

THE LINK BETWEEN MITOCHONDRIA AND INFLAMMATION: A BRIEF REVIEW

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ABSTRACT – Inflammation plays a central role in various diseases, including autoimmune disorders and viral infections, and can worsen conditions caused by non-inflammatory stressors. Mitochondria, with their bacterial-like properties, are involved in regulating inflammation. Damaged mitochondria release components such as mtDNA into the cytosol, triggering innate immune responses. The DNA sensor cGAS activates the STING pathway, leading to a type I-IFN response and inflammasome activation. MtDNA is also a key activator of the NLRP3 inflammasome via a reactive oxygen species (ROS)-dependent mechanism. Mitochondrial ROS and mtDNA act as damage-associated molecular patterns (DAMPs), which are critical for inflammasome activation and regulate regulated cell death (RCD). Mitochondrial components such as cytochrome c, cardiolipin, and N-formyl peptides can trigger inflammatory responses through various receptors like TLR9 and RAGE. Excessive mtDAMP signaling is tightly regulated to prevent unwarranted inflammation, with mechanisms like apoptosis and autophagy modulating immune responses. Dysregulated mtDAMP signaling contributes to diseases such as Systemic Lupus Erythematosus, Crohn's disease, and Parkinson's disease, and can affect viral infections and cancer progression. Mitochondrial dysfunctions play a significant role in abnormal innate immune responses. Although mitochondrial-targeting therapies for inflammation are largely unexplored, they present a potential avenue for treatment, especially given the limited pharmacological options available. In conclusion, while mitochondria are key regulators of inflammation, further research is needed to fully understand their role and develop effective therapeutic strategies to address mitochondrial dysfunction and its connection to various inflammatory diseases.

KEYWORDS: Mitochondria, Inflammation, cGAS-STING, Inflammasome.

INTRODUCTION

Numerous human diseases, including autoimmune disorders and viral infections, are linked to dysregulated inflammatory responses¹⁻⁴. Conversely, unregulated inflammation may exacerbate the progression, severity and duration of diseases induced by non-inflammatory stressors⁵. The activation of adaptive immunity leads to a robust inflammatory response, contributing to the beneficial effects seen in various cancer treatments⁶⁻¹⁰. Additionally, several elements of the molecular pathways that trigger inflammation play a role in embryonic and postembryonic development¹¹. Immune and non-immune cells possess pattern recognition receptors (PRRs), which are generally activated to initiate inflammation¹². Endogenous molecules known as damage-associated molecular patterns (DAMPs) can activate pattern recognition receptors (PRRs) alongside microbial components linked to infection, the so-called pathogen-associated molecular patterns (PAMPs)¹². DAMPs generally cannot activate PRRs signaling in normal physiological conditions because they have restricted access to the subcellular regions containing PRRs¹³. However, during cellular stress or death, alterations in the permeability of cellular compartments enable DAMPs to engage PRRs, initiating inflammatory responses¹³.

Several lines of evidence suggest the involvement of mitochondria in the regulation of inflammatory pathways. Firstly, a variety of mitochondrial and bacterial proteins exhibit numerous similarities¹⁴. Se-

condly, mitochondrial genome, circular and lacking histone association, is closely related with bacterial genomes¹⁵. Mitochondria possess two membranes that help separate mitochondrial DAMPs (mtDAMPs) from specific PRRs: the inner mitochondrial membrane (IMM) and the outer mitochondrial membrane (OMM)¹⁵. Finally, both necrotic and apoptotic regulated cell death (RCD) are primarily governed by irreversible mitochondrial permeabilization¹⁶. When adaptation to cellular stress is unsuccessful, mitochondria serve as a distinct platform for inflammation, PRRs signaling, and DAMPs redistribution, which is associated with the initiation of regulated cell death (RCD)¹⁶. After damage, mitochondria release their inner components including mtDNA into the cytosol eliciting innate immune cascades¹⁷. The nucleic acid or its components are detected into the cytosol by the DNA sensor cyclic guanosine monophosphate-adenosine monophosphate (cGAMP) synthase (cGAS), which triggers a potent type I-Interferon (type I-IFN) response, through the stimulator of the interferon genes protein (STING). This, in turn, promotes the expression of interferon-stimulated genes (ISGs)¹⁸. MtDNA is also able to activate the inflammasome pathway. Moreover, oxidative stress with production of reactive oxygen species (ROS) has been found to regulate both positively and negatively the IFN response. Aim of this review is to briefly summarize the existing evidence and the molecular bases of mitochondria control on inflammations and the relevance for human diseases.

