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Review

# Mitochondrial Flux, Biogenesis & Autophagy in the Pathophysiology of Innate Immune System Dysfunction

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**Abstract:** Mitochondrial flux, the processes by which the mitochondrial compartment of the cell fuses, fissions and is degraded, underlies a complex spectrum of diseases. Pathological functioning of the innate immune system is underpinned by signalling pathways previously studied for their role reconfiguring cellular metabolic requirements. This review attempts to establish the physiologic state of mitochondrial flux across the cell, explain the process and regulation of mitochondrial biogenesis and autophagic degradation, before examining how disruption of these processes is intrinsic to a number of disease states. Particular attention is paid to how bioenergetic demands of the tissues are modulated in viral SARS-CoV, hepatitis B & C infection and asthma.

**Keywords:** Mitochondrial flux; mitophagy; autophagy; innate immunity; OXPHOS; metabolism; asthma; SARS-CoV-2

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## 1. Introduction

Mitochondria are the primary bioenergetic organelles of cellular metabolism and their function underlies much of the metabolic activity throughout the organism. While their roles in oxidative phosphorylation (OXPHOS), the tricarboxylic acid (TCA) cycle, electron transport chain (ETC), production of reactive oxygen species (ROS) and oxidative or age-related damage are most widely understood, they also hold diverse roles as constituent components of the innate immune system. This review first approaches the role of mitochondrial flux as a central feature of the physiologic mitochondrial compartment – the continuously fusing and fissioning mitochondrial component of the cell – before explaining mechanisms of mitochondrial biogenesis and autophagy. After detailing the regulatory mechanisms that control this process, these topics are explored in the context of specific diseases.

## 2. The physiologic Mitochondrion

### 2.1. Mitochondrial Flux is an Essential Feature of the Mitochondrial Compartment

The physiological state of the mitochondrial compartment of the cell is one of flux. Mitochondrial morphology is heterogeneous and depends on the phenotype and function of the tissue, ranging from dense reticular networks in cells with high OXPHOS requirements to more discrete, small, separated organelles in tissues dependent on anaerobic glycolysis (1,2). It is a dynamic process whereby mitochondria continuously undergo fusion and fission, the “right” configuration being controlled by cellular and extracellular factors, and it is essential to the normal function of the cell.

Fission protein 1 (Fis1) acting in conjunction with dynamin related peptide 1 (Drp1) are the primary fission regulating peptides of the outer membrane. While Fis1 is an outer membrane protein,

Drp1 is a cytosolic peptide recruited to the outer mitochondrial membrane (3,4). Excessive Drp1 activation has been implicated in autosomal recessive juvenile Parkinsonism, which results from failure of mitochondrial fission processes and impaired mitophagy (5,6). Fusion is controlled mainly by GTPases mitofusin 1 and 2 (Mfn1, Mfn2) in the outer membrane and optic atrophy protein 1 (Opa1, also known as Mgm1) in the inner membrane. Their dysfunction has been implicated in diseases such as dominant optic atrophy (7) and Charcot-Marie-Tooth 2A (8).

Morphologically, failure of fusion proteins results in fragmentation of the mitochondrial compartment and disorder of the cellular OXPHOS system (9–11). Cells requiring a highly energy-dense profile display a rich, closely spaced reticular mitochondrial network that provides a key highway for metabolite and waste transport while allowing continued traffic of mitochondrial proteins that are encoded by nuclear genomes (12). Mitochondrial flux is controlled by two distinct and opposing processes – mitochondrial biogenesis (mitogenesis) and autophagy of defective mitochondria (mitophagy).

## 2.2. Mitogenesis

Mitochondrial biogenesis is a complex process requiring extensive crosstalk between nuclear and mitochondrial apparatus. The mitochondrial genome consists of around 16.5 thousand base pairs. 13 peptides are transcribed from mitochondrial DNA (mtDNA) and produced within the mitochondria: 7 of the 45 ETC complex I components, 1 component of the 11 comprising ETC complex III, 3 of the 13 comprising ETC complex IV and 2 of the 18 required for ETC complex V. A further 22 tRNA and 2 mitochondrial ribosomal RNA genes are also present, without which mitochondrial protein transcription and translation could not take place (13). The several thousand other components required to produce functioning mitochondria are derived from nuclear-encoded proteins which must be transcribed, translated, processed, and transported into the mitochondria.

mtDNA is housed within protein nucleoids consisting of high mobility group (HMG) proteins, particularly mitochondrial transcription factor A (TFAM). These proteins assist in structural stability, replication and transcription and are essential to mitochondrial biogenesis (14,15). This is conducted by a mtDNA replication apparatus which, while described in the literature, is nevertheless poorly understood. mtDNA polymerase (Pol $\gamma$ ) is a nuclear encoded protein composed of two subunits, encoded by genes POLG (held at locus 15q25) and POLG2 (held at locus 17q24.1). The process of mtDNA transcription is highly conserved in eukaryotes and is upregulated when cellular OXPHOS demands are increased. Pol  $\gamma$  acts with Twinkle (the mtDNA helicase) and mitochondrial single stranded DNA binding protein (mtSSB) to initiate mtDNA replication (16,17). Failure of Pol  $\gamma$  results in a variety of monogenic hereditary and sporadic disorders including microcerebrohepatopathy, Alpers-Huttenlocher syndrome (a triad of neurodevelopmental regression, seizures and liver failure) and progressive external ophthalmoplegia. Characteristic molecular features of these diseases include multiple mtDNA deletions, cytochrome c deficiency within muscle fibres and gross depletion of mtDNA throughout the body (18,19). Germline failure of mtSSB is lethal in utero while localised inactivation in myocardial tissue results in cardiomyopathy in murine models (17).

