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**MITOCHONDRIAL MECHANISMS IN IMMUNITY AND INFLAMMATORY
CONDITIONS: BEYOND ENERGY MANAGEMENT**

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ABSTRACT

Significance: The growing importance of mitochondria in the immune response and inflammation is multifaceted. Unraveling the different mechanisms by which mitochondria have a relevant role in the inflammatory response beyond the energy management of the process, is necessary for improving our understanding of the host immune defense and the pathogenesis of various inflammatory diseases and syndromes.

Critical issues: Mitochondria are relevant in the immune response at different levels, including releasing activation molecules, changing its structure and function to accompany the immune response, and serving as a structural base for activating intermediates as NLRP3 inflammasome. In this scientific journey of dissecting mitochondrial mechanisms, new questions and interesting aspects arise, such as the involvement of mitochondrial-derived vesicles in the immune response with the putative role of preventing uncontrolled situations.

Recent advances: Researchers are continuously rethinking the role of mitochondria in acute and chronic inflammation and related disorders. As such, mitochondria have important roles as centrally positioned signaling hubs in regulating inflammatory and immune responses. In this review, we present the current understanding of mitochondrial mechanisms involved, beyond the largely known mitochondrial dysfunction, in the onset and development of inflammatory situations.

Future directions: Mitochondria emerge as an interesting and multifaceted platform for studying and developing pharmaceutical and therapeutic approaches. There are many ongoing studies aimed to describe the effects of specific mitochondrial targeted molecules and treatments to ameliorate consequences of exacerbated inflammatory components of pathologies and syndromes, resulting in an open area of increasing research interest.

KEYWORDS

mitochondria; immunity; inflammation; mitochondrial dynamics; mitochondrial-targeted therapeutics

1. INFLAMMATION AND MITOCHONDRIA

Inflammation is commonly defined as a biological response of the immune system that can be triggered by a variety of factors, including pathogens, damaged cells and toxic compounds (Chen et al, 2017), inducing acute or chronic responses and potentially leading to tissue damage or disease. Two complementary immune systems coexist in vertebrates that recognize and eliminate pathogens: innate and adaptive immune systems. Within a short period after activation of the innate immune system, the acute inflammatory response is initiated by immune cells (mainly including neutrophils, natural killer cells, monocytes, and macrophages) enabling secretion of various cytokines and chemokines to recruit other immune cells (as activated T lymphocytes) at the site of infection (Chaplin, 2010). However, if its capacity is exceeded, the adaptive immune system is engaged, and specific T and B cells are activated. If this process is prolonged or inefficient, it progresses to a chronic state of inflammation. In this sense, chronic inflammation is a prolonged, dysregulated, and maladaptive response that involves persistent inflammation and, often, tissue damage (Medzhitov, 2008). This is the basis by which inflammation is also viewed as a driving factor in many diseases (Nathan and Ding, 2010), including atherosclerosis, cancer, heart disorders, autoimmunity, and it is a major contributor to age-related conditions (Netea et al, 2017).

Mitochondria are major players in the innate immune response in antimicrobial defense and sterile inflammation (West, 2017), as active actors in different mechanisms, where they not only provide a platform for various signaling events but also contribute to the effector response (de la Cruz and Kang, 2018; Brokatzky and Hacker, 2022). For example, mitochondria play an important role in the regulation of major elements of innate immune receptor signaling pathways such as RIG I-like helicases receptors (RLR), Toll-like-receptors (TLR), Nuclear oligomerization domain (NOD)-like receptors (NLR). In this sense, mitochondria have several structural and functional characteristics that justify the relevant role of this organelle in immunity and inflammation. They have their own genome (mtDNA) and a characteristically double membrane, being the inner membrane intimately ligated to O₂ metabolism and redox processes through de respiratory chain and production of reactive oxygen species (ROS), and ATP production through the F₁F₀ATP synthase. Apart from being the powerhouse of the cell, the mitochondrion has emerged as a signaling hub intimately involved in the modulation of the inflammatory response (Andrieux et al, 2021). At this stage, is relevant to point out that they are evolutionary endosymbionts that were derived from bacteria, and so might bear bacterial molecular motifs (Zhang et al, 2010).

Although there is consensus about the important role of oxidants in inflammatory processes, mechanisms remain largely unclear. The intricate relationship between oxidative stress, redox

based-mechanisms and inflammation is an area of intense research and evolution. The set of principles that define redox signaling and redox regulation in different processes is nicely and systematically defined in the review published by Jones and Sies (Jones and Sies, 2015). A challenging issue is the involvement of mitochondria, as energy and redox cellular hubs, on processes that may be the cause or consequences of inflammatory situations (Andrieux et al, 2021). The complex role of mitochondria can be analyzed in pathologies where inflammation is relevant actor as in sepsis and endotoxemia. In these situations, mitochondria have been described as not only involved in the initiation of inflammation (through damage-associated molecular patterns -DAMPs- release), but also functionally affected by the inflammatory response leading to dysfunctional mitochondria and decreased ATP production (Vico et al, 2019; Adan-Arean et al, 2021). Also, this elusive insight is trying to be uncovered, for example, in neurodegenerative conditions linked to inflammatory states (dela Cruz & Kang, 2018; Newman & Shadel, 2018; Tang et al., 2014). Considerable efforts are made by redox researchers to decipher these linked areas that are constantly evolving. In this review we discuss emerging research on how the immune response may be regulated and affected through mechanisms involving mitochondria, and the profound link between inflammation and mitochondrial function and structure. A special highlight is provided to the role of DAMPs and the therapeutic potential of targeting mitochondria in inflammatory situations. In this sense, current understanding of mitochondrial mechanisms involved, beyond the largely known mitochondrial dysfunction, in the onset and development of inflammatory situations is presented.

2. TRIGGERING IMMUNE RESPONSES: THE ROLE OF DAMPs

Immune system activation occurs not only due to external stimuli, but also due to endogenous molecules (Netea et al, 2020). As such, mitochondrial constituents might play as DAMPs that could trigger innate immune responses during pathological insults (Zhang et al, 2010; dela Cruz and Kang, 2018; Grazioli and Pugin, 2018). Mitochondrial DAMPs (mtDAMPs) are potent immunological activators probably due to the bacterial ancestry of mitochondria, and include not only proteins but also DNA or lipids (Zhang et al, 2010). In other words, when mitochondria are stressed or dysfunctional, they may produce a variety of DAMPs which may function as drivers of inflammatory responses (Fig. 1), and if their presence is sustained in time they may lead to pathological situations. In this sense, current evidence indicates that uncontrolled and excessive release of mitochondrial DAMPs is associated with the process severity, has prognosis value in human diseases, and contributes to the dysregulated process observed in numerous inflammatory and autoimmune conditions (Grazioli and Pugin, 2018). Interestingly, Nicolas-Avila et al described a

non-canonical route for elimination of damaged mitochondria through a network of resident macrophages surrounding cardiomyocytes thus preventing DAMPs release (Nicolas-Avila et al, 2020). Failure to properly eliminate them results in inflammasome activation and autophagy arrest.

Mitochondrial DAMPs include mtDNA, ATP, mitochondrial transcription factor A (TFAM), N-formyl peptide, succinate, cardiolipin (CL), and cytochrome c (cyt c) (Fig. 1). In the last years, the *in vivo* occurrence of mitochondrial double-stranded RNA led to its description as DAMPs triggering interferon type I response (Dhir et al, 2018; Pajak et al, 2019). Considering mtDNA as an example, it contains 37 genes coding for 2 ribosomal nucleic acids, 22 transfer RNAs, and 13 essential protein subunits of the oxidative phosphorylation system (Andersson et al, 2003). If compared with nuclear DNA, it presents low or absent methylation levels and increased susceptibility to oxidative damage (Andersson et al, 2003; Mehta et al 2017; Guitton et al, 2022). Its association into protein-DNA complexes (nucleoids) under the control of TFAM (Grazioli and Pugin, 2018) renders protection from oxidative damage. MtDNA release pathways include passive mechanisms, as in necroptosis and apoptosis (Linkermann and Green, 2014), and active mechanisms, as through mitochondrial-derived vesicles (MDV) (Islam et al., 2012). Free mtDNA can be recognized by three important pattern recognition receptors (PRR) of the innate immune system: TLR9, inflammasomes and type I interferon response receptor (Grazioli and Pugin, 2018; Patergnani et al, 2020). In these cases, interaction of mtDNA with its receptors trigger a pro-inflammatory response (de Gaetano et al, 2021). Another interesting example is CL, a lipid dimer consisting of two phosphatidyl groups bridged by glycerol localized in the inner mitochondrial membrane. It has relevant functions in mitochondrial respiration and mitochondrial biogenesis (Chicco and Sparagna, 2007; Claypool and Koehler, 2012). Moreover, several reports highlighted the close interaction that exists between CL and cyt c (Rice et al, 2021). ROS-mediated CL peroxidation causes the detachment of cyt c from the inner membrane, probably inducing apoptosis. CL can induce inflammation by its binding to NLRP3 inflammasomes (Iyer et al, 2013). In the same way, interference with CL synthesis has been shown to inhibit NLRP3 inflammasome activation (Liu et al, 2019). Additionally, CL can stimulate the activation and proliferation of CL-responsive $\gamma\delta$ T cells (Dieudé et al, 2011). As a whole, it has become increasingly evident that mtDAMPs play a critical role in sterile inflammation and in various diseases such as those characterized by chronic inflammation. Although an increasing number of studies have demonstrated that mitochondrial DAMPs can be actively released by non-necrotic cells exposed to an external stimulation (Katsumi et al, 2019; Murao et al, 2021), the mechanisms for extracellular release *via* MDV or autophagy requires further clarification. Is important to point out that therapeutics designed to target mitochondrial DAMPs and their related signaling pathways are promising in various inflammatory and auto-immune diseases. Moreover, the measurement of

mitochondrial DAMPs in body fluids as a biological marker of a disease may also be useful for prognostic value (Fucikova et al, 2015; Huckriede et al, 2021). The future direction in this idea is to analyze mtDAMPs impact in the initiation and progression of related diseases. Recent advances in mitochondrial biology have enabled researchers to rethink the mitochondrial role in acute and chronic inflammation and related disorders. As such, mitochondria have important roles as centrally positioned signaling hubs (besides the classical view as cellular energy hubs) in regulating inflammatory and immune responses.

