

1 **Mitochondrial calcium: mechanisms, regulation and functions in**
2 **physiology and disease**

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Abstract

Calcium ions (Ca^{2+}) constitute one of the most versatile signalling molecules with many physiological functions, prominently including muscle contraction, neuronal excitability, cell migration and growth. By uptaking and releasing Ca^{2+} mitochondria serve as important regulators of cellular Ca^{2+} . Mitochondrial Ca^{2+} has also other important functions, such as regulation of mitochondrial metabolism and ATP production and cell death. In recent years, the identification of the molecular machinery regulating mitochondrial Ca^{2+} accumulation and efflux has expanded the number of conditions that are strongly associated with the functions of mitochondrial Ca^{2+} channels or transporters. Indeed, several physiological and pathological processes have now been linked to alterations in mitochondrial Ca^{2+} levels. Thus, understanding the mechanisms of mitochondrial Ca^{2+} regulation and function in different cell types is an important task in biomedical research with the mitochondrial Ca^{2+} machinery emerging as a novel target for the treatment of several disorders.

Keywords: Calcium (Ca^{2+}) signaling, homeostasis, MCU complex, cell death, inflammation, cancer, ion channels, heart, metabolism

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[H1] Introduction

The two adjectives most commonly used to define calcium (Ca^{2+}) signaling are “universal” and “versatile”¹. The universality of Ca^{2+} as a signalling molecule derives from its ubiquity as an intracellular second messenger that controls a wide range of critical processes, whereas the versatility of Ca^{2+} depends on its ability to generate signals with largely different spatial and temporal forms (BOX 1). Among the many organelles, mitochondria play major roles as both regulators and decoders of Ca^{2+} inputs. Due to their intrinsically dynamic nature, mitochondria can localize at specific positions throughout the cell, shaping the Ca^{2+} response in a strategic fashion and acting as Ca^{2+} -dependent effectors of a vast range of processes, such as energy production and cell death.

As described by Ernesto Carafoli in a fascinating historical review², the first indirect evidence of Ca^{2+} transport inside mitochondria dates back to 1953 (REF ³), but the concept that isolated mitochondria could take up high levels of Ca^{2+} by using ATP-derived energy emerged only in the 1960s with observations made by two independent groups^{4,5}. Since then, mitochondria have been thought of as well-defined structures capable of accumulating large amounts of Ca^{2+} ions inside their matrix. Over the past sixty years, intense research in the Ca^{2+} field defined the basic features of mitochondrial Ca^{2+} handling and clearly established the role of mitochondria in the regulation of cellular Ca^{2+} homeostasis, as well as specific functions of mitochondrial Ca^{2+} uptake. At resting conditions, the Ca^{2+} concentration ($[\text{Ca}^{2+}]$) inside mitochondria approaches the values measured in the bulk cytoplasm (100-200 nM), but during stimulation with $[\text{Ca}^{2+}]$ -increasing agents, mitochondria accumulate 10–20-fold more Ca^{2+} than the cytosolic compartment. The sources of Ca^{2+} required for such $[\text{Ca}^{2+}]$ rises are external, represented by the extracellular milieu ($[\text{Ca}^{2+}]$ of ~ 1 mM) from where Ca^{2+} is taken up by plasma membrane channels (the prevailing mechanism in neurons and other excitable cells) or internal via the release of Ca^{2+} from internal sources — endoplasmic reticulum (ER) or sarcoplasmic reticulum (SR) in muscle cells and the Golgi apparatus — via different classes of intracellular channels (e.g., the inositol 1,4,5 trisphosphate receptor (IP3Rs) or ryanodine receptors (RyRs). These intracellular Ca^{2+} stores are loaded with Ca^{2+} ($[\text{Ca}^{2+}]$: >500 μM) at the expense of ATP hydrolysis via the activity of a Ca^{2+} pumps (sarco/endoplasmic Ca^{2+} ATPase, or SERCA, and the secretory pathway Ca^{2+} -transport ATPases, or SPCAs). The reduction of ER intraluminal Ca^{2+} results in a massive Ca^{2+} entry from the extracellular space, a mechanism known as capacitative Ca^{2+} influx or SOCE (store-operated Ca^{2+} entry), aimed to provide Ca^{2+}

73 for the refilling of the ER and regulate a wide number of signaling functions by increasing the
74 cytosolic $[Ca^{2+}]^6$ (Fig.1).

75 The close proximity of mitochondria to such Ca^{2+} pools, in particular the ER, and the presence
76 of a highly Ca^{2+} -selective channel located at the inner mitochondrial membrane (IMM),
77 explain how large amounts of Ca^{2+} could enter these organelles. Ca^{2+} uptake is driven by a
78 **membrane potential** difference ($\Delta\Psi$), generated by the **respiratory chain**, which provides
79 the thermodynamic force required for positively charged ions to enter the matrix. However,
80 Ca^{2+} does not remain inside mitochondria but rather is rapidly extruded into the cytoplasm
81 through a complex system of Ca^{2+} antiporters, restoring the basal state level. Thus, the
82 coordination of this highly sophisticated Ca^{2+} machinery, which consists of different pumps,
83 channels and auxiliary proteins, is crucial for the maintenance of mitochondrial Ca^{2+}
84 homeostasis, which in turn further demonstrates the impact of the mitochondrial
85 compartment in the regulation of cellular Ca^{2+} signaling.

86 In this review, we will focus on the physiological role of mitochondrial Ca^{2+} and its
87 deregulation in several pathological contexts. Moreover, we will describe the molecular
88 details of the different Ca^{2+} transporters and provide mechanistic insight into the related
89 regulatory pathways of mitochondrial Ca^{2+} exchange, discussing the most recent discoveries
90 and the many unanswered questions and conflicting interpretations.

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92 **[H1] Mitochondrial Ca^{2+} entry**

93 The continuous development of methods for measuring $[Ca^{2+}]$, based on either luminescent or
94 fluorescent probes (BOX 2), has enabled the characterization of the intrinsic mechanisms
95 regulating mitochondrial Ca^{2+} handling. To reach the internal matrix region, cytosolic Ca^{2+} has
96 to cross two membranous systems, the outer mitochondrial membrane (OMM) and the IMM,
97 which both harbour protein pores enabling regulated Ca^{2+} uptake (Fig. 2).

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99 ***[H3] The mitochondrial calcium channels***

100 The first barrier, the OMM, is considered highly permeable to Ca^{2+} ions, and this permeability
101 is ensured by high expression of the OMM protein VDAC (voltage-dependent anion channel),
102 which forms membrane pores and represents the first molecular interface between
103 mitochondria and Ca^{2+} stores (the ER/SR and the extracellular space). VDAC porins exist in
104 three subtypes (from 1 to 3), which are expressed more or less ubiquitously but vary in their
105 isoform ratios and sub-mitochondrial distribution among tissues⁷. Recent findings have

106 confirmed the key role of VDACs in mitochondrial Ca^{2+} transfer across the OMM in different
107 contexts^{8,9}, leading to a high $[\text{Ca}^{2+}]$ in the intermembrane space (IMS) (Fig. 2a).

108 The channel responsible for Ca^{2+} passing through the IMM is termed the mitochondrial
109 calcium uniporter (MCU). It is now firmly established that the MCU is a macromolecular
110 complex composed of pore-forming subunits and regulatory proteins¹⁰⁻¹² (Fig. 2b). The
111 molecular characterization of the entire complex was made possible by studies, which
112 simultaneously identified the *bona fide* channel component MCU (previously known as
113 CCDC109a)^{13,14}. The other elements of the holocomplex are the MCU regulator MCUB (also
114 known as CCDC109b)¹⁵ and the IMS-resident protein MICU1 (REF¹⁶), which binds to its
115 paralogue MICU2 (REF¹⁷) to form heterodimeric structures^{18,19} associated with MCU through
116 the single-pass membrane protein SMDT1 (later renamed EMRE, or essential MCU
117 regulator)²⁰. Notably, additional components of the complex have been described, including
118 MICU3 (REF¹⁷) and MICU1.1, a MICU1 splicing variant with higher Ca^{2+} -binding affinity than
119 MICU1²¹, which are tissue-specific members of the uniporter and are expressed in the central
120 nervous system and skeletal muscle, respectively.

121 The working model of the uniporter is the product of extensive research: after passing
122 through VDACs, incoming calcium is first handled by MICU1-2 dimers, due to their strategic
123 IMS localization and the presence of two Ca^{2+} -binding EF-hand domains in both the MICU1
124 and MICU2 amino acid sequences. Loss-of-function studies have definitively demonstrated
125 that MICU1-2 dimers are the gatekeepers of the uniporter, setting the Ca^{2+} threshold for MCU
126 activation and limiting the detrimental accumulation of Ca^{2+} inside the matrix under basal
127 (unstimulated) conditions²²⁻²⁴. Thus, by sensing the IMS Ca^{2+} levels, MICU1/2 proteins gate
128 the activity of the pore, allowing mitochondrial Ca^{2+} uptake exclusively at high $[\text{Ca}^{2+}]$.
129 However, while MICU2 is *per se* a genuine inhibitor of the uniporter, reducing mitochondrial
130 Ca^{2+} entry at both low and high cytosolic $[\text{Ca}^{2+}]$ ^{18,19}, the mechanistic role of MICU1 is currently
131 debated, since it has been suggested to be a purely stimulatory subunit¹⁸ or to play a dual role,
132 inhibiting entry at low $[\text{Ca}^{2+}]$ and cooperating with MCU when the $[\text{Ca}^{2+}]$ rises²².