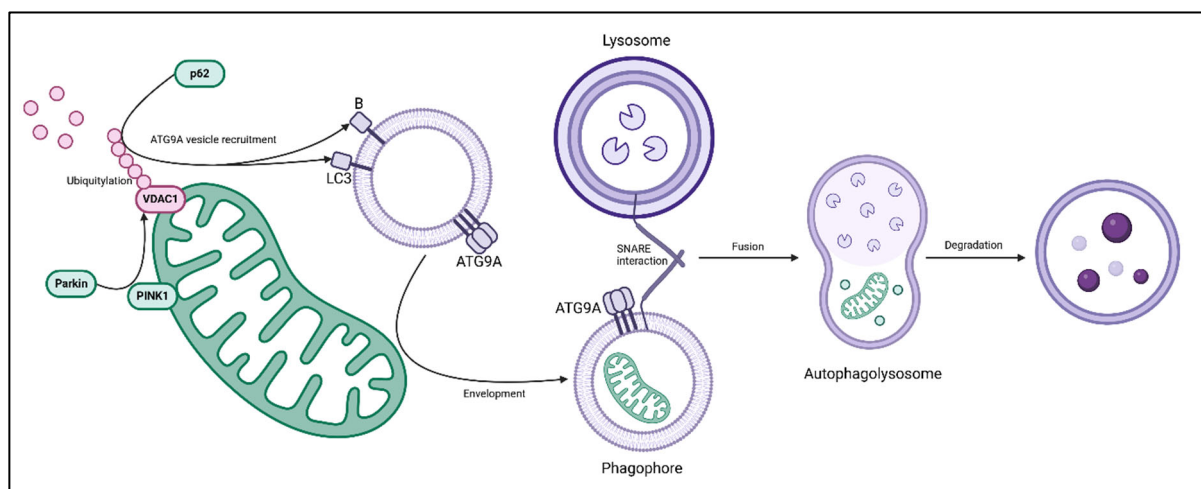
## 2.3. Mitophagy

Mitophagy is the autophagic process by which mitochondria are degraded and recycled into their component parts. When mitochondria malfunction, damage associated molecular patterns (DAMPs) such as mtDNA and ROS are produced. Recognised by a host of pattern recognition receptors (PRRs), defective mitochondria are then selectively sequestered for disposal via lysosomal degradation (20).

Phosphatase and tensin homolog (PTEN) induced kinase 1 (PINK1) – Parkin interaction constitutes the classic mitophagy pathway. PINK1 is a serine/threonine kinase containing mitochondrial targeting sequence, bearing mitochondrial membrane side and a cytoplasmic facing kinase (21), and it is activated by depolarisation of the mitochondrial membrane (22,23). Parkin (so named for its aetiologic role in the pathogenesis of several variants of autosomal recessive hereditary Parkinson disease (5,6)) is a cytosolic E3 ubiquitin ligase which locates to the mitochondrial

membrane when activated by PINK1. Activated Parkin chain-ubiquitylates N-terminally fused lysine residues on voltage dependent anion channel 1 (VDAC1) (21,22), along with Mfn1 and Mfn2 (21,24,25), resulting in the recruitment of autophagic adaptor protein p62 (also referred to as sequestosome-1 or SQSTM1). p62 is the link between the ubiquitylation pathway proteins PINK1-Parkin and the autophagy related (ATG) proteins subsequently responsible for vesicle interactions and lysosomal envelopment of the organelle. p62 interacts with ATG8 homologues LC3 and B of the phagophore vesicle complex (26), allowing the defective organelle to be enveloped by the expanding phagophore membrane. At this point, activation of ATG9a allows fusion of the phagophore with the lysosome via SNARE-SNARE protein interaction (27), resulting in the introduction of proteolytic enzymes and organelle degradation within the autolysosome (28), as described in Figure 1.

Parkin independent mitophagy is less well explored and appears to function via proteins involved in physiologic mitochondrial flux. Parkin knockout cells with defective mitochondria produce mitophagy by PINK1 interaction with Drp1, resulting in fracture of the outer mitochondrial membrane and chain-ubiquitylation of the inner membrane (29). In Drp1 and Opa1 knockout ("mitochondrial stasis") hepatocytes, p62 recruits cullin-RING scaffold protein associated ubiquitin ligases Keap1 and Rbx1, allowing an alternative PINK1-Parkin independent method of ubiquitylation (30). An alternative method has been demonstrated in hypoxic cells. BNip3 and Nix (members of the Bcl-2 pro-apoptotic protein family (31)) prevent hypoxia inducible factor 1 $\alpha$  (HIF-1 $\alpha$ ) stabilisation, resulting in the degradation of Mfn1, Mfn2 and translocase of outer membrane protein 20 (TOM20). This prevents fusion, continued use of damaged organelle segments and failure of mitochondrial membrane integrity (32). It remains to be seen whether Parkin independent mitophagy pathways occur concurrently to classic PINK1-Parkin autophagy or are truly independent of it and only occur when components are defective.