3.MITOCHONDRIAL REGULATORY POINTS AND IMMUNE CELL FATE

3a. Mitochondrial regulatory points

Recent studies have shown that mitochondrial metabolism has an essential role in controlling the fate of immune cells. From T cells to macrophages, mitochondria play a key role in the various metabolic pathways that define each immune cell subset (van der Windt et al, 2012; O’Neill et al, 2016; Mehta et al, 2017; Sugiura et al, 2022). At this point, it is important to analyze how mitochondrial metabolism dictates the function and fate of immune cells beyond its role in generating ATP. In this central position, mitochondria emerge with various metabolic points plausible to be importantly regulated (Fig. 2) and that may determine immune cell function. The knowledge and analysis of mitochondrial hot points plausible of being regulated open important directions for developing directed therapeutics based on functional regulation.

One of the regulatory points is represented by the glycolysis pathway (producing pyruvate from glucose). In a further step, pyruvate can either be secreted as lactate or enter mitochondria and be oxidized to acetyl-CoA by pyruvate dehydrogenase. This last process can be negatively regulated by pyruvate dehydrogenase kinase. To enter the tricarboxylic acid (TCA) cycle, acetyl-CoA needs to be condensed with oxaloacetate to produce citrate. In the final step, reducing equivalents are formed (NADH and FADH₂) allowing the regeneration of oxaloacetate. T cell activation by the stimulation T cell receptor (TCR), activates signaling pathways and transcription factors that, in turn, increase the flux of metabolites through glycolysis and the TCA cycle (Wang et al, 2011). It has been shown that pharmacological or genetic inhibition of glycolysis limits TCR-dependent T cell proliferation (Chang et al, 2013). Macrophage polarization is also important at this point. In this sense, M₁ macrophages display an increased glycolytic flux that is characterized by a high rate of lactate production that has been shown to be necessary for its pro-inflammatory functions (Griffiths et al, 2017; Haschemi et al, 2012). It was observed that increased lactate produced in M₁ macrophages, can cause epigenetic modifications leading to a M₂ phenotype and resolution of the

inflammatory situation (Zhang et al, 2019). Moreover, M₁ macrophages have a unique TCA cycle that is described to be broken at two points: at isocitrate dehydrogenase and at complex II, allowing not only the occurrence of reverse electron transfer (RET) but also the net increase of NO production from glutamate. On the contrary, M₂ macrophages display lower levels of glycolytic flux and an unbroken TCA cycle (Jha et al, 2015). One interesting situation to highlight is that in activated macrophages the occurrence of the production of itaconate from aconitate, blocks succinate-mediated inflammatory processes (O'Neill et al, 2019).

Another regulatory point includes the exportation of citrate to cytoplasm to regenerate acetyl-CoA and oxaloacetate through the citrate shuttle, which in turn produces *de novo* fatty acids through fatty acid synthase (FAS). Alternatively, fatty acid oxidase (FAO) can catalyze the inverse process, a reaction taking place in mitochondria (Almeida et al, 2021; Zhu et al, 2022). This division of fatty acid catabolism in mitochondria and fatty acid anabolism in the cytoplasm helps to compartmentalize reactions and to prevent futile cycles. Regarding this decision point, it is worth to note that T cells increase citrate transport into the cytoplasm through the citrate shuttle to increase the cytosolic levels of acetyl-CoA (Mehta et al, 2017), a required situation for histone acetylation and interferon γ (IFN γ) production. Fatty acid trafficking is necessary for M₂ macrophages activation as the treatment with etoxomir (pharmacological inhibitor of FAO) prevents its activation (Vats et al, 2006). Also, it has been suggested that fatty acid acquirement by M₂ macrophages could be used to activate this type of macrophages specific gene expression profiles in an independent manner from mitochondrial metabolism (Mehta et al, 2017). Interestingly, it was shown that FAO positively regulates mitochondrial spare respiratory capacity in CD8⁺ T cells and, therefore, favors cellular survival (Nomura et al, 2016).

Another interesting regulatory point is the electron transport chain (ETC) (that is analyzed in the following item) and the production of mtROS from it, through the partial reduction of O₂ to superoxide. The important role of mtROS in T cell activation is supported by evidence indicating that T cell activation requires the recruitment of mitochondria to the immune synapse (Sena et al, 2013). Moreover, Zhang et al. showed that activated T cells inhibit the formation of the mitochondrial permeability transition pore (mPTP) probably to prevent increased mtROS leakage from mitochondria (Zhang et al, 2016). An interesting aspect of this regulatory point is the concept called mitohormesis, where a mild increase of ROS described as the hormetic stressor can lead to a sublethal stress (Calabrese et al, 2007), thus triggering the activation of a retrograde mitochondria-to-nucleus signaling mechanisms and the vitagene network (Calabrese et al, 2010; Yun and Finkel, 2014; Fischer and Ristrow, 2020). This process was described to be plausible to occur in macrophages

leading to metabolism reprogramming as a mechanism to restrain inflammation through tolerance (Timblin et al, 2021).

And last but not least, ATP production and maintenance of the mitochondrial inner membrane potential also represent an important regulatory point that is plausible to be regulated during the activation and fate of immune cells (Faas et al, 2017), and is discussed in the following section.

3b. The relevance of electron transport chain in immune cells

In immunometabolism, the importance of the ETC has drifted from bioenergetics to its regulatory and signaling pathways (Glancy et al, 2020; Yin and O'Neill, 2021; Preau et al, 2021). The origin of this change was the description of cyt c, part of the ETC, as a driver of apoptosis. This finding resignified the importance of the ETC beyond energy management. In Fig. 3, the main roles and involvement are summarized for each respiratory complex. The description and characteristics of the ETC is beyond the scope of this review and has been largely reviewed elsewhere (Acín-Pérez et al, 2020; Nolfi-Donagan et al, 2020; Vercellino and Sazanov, 2022).

The ROS produced by *complex I* significantly impact the immune system. For example, in response to LPS macrophages can shift from oxidative phosphorylation to glycolysis while also increasing succinate levels (Mills et al, 2016). This pathway can activate hypoxia-inducible factor 1 α (HIF1 α), a key transcription factor in the expression of proinflammatory genes, that in turn can lead to the increased production of interleukin 1 β (IL-1 β) (Mills et al, 2016). In this way, treatment with metformin or rotenone (complex I inhibitors) was shown to reduce pro-IL-1 β production and to increase the anti-inflammatory IL-10 production in macrophages (Xian et al, 2021). Complex I is also implicated in lymphocyte activation, proliferation, and function. Its activity is required in proliferating cells as it maintains an appropriate NAD⁺/NADH ratio to support aspartate and nucleotides biosynthesis (Sullivan et al, 2015). Moreover, blocking complex I with rotenone inhibited proliferation in T effector cell subsets, and aspartate supplementation partially restored the proliferative capacity of rotenone pretreated T_H1 cells (Bailis et al, 2019). In another study, it was observed that in CD8⁺ T cells, rotenone inhibited T cell cytotoxicity based on the measurement of decreased production of IFN γ and tumor necrosis factor α (TNF α) and degranulation (Yi et al, 2006).

As previously stated, *complex II* has been implicated in M₁ macrophage activation. Also, accumulated succinate can also be exported from mitochondria to cytosol where it can inhibit PHD activity to stabilize HIF1 α (Tannahill et al, 2013). This effect of complex II is strengthened by the use of dimethyl malonate, a potent inhibitor of succinate oxidation by complex II, inhibiting LPS-activated macrophages IL-1 β production but increasing IL-10 production (Mills et al, 2016). Interestingly,

reduced IFN γ production by T_H1 cells was observed through complex II activity inhibition using, for example, thenoyltrifluoroacetone, 3-nitropropionic acid or atpenin 5 (Bailis et al, 2019).

Complex III is another important mtROS producer besides complex I in the ETC. MtROS produced through Q site of complex III are important activators of HIF1 α (Mansfield et al, 2005), which is widely expressed in innate and adaptive immune cells including macrophages, neutrophils, and lymphocytes. Analyzing the specific importance of complex III, it has been described that the loss of RISP (Rieske iron-sulfur protein) leads to impaired differentiation of hematopoietic stem cells with histone hypoacetylation due to reduced citrate levels (Ansó et al, 2017). Also, functional complex III is required for antigen specific CD4⁺ T cell activation (Weinberg et al, 2019). A specific mutation of complex III in T cells allowed Sena et al. to demonstrate that mtROS produced at complex III were required for IL-2 production through the activation of NFAT (nuclear factor of activated T cells), and antigen-specific proliferation. In this way, complex III seems to be essential for the correct development of T cells (Sena et al, 2013).