MATERIALS AND METHODS

This review was created investigating PUBMED databases using the following terms: mitochondria AND inflammation OR mitochondria AND apoptosis OR mitochondria AND caspases OR mitochondria AND inflammasome OR mitochondria and autophagy. A total of 1313 papers were selected. The resulting list of publications was disposed of all articles without information relevant to the outcomes of interest by screening of abstracts. In total, 115 publications were included in the qualitative data analysis.

cGAS-STING SIGNALING PATHWAY

Among the mitochondrial DAMPs, mtDNA leaked into the cytosol can function as endogenous ligand for cGAS and induce cGAS-STING signaling-mediated inflammation¹⁸. Mitochondrial RNA species in cytosol can lead to IFN induction as well, through the activation of the mitochondrial antiviral-signaling protein (MAVS): therefore, outside the mitochondrion, nucleic acids can be the cause of various inflammation-related diseases¹⁹. MtDNA enters the cytosol due to mitochondrial outer membrane permeabilization (MOMP) or other mitochondrial dysfunctions^{20,21}. Apoptotic caspases, however, significantly inhibit this process²²⁻²⁴ (Figure 1, panel A).

MtDNA, naked double-strand (ds) DNA, and dsDNA associated with proteins that induce specific curvature – such as high mobility group box 1 (HMGB1) and TFAM, a mitochondrial transcription factor – are potent activators of cGAS: in contrast, histone-bound nuclear dsDNA exhibits weak activation of cGAS^{25,26}. These findings indicate a system that prevents unnecessary activation of cGAS under normal conditions while remaining able to start inflammatory reactions in critical situations^{27,28}. Intracellular viral infections frequently lead to mitochondrial dysfunction and/or MOMP, ultimately resulting in the release of mtDNA, which is particularly relevant in the context of pathogen virulence²⁹⁻³³. Two proteins, BAX1 and BAK1, are usually responsible for triggering the release of mtDNA during MOMP, leading to a loss of soluble electron transport chain components like cytochrome c^{34,35}. This affects mitochondrial respiration and hampers the maintaining of metabolic balance across the IMM³⁶. In this context, the pores formed by BAX and BAK1 in the OMM cause the expulsion of the IMM into the cytosol, resulting in its degradation and the release of mtDNA^{34,35}. A considerable amount of mtDNA that exits mitochondria seems to remain associated with the permeabilized organelles rather than circulating freely in the cytoplasm³⁴. Recent research indicates that the relative levels of BAK1 and BAX significantly regulate the rate of mtDNA release during MOMP^{36,37}. A variety of physiological and pathological contexts have documented “minority MOMP,” in which only a few mitochondria of the cell experience MOMP and there is no involvement of RCD^{38,39}. The activation of DNA fragmentation factor subunit- β (DFFB)³⁸ induces DNA damage, while mtDAMPs^{40,41} facilitate inflammatory responses. Additionally, mitochondrial fusion resulting from BCL-2 redistribution⁴² actively inhibits this type of MOMP and this may additionally stimulate inflammatory pathways. Recent reports indicate that mtDNA release may occur independently of BAK1/BAX, for example through execution of large macropores at the mitochondrial membrane by voltage-dependent anion channel (VDAC) oligomers^{43,44} (Figure 1, panel B).