**Figure 1.** The PINK1-Parkin Pathway.

Phosphatase and tensin homolog induced kinase 1 (PINK1) is a mitochondrial membrane bound protein. On depolarisation of the mitochondrial membrane, PINK1 recruits cytoplasmic Parkin protein, an E3 ubiquitin ligase. When activated, Parkin chain-ubiquitylates lysine residues on voltage dependent anion channel 1 (VDAC1). This signals p62, which interacts with autophagy related protein 8 (ATG8) homologues LC3 and B, resulting in envelopment of the defective organelle within an ATG9a phagophore. SNARE-SNARE interaction with lysosomes causes phagophore-lysosomal fusion and results in the formation of the autophagolysosome, the contents of which are subsequently degraded. (Created in BioRender.com)

### 3. Regulation of Flux and Metabolism

#### 3.1. The PPAR-PGC-1 Axis

Nuclear transcription factors peroxisome proliferator-activated receptors (PPAR) hold a central role in determining the metabolic profile of cells and tissues. PPAR isoforms have heterogeneous expression throughout the organism, their different localisation allowing fine control of the metabolic needs of the tissue (33). Activated PPAR $\gamma$  and PPAR $\beta$  stimulate nuclear transcription of OXPHOS proteins and ETC subunits, along with stimulating mitochondrial transcription of mtDNA encoded genes (34). Nuclear stimulators of PPAR $\gamma$  include thyroid hormone T3 (35–37), prostaglandin J2 (33), long chain fatty acids (38) and thiazolidinedione pharmaceuticals such as rosiglitazone (39). Within the nucleus PPARs exist as a heterodimer bound to retinoid X receptor (RXR) which, on ligand activation, binds PPAR-responsive regulatory elements within the genome activating transcription (40). With regards to PPAR $\gamma$  (and to a certain extent PPAR $\alpha$  (41)), this includes fatty acid binding protein 2 (aP2), acyl-CoA binding protein (ACBP), lipoprotein lipase (LPL), fatty acid translocase/transport protein (FAT/FATP also known as cluster of differentiation 36 or CD36), acyl-CoA synthetase (ACS), glycerol kinase (GyK), insulin receptor substates 1 and 2 (IRS1 and IRS2) and glucose transporter 4 (Glut4). The net result of this is increased mobilisation of fats and fatty acids, their import to the cell, processing into usable metabolites and eventually, oxidative phosphorylation (33). Acting via a similar mechanism, PPAR $\delta$  acts in skeletal muscle to upregulate cytochrome c, uncoupling proteins 2 and 3 (UCP2 and UCP3) (42) along with TCA cycle proteins succinate dehydrogenase and citrate synthase, resulting in a shift towards muscle fibres with higher OXPHOS potential (43).

PPAR isoforms act with PPAR $\gamma$  coactivator 1 (PGC-1) to provide upregulation of diverse mitochondrial functions. In brown fat tissue, this is most prominently the upregulation of uncoupling protein 1 (UCP1), essential for thermogenesis (44). While PPARs act mainly to induce transcription of proteins responsible for lipid metabolism, the TCA cycle and OXPHOS components, PGC-1 is the primary nuclear stimulator of mitogenesis, ultimately marshalling over 1100 nuclear genes via several downstream transcription factors (45–47). Well studied targets of the PPAR $\gamma$ -PGC1 axis include nuclear respiratory factor 2 (NRF2), which activates TFAM to upregulate mtDNA replication and transcription (48), and UCP2 and paraoxonase-2 (PON2), which allow enhanced action to mitigate the production of reactive oxygen species produced within mitochondria (47).

#### 3.2. The Role of AMPK, Sirtuins and mTOR

The major link element between lipid metabolism, TCA proteins, mitogenesis and mitophagy are NAD-dependent deacylase sirtuin proteins, themselves activated by AMP-protein kinase (AMPK) and mammalian target of rapamycin (mTOR). These pathways are highly conserved from single celled eukaryotes to mammals and have a complex role in the integration of nutrient sensing, metabolic demands and cell stress or damage, and their outcomes converge on mitophagy, mitogenesis and cell proliferative processes.

AMPK is activated when the AMP/ATP ratio increases within in the cell, indicating low balance of ready-use energy. AMPK is a major stimulator of mitochondrial flux, mitophagy and mitogenesis and it is through this mechanism that cells with low energy balance, increased ROS and stress act to repair and replace defective components of the mitochondrial compartment (49).

