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Neither too much nor too little: mitochondrial calcium concentration as a balance between physiological and pathological conditions

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Ca²⁺ ions serve as pleiotropic second messengers in the cell, regulating several cellular processes. Mitochondria play a fundamental role in Ca²⁺ homeostasis since mitochondrial Ca²⁺ (mitCa²⁺) is a key regulator of oxidative metabolism and cell death. MitCa²⁺ uptake is mediated by the mitochondrial Ca²⁺ uniporter complex (MCUc) localized in the inner mitochondrial membrane (IMM). MitCa²⁺ uptake stimulates the activity of three key enzymes of the Krebs cycle, thereby modulating ATP production and promoting oxidative metabolism. As Paracelsus stated, "Dosis sola facit venenum,"in pathological conditions, mitCa²⁺ overload triggers the opening of the mitochondrial permeability transition pore (mPTP), enabling the release of apoptotic factors and ultimately leading to cell death. Excessive mitCa²⁺ accumulation is also associated with a pathological increase of reactive oxygen species (ROS). In this article, we review the precise regulation and the effectors of mitCa²⁺ in physiopathological processes.

KEYWORDS

mitochondria, calcium, mitochondrial calcium uniporter (MCU), cell death, metabolism

1 Introduction

Intracellular calcium ions (Ca²⁺) serve as a widespread second messenger, regulating a multitude of cellular functions such as gene expression, metabolism, muscle contraction, synaptic plasticity, cell proliferation, and death. The intricate control of Ca²⁺ signaling enables cell-specific control of these biological processes in space and time (Berridge, 2001). There are several sources of Ca²⁺ that cooperate to elevate the concentration of Ca²⁺ in the cytosol [(Ca²⁺)_{cvt} ~ 100 nM]. These sources encompass Ca²⁺ from the extracellular milieu $[(Ca^{2+})_{ext} \sim 1 \text{ mM}]$, and intracellular Ca²⁺ reservoirs, primarily the endoplasmic reticulum (ER)-recognized as the sarcoplasmic reticulum (SR) in striated muscle cells [(Ca²⁺)_{ER/SR} $> 100 \,\mu$ M] (PMID: 8036248; PMID: 16371601). In this context, mitochondria play a pivoltal role. Indeed, in response to an increase in [Ca²⁺]_{cvt}, mitochondria can uptake Ca²⁺ through a process that depends on three prerequisites. 1) The electrochemical proton gradient ($\Delta \mu H^+$), generated by the translocation of H⁺ ions across the inner mitochondrial membrane (IMM) due to the activity of the electron transport chain (ETC). It comprises the membrane potential difference ($\Delta \Psi$) and the H⁺ concentration difference (ΔpH), with $\Delta \Psi$ being predominant (Mitchell and Moyle, 1967). The negative $\Delta \Psi$ (~-180 mV) represents the driving force for Ca²⁺ accumulation within the mitochondrial matrix. 2) The microdomains

between ER/SR and the plasma membrane with the mitochondria. Mitochondria are closely located to ER/SR Ca^{2+} channels (inositol-1,4,5-triphosphate-receptors [Ins(1,4,5)P₃Rs] and ryanodine receptors (RYRs), as well as plasma membrane Ca^{2+} channels (store-operated channels and voltage-operate channels). This enables mitochondria to promptly sense microdomains of high [Ca^{2+}]_{cyt} (Rizzuto et al., 1998; Csordás et al., 1999; Szalai et al., 2000). 3) The presence of the mitochondrial Ca^{2+} uniporter (MCU) complex in the IMM, a sophisticated mechanism that enables Ca^{2+} entry into the mitochondrial matrix (discussed in the next paragraph).

In this review, we will provide a brief overview of the structure and function of the MCU complex. We will then focus on the regulators of mitCa²⁺. Specifically, we will discuss the role of mitochondria as cytosolic Ca²⁺ buffers and the role of mitCa²⁺ in the regulation of oxidative metabolism, cell death, and ROS production.

2 Structure and function of the MCU complex

The MCU complex is composed of the pore-forming subunit, MCU, its dominant-negative form, MCUb, the essential MCU regulator (EMRE), the mitochondrial Ca²⁺ uptake regulatory subunits (MICU1, MICU2, and MICU3), and potentially by the MCU regulator 1 (MCUR1) (Figure 1).