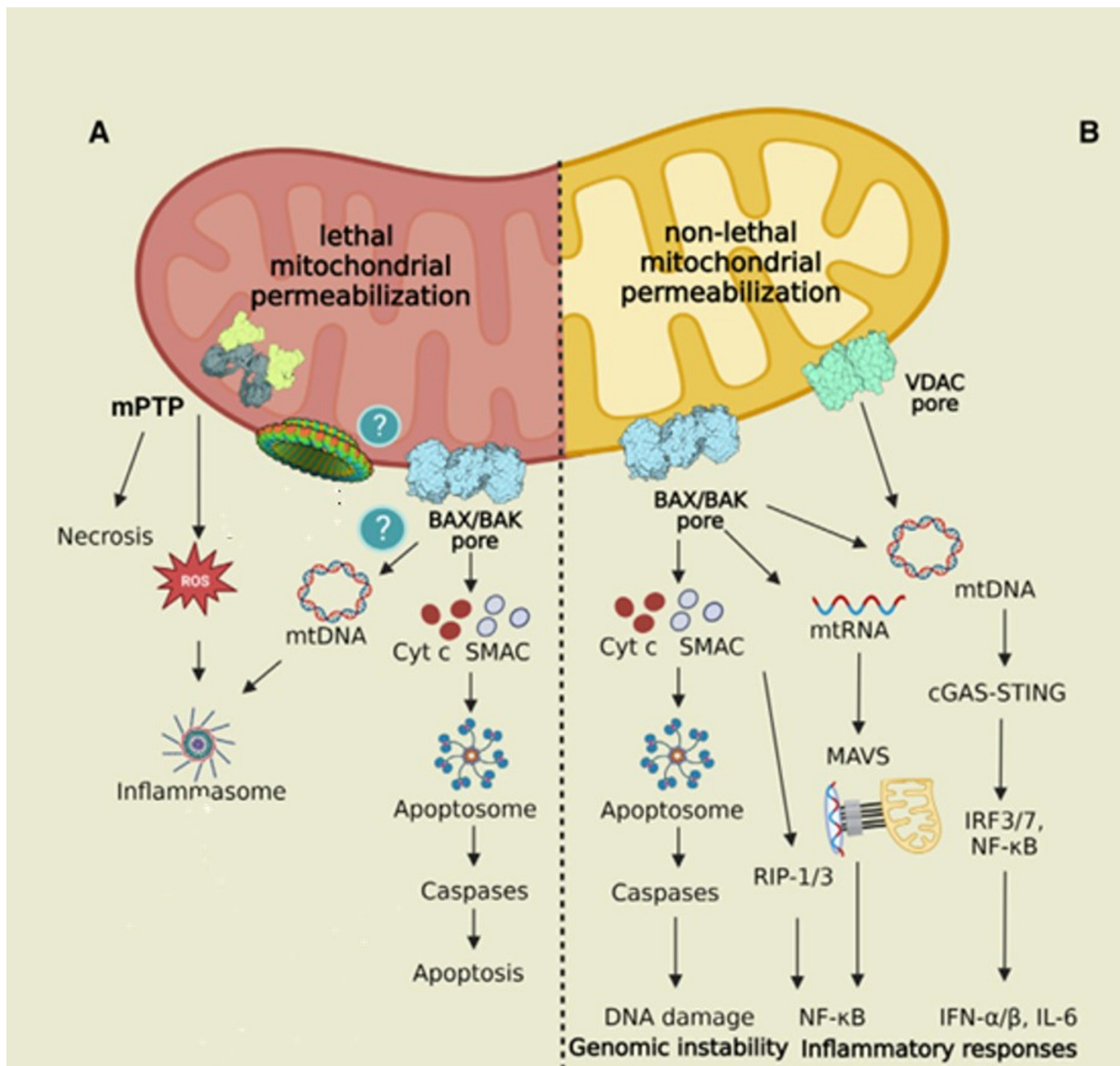


Figure 1. Mitochondrial permeabilization in cell death and inflammation.

When mitochondrial pores open, mitochondrial contents enter the cytosol, which can cause cell dismissal (A) or non-lethal inflammatory signaling (B). BAX and BAK help generate persistent protein-lipid holes at mitochondria during apoptosis, releasing apoptogenic substances.