Sirtuins are responsible for deacylation of histone proteins and are heavily linked to ageing processes. Of the seven sirtuin homologues known in mammalian cells, Sirt2 has been best studied for its role in longevity and is primarily localised within the nucleolus where it promotes genome stability in mitotically active cells (50,51). Genome sequencing of Sirt3, 4 and 5 appear to show mitochondrial targeting signals and confocal laser scanning microscopy of proteins tagged with MitoTracker red show localisation within the mitochondrial compartment (52,53). Sirt3 translocates to the mitochondrial compartment from the nucleus at times of cellular stress, such as when DNA damage occurs (54). Deacylation targets of Sirt1, Sirt3 and Sirt5 include PGC-1 $\alpha$  in the nucleus (55) and BNip3 (56), Opa1(57) and Parkin (58) in the mitochondria, while AMPK also activates PINK1 and

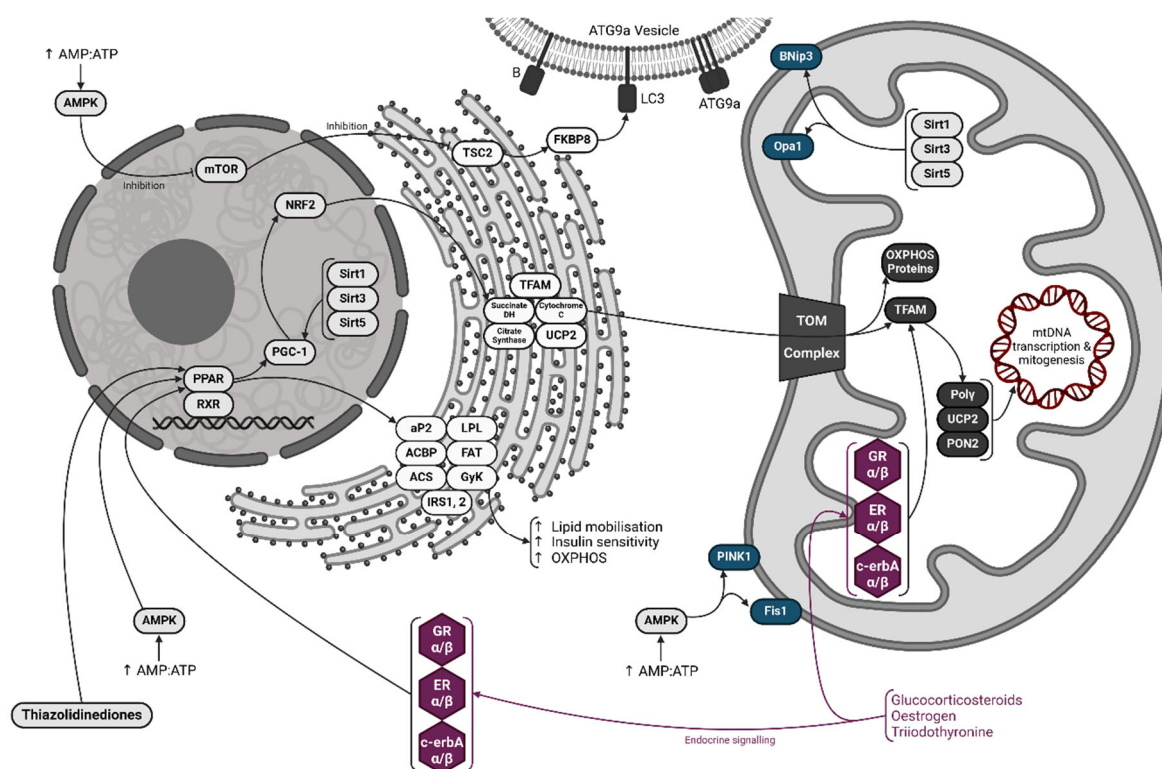
Fis1 (59). PINK1 and the PINK1-Parkin pathway appear to play an important role in mediating mitochondrial flux – overexpression of PINK1 results in increased Drp1 activation and fragmentation of mitochondrial compartment while underexpression of PINK1 results in excessive fusion (60).

Mammalian target of rapamycin (mTOR) is a serine/threonine kinase complex which in its active state stimulates ribosome biogenesis, protein synthesis and metabolism via the IRS-PI3K pathway, while inhibiting mitophagy. It is a major regulator of cellular growth and anabolism and, via interaction with a number of signalling pathways, responds to insulin stimulation and cellular energy levels (61). mTOR signalling has been well documented owing to interaction with apoptotic apparatus via the PI3K/Akt/mTOR signalling cascade (62). With regards to mitophagy, mTOR acts via the phosphorylation of tuberous sclerosis complex 2 (TSC2), maintained within endoplasmic reticular linkages to mitochondria, to negatively interact with FK506 binding protein 8 (FKBP8), which when active initiates LC3 vesicle-dependent autophagy (63). In nutrient starvation, AMPK inactivates mTOR, allowing unopposed FKBP8 action, upregulating mitophagy (64). Previously assumed to be separate processes, significant crosstalk exists between the PI3k/Akt/mTOR cascade and the unfolded protein response (UPR), which mediates metabolic and apoptotic response to endoplasmic reticular stress. Collectively, mTOR and the UPR provide the integration pathways to balance organismal metabolic requirements with nutrient availability. Unfavourable growth conditions or hypoxia produce UPR activation and mTOR inactivation, upregulating mitophagy, reducing the OXPHOS requirements of the cell, and balancing the metabolic requirements of the tissue with the nutrients available (65).