133 The pore-forming subunit MCU forms pentameric structures *in vitro*²⁵, and its activity is
134 strictly dependent on EMRE, since mammalian MCU does not transport Ca^{2+} in an EMRE
135 knockout (KO) background²⁰. Although it was originally proposed that EMRE might control
136 MCU by sensing the $[\text{Ca}^{2+}]$ in the matrix through its C-terminal domain²⁶, subsequent, and in
137 our biased opinion more convincing, observations revealed that the C-terminus of EMRE is
138 located in the IMS, rather than the matrix^{27,28}, connecting the MICU1-2 sensors to MCU and
139 thus regulating Ca^{2+} entry²⁸. MCU is negatively regulated by its paralogue MCUB¹⁵, though

140 overexpression of MCUb in *Trypanosoma cruzi* does not have a dominant negative effect on
141 MCU²⁹.

142 This characterization of the function of the MCU complex fulfills all the properties that were
143 attributed to the uniporter several years before its molecular discovery, such as sensitivity to
144 Ruthenium red (RR) inhibition, a high Ca²⁺ selectivity³⁰, induction of Ca²⁺ uptake only in
145 energized mitochondria, and a low Ca²⁺ affinity (apparent K_D of 20-30 μM)³¹. This implies that
146 the function of the MCU complex completely relies on two main parameters, the
147 mitochondrial membrane potential and the [Ca²⁺] in the area surrounding the channel.

148

149 ***[H3] Mitochondrial membrane potential as a driving force for calcium uptake***

150 After the acceptance of the **chemiosmotic theory**, it was postulated that the driving force for
151 Ca²⁺ entry is the proton electrochemical gradient potential, generated by the serial reduction
152 of electrons through the respiratory electron transport chain (ETC). The reductive transfer of
153 electrons through respiratory complexes I-IV produces the energy required to pump H⁺ ions
154 against their concentration gradient in the IMS, resulting in a ΔΨ of 150-180 mV (negative
155 inside, thus favoring cation entrance) (Fig. 2c). As proof of this concept, dinitrophenol and
156 carbonyl cyanide-p-trifluoromethoxyphenylhydrazone (FCCP), two uncouplers of oxidative
157 phosphorylation, dissipate the membrane potential across the IMM, thereby almost resetting
158 the ΔΨ and abolishing Ca²⁺ entry via the uniporter^{32,33}.

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160 ***[H3] The role of ER-mitochondria tethering in mitochondrial calcium uptake***

161 The participation of mitochondria in many Ca²⁺ signaling pathways depends on close
162 interactions with the ER calcium store, and the ensuing formation of ER-mitochondria contact
163 sites. The distance between the ER and the mitochondrion at these sites varies between 10
164 and 60 nm³⁴, and the ER associates more frequently with mitochondria than with other
165 organelles^{35,36}. This allows mitochondria to be exposed, upon the opening IP3R to
166 microdomains of high [Ca²⁺] that are necessary to induce Ca²⁺ accumulation through the low-
167 affinity MCU complex.

168 These synaptic-like associations, called mitochondria-associated membranes (MAMs)³⁷, are
169 small enough to allow contact between proteins on the surface of both organelles and ensures
170 that upon agonist Ca²⁺ mobilization, the [Ca²⁺] on the cytosolic surface of the OMM reaches
171 levels 10-fold higher than those in the bulk cytosol³⁸ (Fig. 2a). Conversely, the [Ca²⁺] to which
172 the OMM is exposed during SOCE is similar between mitochondria located near the plasma
173 membrane and those located in other intracellular areas. However, mitochondria can also

174 form associations with the plasma membrane called plasma membrane-associated
175 mitochondria (PAM)³⁹, where mitochondria are exposed to a 3-fold higher [Ca²⁺] upon
176 activation of voltage-gated Ca²⁺ channels in the plasma membrane³⁸.

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178 **[H1] Mitochondrial Ca²⁺ efflux**

179 Historically, two major systems have been postulated to extrude Ca²⁺ from the matrix: the
180 sodium (Na⁺)/Ca²⁺ exchanger (mNCX) and the H⁺/Ca²⁺ (mHCX) exchanger. The first appears
181 to be the predominant antiporter in excitable tissues (heart, brain), whereas the latter mainly
182 leads to Ca²⁺ release in non-excitable tissues (liver, kidney). The stoichiometry of mNCX-
183 driven transport is defined as electrogenic, with 3 (or 4) Na⁺ for 1 Ca²⁺ (REF ⁴⁰), whereas the
184 exchange ratio of mHCX is electroneutral (2 H⁺ for 1 Ca²⁺)⁴¹ (Fig. 2d). Thus, the two Ca²⁺ efflux
185 systems mediate the extrusion of matricial Ca²⁺ toward the IMS, reaching the cytosolic
186 compartment by the VDAC channels or additional Ca²⁺ extruding mechanisms located at OMM,
187 such as the NCX family member NCX3 (REF ⁴²). Although Na⁺-dependent and Na⁺-independent
188 Ca²⁺ exit mechanisms have been described since the 1970s, the molecular identities of the
189 different components of mitochondrial Ca²⁺ efflux were revealed only a few years ago.

190 In 2010 it was shown that mNCX is a gene product of mammalian *SLC8B1* (REF ⁴³), most
191 frequently known as NCLX, since it catalyzes not only Na⁺/Ca²⁺ exchange but also lithium
192 (Li⁺)-dependent Ca²⁺ transport. This unique property, which was originally ascribed to the
193 mNCX⁴⁴, together with i) NCLX mitochondrial localization, ii) sensitivity to the classical mNCX
194 inhibitor CGP-37157, and iii) alteration of mitochondrial Ca²⁺ efflux in multiple cell types
195 lacking NCLX activity^{43,45-47}, definitively demonstrates that NCLX is the mitochondrial
196 Na⁺/Ca²⁺ exchanger.

197 While the molecular nature of the mNCX is generally accepted today, the identity of the
198 H⁺/Ca²⁺ antiporter is more controversial. In 2009 it was demonstrated that the IMM protein
199 LETM1 (leucine zipper EF-hand containing transmembrane protein 1) acts as a H⁺/Ca²⁺
200 exchanger in both *Drosophila* and mammalian cells, as well as in proteoliposomes⁴⁸.
201 Moreover, the authors suggested that LETM1 might promote mitochondrial Ca²⁺ entry under
202 certain conditions, functioning as a high-affinity Ca²⁺ uptake system alternative to the MCU
203 complex⁴⁸. This concept has been confirmed by others^{49,50}, but the huge advances in the
204 understanding of the mechanisms of the uniporter have decreased the interest in such
205 observations.

206 The role of LETM1 in matricial Ca²⁺ release has also been questioned⁵¹; indeed, LETM1 was
207 first reported as a K⁺/H⁺ exchanger⁵²⁻⁵⁴, and some LETM1-related features described in initial

208 studies, such as a stoichiometry of 1 H⁺ for 1 Ca²⁺ and sensitivity to the MCU inhibitor RR⁴⁸,
209 conflict with those originally described for the mHCX. Novel findings obtained with a highly
210 purified LETM1-containing liposome system partially clarified these issues, suggesting
211 electroneutral transport of Ca²⁺ and insensitivity to RR and CGP-37157, thereby reaffirming
212 that LETM1 is the mHCX⁵⁵. Moreover, LETM1 might oligomerize in hexameric structures, thus
213 acting as a transporter, even though it only contains a single transmembrane helix⁵⁶.
214 However, due to the numerous conflicting results, including opposite mitochondrial Ca²⁺
215 levels observed in LETM1-silenced cells^{45,48,50,56,57}, more experimental evidence is required to
216 firmly establish the functional role of LETM1 as a component of the mitochondrial Ca²⁺ efflux
217 machinery.

218 Importantly, mHCX and mNCX could not be the unique molecular pathways aimed to extrude
219 Ca²⁺ from the mitochondrial matrix. It has also been proposed that, under certain conditions,
220 the transient opening of the mPTP (mitochondrial permeability transition pore) might
221 represent an alternative Ca²⁺ efflux pathway⁵⁸, although other observations question this
222 hypothesis⁵⁹.

223

224 **[H1] Regulation of Mitochondrial Ca²⁺**

225 Molecular studies have revealed that the heterogeneity of the mitochondrial Ca²⁺ machinery is
226 associated with an equally variable regulatory system, which operates at multiple levels to
227 maintain physiological Ca²⁺ homeostasis. Indeed, many proteins have been reported to be
228 genuine regulators of Ca²⁺ uptake by acting on specific molecular targets or controlling
229 essential mitochondrial functions (Table 1).

230 Due to its strategic position, VDAC is the preferential target for endogenous proteins located
231 at the interface between mitochondria and the cytoplasm, including the **Bcl-2 family**
232 members⁶⁰. For example, Bcl-xL interacts with VDAC1 and VDAC3, but not VDAC2, shaping
233 mitochondrial Ca²⁺ entry by favoring Ca²⁺ transfer across the OMM⁶¹. VDAC gating requires a
234 voltage-dependent transition between the closed and open states, but the closed VDAC
235 conformation shows higher cation-selectivity and Ca²⁺ permeability⁶². Thus, Bcl-xL should
236 promote VDAC closure, as previously suggested⁶³, thereby enhancing mitochondrial Ca²⁺
237 accumulation. However, this aspect remains largely unclear, since it has been reported that i)
238 Bcl-xL promotes the open VDAC state, rather than the closed configuration⁶⁴; ii) VDAC could
239 assume a cation-selective open conformation⁶⁵; and iii) it has been reported that Bcl-xL
240 inhibits VDAC1 activity, thus lowering, rather than increasing, the mitochondrial [Ca²⁺]⁶⁶.