Knockdown of cytochrome oxidase or *complex IV* in macrophages was shown to increase the production of IL-1 β , IL-6, and TNF α , and M₁ polarization and phagocytosis processes (Angireddy et al, 2019). Importantly, it has been shown that in NK cells complex IV is required for antigen-specific amplification (Mah-Som et al, 2021). The non-structural component COX10 is commonly studied to unravel the mechanism by which complex IV is associated with the immune system. T cell specific knockdown of this component was described to impair T cell activation, demonstrating that is important for T cell exit from quiescence acting as a metabolic checkpoint for cell fate decisions following activation (Tan et al, 2017).

Although *F₁F_o-ATP synthase* is not strictly part of the mitochondrial respiratory chain, it is important to briefly discuss its importance based on its main activity as ATP producer. For example, in polarized macrophages, inhibition of ATP synthesis or decreased ATP levels can suppress both M₁ and M₂ activity (Mills et al, 2016; Qin et al, 2020). Also, it was shown that oligomycin (*F₁F_o-ATPase* synthase inhibitor) can decrease LPS-induced IL-1 β levels in M₁ macrophages and suppress arginase activity in M₂ macrophages (Mills et al., 2016). At this point, ATP production and the maintenance of membrane potential are necessary in a context of immune cell activation and differentiation, processes that are directed by energy expenditure and maintained mitochondrial function (Mehta et al, 2017; Stanzani et al, 2019; Vico et al, 2019).

Considering the mitochondrial respiratory chain as a whole, it is important to recognize its therapeutic potential. This observation is based on its importance in the activation and modulation of the inflammatory response, as center of cellular energy metabolism, regulating the levels of NADH, FADH and ATP associated to the Krebs cycle, fatty acid oxidation, aminoacid oxidation, and

pyrimidine biosynthetic pathway, and the maintenance of cellular redox balance (Yin and O'Neill, 2021). Nevertheless, researchers should not set aside the importance of the spatial organization of the respiratory chain in supercomplexes for the functional and regulatory aspects on the activation of the immune response.

4. THE ROLE OF MITOCHONDRIA ON NLRP3 INFLAMMASOME ACTIVATION

The NLRP3 inflammasome is a multiprotein complex, composed of three protein subunits: a sensor molecule (NLRP3), an adaptor protein (ASC), and an effector protein (caspase-1) (Rathinam and Fitzgerald, 2016) (Fig. 4). While NLRP3 inflammasome activity is a necessary component of the innate immune response, its excessive activation can lead to the inflammatory form of cell death called pyroptosis (Swanson et al, 2019). The discovery of the NLRP3 inflammasome and pyroptotic cell death in the last decade has shown the increasing relevance of mitochondria as key players in the inflammatory response (Jo et al, 2016; Huang et al, 2022). Mitochondria are actively involved not only in activation pathways, but also as docking sites in the activation process (Swanson et al, 2019). In this sense, DAMPs act as one of the links between mitochondria and inflammation, and are recognized by the cytoplasmic nucleotide-binding domain leucine-rich repeat-containing receptors (NLRs) (Gong et al, 2020). These NLRs recognize a wide spectrum of intracellular inflammatory stimuli. There are four classes of NLRs (NLRP1, NLRP3, NLRC4 and AIM1) that sense a variety of inflammatory signals to mediate caspase-dependent activation of cytokines (Sandhir et al, 2017). The most common and largely studied is NLRP3 and is normally localized in the cytosol. NLRP3 inflammasome structure is a complex association of cytosolic NLRP3, ASC (apoptosis associated speck-like protein containing a CARD), and caspase 1 (Gilkerson and Matoron, 2014); Fig. 4 shows its structure and activation, emphasizing the activating signals involved and the main consequences observed. Briefly, upon activation, NLRP3 recruits ASC and pro-caspase 1, which in turn becomes activated in caspase 1 being the responsible for the activation of IL-1 β and IL-18 (Yang et al 2019; Huang et al, 2021).

One of the most important interactions of mitochondria with NLRP3 inflammasome is its role in the signaling events for proper activation (Billingham et al, 2022). It has been described that DAMPs leaked from damaged mitochondria can activate the innate immune response through the assembly of the multimeric protein complex inflammasome, ultimately leading to the generation of biologically active cytokines (IL-1 β and IL-18) (Ge et al, 2020; Liu et al, 2019; Pandey et al, 2021; Sugiura et al, 2014). This, in turn, may lead to pyroptosis (Bouhamida et al, 2022; Sandhir et al, 2017). Interestingly, since mtDNA and mtRNA metabolism are implicated in NLRP3 inflammasome activation (Shimada et al, 2012; Zhong et al 2019; Hsu et al, 2023), their involvement in the

pathogenesis of inflammatory syndromes (as sepsis) is not surprising. Moreover, NLRP3 polymorphisms can be used as a risk estimate for the development of sepsis and inflammatory associated pathologies, highlighting the relevant role of inflammasome activation (López-Armada et al, 2013; Schunk et al, 2021).

Mitochondrial dynamics emerges as a key regulator for NLRP3 inflammasome activation. It has been shown that Drp1 knockdown that results in aberrant mitochondrial elongation, increases NLRP3-dependent caspase 1 activation and IL-1 β secretion in mouse bone marrow-derived macrophages (Park et al, 2015). Moreover, in the presence of carbonyl cyanide m-chlorophenyl hydrazone (chemical inducer of mitochondrial fission) effectively decreases NLRP3 inflammasome assembly and activation. Moreover, it has been shown that mitofusin 2 (Mfn 2, mediator of mitochondrial fusion) is involved in its activation (Ichinohe et al, 2013). It is interesting to note that SESN2 (sestrin 2, a stress-inducible protein) has been described to control NLRP3 inflammasome activation probably by increased removal of damaged mitochondria through mitophagy (Kim et al, 2016). In line with this observation, it was described that autophagy can control inflammation through macrophage-disruption of apoptotic corpses or inhibiting NLRP3 inflammasome activation by removing damaged mitochondria (López-Armada et al, 2013). Conversely, inhibition of mitophagy results in spontaneous inflammasome activation (Nakahira et al, 2011).

In addition to the role of mitochondria in signaling events for inflammasome activation, there is increasing evidence that mitochondria are also important as docking sites in the activation process. This contribution of mitochondria in NLRP3-mediated inflammation is demonstrated by the recruitment in the cytoplasm of macrophages in a process mediated by microtubules (Misawa et al, 2013). In this sense, microtubule-driven apposition of ASC on mitochondria to NLRP3 on the endoplasmic reticulum was observed to contribute to inflammasome activation (Misawa et al, 2013). Nakahira and col. observed that NLRP3 relocates to mitochondria following stress (Nakahira et al, 2015). During activation NLRP3 and ASC redistribute to the perinuclear space where endoplasmic reticulum colocalize with mitochondria-associated membranes (MAMs). Taking these observations together, it is viewed that MAMs allow physical interaction between Inflammasome and its ligands. The emerging role of MAMs as modulators of innate immunity is further supported by evidence showing that abnormalities on ER-mitochondria relationships correlates with the inflammation severity in pathologies with an inflammatory component such as cancer, diabetes, and obesity (Pereira et al, 2022).

Regarding the physical interaction between NLRP3 and mitochondria for inflammasome activation, it is worth to describe the implication of three molecules as connection points. One of these relevant molecules appears to be the phospholipid CL that, apart from serving as binding site

for molecules related to autophagy and apoptosis (Dudek, 2017), also binds NLRP3 and caspase 1 (Swanson et al, 2019). Another example is the mitochondrial antiviral signaling protein (MAVS), which is an adaptor in RNA sensing pathways. Its presence is important for NLRP3 inflammasome activation during RNA viral infections (Swanson et al, 2019). MAVS recruits NLRP3 and locates it to mitochondria for inflammasome activation (Subramanian et al, 2013). Importantly, MAVS appear to be a non-essential protein for inflammasome activation induced by other stimuli. Lastly, Mfn 2 was found to be important in this type of mechanism (Swanson et al, 2019). It was shown that during viral infection, Mfn 2 is required for the formation of a complex with MAVS to support the localization of NLRP3 to mitochondria (Ichinohe et al, 2013).

This item reveals the relevance of the nature of the different types of involvement of mitochondria in the mechanism of NLRP3 inflammasome activation. A greater understanding of the underlying mechanisms on the activation process as docking site for assembly and further activation of NLRP3 inflammasome opens an exciting target for pharmacological interventions. Moreover, mitochondria are also involved in the activation (through mtDNA) of others signal transduction cascades involved in inflammation as the one including cyclic GMP-AMP synthase (cGAS) and the stimulator of the interferon response cGAMP interactor 1 (STING1) (Marchi et al, 2022).