### 3.3. Direct Action Via Mitochondrial Receptors

Direct regulatory action on mitochondria is established in the literature, although poorly understood, and there remains much scope for future research. In macrophages, glucocorticoid action causes increased polarisation of the mitochondrial membrane, import of TCA cycle metabolites and upregulation of mitochondrial biogenesis (66). Steroid and thyroid hormone receptors are found within the mitochondrial matrix, all nuclear encoded yet allowing for direct endocrine action within the mitochondria. Two major mitochondrial isoforms of the glucocorticoid receptor (GR), GR $\alpha$  and GR $\beta$  have been detected, two isoforms of the oestrogen receptor (ER), ER $\alpha$  and ER $\beta$  along with two isoforms of the thyroid receptor c-erbA $\alpha$  and c-erbA $\beta$  (67).

New studies indicate that on ligand binding, cytoplasmic glucocorticoid receptors interact with pyruvate dehydrogenase complex proteins and translocate to within the mitochondrial compartment of the cell, where they upregulate TCA cycle activity (66). It was noted in 1977 that isolated rat mitochondria respond to thyroid hormone T3 stimulation with increased OXPHOS activity (68) and the presence of matrix receptors for these hormones explains this finding. In addition to acting on nuclear transcription factors, T3 and steroid hormone administration results in increased mitochondrial genome expression by acting on c-erbA receptors to activate TFAM, increasing transcription of mitochondrial protein subunits (35).



**Figure 2.** Control of Flux, Mitophagy, Mitogenesis & Metabolism.

Peroxisome proliferator-activated receptors (PPARs) are nuclear transcription factors responsible for control of lipid metabolism, oxidative phosphorylation (OXPHOS) and mitochondrial biogenesis. On ligand binding, PPARs associate with the retinoic acid X receptor (RXR) and bind PPAR-associated regulatory elements of the genome. This stimulates the production of proteins such as fatty acid binding protein 2 (aP2), acyl-CoA binding protein (ACBP), lipoprotein lipase (LPL), fatty acid translocase/transport protein (FAT/FATP also known as cluster of differentiation 36 or CD36), acyl-CoA synthetase (ACS), glycerol kinase (GyK), insulin receptor substates 1 and 2 (IRS1 and IRS2). The net result of this is increased lipid mobilisation, insulin sensitivity and OXPHOS.

PPARs also control PPAR coactivator 1 (PGC-1) homologues, which are the master regulators of mitochondrial biogenesis. Acting via nuclear respiratory factor 2 (NRF2), they upregulate production of key OXPHOS proteins including succinate dehydrogenase (succinate DH), cytochrome c, citrate synthase and uncoupling protein 2 (UCP2). These proteins are conveyed to the mitochondrial compartment through dense networks of endoplasmic reticulum before entering the organelle through translocase of outer membrane (TOM) complexes. PGC-1 homologues also stimulate production of mitochondrial transcription factor A (TFAM), which upregulates mtDNA polymerase ( $\text{Poly}\gamma$ ). Along with UCP2 and paraoxonase-2 (PON2),  $\text{Poly}\gamma$  increases replication and transcription of mitochondrial DNA (mtDNA), production of mtDNA encoded OXPHOS proteins and mitogenesis.

Adenosine monophosphate kinase (AMPK) is activated when the AMP:ATP ratio within the cell increases – a key indicator of low energy balance. AMPK is a modulator of lipid metabolism, mitochondrial flux and mitogenesis. Acting on PPARs, it increases lipid mobilisation, insulin sensitivity and OXPHOS; while downstream it also increases mtDNA replication and transcription via the PPAR-PGC-1 axis. Active AMPK also inhibits mammalian target of rapamycin (mTOR). In its resting state, mTOR constitutively inhibits tuberous sclerosis protein 2 (TSC2). When mTOR is inactivated by AMPK, TSC2 is free to interact with FK506 binding protein 8 (FKBP8), which is an activator of microtubule-associated protein 1A/1B-light Chain 3 (LC3), a membrane bound protein present in autophagy related protein 9a (ATG9a) vesicles, required for phagophore formation. Active AMPK also stimulates phosphatase and tensin homolog induced kinase 1 (PINK1), a key component of PINK1-Parkin mitophagy, and fission protein 1 (Fis1), required for proper fission during

mitochondrial flux. Increased flux and mitophagy augments increased mitogenesis, lipid mobilisation and OXPHOS – the mitochondrial component of the cell is renewed, balancing the metabolic capabilities with organismal requirements.

Sirtuin (Sirt) proteins are linked to ageing and longevity and in their core role deacylate histone proteins, allowing genes to be transcribed. In the nucleus Sirt1, 3 and 5 activate PGC-1 homologues, leading to increased mitogenesis. Within the mitochondria, their secondary role includes upregulating flux proteins optic atrophy 1 protein (Opa1) and Bcl-2 Interacting Protein 3 (BNip3).