241 Several intra-mitochondrial proteins have been suggested to regulate Ca²⁺ signaling by
242 altering the MCU complex functions. The first in chronological order is MCUR1 (MCU regulator
243 1, also known as CCDC90a). It has been shown that MCUR1 binds MCU at the matrix interface
244 and that MCUR1 knockdown abolishes Ca²⁺ uptake in intact cells⁶⁷. The interaction between
245 MCU and MCUR1 has been reported in other studies⁶⁸⁻⁷⁰, and MCUR1 was recently proposed
246 to have a role as a scaffold factor in the assembly of the uniporter complex⁷¹. Conversely,
247 when a proteomic assay was used to identify components of the MCU complex, MCUR1 was
248 not recognized²⁰, and the yeast *Saccharomyces cerevisiae*, which lacks any uniporter activity,
249 possesses an MCUR1 ortholog, named fmp32, suggesting a function for MCUR1 outside the
250 MCU complex. Moreover, MCUR1/CCDC90a has been described as a co-factor in the assembly
251 of the respiratory chain, rather than the uniporter, indicating that the reduction of Ca²⁺ uptake
252 observed in MCUR1-deleted cells may be due to alteration of the mitochondrial membrane
253 potential⁷². Therefore, the idea that the MCUR1-related Ca²⁺ defect, ascribed to modulation of
254 MCU function, is secondary to mitochondrial membrane depolarization caused by respiratory
255 chain disorders cannot be ruled out. Notably, in hepatocarcinoma cells, MCUR1 appears to
256 regulate Ca²⁺ entry in an uniporter-dependent manner, although forced MCUR1 silencing
257 induces a decrease in $\Delta\Psi$ ⁷³. This mitochondrial potential drop has been attributed to a
258 concomitant trigger of apoptosis⁷³, but, in our opinion, it is inconsistent with exclusive
259 inhibition of MCU activity, since genetic manipulation of the pore-forming subunit has never
260 been linked to cell death induction.

261 Similarly to MCUR1, SLC25A23 has been proposed as a novel regulator of the uniporter⁷⁴,
262 although it has a homolog in yeast (Sal1) and was originally described as a Ca²⁺-regulated
263 mitochondrial ATP-Mg/Pi carrier^{75,76}. Other proteins, including canonical transient receptor
264 potential 3 (TRPC3)⁷⁷ and uncoupling protein 2-3 (UCP2-3)⁷⁸, are involved in mitochondrial
265 Ca²⁺ accumulation, most likely through MCU complex-independent mechanisms.

266 Several regulatory factors, shown in Table 1, have been reported to maintain the correct
267 distance between the ER and mitochondria, thereby ensuring proper Ca²⁺ transfer.
268 Particularly worthy of mention are two OMM proteins, mitofusin-2 (MFN2) and PDZD8. MFN2
269 was originally characterized as an ER-mitochondria tether⁷⁹, but its role was strongly
270 contested⁸⁰, and it is still unclear whether MFN2 promotes or inhibits ER-mitochondria
271 contacts. PDZD8, previously known as a regulator of retroviral infection⁸¹, has recently been
272 described as the long-sought mammalian ortholog of the yeast Mmm1 protein, which is a
273 component of the ER-mitochondria encounter structure at ER-mitochondria contact sites and
274 coordinates Ca²⁺ exchange exclusively via its ER-mitochondria tethering role⁸².

275 Post-translational modifications represent additional layers in the regulation of mitochondrial
276 Ca^{2+} handling. The first example of phosphorylation events capable of finely tuning
277 mitochondrial Ca^{2+} homeostasis is attributed to the PKC family⁸³. Recently, a regulatory
278 pathway for Ca^{2+} efflux has been identified⁸⁴: both PINK1 and PKA positively regulate NCLX,
279 and inhibition of Ca^{2+} release in PINK1 KO cells could be reverted by PKA-mediated NCLX
280 phosphorylation⁸⁴. Intriguingly, PINK1 is also able to boost mitochondrial Ca^{2+} extrusion by
281 phosphorylating LETM1, the putative mHcX, at Thr192 (REF ⁸⁵).

282 Both VDAC function and interactions with other molecular partners are affected by multiple
283 phosphorylation events. In high-fat conditions, GSK3-mediated VDAC phosphorylation at a
284 threonine residue is drastically reduced, and its permeability to Ca^{2+} is increased, leading to
285 disruption of the VDAC–Bcl-xL complex⁸⁶.

286 The uniporter complex is also subjected to phosphorylation events. The proline-rich tyrosine
287 kinase 2 (Pyk2) can target MCU, promoting the formation of tetrameric channels⁸⁷. In
288 addition, during heart disease, a matricial pool of Ca^{2+} /calmodulin-dependent protein kinase
289 II (CaMKII) phosphorylates MCU at two sites (Ser57 and Ser92), resulting in a higher Ca^{2+}
290 response⁸⁸. Interestingly, phosphorylation of the N-terminal residue 92 seems to be critical
291 for MCU activity⁶⁸. However, subsequent electrophysiological studies failed to confirm the
292 regulatory effect of CaMKII on MCU⁸⁹.

293 No phosphorylation events have been associated with the other uniporter complex
294 components, although MICU1 can be methylated by protein arginine methyl transferase 1
295 (PRMT1)⁹⁰. Moreover, the m-AAA protease (AFG3L2/SPG7) has been shown to degrade
296 unassembled EMRE, thus ensuring the correct stoichiometry between the different complex
297 subunits and preserving uniporter activity^{91,92}. Overall, these observations demonstrate that
298 mitochondrial Ca^{2+} uptake and efflux are regulated on multiple levels. An aberration in a
299 single regulatory mechanism could result in the harmful remodeling of Ca^{2+} mitochondrial
300 Ca^{2+} fluxes, which in turn can lead to changes in cellular Ca^{2+} homeostasis and specific
301 pathological phenotypes (see next sections). Therefore, it is not surprising that multiple
302 disease-associated micro-RNAs are emerging as crucial players in the control of
303 mitochondrial $[\text{Ca}^{2+}]$. Indeed, decreases in the gene expression of both VDAC, by miR-7 (REF
304 ⁹³) and miR-29a⁹⁴, and MCU, by miR-25 (REF ⁹⁵⁻⁹⁷), miR-138 (REF ⁹⁷), miR-1 (REF ⁹⁸), and miR-
305 340 (REF ⁹⁹), are thought to be key molecular events underlying different pathological
306 contexts.

307

308 **Mitochondria in Ca^{2+} Homeostasis**

309 Three main functional roles have been attributed to mitochondrial Ca^{2+} uptake: i) stimulation
310 of ATP production by activation of **mitochondrial dehydrogenases**, ii) regulation of cell
311 death and iii) spatiotemporal remodeling of intracellular Ca^{2+} . The first two aspects have
312 obvious implications in multiple physio-pathological processes and will be discussed in the
313 section below.

314 Numerous correlative studies performed in different cellular types have suggested that
315 mitochondria shape the intracellular Ca^{2+} response both locally and in the bulk cytoplasm.
316 However, these observations have been obtained using chemical compounds with low
317 specificity or having a strong impact on mitochondrial functions and thus on the whole
318 cellular metabolism, producing some spurious and controversial results¹⁰⁰. The molecular
319 characterization of Ca^{2+} influx and efflux pathways has provided new evidence supporting the
320 concept that mitochondria can act as cytosolic Ca^{2+} -buffering systems. During IP₃-mediated
321 ER Ca^{2+} release, the peak amplitude of the cytosolic Ca^{2+} response is significantly lower in
322 cells where the mitochondrial Ca^{2+} uptake capacity was increased by MCU over-expression¹⁴.
323 Notably, the elevated cytoplasmic Ca^{2+} levels observed in PDZD8-depleted neurons, where
324 ER-mitochondria tethering is disrupted, could be related to reduced mitochondrial Ca^{2+}
325 buffering activity⁸². Similar findings have been obtained in NCLX-silenced **astrocytes**¹⁰¹,
326 although this effect is more pronounced upon capacitative Ca^{2+} influx, rather than after ER
327 Ca^{2+} depletion. Thus, mitochondria promptly take up cytoplasmic Ca^{2+} , regardless of whether
328 it derives from internal stores (ER) or the extracellular space.

329 The knockdown of both UCP2 and MCU, with consequent reduction of mitochondrial Ca^{2+}
330 uptake, strongly inhibits SOCE by limiting aggregation of STIM1 and activation of ORAI1, the
331 pore-forming subunit of the CRAC (Ca^{2+} release-activated Ca^{2+} channels) at the plasma
332 membrane¹⁰². These findings reveal that the Ca^{2+} buffering capacity of mitochondria
333 positioned at the opening of IP₃Rs could represent a pivotal mechanism in the modulation of
334 SOCE, as previously suggested¹⁰³.

335 The cytosolic $[\text{Ca}^{2+}]$ could also affect the function of both ER-resident proteins (IP₃R)¹⁰⁴ and
336 store-operated Ca^{2+} channels¹⁰⁵, thus implying a regulatory role for mitochondria due to the
337 buffering of local Ca^{2+} rises. High cytosolic Ca^{2+} levels in the area surrounding the channels
338 inhibit their activity, further reducing Ca^{2+} release through the IP₃R or Ca^{2+} entry by ORAI1.
339 The strategic positioning of mitochondria lowers the $[\text{Ca}^{2+}]$, preventing negative feedback and
340 sustaining channel activity. Indeed, MCU loss induces inefficient mitochondrial Ca^{2+} buffering
341 capacity, which in turn limits CRAC function by enhancing Ca^{2+} -mediated slow inactivation of
342 the channels¹⁰⁶. Accordingly, the number of cytosolic Ca^{2+} oscillations, generated by discharge

343 of Ca²⁺ from IP₃-sensitive stores, is significantly lower in MCU knockdown cells, which reflects
344 IP₃R inhibition due to impaired mitochondrial Ca²⁺ uptake¹⁰⁶. Overall, by controlling Ca²⁺
345 channel functions and collecting large amounts of Ca²⁺ in specific subcellular areas,
346 mitochondria have the ability to preclude the propagation of Ca²⁺ waves, thereby regulating
347 specific cellular processes that depend (or that are regulated) by Ca²⁺ (REF ¹⁰⁷). For example,
348 in neonatal cardiomyocytes, reducing mitochondrial Ca²⁺ uptake results in a prominent
349 increase in the amplitude of beat-to-beat cytosolic Ca²⁺ oscillations, which in turn contributes
350 to extend the contraction¹⁰⁸.