MCU is a highly conserved and ubiquitously expressed 40 KDa protein localized at the IMM. Structurally, MCU consists of two transmembrane domains separated by a short loop facing the intermembrane space (IMS). This loop is highly conserved due to the presence of negatively charged amino acids ("DIME" motif, composed of acidic residues), which are crucial for Ca²⁺ selectivity

(Baughman et al., 2011; De Stefani et al., 2011). Consistent with its role of highly selective Ca²⁺ channel, downregulating MCU leads to a substantial reduction in mitCa2+ uptake without affecting the mitochondrial $\Delta \Psi$. Conversely, overexpression of MCU significantly enhances mitCa²⁺ uptake (De Stefani et al., 2011; Chaudhuri et al., 2013). Cryo-EM and X-ray diffraction structure analysis revealed that MCU arranges in a tetrameric architecture (Baradaran et al., 2018; Fan et al., 2018; Nguyen et al., 2018; Yoo et al., 2018), confuting a previously proposed pentameric structure of MCU (Oxenoid et al., 2016).

MCUb is an alternative isoform of MCU located in the IMM, where it forms hetero-oligomers with MCU (Raffaello et al., 2013). MCUb shares 50% sequence homology with MCU and has a similar structure: two transmembrane domains linked by a short loop. However, a crucial difference exists between these two pore-forming subunits. The MCUb protein sequence contains an amino acid substitution in the loop region (E256V) that neutralizes a negative charge, resulting in a significant reduction in the channel conductivity (Raffaello et al., 2013). In cells, overexpression of MCUb causes a reduction in mitCa²⁺ uptake when stimulated with a Ca²⁺ mobilizing agonist, while silencing MCUb strongly increases mtCa²⁺ uptake. This indicates that MCUb negatively affects Ca²⁺ entry through the MCU complex (Raffaello et al., 2013). The expression levels of MCUb vary significantly among different mammalian tissues, suggesting that the MCU/MCUb ratio might impact the physiological ability of mitochondria of specific tissues to uptake Ca2+. For instance, cardiomyocytes that display a low MCU/MCUb ratio are characterized by low MCU activity (Fieni et al., 2012), while skeletal muscle fibers, which instead exhibit high MCU activity (Fieni et al., 2012), are characterized by a high MCU/ MCUb ratio. Interestingly, in heart MCUb incorporation in the complex is a stress-responsive mechanism to limit mitochondrial Ca²⁺ overload during cardiac injury (Lambert et al., 2019) and in



FIGURE 1

MCU complex structure. The MCU complex is localized in the IMM. It comprises the pore-forming subunit, MCU, and its dominant-negative form, MCUb It consists of the pore-forming subunit, MCU, and its dominant-negative variant, MCUb. MCU is connected to the regulatory subunit MICU1 by the transmembrane protein EMRE. The MICU family also includes MICU1.1, MICU2, and MICU3. MICU proteins detect increases in Ca²⁺ levels through EFhand domains, enabling the channel to open in response to elevated cytoplasmic Ca²⁺ levels. MCUR1 is a potential regulator of channel activity; however, its role is still a subject of debate. skeletal muscle it is induced by caloric restriction, where it increases mitochondrial fatty acid utilization in a PDH-dependent mechanism (Huo et al., 2023). EMRE is a 10 kDa metazoan protein located in the IMM and composed of a single transmembrane domain (Sancak et al., 2013). This subunit connects the pore region to the regulatory subunits, as it is necessary for the interaction of MCU with MICU1 and MICU2 (Sancak et al., 2013). The function of the MCU complex critically relies on EMRE, as demonstrated by experiments on EMRE knockout cells. These experiments show that, in the absence of EMRE, mitCa²⁺ uptake is abolished, similar to the MCU knockout phenotype (Sancak et al., 2013). Also in vivo, EMRE has been shown to be required for mitochondrial calcium uniporter activity (Liu et al., 2020). The proteolytic regulation of EMRE, crucial for MCU complex function, is a finely tuned multi-step process that prevents the assembly of MCU-EMRE channels lacking gatekeeper subunits and, as a result, prevents mitochondrial mitCa²⁺ overload. (König et al., 2016).

The regulatory subunits MICU1, MICU2, and MICU3 are located at the IMS and are responsible for the sigmoidal increase of mitCa²⁺ in response to cytosolic Ca²⁺ levels. When cytosolic Ca²⁺ levels are low, mitCa²⁺ uptake is minimal, while it increases exponentially once the $[Ca²⁺]_{cyt}$ reaches a certain threshold (Vecellio Reane et al., 2020) (Figure 1).