Other than via AMPK or Sirt proteins, the systems can be activated by endocrine signalling by glucocorticosteroids, oestrogen or triiodothyronine (T3). Cytosolic glucocorticoid receptors (GR $\alpha$  and  $\beta$ ), oestrogen receptors (ER $\alpha$  and  $\beta$ ) and T3 receptors (c-erbA $\alpha$  and  $\beta$ ) converge on PPAR signalling. Within the mitochondrion, they activate TFAM, allowing dual nuclear-mitochondrial activation and signalling for metabolic requirements. Thiazolidinediones, which are novel anti-diabetic therapies, also target the PPAR-PGC-1 axis, explaining their efficacy in weight loss and altering metabolic function. (Created in BioRender.com)

#### 4. Mitochondria – A Component of the Innate Immune System

##### 4.1. Inflammatory Cytokine Production

Mitochondrial flux and mitophagy play key roles in regulating inflammatory processes. Failure of the mitochondrial fusion-fission cycle results in depolarisation of the mitochondrial membrane, organelle swelling and the formation of “megamitochondria” (69–72). ROS induced damage and mtDNA are recognised as DAMPs, and their resultant leak into the cytoplasm and extracellular environment causes activation of inflammatory processes. The most important PRRs in mitochondrial contexts are Toll-like receptors (TLRs), particularly TLR9. TLR9 is responsive to mtDNA and expressed both intracellularly in membranous vesicles and extracellularly on macrophages (73). Of further note are retinoic acid inducible gene I (RIG-I), which binds non-cell double stranded DNA (dsDNA) (74), and melanoma differentiation associated protein 5 (MDA5), sensing non-cell RNA (75).

Secretion of pro-inflammatory IL-1 $\beta$  and IL-18 by macrophages is dependent on activation of the “inflammasome”, a cytoplasmic protein-complex responsible for cleavage and activation of caspase-1. “Canonical” inflammasomes consist of pro-caspase 1, an aspartate specific cysteine protease (ASC) adaptor protein and a PRR – in this context, nucleotide-binding oligomerisation domain-like receptors (NOD-like receptors or NLRs) (76). When the NLR is activated, pro-caspase 1 is converted to its active form, allowing enzymatic cleavage of pro-IL-1 $\beta$  and other cytokine progenitors to their active form (77). “Non-canonical” inflammasomes do not depend on NLRs and result in gasdermin D cleavage by caspase-11, allowing IL-1 $\beta$  secretion and pyroptosis (78,79).

Mitochondrial antiviral signalling protein (MAVS) plays a key role as an intermediate between nuclear transcription factors NF $\kappa$ B and interferon regulatory factors (IRFs) and the production of interferons during infection of the cell (74,75). In the resting state MAVS is bound to Mfn2 on the mitochondrial outer membrane. When the RIG-I and MDA5 complex responds to non-cell genetic material, they activate MAVS, which binds to TANK-binding kinase 1 (TBK1) and inhibitor of NF $\kappa$ B kinase  $\epsilon$  (IKK $\epsilon$ ), translocating to the nucleus and activating IRFs to upregulate transcription of interferons. The cyclic GMP-AMP synthase – stimulator of interferon genes (cGAS-STING) pathway is a similar mechanism that responds to the presence of dsDNA converging directly on TBK1 and IKK $\epsilon$  (80,81). TLR9 activation by mtDNA acts via adaptor protein MyD88 and a series of IKK adaptors to converge on NF $\kappa$ B, which when translocated to the nucleus upregulates transcription of pro-inflammatory cytokines TNF $\alpha$ , IL-1 and IL-6 (74).

While mitochondrial ROS have long been recognised as a potential trigger of NLRP inflammasomes, a constitutive level of ROS is also an essential component of the function of the innate immune system (73). Transcription of MAVS is negatively regulated by ROS levels, and constitutive production of ROS by NADPH oxidase enzymes appears to be required for RIG-I mediated activation of IRF3 and production of proinflammatory cytokines (82).



#### 4.2. SARS-CoV-2 Infection and Post-Acute Sequelae

The role of canonical and non-canonical inflammasome activation under viral infection is now well understood, and its core role in SARS-Cov-2 inflammation provides greater understanding of the pathogenesis of COVID-19 while also suggesting novel treatment options. SARS-CoV-2 open reading frames (ORFs) are translated from positive-strand RNA and interfere with autophagic processes, disrupting Parkin ubiquitylation and autophagolysosome fusion. This resultant metabolic derangement, along with suppression of the interferon production RIG-I/MAVS and cGAS-STING pathways, causes failure of innate immune antiviral processes (83–86). Of deeper interest are complex interactions between viral entities and mitochondrial structural and transport proteins. RNA-GPS studies early in the COVID-19 pandemic predicted interactions between viral polypeptides and subunits of ETC complexes I, III and IV (87,88). Fluorescence microscopy located SARS-CoV-2 genetic material within the mitochondrial matrix while indicating a consequent failure of mitophagy (89). Viral accessory protein ORF3c has been demonstrated to utilise TOM20 to locate itself within the mitochondrial compartment of the cell where it too disrupts mitochondrial flux (85). Pathological studies have also found that viral genetic material and polypeptide components of SARS-CoV-2 infection persist within post-mortem specimens (90,91), at times for years (92). The implication is that elements of the SARS-CoV-2 virus can sequester themselves within the mitochondrial component of the organism to evade immune surveillance and response. The inflammatory response to viral invasion, accumulation of defective components of the mitochondrial compartment and failure of tissue OXPHOS systems forms a putative theory for the pathogenesis of post-acute sequelae in SARS-CoV-2 infection (83).