351 However, several aspects require more clarification, including the complex relationship
352 between mitochondrial Ca²⁺ uptake and SOCE. For example, in breast cancer cell lines, it has
353 been observed that abolition of mitochondrial Ca²⁺ accumulation by MCU depletion could
354 reduce¹⁰⁹ or marginally increase¹¹⁰ SOCE. Although different experimental conditions might
355 explain some contradictory results, other important factors should be taken in account,
356 including the number of mitochondria and their subcellular distribution, which could vary
357 substantially depending on cell type or condition^{38,111}, or the impact of other organelles in the
358 local buffering of cytoplasmic Ca²⁺ (REF ^{112,113}). Moreover, NCLX could also mediate redox
359 control of SOCE that is independent from mitochondrial Ca²⁺ buffering capacity. Upon ER Ca²⁺
360 depletion, a rapid rise in cytosolic Na⁺ occurs, promoting NCLX activity and mitochondrial
361 Ca²⁺ efflux, which in turn results in a reduction of matrix [Ca²⁺] and ROS generation. This
362 pathway is essential for sustaining capacitative Ca²⁺ influx, since prolonged ROS production is
363 associated to SOCE inhibition by oxidation of Orai1 at Cysteine 195 (REF ¹¹⁴).

364

365 **[H1] Pathophysiology of Mitochondrial Ca²⁺**

366 The concept that mitochondrial Ca²⁺ is a crucial regulator of cell life and death originates i)
367 from its ability to activate oxidative metabolism, mitochondrial respiration and ATP synthesis
368 by stimulating three Ca²⁺-sensitive matrix dehydrogenases¹¹⁵ and ii) from the fact that
369 intracellular Ca²⁺ deregulation can trigger either necrosis, apoptosis or autophagy¹¹⁶⁻¹¹⁸. This
370 dual role explains how mitochondrial Ca²⁺ has prominent implications in multiple physio-
371 pathological processes. Among them, here we will focus on i) insulin secretion, ii) heart
372 functionality, and iii) inflammation to highlight as, in different tissues, highly differentiated
373 and specialized, mitochondrial Ca²⁺ homeostasis acts as a master regulator of cellular
374 functions. Nevertheless, recent preclinical and clinical data have indicated that mitochondrial
375 Ca²⁺ derangement is a novel feature of cancer pathology (BOX 3).

376 ***[H3] Insulin secretion and links to diabetes***

377 Pancreatic beta cells (β -cells) are the body's sole source of circulating insulin. β -cells are
378 specifically designed to synthesize and store large amounts of insulin¹¹⁹, which is secreted
379 based on the demand of target tissues. In healthy individuals, β -cells sense changes in plasma
380 glucose concentration and respond by releasing corresponding amounts of insulin into the
381 bloodstream. Despite decades of research, the molecular mechanisms underlying the
382 activation of β -cells are not yet clearly defined.

383 Nutrient secretagogues, especially glucose, initiate downstream signals enabling β -cells to
384 break down sugar and release insulin by stimulating mitochondrial energy metabolism¹²⁰. It is
385 assumed that glucose mobilizes Ca^{2+} from the ER store. The consequent formation of Ca^{2+}
386 microdomains at nearby mitochondria permits efficient mitochondrial Ca^{2+} uptake via the
387 MCU complex, followed by Ca^{2+} -triggered ATP production. The resulting shift in the cytosolic
388 ATP:ADP ratio leads to the closure of ATP-sensitive K^+ (K_{ATP}) channels on the plasma
389 membrane of β -cells, eliciting plasma membrane depolarization. Once a threshold potential is
390 reached, voltage-gated Ca^{2+} channels in the plasma membranes of β -cells open, generating
391 individual Ca^{2+} microdomains beneath the plasma membrane¹²¹.

392 The main role of the increase in sub-plasma membrane Ca^{2+} is to permit insulin release¹²²,
393 possibly through the activation and migration of protein kinase C (PKC) β -II to the surface of
394 secretory vesicles localized in that area, although the details of the mechanism are still not
395 fully understood¹²³. Moreover, mitochondria that are strategically situated close to plasma
396 membrane Ca^{2+} channels are able to sense microdomains of high Ca^{2+} concentration in their
397 proximity, take up Ca^{2+} through the MCU complex and fuel the exocytotic process by
398 producing ATP.

399 Thus, the mitochondrial Ca^{2+} machinery plays a fundamental physiological role in glucose-
400 mediated insulin secretion¹²⁴, both by initiating and sustaining the process. In this scenario,
401 the generation of two different types of microdomains with high Ca^{2+} concentrations — at the
402 interface with ER and the plasma membrane — that are associated with two pools of
403 mitochondria allows acceleration of Ca^{2+} -dependent mitochondrial metabolism and the
404 regulation of the two secretion stages independently: mitochondria forming MAMs are
405 fundamental in initiating the secretion process upon the release of Ca^{2+} from ER channels,
406 including RyRs¹²⁵, whereas mitochondria forming PAMs are tightly associated with the cell
407 surface and seem to be more important in sustaining and amplifying the phase of insulin
408 secretion¹²⁴, upon Ca^{2+} entry from the extracellular space (Fig. 3a).

409 Defects in mitochondrial Ca^{2+} homeostasis within pancreatic β -cells, with a consequent
410 reduction of mitochondrial ATP production¹²⁶ and thus impaired insulin secretion¹²⁷, are
411 considered one of the causal factors in the etiology of both type 1 and type 2 diabetes¹²⁸.
412 Chronic ER Ca^{2+} depletion due to leaky RyR channels is responsible for decreased
413 mitochondrial Ca^{2+} uptake and β -cell failure, representing a potent risk factor for the
414 development of diabetes¹²⁵. Therefore, strategies to rejuvenate or replace these cells, as well
415 as those to restore an efficient mitochondrial Ca^{2+} response, represent promising therapeutic
416 approaches for these diseases and their complications. Both the MCU channel⁵⁷ and its
417 regulatory partner MICU1 (REF ¹²⁹) from the MCU complex have been indicated to play a
418 fundamental role in the β -cell feed-forward mechanism of Ca^{2+} entry into mitochondria, which
419 guarantees insulin secretion and thus represents a promising therapeutic target for diabetes.
420 Recently, it has been demonstrated how the enhancement of K^+ flux across the ER membrane
421 through ER-localized TALK-1 channels facilitates Ca^{2+} release from the ER, improving
422 mitochondrial ATP production. These observations revealed TALK-1 as a possible therapeutic
423 target to reduce ER Ca^{2+} handling defects and thus restore correct mitochondrial Ca^{2+}
424 homeostasis in β -cells during the pathogenesis of diabetes¹³⁰.

425

426 **[H3] Cardiac cell functions and heart failure**

427 Calcium is of vital importance in maintaining cardiac cell function during the cardiac cycle
428 (excitation, contraction or diastole, and relaxation or systole). Meanwhile, it also plays a key
429 role in the pathology of heart failure, being responsible for cardiac cell death via apoptotic and
430 necrotic pathways¹³¹.

431 Under physiological conditions, Ca^{2+} signaling in the heart exerts three main functions
432 controlling the so-called excitation-contraction coupling (*EC coupling*), excitation-
433 transcription coupling (*ET coupling*) and excitation-metabolism coupling (*EM coupling*)
434 mechanisms. While EC and ET coupling are governed essentially by cytosolic Ca^{2+} transients
435 that drive contraction and cardiac muscle genes activation or inactivation, mitochondrial Ca^{2+}
436 contributes to local control of oxidative metabolism (EM coupling), generating the ATP
437 needed to power cardiac excitation and contraction during every heartbeat¹³².

438 In mammalian cardiac cells, the cardiac cycle starts with the generation of an automatic
439 **action potential** (AP) in a group of specialized cells, named sinoatrial (SA) nodal cells,
440 responsible for initiating the electrical cardiac impulse needed for contraction. The AP begins
441 with a change in the voltage of the cell membranes of heart cells that becomes more positive,
442 mainly due to the opening of sodium channels, which allow Na^+ to flow into the cell. This

443 depolarization, also called the “funny” current (for its property of being activated by very
444 negative membrane potentials), permits a threshold potential of about -50 mV to be reached,
445 inducing a progressive opening of L-T Ca^{2+} channels (LTCCs) in the sarcolemmal membrane.
446 The consequent cytosolic Ca^{2+} influx through LTCCs is sufficient to regulate and activate
447 mitochondrial functions and thus ATP production¹³³, through the generation of Ca^{2+}
448 microdomains around nearby mitochondria. Calcium influx through LTCCs also triggers Ca^{2+}
449 release from the nearby junctional SR via IP3Rs and RyRs in a process known as Ca^{2+} -induced
450 Ca^{2+} release (CICR), a crucial process for cardiac muscle contraction¹³⁴. The high local
451 cytosolic $[\text{Ca}^{2+}]$ generated during the CICR process initiates contraction by binding **troponin**
452 **C on myofilaments** and contributes to mitochondrial metabolism, permitting Ca^{2+} uptake into
453 mitochondria¹³⁵. A rapid increase in mitochondrial Ca^{2+} is essential for telegraphing the
454 enhanced metabolic demand for ATP to promote oxidative phosphorylation. Thus,
455 mitochondrial Ca^{2+} is fundamental to providing the necessary link between ATP supply and
456 demand during cardiomyocyte contraction (Fig. 3b).