Caspase activation, along with mtDNA, is involved in the cGAS/STING pathway and inflammasome activation. The release of cytochrome c from mitochondria through a mechanism that remains inadequately characterized, potentially establishing a positive feedback loop that enhances apoptosome activation and the caspase cascade. mPTP disrupts electron transport, leading to increased reactive oxygen species (ROS) production, ATP depletion, and subsequent necrotic cell death. In the context of non-lethal mitochondrial permeabilization, mitochondrial content resulting from BAX/BAK-mediated minority mitochondrial outer membrane permeabilization (MOMP) can initiate various pathways, including (1) prooncogenic DNA damage through cytochrome c and sublethal caspase activation; (2) activation of the NF- κ B pathway and maturation of IL-1 β , an inflammatory response mediated by released SMAC; (3) release of mtRNA, which can activate MAVS on the mitochondrial surface, subsequently activating MDA5, leading to TBK1 activation and inflammation; and (4) release of mtDNA in the absence of caspase activation, resulting in robust STING pathway activation for cytokine production and inflammation.

This is particularly true for mild mitochondrial stress, unable to cause MOMP and RCD. The notion that mitochondrial permeability transition pore (MPT) contributes to mtDNA leakage is supported by evidence indicating that various VDAC isoforms modulate MPT-induced regulated necrosis⁴⁵. DsDNA can diffuse through pores of at least 3 nm in diameter⁴⁶ while MPT generates pores ranging from 1.5 to 3

nm⁴⁷. The presence of 1 to 9 open MPT complexes per mitochondrion suggests that MPT functions efficiently. Conversely, the estimated count of BAX-BAK1 oligomers involved in MOMP exceeds 20⁴⁸. Both MPT and MOMP may, therefore, contribute to mtDNA release. In conclusion, the activation of cGAS/STING1 can elicit strong inflammatory responses triggered by mtDNA, especially when the activation of apoptotic caspases is restricted⁴⁹.

INFLAMMASOME SIGNALING

Inflammasomes, which are supramolecular complexes that activate caspases (CASP) 1, 4, and 5, can also be stimulated by cytoplasmic mtDNA, a potent cGAS agonist⁵⁰. Various chemical patterns associated with microorganisms consistently activate the inflammasome, particularly through NLRP3 sensing component⁵¹. MtDNA released during mitochondrial dysfunction is recognized as a key activator of the NLRP3 inflammasome, mainly through ROS-dependent mechanisms⁵¹. For optimal NLRP3 inflammatory signaling, traditional activators such as lipopolysaccharides (LPS) and ATP need the neo synthesis of mtDNA⁵². Experimental methods that reduce mtDNA also impact oxidative phosphorylation by diminishing the levels of specific electron transport chain components⁵³. This indicates that the inhibition of NLRP3 signaling following mtDNA depletion may be occasionally attributed to intracellular ATP deficiency, or at a minimum, may worsen it. Recent studies have shown that the activation of BAX and BAK1 enhances the degradation of the inhibitor of apoptosis protein (IAP), subsequently promoting CASP8-dependent NLRP3 inflammasome activation^{54,55}. Additionally, they initiate a supramolecular complex known as the ripoptosome, which operates independently of NLRP3 and results in the maturation of IL-1 β ⁵⁵.

In summary, mitochondrial ROS and mtDNA serve as essential DAMPs for inflammasome activation, generating a signal cascade able to regulate the molecular mechanisms of RCD.

ADDITIONAL PRO-INFLAMMATORY MOLECULES

Other cellular PRRs include Toll-like receptor 9 (TLR9) and the advanced glycosylation end product-specific receptor (AGER, or RAGE)^{56,57}. Both free and protein-bound mtDNA effectively activate these receptors. Unbound mtDNA acts primarily as an agonist for TLR9, due to its close resemblance to bacterial DNA (the typical TLR9 activator) and the low methylation of CpG islands in the mitochondrial genome^{58,59}. When mtDNA is associated with HMGB1 or TFAM, it exhibits immunostimulatory properties upon interacting with TLR9 or AGER⁶⁰. In response to various stressors, including the onset of inflammation, proteins are translocated from the nucleus to the cytoplasm⁶¹. Recombinant TFAM has been found to enhance cytokine release from primary microglial cells and cultured human monocytes. To activate these pathways, mtDNA must be released into the extracellular space, whether in a protein-bound or unbound form. In lasmacytoid dendritic cells, the activation of endosomal TLR9 have been shown to respond to the accumulation of cytoplasmic mtDNA evocated by slight mitochondrial dysfunction⁶¹.