#### 4.3. Disruption of Mitochondrial Innate Immunity in Hepatitis B & C Infection

Hepatitis B (HBV) is an encapsulated DNA virus, while hepatitis C (HCV) is an RNA virus, yet both result in persistent and progressive liver damage, the outcome of which is hepatic fibrosis, cirrhosis and death. HBV and HCV gain access to the liver via an organ-specific multi-receptor complex, after which the viral particles are unencapsulated, the nucleocapsid is released into the cytoplasm and the viral DNA (HBV) or positive sense viral RNA (HCV) can act as material for translation of viral peptides (93).

HBV enhances its replicative ability by hijacking mitophagic processes, initially by stimulating excessive organelle fission by promoting Drp1, and ultimately by the upregulation of the PINK1-Parkin axis and degradation of Mfn2. The outcome of this process is persistence of the infected cell beyond usual viability, reducing ROS production and maintaining limited OXPHOS activity while using glycolysis metabolites to provide useful substrates for virion production (94,95). In HCV, viral RNA is recognised by RIG-I and MDA5 PRRs, which trigger MAVS assisted IRF and NF $\kappa$ B based interferon response (96). Viral non-structural (NS) proteins NS3 and NS4 are serine proteases that render MAVS ineffective by cleaving it from Mfn2, thus preventing RIG-I/MDA5 signalling (97), while also interfering with essential cofactors of TLR signalling (98). Spread of the virus between hepatocytes results in a state of persistent inflammation in newly infected areas as pro-inflammatory pathways are activated, while chronically infected areas have interferon production suppressed by PRR interference (99).

HCV infection appears to increase mitophagy via an indirect route by suppression of mTOR, which when active suppresses mitophagy (100) or unfolded protein response (UPR) (101) pathways, although whether this occurs in HCV infection to the same extent as in HBV is controversial within the literature (102,103). The converse is true in alcoholic hepatitis (AH), where hepatocytes from AH patients display reduced Drp1 and inactive mitochondrial fission. Electron micrograph studies show the accumulation of megamitochondria, while metabolomic studies show increased ROS, cell stress, cytosolic mtDNA and activation of cGAS-STING interferon signalling (104).

#### 4.4. Nascent Connections Between Mitophagy, Asthma and COPD

Asthma as a disease is characterised by chronic airway inflammation, respiratory symptoms such as coughing and wheezing, varying in intensity over time (105). Inappropriate mitophagy plays a role in the development of asthma in response to particulate matter. Genetic studies indicate that single nucleotide polymorphisms of ATG5 and SQSTM1 genes highly predispose to the development of asthma, while electron micrographs of bronchial biopsy material show increased autophagosome activity in patients with reduced lung function (106). The mTOR pathway appears to play a role in the development of asthma, as evidenced by murine models where mTOR blockade through rapamycin alleviates symptoms of inflammation. Asthmatic mice produced by allergic sensitisation using cigarette smoke extract showed significantly decreased neutrophil count and markers of inflammation when treated with intraperitoneal infusions of rapamycin (107). A similar study showed increased LC3 autophagosome formation in sensitised mice, with autophagy-related double-membrane vesicles more prominent in eosinophils from sensitised mice than in controls (108). Histopathological examination of human large airway epithelial tissue demonstrates increased expression of ATG5 protein in severe cases of asthma with airway remodelling, the changes in correspondence to the severity of the remodelling process (109). As the disease progresses, transforming growth factor  $\beta$  (TGF- $\beta$ ) signalling produces fibrosis while ultimately downregulating PINK1-Parkin autophagic processes, mitophagy and mitogenesis (110).

Similar effects have been demonstrated in COPD, and rapamycin and mTOR blockade remain targets of interest in development of pharmaceutical treatments for pulmonary inflammatory disease (111). The role of the PINK1-Parkin mitophagy pathway in pathogenesis was demonstrated by showing that PINK1 deficiency was protective against cell death and necroptosis in response to cigarette smoke in mouse models (112). A similar study demonstrated the LC3 deficient mice had reduced airspace enlargement in response to cigarette smoke extract than control animals (113).