457 In this context, the MCU is critical for boosting heartbeat frequency by favoring rapid Ca^{2+}
458 mitochondrial uptake during the cardiac cycle¹⁰⁸. Only the generation of well-defined
459 mitochondrial Ca^{2+} microdomains, either at the entrance of voltage-gated Ca^{2+} channels at the
460 plasma membrane (sarcolemma) after LTCC opening or in close proximity to RyRs in the SR
461 during CICR events, can explain mitochondrial Ca^{2+} uptake in cardiac myocytes. Importantly,
462 MCU-enhanced oxidative phosphorylation is also required for reloading SR Ca^{2+} stores and
463 sustaining fight or flight heart rate increases in response to energy demand¹³⁶.

464 To date, it remains controversial whether variations in the mitochondrial $[\text{Ca}^{2+}]$ occur quickly
465 in a beat-to-beat fashion, taking place synchronously with cytosolic Ca^{2+} fluctuations, or
466 whether Ca^{2+} uptake could occur slowly¹³⁷. Undoubtedly, mitochondria sense cytosolic Ca^{2+}
467 signals and transform them into mitochondrial energy production, and they are far from being
468 only passive Ca^{2+} sinks. Thus, there is an emerging consensus regarding the existence of
469 subpopulations of mitochondria exposed to high levels of $[\text{Ca}^{2+}]$ with the ability to take up
470 Ca^{2+} on a beat-to-beat basis¹³⁸. It is possible that the new mechanistic understanding of the
471 MCU functions and advancements in Ca^{2+} measurement technologies (BOX 2) could help solve
472 this disagreement.

473 As mitochondrial Ca^{2+} is fundamental to maintaining the ATP supply in myocardial cells,
474 disrupted cardiomyocyte Ca^{2+} homeostasis is recognized as a major contributor to the heart
475 failure phenotype¹³⁹. Acute heart diseases, i.e., ischemia/reperfusion (I/R) injury, are mainly
476 attributed to mitochondrial Ca^{2+} overload together with increased production of reactive

477 oxygen species (ROS) caused by an overshoot of the mitochondrial respiratory chain activity
478 that, driving the activation of the mitochondrial permeability transition pore (mPTP), lead to
479 necrotic and apoptotic cardiac cell death. Thus, targeting the regulatory systems of
480 mitochondrial Ca²⁺ homeostasis, such as the MCU complex and NCLX, as well as limiting ROS
481 generation and mPTP activation could represent a potential therapeutic strategy to combat
482 these pathologies.

483 The use of mPTP inhibitors, such as cyclosporin A, has been reported in experimental studies
484 to reduce myocardial infarction (MI) size and preserve cardiac function. However, in clinical
485 trials, opposite effects were observed by the same group upon administration of cyclosporin
486 A, thus failing to demonstrate a final and conclusive benefit for clinical outcomes^{140,141}.
487 Therefore, more specific and novel mPTP inhibitors, based on new findings regarding the
488 molecular composition of mPTP¹⁴² are required to translate mPTP inhibition as a
489 cardioprotective strategy into clinical practice.

490 In parallel, other strategies are being explored. Cardiac-specific MCU-KO or dominant
491 negative MCU-expressing mice showed a drastic reduction of mitochondrial Ca²⁺ uptake and
492 were strongly protected against I/R injury¹⁴³⁻¹⁴⁵, revealing MCU as a potential new target for
493 cardioprotective drug design. In agreement with this view, the increased MCU current
494 induced by activation of CaMKII during I/R promotes mPTP opening and myocardial death⁸⁸.
495 Thus, although this pathway is debated (see section above), mitochondrial-targeted CaMKII
496 inhibition might be another strategy to prevent or reduce myocardial death and heart failure.

497 In addition to MCU, it has been recently identified how Ca²⁺ efflux is essential for maintaining
498 cardiac cellular function. Targeting NCLX by increasing its activity is sufficient to prevent
499 mitochondrial Ca²⁺ overload and to limit mPTP opening, with a consequent reduction in MI
500 size and cell death after I/R injury⁴⁷. These data suggest that augmenting Ca²⁺ efflux is another
501 promising therapeutic strategy in this type of disease.

502 Furthermore, ROS-targeted therapies, although they have yielded mixed results in attenuating
503 I/R-induced damage¹⁴⁶, could also be considered an available alternative, possibly in
504 combination with the other aforementioned treatments.

505 Importantly, the regulation of contact sites between the SR and mitochondria also has a role
506 in the cardiac I/R process. In particular, down-regulation of the tyrosine phosphatase
507 PTPIP51 (protein tyrosine phosphatase-interacting protein 51), a crucial regulator of ER/SR-
508 mitochondria contacts (Table 1), protects cardiomyocytes from mitochondrial Ca²⁺ overload
509 and death, highlighting its role as a new therapeutic target during I/R injury¹⁴⁷.

510 In chronic heart failure, a major myocyte dysfunction is related to stasis and accumulation of
511 cytoplasmic Ca²⁺. This defect in failing cells largely results from decreased expression and
512 activity of the SR Ca²⁺-ATPase¹⁴⁸ and increased RyR Ca²⁺ leakage (in particular the type 2
513 receptor RyR2), due to their redox modifications¹⁴⁹ or PKA hyperphosphorylation^{150,151}.
514 The consequent amount of Ca²⁺ that accumulates in the cytoplasm results in continuous and
515 persistent asynchronous mitochondrial Ca²⁺ overload and dysfunction, contributing to heart
516 failure and myocyte cell death. In these conditions, less Ca²⁺ can be released from the SR upon
517 LTCC activation, resulting in a decreased magnitude of Ca²⁺ transients, as well as reduced ATP
518 supply, with a consequent contractile dysfunction¹⁵². At the same time, SR Ca²⁺ leakage is
519 sufficient to induce spontaneous APs and is therefore considered an important trigger for
520 cardiac arrhythmias¹⁵³. Overall, these findings further support that targeting both MCU and
521 NCLX to prevent mitochondrial Ca²⁺ overload in combination with systems to reduce SR Ca²⁺
522 mishandling could represent good strategies for intervention in these types of heart
523 dysfunctions.

524

525 ***[H3]Inflammatory responses and pathological inflammation***

526 The first evidence that mitochondrial Ca²⁺ is important during inflammation dates back more
527 than 30 years¹⁵⁴, but increasing interest in this area has only become evident since the
528 molecular identity of the MCU complex and localization of the **NLRP3 inflammasome** at
529 mitochondria¹⁵⁵ were elucidated.

530 Studies have highlighted how chronic stress enhances mitochondrial Ca²⁺ accumulation,
531 which in turn induces excessive and sustained inflammation. Mitochondrial Ca²⁺ homeostasis
532 is reported to be disrupted in infectious diseases, where MCU seems to be the main player in
533 the regulation of bacteria- and virus-induced activation of inflammation.

534 *Pseudomonas aeruginosa* infection of airway epithelial cells from patients with cystic fibrosis
535 (CF) drives excessive MCU-mediated mitochondrial Ca²⁺ accumulation, which is critical for the
536 activation of a heightened NLRP3-dependent inflammatory response. The relationship
537 between the *P. aeruginosa*-dependent inflammatory response and mitochondrial Ca²⁺
538 perturbation exacerbates the CF pathological phenotype¹⁵⁶. Loss of MCU *in vitro* has been
539 shown to reduce mitochondrial Ca²⁺ uptake and to blunt activation of the NLRP3 inflam-
540 masome induced by *Pseudomonas*¹⁵⁶.

541 MCU-mediated Ca²⁺ overload was also found to be essential for a virus-induced inflammatory
542 response. Indeed, MCU specifically interact with MAVS (mitochondria anti-viral signaling)
543 complexes localized on mitochondria and positively regulates the release of the pro-

544 inflammatory cytokine IFN- β upon viral infection¹⁵⁷. Chronic viral infection is accompanied by
545 ER stress, inducing mitochondrial Ca²⁺ overload through a MCU/MAVS-dependent pathway,
546 with subsequent sustained IFN- β production that contribute to autoimmune diseases.
547 Knockdown or silencing of MCU (or MAVS) reduces mitochondrial Ca²⁺ uptake capacity and
548 significantly decreases virus-induced IFN- β levels¹⁵⁷ and thus the inflammatory status.
549 The importance of regulating MCU under stress conditions, when the risk of Ca²⁺ overload
550 is elevated, has also been reported in a model of the inflammatory response induced after
551 tissue injury/loss in the liver. During liver regeneration after partial hepatectomy, loss of
552 MICU1, the Ca²⁺-sensing regulator of MCU, leads to an enhanced and sustained pro-
553 inflammatory response, associated with mitochondrial Ca²⁺ overload that switches the fate of
554 the cell from proliferation to death¹⁵⁸. The mitochondrial Ca²⁺ overload response is followed
555 by mPTP opening, sensitizing MICU1-deficient hepatocytes to death instead of permitting
556 cell proliferation and regeneration¹⁵⁸.
557 These findings all support the notion that increased Ca²⁺ flux through the uniporter complex
558 fuels important pathogenic pathways related to an inflammatory state, identifying this
559 channel as a potential target in the treatment of inflammation-associated diseases.

