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The ATPase Inhibitory Factor 1 (IF₁) regulates the expression of the mitochondrial Ca^{2+} uniporter (MCU) via the AMPK/CREB pathway



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Calcium ions (Ca^{2+}) are universal intracellular messengers that control a diverse array of cellular functions. The versatility of Ca^{2+} signalling depends on Ca^{2+} interaction with a wide range of sensors and transducers through varied spatiotemporal dynamics, and relies on the presence of intracellular stores enabling the functional organization of Ca^{2+} transients in signalling microdomains [1,2]. Along with the endoplasmic reticulum (ER), mitochondria are fundamental Ca^{2+} -sequestering organelles that act as hubs for Ca^{2+} storage and buffering, thereby tuning the local Ca^{2+} availability and shaping cellular Ca^{2+} signals [3]. The tight control of mitochondrial Ca^{2+} entry and cycling is critical to preserve intracellular Ca^{2+} homeostasis and avoid alterations underlying the development of severe pathological conditions [2]. Hence, furthering the current understanding of the mechanisms that regulate mitochondrial Ca^{2+} handling is crucial to the development of advanced, targeted treatment options.

Mitochondrial Ca²⁺ storage capacity is highly correlated with the bioenergetic state of these organelles. Mitochondrial Ca²⁺ uptake is driven by both high mitochondrial membrane potential $(\Delta \Psi_m)$ and low intramatrix Ca²⁺ concentration ($[Ca^{2+}]_m$), while its rate is regulated by the activity of the mitochondrial Ca²⁺ uniporter complex (MCUC), a specialized channel residing on the mitochondrial inner membrane (MIM) that fully opens at high local intracellular [Ca²⁺] ([Ca²⁺]_i) [4]. Concurrently, intramitochondrial Ca²⁺ is a major regulator of ATP

production, promoting oxidative phosphorylation [5]. Ca^{2+} transients are therefore crucially involved in the control of the F_1F_0 -ATP synthase activity, in combination with its endogenous regulator, the ATPase inhibitory factor 1 (IF₁) [6].

The primary function of IF₁ is to inhibit the reversal of the F₁F_o-ATPsynthase during conditions of impaired $\Delta\Psi_m$. Thus, IF₁ prevents excessive ATP loss, energy imbalance and cell death under ischaemia/hypoxia [6]. Recent studies, including work from our group, have revealed the existence of a large plethora of IF₁ functions, and outlined the pathological implications of its deregulation. We recently uncovered that IF₁ activates a pro-oncogenic mechanism of evasion of apoptosis occurring through optic atrophy 1 (OPA1)-dependent maintenance of cristae shape and preservation of redox balance [7]. We demonstrated that loss of IF₁ activity promotes stress-dependent OPA1 degradation, causing abnormal mitochondrial morphology and impairing cell metabolism. To further explore the impact of IF₁ on mitochondrial function, here we study its role in mitochondrial Ca²⁺ homeostasis.

We previously showed that IF_1 over-expression counteracts typical traits of Ca^{2+} -mediated cell death, such as mitochondrial swelling and permeability transition [8]. Moreover, there is evidence suggesting that OPA1 oligomer destabilization, which is a feature accompanying IF_1 -depletion [7], facilitates mitochondrial Ca^{2+} uptake through cristae