## 5. Conclusions

The mitochondrial compartment plays a central role in our understanding of innate immunity. Rather than considering the metabolic aspects of mitochondria separate from their now well-defined role in the innate immune system, both roles are complementary and essential to the other's proper function. The metabolic phenotype of a tissue is the outward expression of a configuration requirement demanded by systemic and local homeostasis, which is to say that the metabolic role of mitochondria underpin their function within the immune system. Pathological change in tissue is accompanied by change in the metabolic phenotype of component cells, underpinned by changes in the configuration of cellular mitochondria. To this end, we refer not to singular mitochondrion but the mitochondrial compartment of a tissue. This terminology encapsulates the dynamic nature of mitochondrial flux – a highly regulated continuum of fusion-fission events throughout which the bioenergetic and immune components of the cell can remain in balance with the demands of the organism.

Via a complex, cascading network of extra- and intracellular signals the OXPHOS metabolic component of the cell is modulated in response to stress, starvation, pathogenic invasion, and other modalities of disease. Certain invaders such as SARS-CoV-2, HBV and HCV have evolved to take advantage of this apparatus. Our innate antiviral response to both acute and chronic SARS-CoV-2 infection can be characterised as a battle of control over E3 ubiquitin ligases, as viral material attempts to sequester itself within defective organelles that are resistant to proper patterns of mitochondrial flux.

In asthma, autophagic processes are upregulated and correspond to disease severity. Previous treatment methods have focused on targeting inflammatory pathways in the hopes that this would ameliorate the symptoms. While in mild to moderate cases this may prove effective, severe asthma has both a marked deleterious effect on the individual and high mortality. Further studies elucidating the role of mTOR signalling, PINK1-Parkin autophagy and downstream LC3 and ATG5 mediated autophagosome activity are warranted. Greater understanding of the pathophysiology of asthma

enables the development of novel therapeutic interventions that should revolutionise the treatment of a widespread and severely debilitating illness.

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**Availability of data and materials:** Not applicable

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### Abbreviations

**ACBP** - Acyl-CoA Binding Protein  
**AH** - Alcoholic Hepatitis  
**AMPK** - AMP-Protein Kinase  
**ATG** - Autophagy-Related  
**BNip3** - Bcl-2 Interacting Protein 3  
**CD36** - Cluster of Differentiation 36 (also known as FAT/FATP – Fatty Acid Translocase/Transport Protein)  
**cGAS** - Cyclic GMP-AMP Synthase  
**COPD** - Chronic Obstructive Pulmonary Disease  
**DAMPs** - Damage Associated Molecular Patterns  
**Drp1** - Dynamin-Related Protein 1  
**ETC** - Electron Transport Chain  
**FAT/FATP** - Fatty Acid Translocase/Transport Protein (also known as CD36)  
**Fis1** - Fission Protein 1  
**FKBP8** - FK506 Binding Protein 8  
**Glut4** - Glucose Transporter 4  
**GR** - Glucocorticoid Receptor  
**HCV** - Hepatitis C Virus  
**HIF-1 $\alpha$**  - Hypoxia Inducible Factor 1 Alpha  
**HMG** - High Mobility Group  
**HBV** - Hepatitis B Virus  
**IKK $\epsilon$**  - Inhibitor of NF $\kappa$ B Kinase Epsilon  
**IL** - Interleukin  
**IRFs** - Interferon Regulatory Factors  
**IRS** - Insulin Receptor Substrate  
**Keap1** - Kelch-like ECH-associated Protein 1  
**LC3** - Microtubule-associated Protein 1A/1B-light Chain 3  
**LPL** - Lipoprotein Lipase  
**MAVS** - Mitochondrial Antiviral Signalling Protein  
**MDA5** - Melanoma Differentiation Associated Protein 5  
**Mfn1/Mfn2** - Mitofusin 1 / Mitofusin 2  
**mtDNA** - Mitochondrial DNA  
**mtSSB** - Mitochondrial Single-Stranded DNA Binding Protein  
**mTOR** - Mammalian Target of Rapamycin  
**NF $\kappa$ B** - Nuclear Factor Kappa-light-chain-enhancer of Activated B Cells  
**NLRs** - Nucleotide-Binding Oligomerisation Domain-like Receptors  
**NRF2** - Nuclear Respiratory Factor 2  
**OXPHOS** - Oxidative Phosphorylation  
**PINK1** - PTEN Induced Kinase 1

**PON2** - Paraoxonase-2  
**PPAR** - Peroxisome Proliferator-Activated Receptor  
**PRRs** - Pattern Recognition Receptors  
**RIG-I** - Retinoic Acid Inducible Gene I  
**ROS** - Reactive Oxygen Species  
**RXR** - Retinoid X Receptor  
**SARS-CoV** - Severe Acute Respiratory Syndrome Coronavirus  
**SNARE** - Soluble NSF Attachment Protein Receptor  
**SQSTM1** - Sequestrome-1 (also known as p62)  
**TBK1** - TANK-binding Kinase 1  
**TCA** - Tricarboxylic Acid  
**TFAM** - Mitochondrial Transcription Factor A  
**TLR** - Toll-like Receptor  
**TOM** - Translocase of Outer Membrane  
**TSC1/TSC2** - Tuberous Sclerosis Complex 1 / Tuberous Sclerosis Complex 2  
**UCP** - Uncoupling Protein  
**UPR** - Unfolded Protein Response  
**VDAC1** - Voltage Dependent Anion Channel 1

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