560

561 **Future Perspectives**

562 A large body of evidence has accumulated regarding the molecular basis of mitochondrial Ca²⁺
563 homeostasis, a pivotal regulator of many cellular functions: it plays a crucial role in regulating
564 mitochondrial functions and adapting mitochondrial activity to cellular needs but it is also
565 tightly coupled to the cytosolic Ca²⁺ changes induced by a variety of stimuli. Importantly,
566 genetic or environmental alterations in intracellular Ca²⁺ signaling are linked to many human
567 diseases, including common disorders. Thus, a complete understanding of the pathways
568 allowing mitochondrial Ca²⁺ entry and release is crucial for the characterization of the
569 molecular routes that are activated on the basis of different cellular functions of Ca²⁺.
570 Future research will uncover many other aspects of mitochondrial Ca²⁺ homeostasis. In
571 particular, we will attempt to gain a complete understanding of mitochondrial Ca²⁺ regulation.
572 This includes i) the identification of the related functions of the newly discovered accessory
573 proteins and post-translational modifications of mitochondrial Ca²⁺ channels and
574 transporters; ii) a broader investigation of the involvement of mitochondrial Ca²⁺ homeostasis
575 in genomics, proteomics, and metabolomics for a definition of the “omic” signature of
576 mitochondrial Ca²⁺ signaling; and iii) the development of new drugs targeting mitochondrial
577 Ca²⁺ pathways.

578 Moreover, the role of mitochondrial Ca^{2+} signaling in many human disorders will be further
579 clarified through the identification of specific mutations in the proteins responsible for the
580 maintenance of mitochondrial Ca^{2+} homeostasis. For example, considering the role of Ca^{2+}
581 signaling and mitochondria in neurons, the mechanisms of diseases such as multiple sclerosis,
582 Alzheimer's disease, and Parkinson's disease as well as those with more complex phenotypes,
583 such as psychiatric disorders, will be better understood and new therapeutic approaches
584 proposed. Moreover, the contribution of mitochondrial Ca^{2+} in cancer-specific environmental
585 settings will be clarified opening the possibility to modulate mitochondrial Ca^{2+} homeostasis
586 to enhance the efficacy of cytotoxic agents.

587 Finally, the participation of mitochondrial Ca^{2+} in the process of aging¹⁵⁹ and its importance in
588 stem cell biology¹⁶⁰ will produce new and exciting achievements in the future and will attract
589 scientists from other fields to this fascinating and still innovative area of mitochondrial
590 biology.

591

592 **BOX 1**

593 **Calcium as a second messenger**

594 Ca^{2+} ions are ubiquitous second messengers that allow the information conveyed by
595 extracellular and intracellular signals to be translated into an intracellular effect. The
596 versatility and complexity of Ca^{2+} -mediated signaling can be inferred by the simple
597 observation that a rise in cytoplasmic $[\text{Ca}^{2+}]_c$ ($[\text{Ca}^{2+}]_c$) is elicited by a wide variety of molecules
598 and decoded into very different, sometimes opposite effects. To fulfill such a complex
599 signaling role, the $[\text{Ca}^{2+}]_c$ rises follow precise spatiotemporal patterns. Indeed, the study of
600 Ca^{2+} signaling at the single-cell level has revealed the occurrence of spatially controlled rises.
601 The localized rises can remain confined, thereby preventing the inappropriate stimulation of
602 different cellular domains, or gradually diffuse, as in the case of the " Ca^{2+} waves", i.e., the
603 orderly propagations of $[\text{Ca}^{2+}]_c$ rises throughout the cell. The complexity is not limited to
604 spatial organization. Indeed, it is now well known that agonists, such as histamine, ATP or
605 carbachol, can induce, in many cell types, a series of repetitive $[\text{Ca}^{2+}]_c$ increases, commonly
606 referred to as " Ca^{2+} oscillations". Each of these signaling patterns, through the specific
607 recruitment of downstream effectors, is decoded into the appropriate cellular effect.

608 A wide range of mammalian proteins are regulated by Ca^{2+} , classified as buffer or trigger
609 proteins¹⁶¹. Ca^{2+} buffers encompass Calsequestrin and Calreticulin, located at sarcoplasmic
610 and endoplasmic reticulum, respectively, and the cytosolic proteins Calbindin and
611 Calretinin, as well as the relatively slow buffer Parvalbumin. This class of molecules not only

612 cooperate with Ca²⁺ channels, transporters and pumps for shaping the intracellular Ca²⁺
613 signals, but also display multiple functions and physiological roles¹⁶². Trigger proteins include
614 modulators of muscle contraction (Troponin C), proteases (Calpain), kinases (Protein Kinase
615 C, PKC) phosphatases (Calcineurin B), or key mediators of different enzymes (Calmodulin).
616 Most of them possess one or multiple EF-hand calcium-binding motifs and change their
617 conformation upon binding Ca²⁺, two exceptional features that have been employed for the
618 creation of intra-organellar Ca²⁺ fluorescent indicators (see Box 2). Thus, Ca²⁺ binds to a huge
619 number of proteins, affecting their localizations, molecular associations and functions, and it
620 provides an active regulation of vast array of biological processes, such as contraction, gene
621 transcription, and differentiation. The role of Ca²⁺ signals in the intracellular transcriptional
622 activity, by regulating key factors as NFAT and CREB, strengthens its impact on cellular
623 plasticity and long-term changes. In this view, the crucial function of Ca²⁺ in coordinating
624 different cellular events is not limited to variations in its cytosolic levels, but could be
625 extended to changes in Ca²⁺ signaling inside the organelles. For example, lysosomal Ca²⁺
626 activates Calcineurin, which in turn promotes TFEB (Transcription Factor EB) translocation
627 into the nucleus and transactivation of target genes¹¹². After fertilization, mitochondrial Ca²⁺
628 entry sustains ROS production and cell cycle progression in early *Xenopus* embryos¹⁶³. These
629 findings reveal as spatial micro-rearrangements of Ca²⁺ homeostasis have important
630 biological consequences and that aberrations in the intracellular Ca²⁺ machinery could
631 represent the crucial aspect in many pathological scenarios.

632

633 **BOX 2**

634 **Methods for measuring mitochondrial Ca²⁺**

635 There are two main genetically encoded strategies currently used to design functional probes
636 that measure mitochondrial [Ca²⁺]: those based on the calcium-activated photoprotein
637 aequorin and those based on fluorescent protein (FP). Using appropriate mitochondria-
638 targeting signals, aequorin has been directed to both the OMM and IMS, although the most
639 commonly used version is the aequorin chimera targeted to the mitochondrial matrix by the
640 pre-sequence of subunit VIII of cytochrome c oxidase¹⁶⁴. Aequorin provides important benefits
641 over GFP-based indicators, such as a wide dynamic range, a high signal-to-noise ratio, and the
642 ability to emit light upon Ca²⁺ binding rather than requiring potentially damaging light
643 excitation. However, the use of aequorin displays some pitfalls, including low light emission
644 by the photoprotein that renders it inappropriate for imaging Ca²⁺ waves at the single-cell
645 level. These disadvantages have led to the extensive employment of alternative methods, such

646 as FP-based approaches, which combine bright fluorescence with efficient targeting, or
647 synthetic fluorescent dyes, which do not require transfection and are very user-friendly.
648 Rhod-2 AM is the most commonly used chemical probe, although it cannot be precisely
649 targeted to mitochondria, and its measurement exhibits multiple drawbacks¹⁶⁵.
650 Mitochondrial fluorescent Ca²⁺-indicators are based on a calmodulin/Ca²⁺-sensing protein,
651 and they are classified into two families, the first represented by the Förster resonance energy
652 transfer (FRET)-based cameleon type, and the second by an engineered single FP type, such
653 as GCaMP and pericam. Mitochondrial-targeted cameleons (2mt-D2cpv and its variants),
654 consisting of cyan and yellow FPs as the donor and acceptor, linked by calmodulin and the
655 M13 peptide from the myosin light-chain kinase, and mito-pericam, built up by combining a
656 circularly permuted FP and a Ca²⁺-responsive element, allow ratiometric Ca²⁺
657 measurements; the development of mito-GCaMP chimeras, and their derivatives mito-CEPIAs
658 and mito-GECOs, has expanded the spectra for the analysis of mitochondrial [Ca²⁺].
659 Intriguingly, by fusing GFP and aequorin, a new class of ratiometric Ca²⁺ probes, termed GAPs,
660 has been generated¹⁶⁶. GAP indicators have been targeted to various organelles, including
661 mitochondria, but the performance of mito-GAP constructs has not been tested yet by other
662 groups.

663

664 **BOX 3**

665 **Mitochondrial Ca²⁺ in cell death and cancer**

666 There is no doubt that cell death belongs to the numerous cell functions on which Ca²⁺ exerts
667 a complex regulatory role. It has long been known that in neurons and other cell types an
668 unchecked increase in [Ca²⁺]_c can trigger apoptosis¹⁶⁷⁻¹⁶⁹, and likewise, agents able to release
669 Ca²⁺ from intracellular stores have been shown to be pro-apoptotic¹⁷⁰. On the other hand, the
670 inhibition of Ca²⁺ signalling removes a crucial trophic effect and agents, such as ethanol, that
671 block NMDA-dependent Ca²⁺ signalling cause massive neuronal apoptosis during brain
672 development¹⁷¹.

673 As to the site of action of the “apoptotic” Ca²⁺ signal, mitochondria again emerge as a critical
674 site. While transient mitochondrial Ca²⁺ oscillations stimulate metabolism and constitute a
675 pro-survival signal, prolonged mitochondrial Ca²⁺ overload is a fundamental trigger to initiate
676 apoptosis through the opening of mPTP^{116,118}. Indeed, treatment with apoptotic stimuli causes
677 a release of Ca²⁺ from the ER and induces dramatic changes of mitochondrial morphology and
678 release of caspase co-factors. If Ca²⁺ changes are prevented, mitochondrial morphology is
679 preserved, and the cells are protected from apoptosis¹¹⁸.

680 The mitochondrial Ca^{2+} machinery represents thus a key decoding station for cell fate
681 decisions. Several proto-oncogenes and tumor suppressors critically control these decisions
682 by modulating mitochondrial Ca^{2+} homeostasis.