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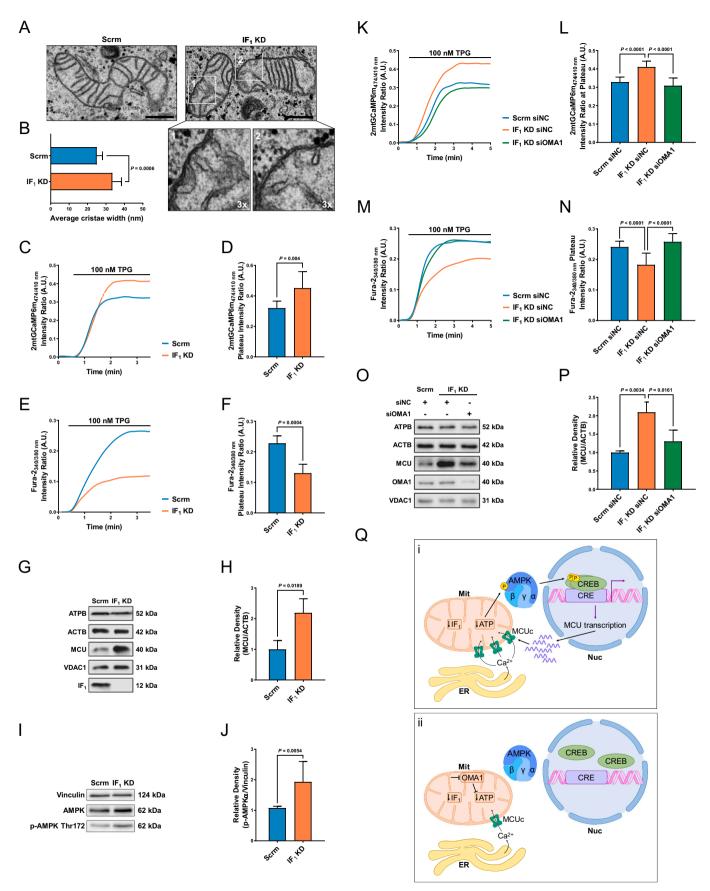
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Fig. 1. IF₁ knock-down enhances mitochondrial Ca^{2+} uptake in HeLa cells via AMPK- and OMA1-dependent upregulation of MCU. (A) Representative micrographs of mitochondrial ultrastructure in Scrm and IF1 KD cells (scale bar: 500 nm). (B) Quantification of average cristae width (Scrm: 24.98 \pm 3.11 nm; IF₁ KD: 33.47 \pm 4.90 nm; $n \ge 15$, N = 3). (C) Representative traces of TPG-induced mitochondrial Ca²⁺ uptake in Scrm and IF₁ KD cells cotransfected with 2mtGCaMP6m and mtRFP, challenged with 100 nM TPG. (D) Quantification of average mitochondrial 2mtGCaMP6m fluorescence ratio at plateau (Scrm: 0.32 \pm 0.05 A.U.; IF₁ KD: 0.45 \pm 0.11 A.U.; $n \ge 15$, N = 4). (E) Prototypical traces of intracellular Ca²⁺ rise following administration of 100 nM TPG in Scrm and IF, KD cells loaded with 5 µM Fura-2 AM and 25 nM MitoTracker™ Red CMXRos. (F) Quantification of average cytosolic Fura-2 AM plateau fluorescence ratio (Scrm: 0.23 ± 0.02 A.U.; IF₁ KD: 0.13 ± 0.03 A.U.; n ≥ 15, N = 4). (G) Representative Western blot of MCU protein levels in Scrm and IF₁ KD cells; ysates were also tested for VDAC1, ATPB and IF1, GAPDH was used as loading control. (H) Bar charts reporting quantitative analysis of MCU protein levels of MCU relative to GAPDH (Scrm: 1.00 \pm 0.29; IF₁ KD: 2.19 \pm 0.46; normalized values, N = 3). (I) Western blotting analysis of cellular protein levels of AMPK α and phospho-AMPKα (Thr172) in Scrm and IF₁ KD cells; vinculin was used as loading control. (J) Densitometry analysis of phospho-AMPKα levels relative to vinculin (Scrm: 1.08 \pm 0.06; IF₁ KD: 2.19 \pm 0.46; N = 5). (K) Prototypical traces of changes in $[Ca^{2+}]_m$ in Scrm and IF₁ KD cells co-transfected with 2mtGCaMP and either an siRNA against OMA1 (siOMA1) or a non-silencing siRNA (siNC), loaded with 25 nM MitoTracker™ Red CMXRos and treated with TPG (100 nM). (L) Quantification of average mitochondrial 2mtGCaMP6m fluorescence ratio at plateau after addition of TPG in the two cell lines (Scrm siNC = 0.33 ± 0.03 A.U.; IF₁ KD siNC = 0.41 \pm 0.03 A.U.; IF₁ KD siOMA1 = 0.31 \pm 0.04 A.U.; $n \ge 20$, N = 3). (M) Representative traces of intracellular Ca²⁺ dynamics following TPG treatment (100 nM) in Scrm and IF₁ KD cells. (N) Column diagram of average cytosolic Fura-2 AM fluorescence ratio at plateau (Scrm siNC = 0.24 ± 0.02 A.U.; IF₁ KD siNC = 0.18 \pm 0.04 A.U.; IF₁ KD siOMA1 = 0.26 \pm 0.03 A.U.; $n \ge$ 30, N = 3). (O) Representative Western blot of MCU protein levels in Scrm and IF₁ KD cells transfected with either siNC or siOMA1; ATPB, GAPDH (loading control), OMA1 and VDAC1 were also detected. (P) Quantification of MCU expression levels relative to GAPDH (Scrm siNC = 1.00 ± 0.04 ; IF₁ KD siNC = 2.10 ± 0.29 ; IF₁ KD siOMA1 = 1.30 ± 0.31 ; N = 3). (Q) Proposed model for IF₁-dependent control of mitochondrial Ca²⁺ uptake: in IF₁-depleted cells (i), the decline in cellular ATP levels induces the AMPK-mediated, CREB-dependent transcription of genes encoding the MCU complex, causing increased mitochondrial Ca²⁺ uptake following emptying of the ER stores; knocking-down OMA1 blocks reverts excessive mitochondrial Ca^{2+} entry activated by IF₁ loss (ii).