5. MITOCHONDRIA QUALITY CONTROL AND MITOCHONDRIAL ARCHITECTURE

The importance of maintaining a healthy and functional mitochondrial population and the close relationship between structure and ultrastructure with mitochondrial function is evidenced by the coexistence of multiple interconnected mechanisms that manage mitochondrial homeostasis to guarantee the maintenance of cellular bioenergetics in the face of different stimuli. Relevant mechanisms responsible for maintaining mitochondrial homeostasis (in number and quality) are mitochondrial biogenesis, fusion, and fission events, mitophagy, and production of MDVs, and are the basis of the global process of mitochondria quality control (Giacomello et al, 2020; Diao and Gustafsson, 2022; Xia et al, 2022). Mitochondrial shape is fundamental for mitochondrial metabolic activity (Giacomello et al, 2020). For example, in fused organelles ATP production and matrix content exchange are facilitated. On the contrary, fissioned organelles may produce more ROS and may be metabolized through mitophagy. Also, mitochondrial fragmentation is necessary for equivalent distribution of components during cell division. It should be noted that these events do not occur independently and that their correct integration will ultimately preserve the mitochondrial functional activity in cells (Fig. 5). Current evidence places mitochondrial function and molecules involved in its homeostasis at the center of the immune response in inflammatory situations, either

related to effector cells of this response, such as macrophages (Sancho et al, 2017) and T cells (Steinert et al, 2021), or in injured cells due to the inflammatory condition.

5.a Mitochondrial biogenesis

This process can be described as the event by which a cell increases its mitochondrial mass, a process that is not only linked to cell division but can also be induced by different stimuli such as high energy requirements, physical training, increased NO levels, and increased ROS production among others. Mitochondrial biogenesis requires the coordinated interaction of nuclear DNA and mtDNA through the activation of different transcription factors to carry out the *de novo* synthesis of mitochondrial proteins and mtDNA. The key transcription factor that regulates mtDNA transcription corresponds to the peroxisome proliferator-activated receptor-gamma coactivator (PGC1) family of transcription factors. Briefly, PGC1 α is activated either by phosphorylation via AMPK (Ke et al, 2021), or by deacetylation by SIRT1 (Majeed et al, 2021). This situation, in turn, leads to the activation of several transcription factors, being the most relevant the nuclear respiration factors (Nrf1 and Nrf2), PPAR and TFAM, finally leading to mtDNA transcription and replication. Specifically, Nrf1 and Nrf2 are the main transcription factors that activate the expression of nuclear genes related to mitochondrial respiratory function (Ke et al, 2021), while TFAM regulates mtDNA replication and transcription, coordinates the assembly of the mitochondrial DNA, and regulates mtDNA copy number (Luo et al, 2021).

Although the relevance of mitochondrial biogenesis during the immune response in inflammatory events is constantly increasing, the unraveling of the molecular mechanisms that activate and drive this process is still ongoing. It has been shown that during bacterial infection PGC1 β is activated in mouse macrophages, increasing mitochondrial function and mtROS production (Sancho et al, 2017), with ultimately bactericidal activity. In contrast, PGC1 β -deficient macrophages showed decreased bactericidal capacity (Sancho et al, 2017). In line with this observation, it was described the importance of PGC-1 β for the efficient organization and packing of ETC components in dendritic cells (Guak et al, 2022). More recently, Dumauthioz et al. showed that PGC1 α overexpression favors the formation of resident CD8 memory T cells (Dumauthioz et al, 2021). It has been described that TFAM is not only involved in the initiation of mtDNA transcription, but also preserving the structural stability of mtDNA as well (West et al, 2016; Li et al, 2019). Interestingly, TFAM deficiency in mice has been shown to induce mtDNA stress, which stimulates cytosolic antiviral innate immune responses in both mouse embryonic fibroblasts and bone marrow-derived macrophages (West et al, 2016; Luo et al, 2021). Finally, inflammatory processes such as endotoxemia have been described to affect mitochondrial biogenesis in cells of the innate or

acquired response. For example, increased expression of PGC1 α and TFAM has been observed in a model of acute endotoxemia both in rat cardiomyocytes (Vanasco et al, 2014) and rat brain cortex (Adán Areán et al, 2021), once again underlining the role of mitochondrial homeostasis as response to inflammatory injury.

5.b Fusion and fission

Mitochondria form networks that during cell life undergo continuous antagonistic fusion and fission events (Bereiter-Hahn and Vöth, 1994). As detailed description of these processes is not the aim of this review, only a brief and introductory reference is included. In mammals, mitochondrial fusion is mainly regulated by the proteins Opa1 (optic atrophy 1, an inner mitochondrial membrane GTPase) (Cipolat et al, 2004), and by the outer membrane GTPases or Mfn 1 and 2 (Santel and Fuller, 2001); while mitochondrial fission is mainly controlled by the cytosolic protein Drp1 (dynamin-related protein 1, a GTPase), where its translocation from the cytoplasm to the mitochondria is an essential step in organelle fragmentation (Smirnova et al, 2001). Although pro-fission proteins (such as Drp1, Fis1) and pro-fusion proteins (such as Mfn1, Mfn2, and Opa1) have been described to act independently in fission and fusion mechanisms (Detmer and Chan, 2007), emerging evidence suggests the existence of crosstalk between fission and fusion machinery. In this sense, the importance of Fis1 in the bidirectional regulation of mitochondrial fusion and fission machinery has been demonstrated, since it is not limited to mitochondrial fission promotion; it can also actively inhibit mitochondrial fusion (Yu et al, 2020). Since Opa1 is also involved in the biogenesis of mitochondrial cristae and respiration, it has been a relevant subject of study in recent years. Sanchez Rodriguez et al (Sánchez-Rodríguez et al, 2022) found that selective removal of Opa1 causes important alterations in macrophage activation and polarization, through decreased IL-6 and TNF α release, reduced NO burst, and macrophage polarization towards M₁. Moreover, Drp1 silencing in macrophages decreased mitochondrial fragmentation and production of TNF α after stimulation with LPS, while the production of IL-6 and IL-1 β was observed increased (Gao et al, 2021). Generalizing, infection with bacterial pathogens is generally associated with a fragmented mitochondrial population, while viral infection leads to mitochondrial fusion in macrophages (Tiku et al, 2020). However, both mitochondrial fission and fusion in macrophages are promoted in a context-dependent manner, setting the importance to unravel these complex mechanisms and the molecules involved that interact during the immune response and inflammatory processes.

Interestingly, efferocytosis, defined as the clearance of apoptotic cells by macrophages is necessarily related to mitochondrial fission (Doran et al, 2020). Apoptotic cell uptake by macrophages triggers mitochondrial fission induced by Drp1, enabling efficient apoptotic cell

degradation in phagosomes, and release of calcium-mediated vesicular trafficking, ultimately leading to the resolution of the inflammatory situation (Wang et al, 2017).

5.c Mitophagy

Mitophagy (or autophagy of damaged mitochondria), is viewed as a mechanism involved in mitochondrial quality control by selectively degrading non-functional mitochondria (Vincow et al, 2013). Several studies, using different cell models, have shown that the dissipation of the mitochondrial membrane potential would be the signal selectively recognized by PINK1 (PTEN-induced kinase 1, a protein involved in initiating this selective autophagy process) (Jin et al, 2010; Kondapalli et al, 2012). Briefly, under basal conditions PINK1 protein n-terminal region is transferred across the outer mitochondrial membrane (OMM) to the inner mitochondrial membrane (IMM), with the kinase domain located closer to the C-terminal region protruding towards cytosol. PINK1 is then cleaved by IMM-linked proteases and subsequently degraded by the proteasome, leading to undetectable basal levels of PINK1 under physiological conditions (Ge et al, 2020). Stressors such as membrane depolarization, or mitochondrial complexes dysfunction lead to accumulation of PINK1 in the OMM by impairing intermembrane transport from the N-terminal domain to the IMM. Subsequent homodimerization of PINK1 in OMM leads to autophosphorylation, promoting activation and recruitment of E3-Parkin ubiquitin ligase, initiating the mitophagic pathway of these mitochondria (Narendra et al, 2008; Suen et al, 2010; Wai and Langer, 2016). Defective removal of damaged mitochondria leads to hyperactivation of inflammatory signaling pathways and subsequently to chronic systemic inflammation and development of inflammatory diseases. Although the crosstalk between mitophagy mechanisms and host defense has been established only recently, a growing body of evidence supports the importance of their coordination (Gkikas et al, 2018). Interestingly, it has been described that the nitrosylation of PINK1 reduces the translocation of Parkin to the mitochondrial membrane, producing the accumulation of damaged mitochondria, observed in Parkinson's disease with chronic inflammatory characteristics (Oh et al, 2017). In recent years, new actors in mitophagy processes have been described. Among them, BCL2 interacting protein 3 (BNIP3) has been described as an important inducer of mitophagy in inflammatory, hypoxic and exercise conditions. However, the regulatory role of BNIP3 in mitochondrial dysfunction and mitophagy is complex and multifaceted and is currently under study (Gao et al, 2020). Also, it has been described that vacuole membrane protein-1 (VMP1) would be involved as a necessary agent to trigger mitophagy in the inflammatory process occurring in acute pancreatitis (Vanasco et al, 2021). It is worth to note that the accumulation of damaged mitochondria as a consequence of imbalance of quality control mechanisms, leads to the release of DAMPs (Zhang et al, 2010) as

analyzed in previous sections of this review. Consequently, pathways involved in the synthesis of different early-phase inflammatory mediators such as TNF α , ILs, IFN γ and ROS/RNS are activated (Geto et al, 2020; Roh and Sohn, 2018). For example, Irazoki et al. found that alterations in mitophagy flux and lysosomal function caused by decreased BNIP3 led to the accumulation of autolysosomes with undegraded cargo, favoring the interaction between mtDNA and TLR9 leading to NF κ B induction and inflammation (Irazoki et al, 2022). Macrophages deficient in LC3 and Beclin1 have been reported to display an accumulation of defective mitochondria, disturbing cytosolic levels of mtDNA that induce NLRP3 activation, and IL-1 β secretion (Nakahira et al, 2011; Zhou et al, 2011). In this direction, Zhong et al. found that mitophagy deficiency associated with aging in macrophages, caused by the decrease in mitochondrial ubiquitination mediated by the PINK1/Parkin pathway, produces the accumulation of damaged mitochondria, favors the release of mtDNA to the cytosol and increases STING activation that signals for age-associated chronic sterile inflammation (Zhong et al, 2022).