Four additional mitochondrial components – cytochrome c, cardiolipin, N-formyl peptides, and SMAC – have the potential to trigger inflammatory responses. In cultured human microglial cell models, extracellular cytochrome c demonstrates immunostimulatory effects that are dependent on TLR4⁶². It has been suggested that recombinant cytochrome c may induce arthritis in mice through mechanisms involving neutrophils and monocytes⁶³. Also, ATP⁶⁴ and haem⁶⁵, produced by mitochondria, have been associated with various immunomodulatory effects when released extracellularly, including the activation of endothelial cells and microglia, as well as the release of IL-1 β by macrophages⁶⁶. These processes are mediated by NLRP3-dependent CASP1 activation, alongside NLRP3-independent activation of CASP4 and CASP5, in conjunction with regulated cell death (RCD)⁶⁷. Haem functions as an agonist for TLR4 and AGER⁶⁵.

Cardiolipin is generally found in the mitochondrial matrix, while N-formyl peptides are in the IMM. Structural disruption caused by late-stage RCD results in cellular fragments that retain mitochondria. These fragments persist in degrading within the extracellular environment until they are internalized by specialized phagocytes⁶⁸. Extracellular cardiolipin interacts with specific T cells, causing expression of the MHC class I-like molecule CD1d on antigen-presenting cells^{69,70}. When released extracellular due to end-stage RCD, N-formyl peptides activate neutrophils by binding to formyl peptide receptor 1⁵⁶. SMAC (diablo IAP-binding mitochondrial protein) plays a role in triggering antitumor immune responses and can directly alter T cell immunological responses⁷¹.

REGULATION OF EXCESSIVE mtDAMP SIGNALING

Regulation of mtDAMP signaling is critical due to the involvement of MOMP in cellular differentiation, embryonic and postembryonic development, tissue homeostasis²⁸. Consequently, multiple mechanisms have evolved to mitigate unwarranted inflammation triggered by mitochondria.

Apoptosis

During apoptosis, extensive MOMP leads to the formation of a cytosolic supramolecular platform that includes CASP9. CASP9 in turn activates CASP3, CASP6, and CASP7, playing a relevant role in regulating the kinetic of RCD and immunological manifestations^{19,72}.

Additionally, caspases trigger the externalization of phosphatidylserine on the surfaces of dying cells, which stimulate phagocytosis and the clearance of these cells^{73,74}. Without an active phagocytic system and with inactive caspases, the shift from MOM to cell death is delayed⁷⁵. This postponement may create an extended timeframe for the production and release of pro-inflammatory factors following MOMP⁷⁵.