enlargement [9]. Interestingly, stable IF1 knock-down HeLa cells (IF1 KD), which were prepared for transmission electron microscopy (TEM) imaging as previously described [7], showed a significant increase in cristae width, particularly at the crista junctions (Fig. 1A, B). This characteristic, which is consistent with reduced OPA1 stability in IF1depleted cells [7], might also underlie alteration in molecular diffusion across the MIM [10]. To test the hypothesis that IF₁ regulates mitochondrial Ca²⁺ handling, stable control (Scrm) and IF₁ KD HeLa cells were treated with the sarco/endoplasmic reticulum Ca²⁺-ATPase (SERCA) inhibitor thapsigargin (TPG, 100 nM), which causes the passive release of Ca²⁺ from the ER and allows to study mitochondria-ER coupling. Cells were co-transfected with mitochondria-targeted GCaMP6m (2mtGCaMP6m), a green fluorescent ratiometric Ca²⁺ indicator, and red fluorescent protein (mtRFP), to monitor mitochondrial Ca²⁺ uptake after administration of TPG. Despite the absence of variations in the basal intramitochondrial Ca^{2+} levels (SFig. 1A), the amplitude of TPG-elicited mitochondrial Ca^{2+} entry was around 30% higher in IF₁ KD cells (Fig. 1C, D). Moreover, IF₁ loss disturbed wholecell Ca²⁺ homeostasis, as confirmed by the lower levels of Ca²⁺ retained in the cytosol (monitored by loading cells with 5 µM Fura-2 AM, a ratiometric fluorescent Ca²⁺ sensor, and 25 nM MitoTracker[™] Red CMXRos; Fig. 1E, F). This was recapitulated in cells treated with the Ca^{2+} mobilising agonist histamine (His, 100 μ M; SFig. 1B–E). Since IF₁ KD cells are characterized by higher $\Delta \Psi_m$ and impaired ATP synthesis at resting conditions [11], the increase in mitochondrial Ca^{2+} influx might represent an adaptive mechanism to maximize ATP production through stimulation of oxidative phosphorylation.

We then investigated the molecular determinants driving enhanced mitochondrial Ca²⁺ uptake in IF₁-depleted cells, starting from MCUC. Quite unexpectedly, IF₁ KD induced a significant upregulation of the pore forming subunit of the complex, MCU (Fig. 1G, H), without affecting mitochondrial mass (SFig. 1F, G). To dissect a potential MCUdependent mechanism augmenting mitochondrial Ca^{2+} entry in IF₁ KD cells, we looked at changes in mRNA levels of the different MCUC components. Likewise, IF1 KD cells showed a nearly 1.6-fold increase in MCU transcript levels, which was matched by a similar increase in the expression of all other subunits (SFig. 1H). Additional analysis of the expression ratio of each MCUC subunits to MCU revealed no alterations in the stoichiometry of the complex between Scrm and IF1 KD cells (SFig. 1I), which suggests that the latter have a higher content of fully functional, non-constitutively active MCUC. To further examine the mechanism leading to MCU upregulation in IF1 KD cells, we then monitor the expression levels and activation state of cAMP response element-binding protein (CREB), which is a known transcriptional regulator of MCU transcription [12], and its upstream regulator 5'