5d. Mitochondrial-derived vesicles

It is worth discussing the important emerging role of MDVs in mitochondrial quality control and its potential involvement in the immune response and inflammatory situations. These vesicles were firstly identified by Neuspiel in 2008 (Neuspiel et al, 2008) and were observed as budding from mitochondria as single or double membrane structures including mitochondrial outer and inner membrane with matrix content. It was described that its main function is to carry specific material between mitochondria and other organelles including lysosomes where they are degraded (Sugiura et al, 2014; Todkar et al, 2021). To undoubtedly define these structures, they must be formed in the absence of Drp1, its diameter should be between 70 and 150 nm, and they have to carry selective cargo (Neuspiel et al, 2008; Schumann and Subramani, 2008). Interestingly, MVDs are early formed during mitochondrial stress, before the occurrence of mitophagy, thus regulating mitochondrial mass in a rapid fashion (Peng et al, 2022).

It has been previously presented that mitochondria can release DAMPs thus activating the innate immune system. Taking this into account, MDVs not only participate as actors in mitochondrial quality control processes and communication between cells (Sugiura et al, 2014), but prevents the secretion of DAMPs by wrapping them for degradation as well. However, when lysosomes are overwhelmed with the degradation process, immune responses can be triggered. In the same way, Todkar et al. showed that the cargo selectivity depends on the different MDV targeting pathways; Opa1 and sorting nexin 9 (Snx9)-dependent MDVs are required to target mitochondrial proteins to extracellular vesicles, while parkin (in Parkinson's disease with a chronic

inflammatory component) blocks this process by directing damaged mitochondrial content to lysosomes (Todkar et al, 2021). This observation shows that the formation of MDVs containing, for example, damaged oxidized proteins is stimulated by the PINK1/Parkin pathway (McLelland et al, 2014).

6. THERAPEUTIC TARGETING

Throughout the present review mitochondria have been identified to play a central role in a wide range of mechanisms associated with cellular homeostasis relevant for immune processes, such as (a) provide the majority of the cellular energy coupling the oxidation of fatty acids and pyruvate with the production of ATP by the ETC, (b) production and regulation of mtROS which are highly involved in the redox metabolism, (c) maintain the Ca^{2+} levels, (d) cell fate and differentiation through the mtPTP, among others (Wallace, 2005; Magnani et al, 2020; Marchi et al, 2022; Hu et al, 2022). Failure of those mitochondrial functions are relevant from the pathophysiological perspective as they are involved in the initiation and progression of numerous inflammatory diseases. Therefore, maintenance of mitochondrial network integrity and function arose as a hallmark in the development of new therapeutic strategies aiming to ameliorate an exacerbated inflammatory response (van der Windt et al, 2012; Chellappan et al, 2022). The present section intends to overview recent progress on the pharmacological approaches and the mitochondria-targeted strategies proposed to improve its function, to highlight their potentially clinical impact in inflammation and inflammatory-associated syndromes.

6a. Modulation of the ETC function

Mitochondrial-targeted treatments aiming to restore or enhance electron transfer have been proposed. Increasing the reducing equivalents feeding into the electron transfer chain may help to bypass complexes dysfunction in order to improve mitochondrial energy production. For example, succinate enhance electron transfer from complex II to complex III when complex I is blocked, or the use of menadione allows the direct transfer of reducing equivalents directly to complex IV in patients with a complex III defect (Wallace et al, 2010; Saeb-Parsy et al, 2021). Based on similar mechanisms, reduced cofactors NADH and $FADH_2$ availability could be increased by treatment with dichloroacetate, and thiamine (vitamin B1). Both compounds act as a mitochondrial pyruvate dehydrogenase kinases (PDK) inhibitor, reducing PDK function and leading to pyruvate dehydrogenase complex (PDHC) activity. This effect increases the catabolism of pyruvate to acetyl-CoA, entering the Krebs cycle and generating reduced cofactors, resulting in a characteristic reversed glycolytic phenotype of cancer cells (El-Hattab et al, 2017; Zeng et al, 2021; Yang et al, 2022; Lee et

al, 2022). Also, PDHC increased activity exert a protective strategy through the release regulation of inflammatory mediators switching the metabolism in response to stressors such as sepsis (Zeng et al, 2021).

Regarding the mitochondrial respiratory chain complexes dysfunction, partial inhibition of the respiratory chain complexes activity with small molecules emerged as a promising mitochondrial-related therapeutic strategy. Dimethyl malonate (DMM) is a cell permeable complex II inhibitor that directly inhibits succinate oxidation. Accumulation of succinate has been proved to limit the anti-inflammatory cytokine IL-10 production in macrophages (Scialò et al, 2017). Administration of DMM leads to a decrease mtROS production from complex I by reverse electron transport, which are required for the expression of IL-1 β and a range of proinflammatory cytokines (Mills et al, 2017; Xu et al, 2018; Yin and O'Neill, 2021), showing the importance of mitochondrial complex II in the oxidative damage mechanisms and initiation and progression of an inflammatory response under different pathologies like cardiac arrest or liver injury (Yin and O'Neill, 2021). Metformin presents similar outcomes as it inhibits mitochondrial complex I blocking also the reverse electron transport from complex II boosting the anti-inflammatory response (Tsuji et al, 2020). Metformin, a widely utilized type 2 diabetes treatment, is a safe and inexpensive drug, and these features have led investigators to consider evaluating this drug in several studies to extend its potentially beneficial anti-inflammatory effects (Mehta et al, 2017). Interestingly, it was described that its mechanism may be related to the occurrence of mitohormesis and the consequent activation of peroxiredoxins by a mild increase in mitochondrial ROS production (Renis et al, 1996; De Haes et al, 2014).

Another therapeutic strategy aiming to compensate for lack of efficiency in ATP production by increasing cofactors oxidation, decreasing ROS production, and increasing AMPK expression is the uncoupling approach, by use of small molecule mitochondrial uncouplers, genetic methods to increase the expression of uncoupling proteins or compounds that can modulate the activity of uncoupling proteins (Hass and Barnstable, 2021). Protonophores such as DNP and FCCP, are able to pass through the mitochondrial inner membrane and increase the proton transport into the matrix initiating changes in the membrane potential required for the ATP production (Childress et al, 2018) leading to metabolic parameters improvement. Considering that off-target effects, such as depolarization of the plasma membrane, were described after the administration of this compounds (Goedeke and Shulman, 2021), research has focused on controlled release formulation plus specific targeting in order to reduce toxicity (Childress et al, 2018).

6b. Mitochondrial antioxidants and ROS scavengers

Supplementation with several natural antioxidants or compounds with antioxidant activity, such as Coenzyme Q (CoQ), vitamins E, C, and lipoic acid were proved to ameliorate oxidative damage as they provide an electron sink (Vanasco et al, 2008; Oliver and Reddy, 2019). To improve efficiency, compounds like CoQ and vitamin E were covalently linked to the lipophilic triphenylphosphonium cation (MitoQ, MitoVit E) which is electrostatically attached to the negatively charged mitochondrial matrix which confers the ability to cross the phospholipid bilayers redirecting it to the matrix that leads to its accumulation many hundred-fold (Bhatti et al, 2017; Capeloa et al, 2022; Sang et al, 2022). Once inside the mitochondria their mechanism of action has been described as reduction of mtROS levels resulting in not only a decreased oxidative insult to macromolecules but affecting the redox signaling pathways as well (Yan et a., 2020; Weissman and Maack, 2021). Metabolic antioxidants like lipoic acid have shown relatively low toxic effects as they can be included in the cellular redox homeostasis response. However, this also represents a disadvantage as it results in a short period of time where these antioxidants can act as mtROS scavengers (Wallace, 2005; El-Hattab et al, 2017). Preventing oxidative damage using mitochondrial-targeted antioxidants has also been extensively proved as an effective therapy for diabetes and its related chronic inflammation (Rovira-Llopis et al, 2018). Of note, mitohormesis and vitagenes activation should be taken into account when analyzing the effect of the supplementation with antioxidants as it might represent an innovative approach in therapeutic intervention (Calabrese et al, 2008; Calabrese et al, 2010).

In the immunometabolism research field, a new generation of mtROS suppressors are also being developed, showing their ability to improve redox signaling (Mehta et al, 2017). S1QELs and S3QELs, which are novel compounds that selectively prevent the excess of complex I-dependent and complex III-dependent ROS production, respectively (Scialo and Sanz, 2021). Therefore, they emerge as potential therapeutic molecules for the treatment of diseases that involve mitochondrial ROS-triggered aberrant inflammation.