MICU1, the first subunit of the MCU complex to be identified in 2010, is a 54 KDa protein located in the IMS (Perocchi et al., 2010). The presence of two EF-hand Ca²⁺-binding domains at the N-terminal sequence enables MICU1 to regulate the activity of the MCU in a Ca²⁺-dependent manner. It was proposed that at low $[Ca^{2+}]_{cyt}$ levels, MICU1 keeps the channel closed to prevent continuous Ca²⁺ entry inside the mitochondrial matrix, which could lead to mitCa²⁺ overload if sustained over time. However, when a certain threshold of $[Ca^{2+}]_{cyt}$ is reached, MICU1 was proposed to act as a cooperative activator of MCU, explaining the exponential increase of mitCa²⁺ uptake (Mallilankaraman et al., 2012b; Csordás et al., 2013).

Two paralogs of MICU1 were later discovered: MICU2 and MICU3 (Plovanich et al., 2013). MICU2 exhibits a comparable expression pattern to MICU1, is also located in the IMS, and contains two EFhand Ca2+-binding domains. MICU2 directly interacts with MICU1 and forms obligate heterodimers, which are stabilized by a disulfide bond. In various cell types, the loss of MICU1 also results in the depletion of MICU2 protein, suggesting that the protein stability of MICU2 is dependent on the presence of MICU1, in a mechanism that is not yet fully elucidated (Patron et al., 2014; Debattisti et al., 2019). Different models have been proposed to explain how the activity of the MCU channel is regulated by MICU1-MICU2 heterodimers. According to Patron et al., the channel is controlled by a gatekeeper mechanism, where MICU2 keeps the channel closed at resting conditions (Figure 1, left panel) (Patron et al., 2014). However, when the concentration of Ca2+ reaches a certain threshold, conformational changes in the dimers lead to the release of MICU2 inhibition, which results in an increased MICU1-mediated mitCa²⁺ uptake (Patron et al., 2014) (Figure 1, right panel). Kamer et al. proposed an on-off switch model for the channel activity. Both MICU1 and MICU2 act as gatekeepers and cooperatively bind Ca2+ with high affinity to lead to mitCa²⁺ uptake. In this model, in the absence of MICU2, MICU1 can keep the channel closed at low Ca2+

levels (Kamer et al., 2017). Another study suggests that the main role of MICU2 is to regulate the Ca^{2+} threshold of the MICU1-mediated channel activation (Payne et al., 2017).

It has been shown that skeletal muscle expresses a unique MCU complex. Indeed, this tissue expresses an alternative splicing variant of MICU1, known as MICU1.1 (Vecellio Reane et al., 2016). This variant has an extra exon that encodes a short sequence of four amino acids. When it forms dimers with MICU2, MICU1.1 activates the channel at a lower Ca^{2+} level compared to MICU1-MICU2 heterodimers. This is especially important in skeletal muscles, as it helps to maintain high ATP production (Vecellio Reane et al., 2016).

MICU3, the other paralog of MICU1, similarly to MICU2 is located in the IMS and contains two EF-hand Ca^{2+} -binding domains (Plovanich et al., 2013). However, unlike MICU1 and MICU2 that are ubiquitous proteins, it is mainly expressed in the nervous system where it exclusively forms heterodimers with MICU1 (Plovanich et al., 2013; Patron et al., 2019). It acts as a positive channel regulator due to its reduced gatekeeping activity compared to MICU1. This ensures a more rapid opening of the channel in response to fast cytCa²⁺ increases, as it occurs in stimulated neuronal cells (Plovanich et al., 2013; Patron et al., 2019).

A possible regulator of the complex is MCUR1, a 35 kDa protein located in the IMM (Adlakha et al., 2019). This protein interacts with MCU and its silencing leads to reduced mitCa²⁺ uptake and ATP production (Mallilankaraman et al., 2012a). However, these effects were proposed to be mediated by its role as an assembly factor of the cytochrome-c oxidase (Paupe et al., 2015). In light of these conflicting results, further studies are needed to clarify the role of MCUR1 in the control of mitCa²⁺ homeostasis.

