload perturbs mitochondrial physiology,

causing ROS generation, mPTP opening and the initiation of cell death. In this context, Ca^{2+} levels might be ideal triggers of mitophagy and could be considered one of the first intracellular mechanisms to avoid apoptosis through the elimination of potentially dangerous elements.

When Does Mitochondrial Ca^{2+} Intervene in the Mitophagy Process?

During the course of evolution, the mitochondria have developed biological pathways with molecular targets and critical checkpoints to monitor their health. The molecular clarification of involved molecular players and their mechanisms in mitochondrial fate, have highlighted the crosstalk between two important biological processes, mitochondrial-targeted autophagy and mitochondrial-related apoptosis. Both processes have similar molecular targets that trigger and modulate their occurrence. Indeed, they are linked by the Ca^{2+} ion, since it represents an important modulator of both cellular processes, acting on their common molecular targets.⁸⁴⁻⁸⁷

To date, the role of Ca^{2+} in mitophagy remains obscure. How does mitochondrial Ca^{2+} stimulate the selective removal of damaged organelles? Does it reduce the efflux of caspase cofactors? Is Ca^{2+} crosstalk with the ER involved? We attempt to answer these questions by discussing recent findings.

During apoptosis, by acting in synergy with a variety of cellular stress conditions, the mitochondrial Ca^{2+} overload is a key “author” of mPTP opening, thus inducing large-scale mitochondrial alterations. If mitochondrial Ca^{2+} loading is prevented (e.g., by loading an intracellular Ca^{2+} buffer), then the Ψ_m and mitochondrial morphology are preserved, and the cells are protected from apoptosis. Mitophagy is generally preceded by the MPT, followed by mitochondrial fission, hence indicating that the regulation of mitochondrial shape is an essential aspect of mitochondrial quality control.³⁹

The Ψ_m represents a very large driving force for Ca^{2+} accumulation and permits Ca^{2+} -entry through MCU. Mitochondrial Ca^{2+} transduction constitutes a fundamental mechanism to regulate cell survival and metabolism, but indirect evidence suggests that it is also pivotal for mitophagy. As previously reported, PINK1 leads to increased mPTP opening, which, in turn, is primarily induced by oxidative stress and/or elevated mitochondrial Ca^{2+} . This observation is consistent with a recent study that showed that loss of PINK1 reduces the activity of the mitochondrial $\text{Na}^+/\text{Ca}^{2+}$ exchanger.⁸⁸ Impaired mitochondrial $\text{Na}^+/\text{Ca}^{2+}$ exchanger activity in *Pink1* KO cells may lead to the accumulation of mitochondrial Ca^{2+} , which opens the mPTP. In this context, the mPTP may serve as a Ca^{2+} -activated, Ca^{2+} -releasing channel. These studies support an important function for PINK1 in regulating mitochondrial activity under stress conditions. The loss of Ψ_m and mitochondrial integrity in a neuronal cell model of PD are partially recovered by treatment with cyclosporin A and fully rescued by treatment with ruthenium red, an inhibitor of MCU, indicating that mitochondrial Ca^{2+} uptake is once again involved.⁸⁹ Moreover, recent work has suggested that an increase in mitochondrial Ca^{2+} content may influence the autophagic

pathway.^{90,91} Pharmacological blocking of MCU activity alters the autophagic level, and the negative regulation of ITPR produces the same effects as the inhibition of the MCU in autophagy.¹⁰ In autophagy, Ca^{2+} may have a dual role, pro- and anti-autophagic, and autophagy is dependent on both ER Ca^{2+} levels and ITPR activity.¹⁰ Although there is no direct evidence, these data suggest that mitophagy could be affected by Ca^{2+} and its effectors.

The anti-apoptotic proteins BCL2 and BCL2L1/Bcl-xL mediate the decrease in ER Ca^{2+} levels and Ca^{2+} release, thus protecting the cell from apoptosis.⁹² These proteins also inhibit autophagy by lowering ER Ca^{2+} levels⁹¹ and by interacting with both ITPR and the autophagic protein BECN1. Thus, the proteins have both anti-apoptotic and anti-autophagic roles. Interestingly, BCL2 inhibits autophagy only when localized to the ER membrane⁹³ as indicated by the dynamic interaction between AMBRA1 and BCL2 at the mitochondria,⁹⁴ where the interaction regulates BECN1-dependent autophagy and apoptotic cell death. The relationship with ER Ca^{2+} stores points to a role for ER Ca^{2+} in mitophagy. Ca^{2+} accumulation in the mitochondrial matrix requires a close morphofunctional coupling between mitochondria and Ca^{2+} stores such that if the interaction is impaired, the alterations could trigger the mitophagy machinery. For example, an early event in mitophagy is that PARK2 trafficks to the OMM, where it ubiquitinates different mitochondrial targets, such as MFNs,⁹⁵ DNMI1,⁹⁶ VDAC1,⁹⁷ and BCL2,⁹⁸ that are well-known mitochondrial Ca^{2+} -sensing proteins involved in strategic events that monitor functional interorganelle Ca^{2+} flux. In addition, PINK1 phosphorylates RHOT1, promoting its proteasomal degradation and triggering PARK2.⁴⁴ These findings emphasize the pivotal role of crosstalk between the ER and mitochondria in mitophagy because RHOT1 is a Ca^{2+} -sensitive regulator of ER-mitochondria contact sites,⁴⁵ mitochondrial Ca^{2+} signaling and motility and fusion-fission dynamics of mitochondria.³⁵ Recent studies have shown that SNCA can associate with mitochondria and that its accumulation increases mitochondrial Ca^{2+} levels and, as a consequence, oxidative damage, depending on both its expression and intracellular distribution.^{99,100} Moderate levels of SNCA overexpression enhance mitochondrial Ca^{2+} homeostasis by augmenting ER-mitochondria contact sites, whereas SNCA loss-of-function impairs mitochondrial Ca^{2+} levels and enhances the autophagic process.

Specific studies are still required to define the mitophagic scenery and determine how mitochondrial Ca^{2+} actively participates in triggering and/or modulating mitophagy, thus giving cells the option to follow either the apoptotic or autophagic pathway. Nevertheless, some evidence supports a model where BNIP3 induces selective removal of mitochondria in cardiac myocytes in an independent Ca^{2+} -, ROS generation-, and mPTP opening-dependent manner.¹⁰¹

In this context, yeast cells may represent a suitable model for further identification of proteins and/or cell effectors involved in mitophagy.⁴¹ The role of Ca^{2+} in yeast metabolism and processes controlling cell survival, such as apoptosis and autophagy, still needs to be elucidated. However, there is increasing evidence that changes in ROS production, Ψ_m and mitochondrial morphology dynamics are either stimuli or consequences of mitophagy in yeast,

thus suggesting that a conserved mitophagic mechanism might be shared at least partially in both yeast and mammalian cells.

Future studies will identify this direct link, opening new avenues for investigation and pharmacological intervention, especially for those diseases where the selective removal of mitochondria is one of the critical steps in the pathogenesis of the disorder.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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