6c. Regulation of mitochondrial biogenesis and turnover

As previously described, mitochondrial biogenesis is a fundamental pathway required to maintain a healthy mitochondrial population and proper organelle function with PGC1 α as nodal regulator. If intracellular ROS levels increase, PGC1 α is directly phosphorylated by AMPK thus mediating mitochondrial biogenesis (Palikaras et al, 2017; Whitley et al, 2019). For example, decreased mRNA expression of several genes associated with oxidative phosphorylation has been described in diabetic patients, including genes regulated by PGC1 α and nuclear respiratory factors (Rocha et al, 2020). Metformin promotes the activation of AMPK and PGC1 α , and was observed

associated to the reduction of mitochondrial complex I-ROS production (Yan et al, 2020). Besides biogenesis, mitochondrial dynamics also offers regulatory targets. Proper control of mitochondrial dynamics regulating mitochondrial fission and fusion provides a window for therapeutic intervention. Small molecules can modulate Drp1, Opa1 or Mfn activity. Drp1 inhibitor mdivi-1 is the most studied molecule that specifically inhibited the GTPase activity of Dnm1 and abolished its assembly. Treatment with mdivi-1 rebalance mitochondrial morphology in disease models associated with excessive mitochondrial division, improving mitochondrial metabolic function, and reducing the cell death (Bordt et al, 2017; Li et al, 2018; Hernandez-Resendiz et al, 2020;). On the other hand, regulation of the mitochondrial fragmentation machinery with chemical therapeutic approaches such as BGP-15 can also be useful to restore normal mitochondrial dynamics in cells (Szabo et al., 2018). Data obtained in numerous studies suggest that targeting mitochondrial dynamics with small molecules that may directly or indirectly increase mitochondrial fusion activity leads to decreased cell death (Whitley et al, 2019).

There is sufficient evidence *in vitro* and *in vivo* that mitochondria have a relevant role in a wide range of inflammatory diseases. Therefore, as mitochondria can be seen as the powerhouse and regulatory center of immunity, the current aim of pharmacological research studies is to design and evaluate small molecules (Table 1) which are able to modulate the mitochondrial mechanisms involved in cellular immunometabolism. In conclusion, it is important to consider targeting compounds towards mitochondria as the main challenge in order to increase treatments specificity for reducing side effects.

7. CONCLUSIONS AND PERSPECTIVES

Unraveling the different mechanisms by which mitochondria have a relevant role in the inflammatory response beyond energy management of the process, is important for improving our understanding of the host immune defense and the pathogenesis of various inflammatory diseases and syndromes. The relevance of mitochondria as a necessary actor in the inflammatory response should be interpreted and based in its complex nature and the existence of other required actors. Consequently, new questions and interesting aspects arise, such as the involvement of MDV in the immune response with the putative objective of preventing uncontrolled situations.

One intriguing aspect is that mitochondria can be important for the immune response at different levels, including releasing activation molecules, changing its structure and function to accompany the immune response, and serving as a structural base for activating intermediates as in NLRP3 inflammasome. In line with this appreciation, this organelle is plausible of being regulated

and, consequently, emerges as an interesting and multifaceted platform for studying and developing pharmaceutical and therapeutic approaches. There are many ongoing studies aimed to describe the effects of specific mitochondrial targeted molecules and treatments to ameliorate consequences of exacerbated inflammatory components of pathologies and syndromes, resulting in an open area of increasing research interest.

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CONFLICT OF INTEREST

The authors do not present any conflict of interest.

LIST OF ABBREVIATIONS

AIM1	Apoptosis inhibitor of macrophages 1
AMPK	Adenosine monophosphate-activated protein kinase
ASC	Apoptosis associated speck-like protein containing a CARD
ATP	Adenosine triphosphate
BNIP3	BCL2 interaction protein 3
CL	Cardiolipin
CoQ	Coenzyme Q
cGAS	cyclic GMP-AMP synthase
cyt c	Cytochrome c
DAMPs	Damage-associated molecular patterns
DMM	Dimethyl malonate
DNP	2,4-dinitrophenol
dsRNA	double stranded RNA
Drp1	Dynamin-related protein 1
ETC	Electron transport chain
FAO	Fatty acid oxidase
FAS	Fatty acid synthase
FCCP	p-trifluoromethoxyphenylhydrazine
Fis 1	Mitochondrial fission 1 protein
HIF1 α	Hypoxia inducible factor 1 α
IFN γ	Interferon γ
IL	Interleukin

IMM	Inner mitochondrial membrane
LC3	Microtubule-associated protein 1A/1B-light chain 3
LPS	Lipopolysaccharide
MAMs	Mitochondrial-associated membranes
MAVS	Mitochondrial antiviral signaling protein
MDVs	Mitochondrial-derived vesicles
Mfn	Mitofusin
mtDNA	Mitochondrial deoxyribonucleic acid
mtPTP	Mitochondrial transition permeability pore
mtROS	mitochondrial reactive oxygen species
NFκB	Nuclear factor kappa-light-chain-enhancer of activated B cells
NFAT	Nuclear factor of activated T cells
NLR	Nuclear oligomerization domain-like receptor
NLRP	Nod-Like Receptor Protein
NLRC4	Nod-like receptor card domain 4
Nrf1/2	Nuclear respiratory factor 1/2
OMM	Outer mitochondrial membrane
Opa1	Optic atrophy 1
PDHC	Piruvate dehydrogenase complex
PDK	Piruvate dehydrogenase kinase
PGC1α	Proliferator-activated receptor coactivator 1α
PHD	Prolyl hydroxylase

PINK1	PTEN-induced kinase 1
PRR	Pattern recognition receptor
RET	Reverse electron transfer
RISP	Rieske iron-sulfur protein
RLR	RIG I-like helicases receptor
ROS	Reactive oxygen species
SESN2	Sestrin 2
SIRT1	Sirtuin 1
STING	Stimulator of interferon genes
TCA	Tricarboxylic acid cycle
TCR	T cell receptor
TFAM	Mitochondrial respiratory factor A
TLR	Toll-like receptors
TNF α	Tumor necrosis factor α
VMP1	Vacuole membrane protein 1

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Table 1: Metabolic and pharmacological small molecules use to modulate mitochondrial metabolism as potential therapeutic approaches in mitochondrial-initiated inflammatory mechanisms.

Mechanism/Agent	Mitochondrial target	Mechanism	Reference
Modulation of the ETC function			
Succinate		Bypasses complex I	Saeb-Parsy et al, 2021;
Menadione	PDK inhibitor	Bypasses complex II. Increased reduce cofactors	Wallace et al, 2010
Dichloroacetate (DCA)	PDK inhibitor	Increasing PDHC, thereby increasing the catabolism of pyruvate to acetyl-CoA	Yang et al., 2022; Zeng et al., 2021
Thiamine (vitamin B1)		Cofactor of PDHC	El-Hattaba et al., 2017
Dimethyl malonate (DMM)	Complex II inhibitor	leads to a decrease ROS production from complex I by reverse electron transport, impaired proinflammatory cytokine	Scialò et al., 2017
Metformin	Complex I inhibitor	Blocks the reverse electron transport from complex II impairing complex I-ROS production Activates AMPK and PGC1 α promoting mitochondrial biogenesis	Tsuji et al., 2020 Yan et al., 2020
2,4-dinitrophenol (DNP)	Protonophoric	Modulate mitochondrial membrane potential by increasing the	Childress et al., 2018
Carbonyl cyanide p-trifluoromethoxyphenyl (FCCP)	uncouplers	proton transport into the matrix to improve ATP production	

Mitochondrial antioxidants and ROS scavengers

MitoQ	Mitochondrial-	Transfers electrons to complex III. Preserve mitochondrial membrane	Bhatti et al., 2017
MitoVit E	targeted antioxidants Complex I and II	potential, decreased ROS production and organelle damage avoiding excessive cell death	

S1QELs and S3QELs	Mitochondrial ROS suppressors	Prevent excessive ROS production from complex I and complex III	Scialo and Sanz 2021
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Regulation of mitochondrial biogenesis and turnover

mdivi-1	Drp1 protein and complex I	Inhibitor Drp1 and complex I; less fission, improved mitochondrial function	Bordt et al., 2017; Hernandez-Resendiz et al., 2020
BGP-15	Opa1	Stimulated GTPase activity and assembly of Opa1, increasing mitochondrial fission; activated diverse other signaling pathways	Szabo et al., 2018