3 MitCa²⁺ buffering activity

As mentioned in the introduction, the presence of microdomains between mitochondria and ER/SR is an essential prerequisite for mitCa²⁺ uptake. Rapid changes in $[Ca^{2+}]_{cyt}$ occurring at these sites provide regulatory feedback on ER/SR Ca²⁺ channels (Rizzuto et al., 2012).

This buffering function is particularly relevant for Ins(1,4,5) P₃Rs. The opening of these channels is inhibited by low and high $[Ca^{2+}]_{cyt}$ while intermediate $[Ca^{2+}]_{cyt}$ promotes their activity. An initial increase in $[Ca^{2+}]_{cyt}$ enables the opening of the $Ins(1,4,5)P_3Rs$, thereby promoting the release of Ca^{2+} from the ER. MitCa²⁺ buffering plays a crucial role in sustaining and prolonging the release of Ca^{2+} by reducing the $[Ca^{2+}]_{cyt}$ near the $Ins(1,4,5)P_3Rs$. This prevents the negative feedback associated with high $[Ca^{2+}]_{cyt}$ (Hajnóczky et al., 1999).

While the bell-shaped effect of $[Ca^{2+}]_{cyt}$ on $Ins(1,4,5)P_3Rs$ is commonly observed, there are some exceptions to this regulation with physiological relevance. One such exception is observed in rat cortical astrocytes, where the predominant isoform of the channel is $Ins(1,4,5)P_3R2$. This isoform is positively regulated only by high $[Ca^{2+}]_{cyt}$ leading to limitations on mitochondrial involvement in the propagation of calcium waves (Boitier et al., 1999).

MitCa²⁺ buffering activity also holds particular significance in cardiac physiology. In neonatal cardiac cells, mitCa²⁺ uptake shapes the amplitude of Ca²⁺ peaks, as evidenced by genetic manipulation of MCU. Downregulation of MCU results in amplificated cytCa²⁺

peaks during spontaneous oscillations, while MCU overexpression has the opposite effect. Additionally, mitochondria buffer Ca²⁺ peaks by taking up Ca²⁺ released during systole and releasing it back into the cytosol during diastole (Drago et al., 2012).

MitCa²⁺ buffering capacity is also influenced by mitochondrial positioning in a defined subcellular domain. This is strongly evident in pancreatic acinar cells, where a "mitochondrial belt" separates the apical secretory pole from the basal pole containing the nucleus. Under normal conditions, this mitochondrial belt prevents the spreading of Ca^{2+} waves from the apical to the basal region. However, in pathological conditions where mitochondrial buffering capacity is overwhelmed, Ca^{2+} waves propagate to the basal region, leading to transcriptional events in the nucleus (Tinel et al., 1999; Sutton et al., 2003).

The role of mitochondrial positioning in regulating Ca^{2+} buffering is also observed in neurons. Specifically, mitochondria located at the synapse modulate cyt[Ca²⁺], strongly affecting neurotransmitter release (Billups and Forsythe, 2002; David and Barrett, 2003).

Overall, mitochondria possess an efficient Ca^{2+} buffering capacity that regulates cellular Ca^{2+} signals through the modulation of Ca^{2+} channels and their subcellular positioning.

4 MitCa²⁺ regulation of metabolism

In the 1960s and 1970s, research carried out in Bristol revealed the pivotal role of mitCa²⁺ in regulating aerobic metabolism. Specifically, it was demonstrated that Ca²⁺ ions directly activate four mitochondrial dehydrogenases, namely, α -ketoglutarate dehydrogenase (α -KGDH), isocitrate-dehydrogenases (IDH), FAD-linked glycerol phosphate dehydrogenase (GPDH), and indirectly, through its Ca²⁺-dependent phosphatase, pyruvate dehydrogenase (PDH) (Denton, 2009) (Figure 2, left panel). Significantly, the

activation of these enzymes enhances the availability of NADH, promoting the electron flow through the respiratory chain complexes and, consequently, ATP synthesis. This is particularly relevant under increased ATP demand in stimulated cells.

- α-Ketoglutarate dehydrogenase (α-KGDH)

 α -KGDH is an enzyme of the Krebs cycle responsible for converting α -ketoglutarate to succinyl-CoA. It comprises a complex of multiple enzymes with the core predominantly composed of dihydrolipoamide succinyl-transferase (E2) subunits, linked to 2-oxoglutarate decarboxylase (E1) and dihydrolipoamide dehydrogenase (E3) subunits (Yeaman, 1989). Ca²⁺ ions directly influence this enzyme by decreasing the K_m for α -ketoglutarate (McCormack and Denton, 1979).