Autophagy

The sublethal MOMP induces mitophagy, facilitating the clearance of permeabilized or dysfunctional mitochondria via lysosomes^{76,77}. This process diminishes the availability of mitochondrial components, such as mtDNA and ROS for PRRs signaling or release into the extracellular environment during RCD. Mitophagy is able to either completely or partially suppress the cGAS signals generated by MOMP⁷⁸. Increased cytosolic mtDAMP availability is frequently associated with genetic or pharmacological methods that suppress autophagy or diminish lysosomal degradation, mediated by enhanced signaling through TLR9, cGAS, and the inflammasome⁷⁹. Experimental methods aimed at specifically inhibiting mitophagy, rather than autophagy broadly, have yielded comparable results. Active inflammasome signaling has been shown to trigger an NF- κ B-dependent response that facilitates the autophagic removal of inflammasomes and the mitophagic removal of permeabilized mitochondria, likely serving as components of an adaptive pathway aimed at restoring inflammatory and cellular homeostasis⁸⁰. Activation of the effectors of STING1 cascade is reported to enhance mitophagy through a comparable mechanism, particularly in the initial stages^{81,82}. The key mitophagy gene PRKN has been shown to facilitate the ubiquitylation-dependent deactivation of BAK1, thereby contributing to the restoration of cellular homeostasis during sublethal MOMP^{83,84}. Mitophagy inactivation occurs alongside significant inflammatory responses resulting from irreversible mitochondrial dysfunction, partially due to CASP1-dependent cleavage of PRKN triggered by intense inflammasome activity⁸⁵. The packaging of mtDAMPs into mitochondria-derived vesicles (MDVs), released during mitochondrial quality control, may be inhibited by PRKN-dependent mitophagy, preventing potential inflammatory responses in adjacent cells⁸⁶. These processes necessitate the suppression of mitophagy to proceed unregulated, potentially involving a feedforward loop that links significant mitochondrial dysfunction to substantial inflammasome activation and CASP1-dependent PRKN degradation⁸⁷. During immunogenic cell death, autophagy is essential for effective ATP secretion and subsequent immunostimulation. This is primarily because effective autophagic responses can sustain intracellular ATP levels instead of directly affecting mitochondria. Apoptosis and autophagy represent molecular systems that have facilitated the retention of potentially harmful inflammatory signals during the co-evolution of mitochondria and host cells. Eukaryotic cells, however, manage inflammatory responses initiated by mitochondria through alternative mechanisms, such as the apparent mutual inhibition of cGAS and inflammasomes^{88,89}.

EXCESSIVE mtDAMP SIGNALING IN HUMAN DISEASES

Patients with systemic lupus erythematosus (SLE) exhibited increased blood levels of oxidized mtDNA with activation of type I interferon responses⁹⁰. A greater risk of Crohn's disease is associated with pathogenic variants in *ATG16L1* gene, encoding a vital component of the autophagy machinery. This aligns with the role of ATG16L1 protein in preventing inflammation and the build-up of damaged mitochondria, which contributes to the function of Paneth cells⁹¹. Individuals diagnosed with Crohn's disease

exhibit dysfunction in Paneth cells within their ileal tissue⁹², as confirmed in mice models^{93,94}. Patients diagnosed with silicosis or interstitial lung disease exhibit elevated levels of CXCL10, a chemokine stimulated by type I interferon signaling⁹⁵. Additionally, there are increased levels of STING1 and phosphorylation of its associated effectors, TBK1 and IRF3⁹⁵. Chronic obstructive pulmonary disease is associated with elevated levels of circulating mtDNA, inflammatory cytokines and ROS overproduction⁹⁶. Patients with acute kidney injury show hyperactivation of STING1 in their renal tubules⁹⁷. In chronic kidney disease, lower levels of TFAM expression correlate with CGAS and STING1 overexpression⁹⁸. The co-deletion of *Pink1* and *Prkn* disrupts mitophagy, worsening acute renal injury induced by ischemia in mice⁹⁹. Missense mutations in *PINK1* and *PRKN* cause familial Parkinson's disease and are associated with elevated blood levels of inflammatory cytokines and mtDNA¹⁰⁰. Microglial cells that ingest mtDNA from deceased neurons trigger inflammatory responses associated with Alzheimer's disease¹⁰⁰. Furthermore, post-mortem cerebral tissues from patients with Alzheimer's disease show signs of mitophagy suppression and accumulation of damaged mitochondria. Stimulation of mitophagy has been shown to mitigate the progression of the disease in a rat model of Alzheimer's disease¹⁰¹. These findings strongly suggest a potential link between mitochondrial dysfunction and various inflammatory diseases.

For primary mitochondrial diseases, mutations in *PNPT1* gene, involved in mitochondrial double stranded RNA suppression, causes a neurodegenerative disorder characterized by the accumulation of these RNA species in patients' fibroblasts, resulting in an enhanced type I-IFN response¹⁰². These species subsequently activate the RLR melanoma differentiation-associated protein 5 (MDA5; also referred to as IFIH1) through BAX-BAK1-mediated MOMP¹⁰².

Recently, defects in *ATAD3A*, a mitochondrial protein involved in mtDNA maintenance, and dysfunction in *TOP1MT*, a regulator of mtDNA, have been reported to produce an enhanced interferon response^{103,104}.