683 By either controlling Ca^{2+} signals arising from the ER (e.g., PML, PTEN, p53, Akt) or directly
684 modifying the activity of mitochondrial proteins involved in Ca^{2+} homeostasis (e.g., FHIT,
685 STAT, Fus1), they are able to modulate anti- or pro-apoptotic signals, preventing or
686 facilitating mitochondrial Ca^{2+} overload.

687 In response to different stress signals, tumor suppressors and proto-oncogenes act at the ER
688 level by modulating Ca^{2+} store content and/or Ca^{2+} dynamics (e.g., Ca^{2+} leakage, Ca^{2+} uptake
689 and Ca^{2+} release)¹⁷², while at mitochondria, by affecting the MCU complex or LETM1 activities,
690 they regulate the mitochondrial Ca^{2+} threshold^{173,174}.

691 During the past few years, it has become evident that the failure of this tuned mitochondrial
692 Ca^{2+} signaling is a hallmark of cancer cells that favors their survival and augments their
693 resistance to cell death.

694 Inactivating mutations in tumor suppressor genes or hyper-activation of oncogenes lead, in
695 many types of cancer, to diminished mitochondrial Ca^{2+} uptake and therefore increased pro-
696 survival potential, with a consequent inhibition of apoptosis and uncontrolled cell
697 proliferation.

698 Restoring proper mitochondrial Ca^{2+} signaling could therefore be a promising avenue for re-
699 sensitizing cancer cells to their intrinsic pro-apoptotic signaling mechanisms and to
700 anticancer therapeutic interventions. Indeed, many chemotherapeutic agents, as well as
701 photodynamic therapy^{175,176}, exert their cytotoxic effects via ER-mitochondrial Ca^{2+} signaling,
702 and therefore their action is completely abolished in cancer cells displaying altered Ca^{2+}
703 kinetics.

704

705 **Figure Legends**

706 **Figure 1: Intracellular Ca^{2+} signaling**

707 In the cartoon is reported a basic overview of calcium signaling.

708 The ER is the major intracellular Ca^{2+} storage organelle. The sarco/endoplasmic-
709 reticulum Ca^{2+} -ATPase SERCAs actively pump Ca^{2+} into the store. The dynamic release of Ca^{2+}
710 from the ER is mediated by the ryanodine receptor (RyR) and the inositol 1,4,5-triphosphate
711 receptor (IP3R). Ca^{2+} released from the ER is captured by the nearby mitochondria located in
712 close contact with the ER through the voltage-dependent anion channel VDAC and the MCU
713 complex, activating cell metabolism.

714 The depletion of the ER results in the translocation of the transmembrane Ca²⁺ sensor protein,
715 stromal interaction molecule 1 (STIM1) to the junctions between ER and the plasma
716 membrane where it binds and activates the Ca²⁺ channel protein Orai1 for store-operated Ca²⁺
717 entry (SOCE). The intracellular Ca²⁺ influx is also mediated by TRP channels, most of them are
718 activated by the depletion of Ca²⁺ from the ER, whereas the plasma membrane Ca²⁺ ATPase
719 (PMCA) function to export Ca²⁺ from the cytosol and maintain the intracellular Ca²⁺
720 concentration at the basal value for proper cell signaling. Beside ER, lysosomes have been
721 recently recognized as the second largest store of intracellular Ca²⁺ that are able to release
722 Ca²⁺ through the TRPML1 channel, crucial for maintaining a correct lysosomal membrane
723 trafficking.

724

725 **Figure 2: The Mitochondrial Ca²⁺ Uptake Pathway**

726 The formation of high [Ca²⁺] microdomains between the endoplasmic reticulum (ER) and
727 mitochondria is critical for ensuring proper Ca²⁺ entry into the mitochondrial matrix. **a)** The
728 correct distance between the ER and mitochondria (~50 nm) is preserved by different
729 regulators, including mitofusin-2 (MFN2), PDZD8 and the complex VAPB (vesicle-associated
730 membrane protein-associated protein B)-PTPIP51 (protein tyrosine phosphatase-interacting
731 protein 51). Once released by inositol 1,4,5 trisphosphate receptors (IP3Rs), the ER Ca²⁺
732 enters into mitochondria through the OMM (outer mitochondrial membrane) protein VDAC
733 (voltage-dependent anion channel) and thus reach the matrix side via the MCU
734 (mitochondrial Ca²⁺ uniporter) complex, located at the IMM (inner mitochondrial membrane).
735 **b)** The MCU complex consists of the pore-forming subunit MCU and the transmembrane
736 proteins MCUB (MCU regulatory subunit b) and EMRE (essential MCU regulator) in
737 association with the intermembrane space (IMS) proteins MICU1 (mitochondrial calcium
738 uptake protein 1) and MICU2. MCUR1 (MCU regulator 1) regulates Ca²⁺ entry from the matrix,
739 but its role as a specific MCU complex component is highly controversial. **c)** The activity of the
740 electron transport chain (ETC) results in the pumping of H⁺ ions outside the mitochondrial
741 matrix, thereby generating an electrochemical proton gradient. This gradient consists of two
742 components: the difference between the cytosolic and matrix pH and the membrane potential
743 difference ($\Delta\Psi$), which is maintained at approximately -180 mV and represents the driving
744 force for mitochondrial Ca²⁺ uptake. **d)** Mitochondria contain both Na⁺-dependent and Na⁺-
745 independent mechanisms for Ca²⁺ extrusion toward the cytoplasm. The molecular nature of
746 the Na⁺/Ca²⁺ exchanger (mNCLX) has been identified in NCLX, an IMM protein containing 13
747 transmembrane domains and catalyzing K⁺-independent electrogenic transport. LETM1

748 (leucine zipper EF-hand containing transmembrane protein 1) has been proposed as the
749 H^+/Ca^{2+} exchanger (mHCX). It acts as a transporter by forming hexameric structures and
750 pumps Ca^{2+} ions in an electroneutral manner. However, it has been suggested that LETM1
751 works as a K^+/H^+ exchanger, rather than an mHCX. Very recent findings have shown that
752 LETM1 contributes to Na^+ cycling, thus modulating Ca^{2+} fluxes in an indirect way¹⁷⁷.

753 PKA: protein kinase A; PINK1: PTEN-induced putative kinase 1.

754

755 **Figure 3: The role of mitochondrial Ca^{2+} in physio-pathological processes.**

756 The generation of high Ca^{2+} microdomains (MAMs: mitochondria associates membranes (with
757 ER) or PAMs: plasma membrane-associated membranes) is fundamental to permit
758 mitochondrial Ca^{2+} uptake through the MCU complex. This figure proposes a schematic
759 representation of the signals that happen inside the cells in response to **a)** glucose stimulation
760 (pancreatic β cell), **b)** action potential (AP) (cardiac cell) and **c)** infections or tissue injury
761 (epithelial cell). **a)** Glucose [1] induces the release of Ca^{2+} from the ER through inositol 1,4,5
762 trisphosphate receptors (IP3Rs) towards mitochondria [2] that start producing ATP [3]. The
763 increased metabolisms permit the opening of Ca^{2+} channels on the plasma membrane [4] and
764 in turn insulin release [5]. **b)** In the cardiac cell, the AP induces the opening of Na^+ channels on
765 the plasma membrane [1] followed by the opening of L-T Ca^{2+} channels [2]. The cytosolic
766 increased of Ca^{2+} is captured by mitochondria to produce ATP [3] and induces the Ca^{2+} -
767 induced Ca^{2+} release (CICR) with a consequent release of Ca^{2+} from the ER through ryanodine
768 receptors (RyRs) that permits contraction [4] and sustains mitochondrial metabolism and
769 ATP production [5]. **c)** Different chronic stress situations, including tissue damage or infection
770 [1] induce ER stress [2] with a consequent prolonged Ca^{2+} transfer towards mitochondria and
771 mitochondrial Ca^{2+} overload [3].

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782 **Table 1: Regulatory pathways of mitochondrial Ca²⁺**

Regulator	Ca ²⁺ Regulation	Molecular Mechanism	Disease links and reference(s)
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783

784

VDAC channels			
* Bcl-xL	Positive	Interacts with VDAC1-3, probably promoting VDAC closure and calcium permeability	- 61
* Bcl-xL	Negative	Inhibits VDAC1 through its BH4 domain	- 66
GSK3	Negative	Phosphorylates VDAC at a Thr residue	Liver steatosis 86
miR-7	Negative	Reduces <i>VDAC1</i> expression and inhibits mPTP opening	Parkinson's disease 93
miR-29a	- (Probably negative)	Reduces <i>VDAC1</i> expression and improves survival upon ischaemia	Cerebral ischemia 94

785

Uniporter complex			
* MCUR1	Positive	Interacts with MCU, promoting Ca ²⁺ entry	Hepatocellular carcinoma 67-70,73
* SLC25A23	Positive	Interacts with MCU, promoting Ca ²⁺ entry	- 74
PyK2	Positive	Activated PyK2 translocates to mitochondria, phosphorylating MCU and favoring tetrameric channel pore formation	Myocardial death 87
CaMK-II	Positive	Phosphorylates MCU at Ser57 and Ser92	Myocardial death and heart failure 88
miR-25	Negative	Reduces the expression of the pore-forming subunit <i>MCU</i>	Colon and prostate cancer; pulmonary arterial hypertension (PAH) 95-97
miR-138	Negative	Reduces the expression of the pore-forming subunit <i>MCU</i>	Pulmonary arterial hypertension (PAH) 97
miR-1	Negative	Reduces the expression of the pore-forming subunit <i>MCU</i>	Cardiac hypertrophy 98
miR-340	Negative	Reduces <i>MCU</i> expression and inhibits breast cancer cell migration	Breast cancer 99
PRMT1	Negative	Methylates MICU1, allowing the engagement of UCP2/3 in Ca ²⁺ entry	- 90
AFG3L2/SPG7	Negative	Loss of AFG3L2/SPG7 induces the formation of constitutively active MCU-EMRE complexes	Neuro-degeneration 91,92
Mia40	Negative	Mia40 ensures the association of MICU1 with the inhibitory subunit MICU2	- 19