- Isocitrate-dehydrogenases (IDH)

Another enzyme of the Krebs cycle directly activated by Ca^{2+} is IDH, which catalyzes the conversion of isocitrate in α -ketoglutarate. IDH consists of an octamer of three different subunits, with similar structure and molecular weight. Similar to α -KGDH, Ca^{2+} ions directly affect IDH by decreasing the K_m for its substrate isocitrate. However, for IDH, Ca^{2+} ion sensitivity is regulated by the ATP/ADP ratio, with increased sensitivity observed at lower ATP/ADP ratios (Denton et al., 1978; Rutter and Denton, 1988; 1989).

- FAD-linked glycerol phosphate dehydrogenase (GPDH)

This enzyme is located in the IMM and is part of the glycerol phosphate shuttle, along with the cytosolic NAD-dependent glycerol phosphate dehydrogenase. GPDH facilitates the transfer of reducing equivalents from cytosolic NADH to



MitCa²⁺ uptake homeostasis. Under normal physiological conditions, the mitCa²⁺ enhances oxidative metabolism by increasing the activity of the Krebs cycle. Conditions of mitCa²⁺ overload promote the opening of the mPTP, resulting in the release of pro-apoptotic factors that ultimately lead to cell death. Simultaneously, excessive mitCa²⁺ uptake strongly promotes the formation of reactive oxygen species (ROS), contributing to the development of pathological conditions.

mitochondrial FADH₂. Notably, this enzyme contains two EFhand domains, in a region facing the IMS that are responsible for Ca^{2+} binding and increasing its activity (Wernette et al., 1981; MacDonald and Brown, 1996).

- Pyruvate dehydrogenase phosphate (PDP)

The pyruvate dehydrogenase complex (PDC) is a multi-enzyme complex that catalyzes the conversion of pyruvate to acetyl-CoA. The central core of the enzyme consists of dihydrolipoate acetyltransferase (E2) subunits, to which the pyruvate decarboxylase (E1) and the dihydrolipoate dehydrogenase (E3) subunits are attached (Hiromasa et al., 2004). Pyruvate dehydrogenase kinases (PDKs) catalyze reversible phosphorylation of three sites of the E1 subunits, inhibiting PDH activity. This inhibition can be reverted by the action of pyruvate dehydrogenase phosphatases (PDPs). In mammalian mitochondria, there are two isoforms of PDPs: PDP1 and PDP2. Importantly, only PDP1 is activated by Ca²⁺, leading to the dephosphorylation of PDH and its activation (Huang et al., 1998; Karpova et al., 2003).

It has also been proposed that, in addition to the four mitochondrial dehydrogenases, $mitCa^{2+}$ can directly modulate the activity of the ATP synthase (Territo et al., 2000).

Furthermore, the aspartate/glutamate exchangers of the IMM (named SLC25A12 and SLC25A13) contain EF-hand Ca^{2+} -binding sites exposed in the IMS. In response to a rise in cyt[Ca^{2+}], metabolite transport is enhanced, ultimately stimulating ATP production (Lasorsa et al., 2003; Contreras et al., 2007).

5 MitCa²⁺ regulation of cell death

An excessive accumulation of Ca^{2+} ions inside the mitochondrial matrix, referred as to mitochondrial Ca^{2+} overload, is the primary trigger for the opening of the mitochondrial permeability transition pore (mPTP) (Figure 2, right panel). The opening of this channel leads to an unselective increase of the permeability of the IMM, allowing the exchange of small molecules across this membrane. This leads to a rapid collapse of the membrane potential, mitochondrial swelling, and subsequent release of pro-apoptotic mitochondrial components, including cytochrome *c*, ultimately culminating in cell death (Bernardi et al., 2022; Carraro and Bernardi, 2023).