AMP-activated protein kinase (AMPK), the increased activity of which has recently been shown in the heart of IF_1 KO mice [13]. Western blotting analysis revealed a remarkable increase in the degree of both AMPKa and CREB phosphorylation when IF1 is down-regulated (2- and 1.5-fold increase, respectively; Fig. 1I, J + SFig. 2D, F), confirming the involvement of an AMPK-mediated, CREB-dependent mechanism of MCU expression. Of notice, while the total levels of CREB were unchanged between the two cell lines (SFig. 2E), AMPKa expression was significantly higher in IF₁ KD cells (SFig. 2A). This indicates that IF₁ depletion promotes AMPK activity via upregulation of the protein rather than by augmenting the rate of its phosphorylation, which is not affected by changes in IF1 expression (SFig. 2B). Collectively, our data suggest that IF₁ controls MCU expression in resting cells by limiting AMPK-mediated CREB activation, which is enhanced when IF1 expression is down-regulated (SFig. 2G). Considering that AMPK is rapidly activated when ATP production decreases, we compared the total cellular ATP levels between the two cell lines. As expected, IF1 KD cells showed a nearly 40% decrease in cellular ATP levels (SFig. 2C), pointing to ATP depletion as the driving mechanism for increased AMPK activity.

Mitochondrial Ca²⁺ uptake appears to be facilitated by unfolding of the cristae through alteration of the membrane diffusion barrier [9,10]. This event is prevented by OPA1, the loss of which impairs both cristae structure and Ca²⁺ homeostasis [14]. Under stress conditions, OPA1 degradation occurs rapidly following activation of the mitochondrial zinc metallopeptidase OMA1, which is prevented by IF_1 [7]. Furthermore, a recent study showed that OMA1 KO is protective against MCU upregulation in a murine model of heart failure, with concurrent preservation of cristae integrity and energy metabolism [15]. Considering the increase in cristae width that accompanies IF1 KD, we speculated that the lack of IF₁ might also favour mitochondrial Ca²⁺ accumulation through OMA1-dependent destabilization of OPA1 oligomers. Therefore, we measured intracellular Ca²⁺ mobilization following TPG administration in cells down-regulated for OMA1 (SFig. 3A). Interestingly, OMA1 KD reduced mitochondrial Ca²⁺ uptake in IF₁ KD cells to levels comparable to control cells (Fig. 1K, L), thus restoring the normal TPGinduced cytosolic Ca²⁺ response (Fig. 1M, N). Moreover, knocking down OMA1 inhibited the increase in MCU protein levels induced by IF₁ loss (Fig. 10, P) without affecting mitochondrial content (SFig. 3B,C). OMA1 KD also significantly reduced ATP loss in cells depleted of IF1 (SFig. 3D), further confirming that OMA1 activation critically promotes mitochondrial dysfunction in IF₁ KD cells.

With this work, we demonstrate that IF_1 is required for maintaining mitochondrial Ca^{2+} homeostasis. Our data prove that IF_1 down-regulation triggers an AMPK-mediated mitochondrial signalling response

that results in the CREB-dependent over-expression of MCU, leading to increased mitochondrial Ca²⁺ accumulation following emptying of the ER stores (Fig. 1Qi). We also found that silencing of the mitochondrial protease OMA1 restores normal MCU levels and mitochondrial Ca²⁺ uptake (Fig. 1Qii), indicating that OMA1 is involved in the pathway activated by IF₁ loss and suggesting that the mitochondrial ultrastructure regulates the Ca²⁺ buffering capacity of these organelles. In view of previous observations ascertaining the protective effect of OMA1 loss against cristae aberrations [15], OMA1 inhibition in IF₁ KD cells might favour OPA1-mediated cristae folding and respiratory chain supercomplex assembly, improving both mitochondrial bioenergetics and function.

Collectively, our data confirm that loss of IF₁ impairs mitochondrial Ca^{2+} import with consequences in both cell physiology and pathology. IF₁ loss may facilitate mitochondrial Ca^{2+} overload through alteration of cristae morphology and MCUC activity, contributing to cristae remodelling and mitochondrial swelling. Conclusive evidence confirming that cristae enlargement has a direct effect on mitochondrial Ca^{2+} dynamics is still missing, and the relationship between mitochondrial Ca^{2+} handling and structure is poorly understood. Nevertheless, this work proposes IF₁ as a key player in this pathway, as well as a molecular mediator of the retrograde response that links impaired mitochondrial bioenergetics and structure to alterations in intracellular signalling.

CRediT authorship contribution statement

M.C. and D.F. conceived the idea for the study and designed the experiments. D.F. conducted the experiments and data analysis and wrote the manuscript. G.G. assisted with Ca^{2+} imaging and Western blotting analysis of MCU levels. A.J. and C.T. helped with Western blotting analysis of CREB and AMPK. C.T., A.B and G.S were involved in discussions and commented on the final manuscript.

Declaration of competing interest

There are no competing interests of any nature to report.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.bbamcr.2020.118860.

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