INADEQUATE mtDAMP SIGNALING

Dysfunctional mtDAMP signaling affects the pathophysiology of viral infections and cancer. Inhibition of MOMP or the inflammatory responses induced by MOMP leads to an increase in viral persistence and tumor growth¹⁰⁵. Hyperactivation of autophagy in cancer cells or the production of viral proteins can inhibit several components of cGAS/STING pathway¹⁰⁶. For example, ICP27, a component of HSV-1 pathogenicity, inhibits STING1 and TBK¹⁰⁵. The ability of the latter to activate NF- κ B, rather than IRF3, is essential for the regulation of infection in mice¹⁰⁷. Additionally, the X protein produced by Hepatitis B virus causes degradation of cellular cGAS¹⁰⁸. Under these conditions, the quantitative measurement of mtDAMP signaling's role in promoting pathogen control through the induction of inflammatory responses remains unassessed. Autophagic anomalies resulting in decreased ATP secretion during immunogenic cell death promote malignant transformation, a process closely regulated by immunosurveillance, in various immunocompetent mouse models of early oncogenesis¹⁰⁹. The observed anomalies are associated with myeloid cells dysfunction within the tumor microenvironment, which further facilitates tumoral cells resistance to various chemotherapeutic agents that induce antitumor immunity, such as oxaliplatin and anthracyclines¹¹⁰.

THERAPEUTIC PROSPECTIVE

The overall incidence of primary mitochondrial disease is uncertain but has been estimated to be as frequent as 1 in 5,000 births, causing debilitating, often fatal, diseases and placing a significant financial burden on healthcare and social support services. There is currently no cure for these diseases. Moreover, mitochondrial dysfunctions are increasingly recognized to have important roles in abnormal innate immune responses, and research on this field has expanded dramatically in the last years. Despite an increasing number of studies has highlighted the relationship between secondary mitochondrial dysfunction and inflammation in different pathological conditions (Alzheimer, Multiple Sclerosis, Parkinson and cancer), whether inflammation suppresses or exacerbates disease pathology is still unclear¹¹¹. Primary inflammatory disorders such as SLE are usually treated with drugs targeting PRRs or cGAS-STING cascade (for example STING1 agonists), or blocking the effector phase of inflammation (cytokine-neutralizing drugs). However, as novel mitopathogenic mechanisms are being uncovered across several medical disciplines, an increasing knowledge of the link between mitochondria and innate immune response

and inflammation may also provide new opportunities for diagnosis, therapy, prevention in various domains of medicine. The potential application of mitochondrial-targeting medications for inflammation reduction has in fact been minimally explored. The limited availability of pharmacological treatments targeting mitochondrial functions, such as MOMP and MPT, may be attributed to the nascent stage of research in this field. Research is being conducted on BAX inhibitors as cytoprotective agents to prevent cardiovascular diseases^{112,113}. Pharmacological BAX inhibitors are expected to limit mitochondrial outer membrane permeabilization (MOMP) and consequently mitigate mitochondria-driven inflammatory responses^{112,113}. However, recent studies indicate that these inhibitors may accelerate MOMP-driven mtDNA release, particularly in BAK1-competent cancer cells, without substantially affecting the kinetics of caspase activation. This may offer an opportunity to initiate cGAS signaling before the caspase-dependent cleavage and subsequent inactivation of cGAS¹¹⁴. Cyclosporine A in humans, a medication targeting PPIF with significant MPT-inhibitory properties, is commonly utilized as an immunosuppressive agent for the treatment of autoimmune disorders and the prevention of transplant rejection. Cyclosporine A binds the PPIF-like cytosolic protein PPIA, which subsequently inhibits calcineurin to reduce lymphocyte activity¹¹⁵. However, part of the pharmacological effect of this drug may be related to MPT inhibition, preventing mtDNA leakage and inflammatory cascade.

CONCLUSIONS

In conclusion, while mitochondria are recognized as key regulators of inflammation, further research is necessary to address unresolved issues and overcome existing challenges, with the primary objective of modulating inflammatory responses in patients through the focus on mitochondrial processes.

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