MitCa²⁺ signals in apoptosis are tightly regulated by antiapoptotic B cell lymphoma (BCL-2) proteins. These proteins modulate the ER-to-mitochondria Ca²⁺ transfer by enhancing the ER Ca²⁺ leak, thereby reducing the ER Ca²⁺ level. This reduction diminishes the transfer of Ca²⁺ to mitochondria upon extracellular stimuli (Foyouzi-Youssefi et al., 2000; Pinton et al., 2000; 2001; Palmer et al., 2004). In contrast, pro-apoptotic proteins exert the opposite effects (Scorrano et al., 2003). Another proposed mechanism involves the direct interaction and modulation of BCL-2 with Ca²⁺-releasing channels on the ER membrane, without affecting the ER Ca²⁺ level (Chen et al., 2004; Hanson et al., 2008; Rong et al., 2009). Overall, BCL-2 proteins can modulate the transfer of Ca²⁺ from the ER to the mitochondria by multiple mechanisms, thereby regulating mitCa²⁺ uptake in response to apoptotic stimuli. MitCa²⁺ also plays a significan role in cell survival pathways. Specifically, the regulation of metabolism by mit[Ca²⁺] impacts autophagy. A decrease in mit[Ca²⁺], with the consequent reduction in the stimulation of aerobic metabolism, activates the AMP-activated protein kinase (AMPK), promoting autophagy. Notably, both the knockdown of Ins(1,4,5)P₃Rs or the use of MCU blockers strongly increases autophagosome formation (Cárdenas et al., 2010). Consistent with these findings, silencing MCU, MICU1, or MCUR1 also serves as a potent activator of AMPK and, consequently, autophagy (Mallilankaraman et al., 2012a).

Overall, maintaining cellular homeostasis involves a complex balance between increasing $MitCa^{2+}$ to meet cellular energy demands and minimizing the risk of mitochondrial calcium overload, a condition that promotes cell death.

6 Crosstalk of mitCa²⁺ and ROS production

Under normal physiological conditions, mitCa²⁺ uptake, by fueling oxidative metabolism, generates ROS signals. ROS are natural by-products of oxidative phosphorylation, and their concentration is tightly regulated by antioxidant molecules. Importantly, at low concentrations, ROS can act as a second messenger in the cell (Turrens, 2003). The physiological significance of mitCa²⁺ uptake in stimulating ROS production has been demonstrated in neurons, where it plays a critical role in the initiation of long-term potentiation (LTP), a fundamental form of plasticity. Specifically, MCU inhibition synaptic disrupt potentiation, despite the N-Methyl-d-aspartate (NMDA) receptor-mediated increase in cyt[Ca²⁺] (Kim et al., 2011).

However, in conditions of excessive mitCa²⁺ uptake, mitochondrial ROS production becomes detrimental (Feno et al., 2019). The increase in ROS production can be directly stimulated by the influence of Ca²⁺ on ROS-producing enzymes like α -KGDH and GPDH, or indirectly via nitric oxide synthase (NOS) activation, which generates NO causing an inhibition of complex IV (Görlach et al., 2015). Furthermore, an abundance of ROS is produced when the mPTP opens under conditions of mitCa²⁺ overload, by reverse electron transport (RET) following mitochondrial membrane depolarization (Biasutto et al., 2016).

ROS can cause damage to proteins, DNA, and lipids contributing to the development of diseases such as Duchenne muscular dystrophy (DMD) and cancer (Sies and Jones, 2020).

Loss of dystrophin in DMD leads to muscle membrane permeability and increased $cyt[Ca^{2+}]$. One proposed mechanism suggests that the mitCa²⁺ overload resulting from the substantial rise in $cyt[Ca^{2+}]$ promotes ROS production, ultimately leading to muscle cell death through apoptotic pathways (Dubinin et al., 2020).

In the context of cancer, it has been demonstrated that Akt phosphorylation of MICU1 elevates basal $mitCa^{2+}$ level and, consequently, ROS production, contributing to cancer progression (Marchi et al., 2019).

Taken together, these studies highlight that $mitCa^{2+}$ serves as key regulator of ROS levels, and any dysregulation in $mitCa^{2+}$ homeostasis may lead to excessive ROS production, fostering pathological conditions.

7 Conclusion

MitCa²⁺ uptake supports oxidative metabolism in response to increased cell energy demand, and its buffering capacity influences ER channels and cytosolic functions. Nevertheless, an excessive influx of mitochondrial mitCa²⁺ triggers the opening of the mitochondrial permeability transition pore (mPTP), ultimately culminating in cell death and fostering increased reactive oxygen species (ROS) production. Consequently, the maintenance of mitochondrial Ca²⁺ homeostasis is paramount for cellular functionality and survival.

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