FIGURE LEGENDS

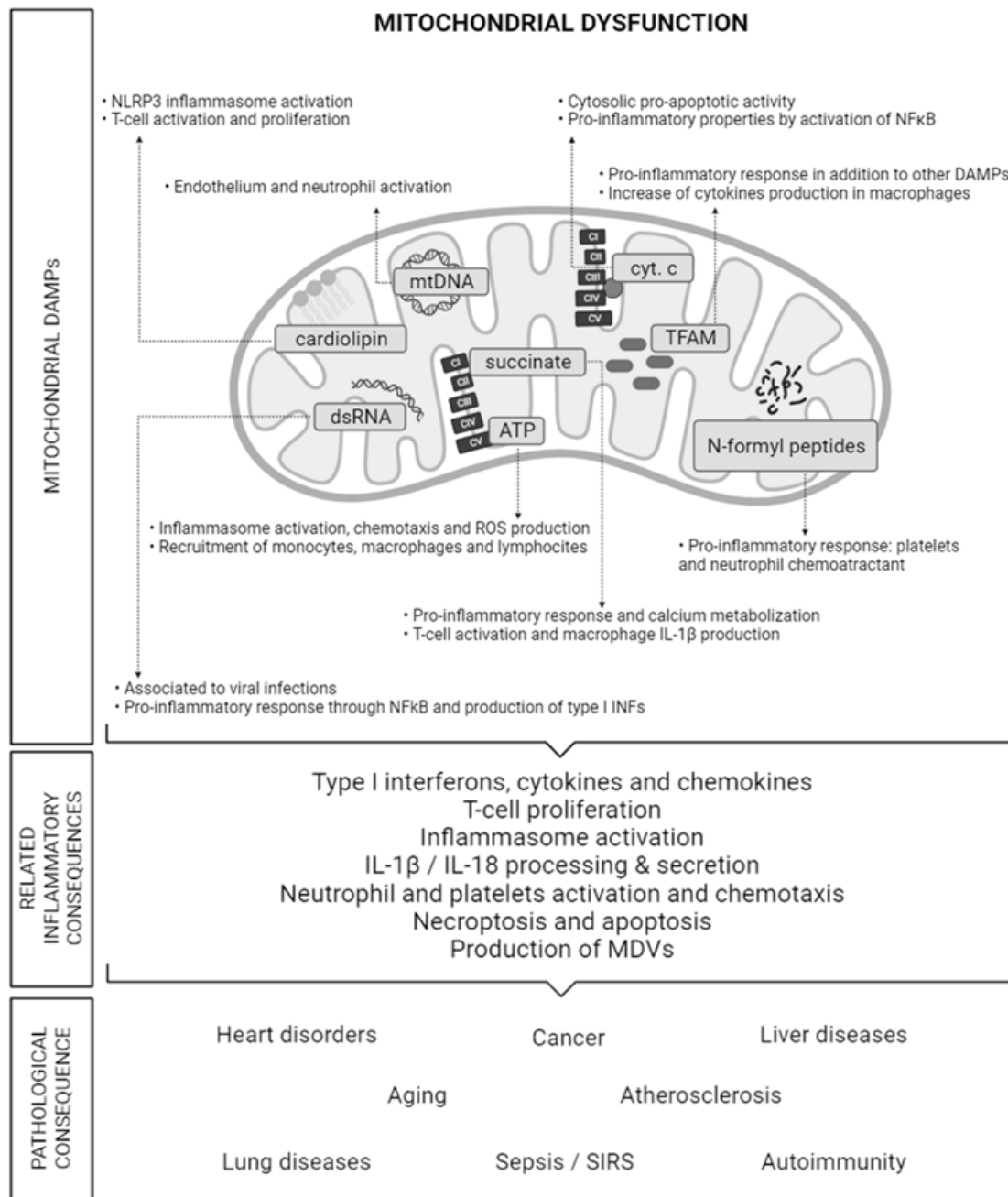


FIGURE 1. Mitochondrial dysfunction, release of DAMPs, and the consequences in the immune system and inflammatory response. The disruption of membrane integrity leads to the release of mitochondrial ligands and DAMPs, as N-formyl peptides, cardiolipin, mtDNA, dsRNA, ATP. Briefly, these DAMPs trigger a wide array of inflammatory responses, including neutrophil activation and migration, inflammasome activation resulting in IL-1 β and IL-18 processing and secretion, and pro-inflammatory cytokine and chemokine production. If sustained in time, this situation may have pathological consequences as cancer, heart disorders, infection, aging, among others.

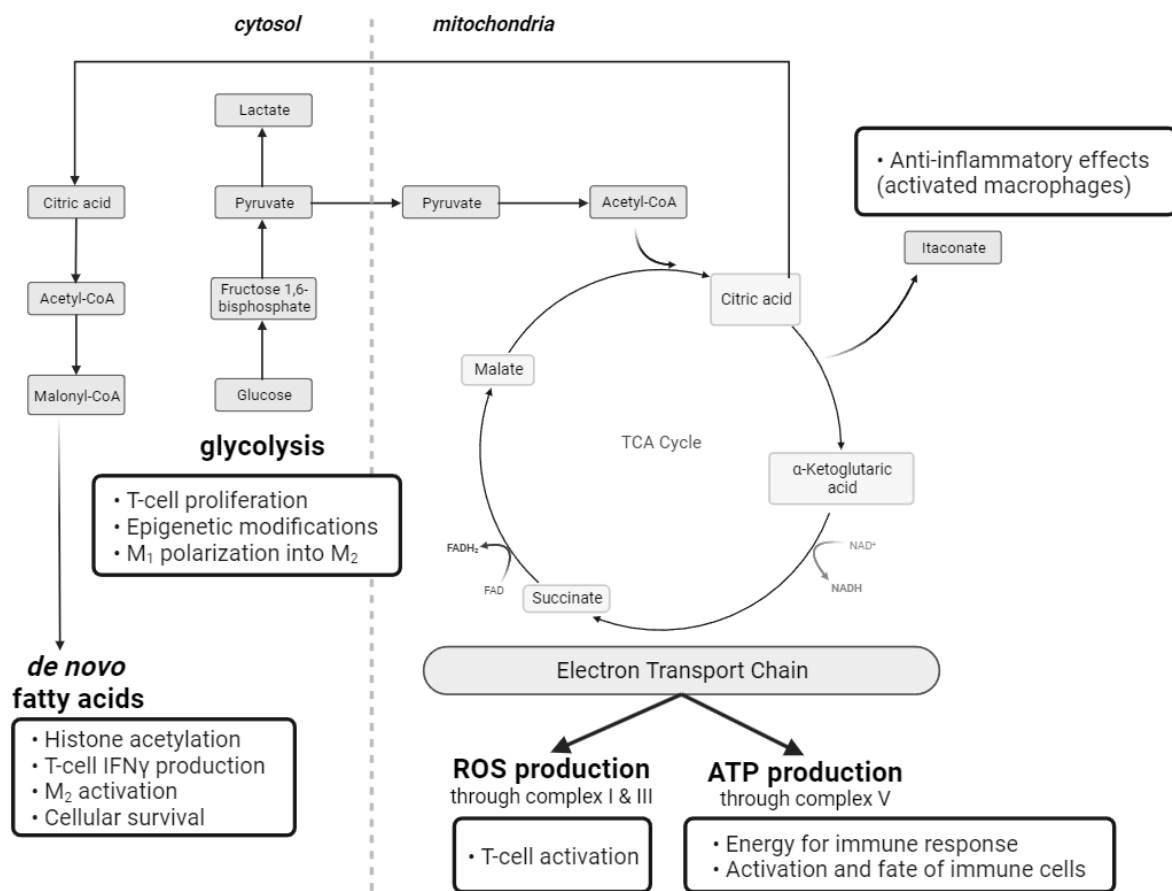


FIGURE 2. Mitochondrial hot points plausible to be regulated with relevant consequences for immune responses. These relevant points include: glycolysis (where pyruvate can either be secreted as lactate or oxidized to acetyl-CoA and enter the TCA cycle), TCA cycle and *de novo* synthesis of fatty acids (through the intermediate production of citrate), mtROS production (through the electron flux leakage and RET), and ATP production (that uses energy provided by the electron transport chain through the maintenance of the inner membrane potential). The importance of these regulatory points on the function and maturation of immune cells, and the inflammatory response are also included.

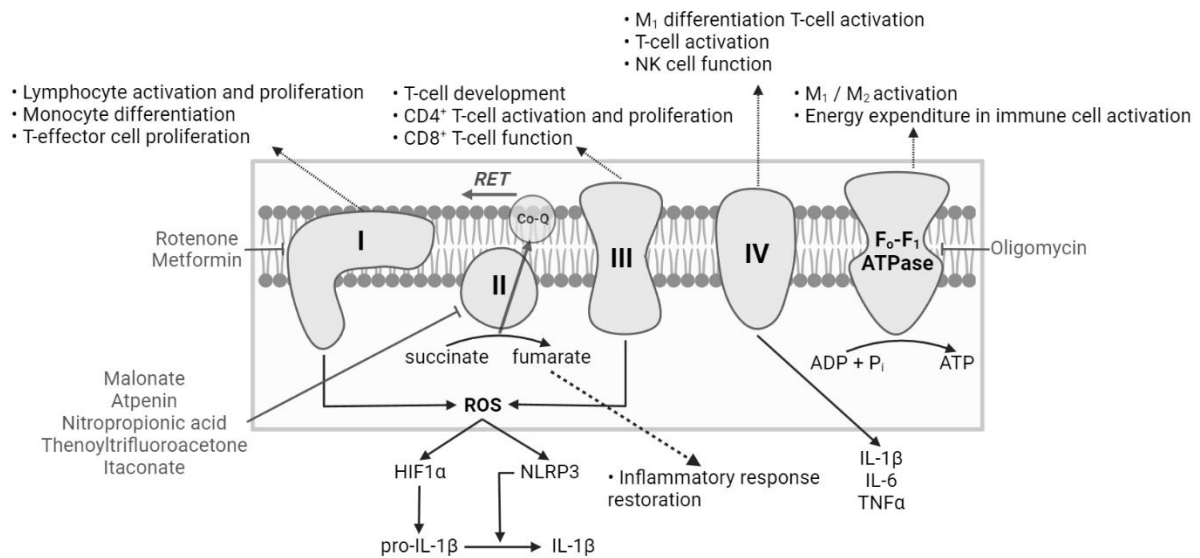


FIGURE 3. The electron transport chain and the regulation of the immune response. As

extensively analyzed in this review, mitochondrial respiratory complexes have implications with immune consequences through the activation and regulation of different mechanisms. In activated macrophages ROS produced at *complex I* can a) activate NLRP3 inflammasome through oxidizing mtDNA and b) stabilize HIF1 α through inhibition of PHD. By both mechanisms IL-1 β production is induced. Complex I is also implicated in lymphocyte activation, proliferation, and function, T cell proliferation, and monocyte differentiation. Its activity is required in proliferating cells as it maintains an appropriate NAD⁺/NADH ratio to support aspartate and nucleotides biosynthesis. Regarding *complex II*, oxidation of succinate to fumarate is decreased. However, in the case of pretrained macrophages this inhibition is not observed, and the inflammatory response is restored (preventing immune paralysis). ROS derived from *complex III* are another major activation signal for HIF1 α that is a master regulator for various immune cell functions. For example, this complex regulates CD4⁺ T cell activation and proliferation, and CD8⁺ T cell function. Inhibition of complex IV promotes M₁ differentiation and the production of proinflammatory cytokines, indicating the anti-inflammatory properties of complex IV. ATP synthase increases the production of IL-1 β produced by M₁ macrophages and induces the differentiation of M₂ macrophages. Also, this complex is involved in T cell fate decisions, and NK cell function. Full lines indicate main effects, dashed lines indicate main effects while being inhibited, and main inhibitors of the respiratory chain are included in the figure.