786

ER-mitochondria tethering			
* MFN2	Positive	MFN2 loss detaches the ER from mitochondria	Charcot-Marie-Tooth neuropathy type 2A (CMT2A); obesity, insulin resistance 79,178
* MFN2	Negative	MFN2 loss increases the ER-mitochondria association	Charcot-Marie-Tooth neuropathy type 2A (CMT2A); obesity, insulin resistance

			80,179
PDZD8	Positive	PDZD8 is a structural and functional ortholog of the yeast ERMES protein MMM1	- 82
PTPIP51	Positive	Interacts with the ER protein VAPB to regulate ER-mitochondria tethering	I/R injury; amyotrophic lateral sclerosis (ALS); Parkinson's disease 147,180-182
GRP75	Positive	Forms a molecular complex with IP3R and VDAC	- 183
FATE1	Negative	Regulates Ca ²⁺ transfer and steroid hormone production	Adrenocortical carcinoma 184
Presenilin-2	Positive	Increases the frequency of Ca ²⁺ hot spots at MAMs	Alzheimer's disease 185
Fis1	Positive	Interacts with Bap31 at the ER, forming a complex to activate the initiator procaspase-8	- 186
PACS-2	Positive	PACS-2 loss detaches the ER from mitochondria	Obesity, insulin resistance 187,188

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Mitochondrial Ca²⁺ efflux			
PINK1	Negative	PINK1 KO cells display reduced mitochondrial Ca ²⁺ efflux. PINK1 increases Ca ²⁺ release by phosphorylating LETM1 at Thr192	Parkinson's disease 84,85
PKA	Negative	Phosphorylates NCLX at Ser258, increasing Ca ²⁺ efflux	Parkinson's disease 84

789

Mitochondrial membrane potential			
* MCUR1 (CCDC90a)	Positive	Acts as a cytochrome c oxidase (COX) assembly factor	- 72
SK2 channel	Negative	Activation of mitochondrial SK2 reduces respiration and ROS formation	- 189

790

791 The * indicates proteins with a controversial role

792 Abbreviations: VDAC (Voltage Dependent Anion Channel), Bcl-xL (B-cell Lymphoma-extra
793 large), GSK3 (Glycogen Synthase Kinase 3), mPTP (mitochondrial Permeability Transition
794 Pore), MCUR1 (Mitochondrial Calcium Uniporter Regulator 1), MCU (Mitochondrial Calcium
795 Uniporter), SLC25A23 (Solute Carrier Family 25 Member 23), Pyk2 (proline-rich tyrosine
796 kinase 2), CaMK-II (Ca²⁺ /calmodulin-dependent protein kinase II), PRMT1 (Protein arginine
797 N-methyltransferase 1), MICU1 (Mitochondrial Calcium Uptake 1), UCP2/3 (Mitochondrial
798 uncoupling protein 2/3), AFG3L2 (AFG3 Like Matrix AAA Peptidase Subunit 2), SPG7 (Spastic
799 paraplegia 7), Mia40 (Mitochondrial intermembrane space import and assembly protein 40),

800 MICU2 (Mitochondrial Calcium Uptake 2), MFN2 (Mitofusin 2), ER (Endoplasmic Reticulum),
801 PDZD8 (PDZ domain-containing protein 8), PTPN51 (Protein tyrosine phosphatase
802 interacting protein 51), VAPB (Vesicle-associated membrane protein-associated protein B/C),
803 GRP75 (Glucose Regulated Protein 75), IP3R (Inositol 1,4,5 Trisphosphate Receptor), FATE1
804 (Fetal and adult testis-expressed transcript protein 1), MAMs (Mitochondria Associated
805 Membranes), Fis1 (Mitochondrial fission 1 protein), Bap31 (B-cell receptor-associated
806 protein 31), PACS-2 (Phosphofurin acidic cluster sorting protein 2), PINK1 (PTEN-induced
807 putative kinase 1), LETM1 (Leucine zipper-EF-hand containing transmembrane protein 1),
808 PKA (Protein Kinase A), NCLX (Sodium/Calcium/Lithium Exchanger), CCDC90a (Coiled- Coil
809 Domain-Containing Protein 90A), COX (Cytochrome c oxidase), SK2 (Potassium
810 intermediate/small conductance calcium-activated channel).

811

812 **Acknowledgments**

813 PP is grateful to Camilla degli Scrovegni for continuous support. PP is supported by the Italian
814 Ministry of Education, University and Research; the Italian Ministry of Health; Telethon
815 (GGP15219/B); the Italian Association for Cancer Research (AIRC: IG-18624); and by local
816 funds from the University of Ferrara. CG is supported by local funds from the University of
817 Ferrara, the Italian Association for Cancer Research (AIRC: IG-19803), the Italian Ministry of
818 Health, and by a Fondazione Cariplo grant. SM is supported by "Fondazione Umberto
819 Veronesi" and the Italian Ministry of Health.

820

821 **Glossary**

822

823 **Membrane potential**

824 The difference in electric potential (measured in mV) between the interior and exterior of a
825 biological membrane, which generates from different concentrations of ions, such as H⁺, Na⁺,
826 K⁺ and Cl⁻.

827

828 **Respiratory chain**

829 The Electron Transport Chain (ETC) consists of four complexes that transfer electrons from
830 NADH and FADH₂ to oxygen, which is reduced to water. Electron flow within these
831 transmembrane complexes leads to the transport of H⁺ across the inner mitochondrial
832 membrane (IMM), generating an electrochemical proton gradient (negative inside the matrix).

833

834 **Chemiosmotic theory**

835 The energy stored in the form of transmembrane electrochemical gradient is used to produce
836 ATP inside the mitochondrial matrix. The protons move back across the IMM through the F₁
837 F_o ATPase enzyme, coupling the electrochemical gradient to ATP production by combining
838 ADP with inorganic phosphate.

839

840 **Bcl-2 family**

841 A large group of evolutionarily-conserved proteins that shares Bcl-2 homology (BH) domains.
842 Bcl-2 family members are deeply involved in cell death regulation, consisting of both anti-
843 (Bcl-2, Bcl-xL) and pro-apoptotic (Bax, Bak) factors.

844

845 **Mitochondrial dehydrogenases**

846 A subclass of oxidoreductase enzymes that oxidizes substrates by transferring H⁺ to electron
847 acceptors, such as NAD⁺, NADP⁺ or FAD. Four dehydrogenases are regulated by Ca²⁺ ions,
848 increasing ATP supply during energy demand, which include: i) the FAD-glycerol phosphate
849 dehydrogenase, which faces the intermembrane space (IMS) of mitochondria; ii) the pyruvate
850 dehydrogenase, iii) the NAD-isocitrate dehydrogenase and iv) the oxoglutarate
851 dehydrogenase, all found in the mitochondrial matrix.

852

853 **Astrocytes**

854 The most numerous and heterogeneous neuroglial cells in the central nervous system,
855 distinguished by a star-like morphology with multiple primary processes originating from the
856 soma. The cytoskeleton of astrocytes is formed by intermediate filaments, commonly used as
857 specific markers for astrocytes identification, such vimentin and GFAP (glial fibrillary acidic
858 protein).

859

860 **Action potential**

861 Consists in a movement of charge sufficient to generate a large and brief deviation in the
862 membrane potential. It is used to communicate information between neurons and from
863 neurons to muscle fibers.

864

865 **Troponin C**

866 A component of the Troponin complex, together with Troponin I and T, which regulates
867 muscle contraction by Ca²⁺ binding. Through its multiple EF-hand domains, Troponin C acts as

868 the Ca^{2+} sensor inside the complex, initiating the cascade of events that leads to contraction of
869 striated muscle by interacting with its partner Troponin I after Ca^{2+} binding.

870

871 **Myofilaments**

872 The principal molecular regulators of contraction in cardiac and skeletal muscles, responsible
873 for force generation and motion. The myofilaments consist primarily of thick filament myosin
874 and thin filament actin proteins, as well as additional components, including Troponin, Titin
875 and Nebulin.

876

877 **NLRP3 inflammasome**

878 Upon activation, the nucleotide-binding oligomerization domain-like receptors family pyrin
879 domain containing 3 (NLRP3) sensor associates with the adaptor molecular apoptosis-
880 associated speck-like protein containing a caspase-recruitment domain (ASC) and the
881 precursor pro-caspase 1, to form the NLRP3 inflammasome complex, leading to activation of
882 caspase-1, secretion of mature pro-inflammatory cytokines and induction of inflammatory cell
883 death (or pyroptosis).

884

885 **Key points**

886

- 887 • **Mitochondria are the master regulators of intracellular Ca^{2+} homeostasis.**
- 888 • **Mitochondrial Ca^{2+} entry and extrusion are regulated by a sophisticated**
889 **molecular toolkit.**
- 890 • **Mitochondria are strictly associated with the Endoplasmic Reticulum (ER), and**
891 **accumulate Ca^{2+} via a multimeric complex, termed Mitochondrial Calcium**
892 **Uniporter, using the potential generated across the inner membrane, reaching**
893 **Ca^{2+} values several fold higher than those of bulk cytosol.**
- 894 • **Mitochondria release Ca^{2+} back to the cytosol via Na^{+} -dependent or -independent**
895 **mechanisms**
- 896 • **Different molecular pathways converge on mitochondria, exerting their**
897 **physiopathological functions through modulation of Ca^{2+} homeostasis.**
- 898 • **Mitochondrial Ca^{2+} channels and transporters are now considered new**
899 **pharmacological targets in different pathological scenarios.**

900

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