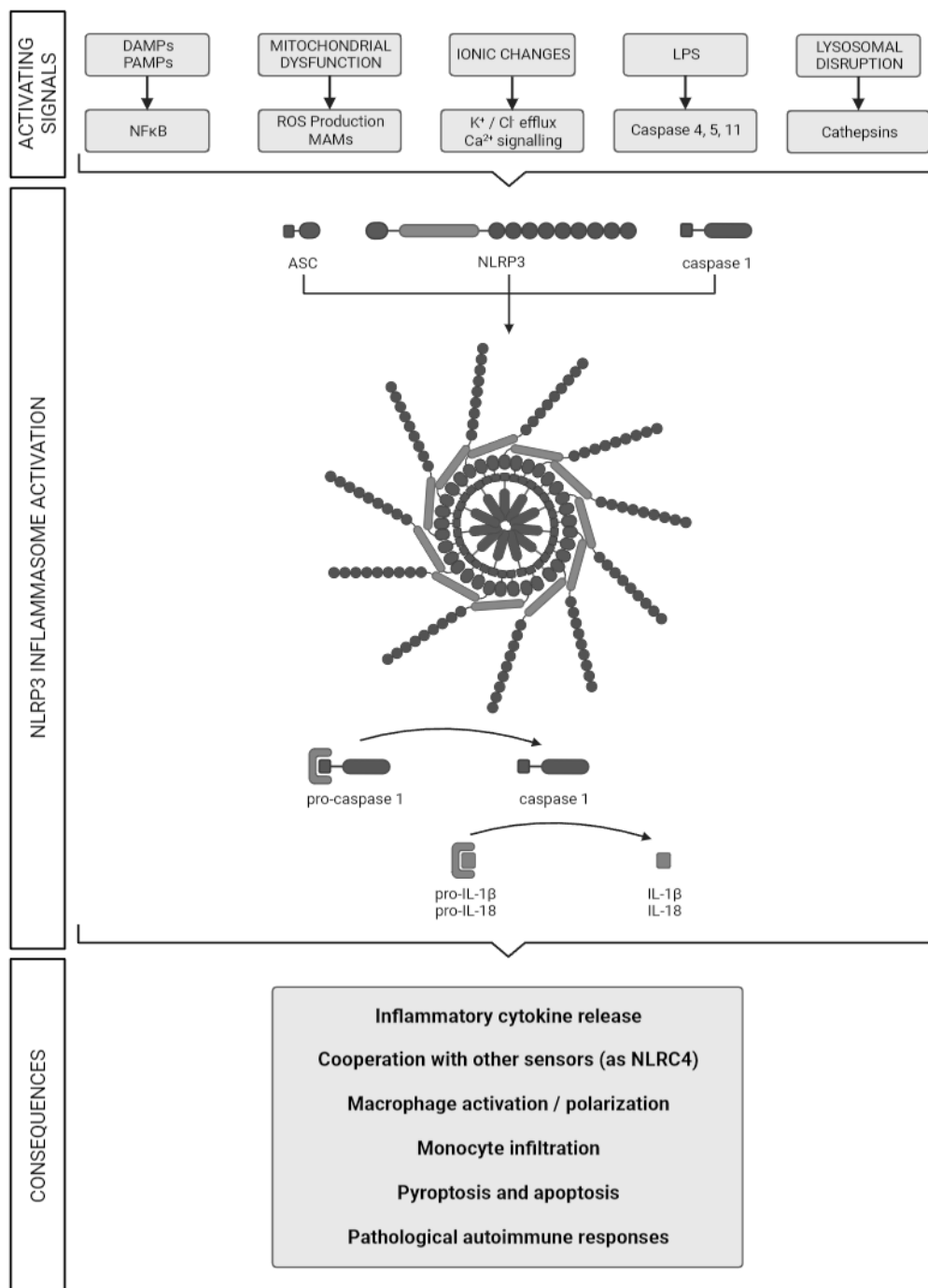


FIGURE 4. Formation of the NLRP3 inflammasome complex. Activation by different stressors of this complex involves constituent molecules as NLRP3, ASC and caspase 1. The activated inflammasome allows the cleavage of pro-caspase 1 into its active form (caspase 1), which in turn cleaves pro-IL-1 β and pro-IL-18 to their active forms (IL-1 β and IL-18, respectively). The immune consequences include: inflammatory cytokines release, macrophage activation and polarization, monocyte infiltration, and pyroptosis, among others.

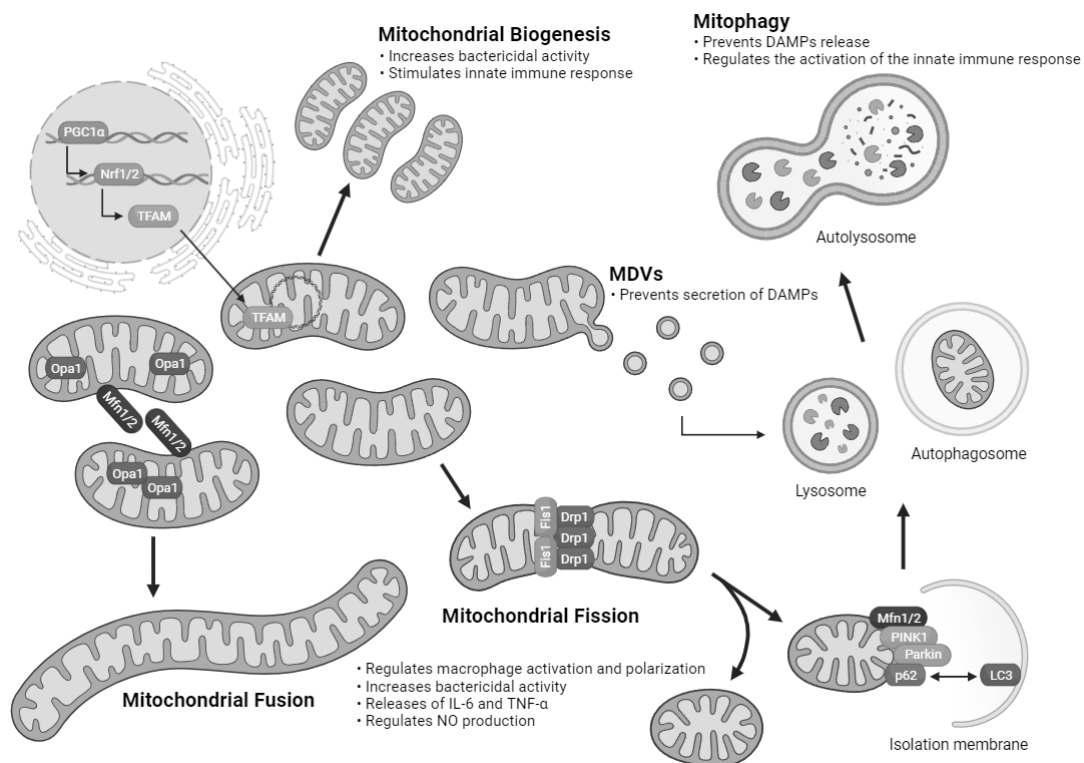


FIGURE 5. Mitochondrial quality control and the coordination of mitochondrial biogenesis, fusion and fission, mitophagy and MDV production. *Mitochondrial biogenesis* needs the activation of PGC1 α . Once activated, PGC1 α binds to Nrf 1/2 to promote expression of several mitochondrial proteins, including TFAM for mtDNA synthesis, ultimately resulting in increased mitochondrial number. In the *fusion* process, outer mitochondrial membrane (OMM) fusion is mediated by Mfn1 and Mfn2, whereas inner mitochondrial membrane (IMM) fusion is mediated by Opa1. Mitochondria *fission* requires the recruitment of Drp1 from cytosol to mitochondria. In Parkin-dependent *mitophagy*, when mitochondria are depolarized in response to various insults, Parkin is translocated to the outer membrane of mitochondria. This process is regulated by PINK1, which is stabilized on depolarized mitochondria. PINK1 either directly phosphorylates Parkin or ubiquitin to promote Parkin translocation or its ligase activity. Once Parkin translocates to mitochondria, it promotes selective mitophagy through mitochondrial ubiquitination and recruitment of autophagy receptor proteins such as p62, which further recruit LC3 positive autophagosomes. *Mitochondria derived vesicles* may be produced even before mitophagy is activated. The segregation of mitochondria to form MDVs is also regulated by PINK1 and Parkin. MDVs are fused with late endosomes and multivesicular bodies and then delivered to lysosomes where they are eventually degraded. Each of these processes, in individual or coordinated fashion, have important regulatory functions for activation, differentiation and function of immune cells.