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Mitochondrial Fusion and Fission: The fine-tune balance for cellular homeostasis

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Abstract

Mitochondria are highly dynamic, maternally inherited cytoplasmic organelles, which fulfill cellular energy demand through the oxidative phosphorylation system. Besides, they play an active role in calcium and damage-associated molecular patterns (DAMPs) signaling, amino acid, and lipid metabolism, and apoptosis. Thus, the maintenance of mitochondrial integrity and homeostasis is extremely critical, which is achieved through continual fusion and fission. Mitochondrial fusion allows the transfer of gene products between mitochondria for optimal functioning, especially under metabolic and environmental stress. On the other hand, fission is crucial for mitochondrial division and quality control. The imbalance between these two processes is associated with various ailments such as cancer, neurodegenerative and cardiovascular diseases. This review discusses the molecular mechanisms that control mitochondrial fusion and fission and how the disruption of mitochondrial dynamics manifests into various disease conditions.

Keywords

Mitochondria; dynamics; fusion; fission; diseases

Introduction

Mitochondria are highly dynamic double membrane-bound organelles found in most eukaryotic cells. They play critical roles in the cells, including energy production through oxidative phosphorylation (OXPHOS), integration of various metabolic pathways, regulation of apoptosis, and maintenance of calcium homeostasis (1). It is believed that mitochondria are the descendants of an ancient prokaryote that underwent an endosymbiotic event with early eukaryotes (2). A mitochondrion consists of an outer membrane, intermembrane space,

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inner membrane, and matrix (Figure 1). The outer membrane contains three integral protein families: translocase of outer mitochondrial membrane (TOMM) complex, sorting and assembly machinery (SAM) complex, and porins. The inner membrane is folded to form cristae, which contains the enzyme complexes responsible for oxidative phosphorylation. The mitochondrial matrix is the site where the tricarboxylic acid (TCA) cycle takes place. It also contains the mitochondrial genome, which is a 16.5 kb double-stranded closed circular DNA. The mitochondrial genome consists of 37 genes that encode 13 OXPHOS proteins, 2 ribosomal RNAs (12S and 16S rRNA), and 22 transfer RNAs (Figure 1). The majority of the mitochondrial proteins (~1500) are encoded by the nuclear genes and are imported into the mitochondria from the cytosol after their synthesis.

Being a vital cellular organelle, maintenance of mitochondrial integrity and homeostasis is extremely critical. Therefore, mitochondria continuously undergo changes in their number and morphology through the processes of fusion and fission. This 'mitochondrial dynamics' helps maintain the pool of mitochondria within a cell and optimal OXPHOS activity by allowing efficient transport and distribution of mitochondrial content. Mitochondrial dynamics is linked to several cellular processes, including cell cycle, apoptosis, cell migration, mitophagy, and reactive oxygen species (ROS) production (3). Therefore, a fine balance between mitochondrial fusion and fission is crucial for cell survival and optimal functioning. Defects in mitochondrial dynamics are linked to many pathological conditions, including cancer, neurodegenerative, and cardiovascular diseases (4,5). This review discusses the molecular insights into the mitochondrial fusion and fission machinery and different disease conditions that develop due to the functional abnormalities in mitochondrial dynamics.

The fusion paradigm and the molecular insight

Mitochondrial fusion joins two mitochondria at the outer and inner membrane interfaces via three membrane GTPases, Mitofusin 1 (MFN1, human chromosome 3q26), Mitofusin 2 (MFN2, human chromosome 1p36), and Optic atrophy protein 1 (OPA1, human chromosome 3q29). These proteins are members of the dynamin-related protein (DRP) superfamily. MFN 1 and 2 are homologs of the drosophila protein fuzzy onion (Fzo) (6), whereas OPA1 is the mammalian ortholog of Mgm1, which is a protein essential for the mitochondrial fusion in yeast (7). Increased fusion is triggered by treatments that inhibit protein synthesis, mammalian target of rapamycin (mTOR) inhibition-induced autophagy, and starvation (8, 9, 10).

Some mitochondria are unable to perform their respiratory function optimally because of mutations in mtDNA induced by reactive oxygen species (11). Therefore, mitochondrial fusion is vital as it allows the exchange of gene products and metabolites between the fusing mitochondria to enhance their overall respiratory function. Likewise, impediment of mitochondrial fusion is associated with the underperformance of mitochondrial function (12). However, a recent study demonstrated that promoting mitochondrial fusion in pancreatic adenocarcinoma cells by overexpression of MFN2 or inhibition of dynamin-related protein-1 (DRP1) led to increased mitophagy, which resulted in a loss of mitochondrial mass and reduced OXPHOS (13). Thus, the true significance of mitochondrial

fusion is elusive and maybe context-dependent, requiring additional in-depth mechanistic investigations.

Outer mitochondrial membrane fusion: role of Mitofusins

The outer mitochondrial membrane fusion is facilitated by two large membrane GTPases- Mitofusin 1 (MFN1) and Mitofusin 2 (MFN2), present on the outer mitochondrial membrane. MFN2 is also present on the endoplasmic reticulum (ER) membrane, where it tethers ER to mitochondria enabling the mitochondrial calcium uptake (14). MFN topology has been described using two models (Figure 2). The classical model of MFN topology suggests that MFNs have two transmembrane domains. However, a recent study has revealed that both MFN1 and MFN2 possess a single transmembrane domain that places the N-terminal GTPase and helical repeat 1 (HR1) domains in the cytoplasm and C-terminal HR2 domain in the mitochondrial intermembrane space (15).

The primary function of Mitofusins is the promotion of docking and fusion of the mitochondrion. At present, a complete understanding of the molecular mechanisms involved in mitochondrial fusion is lacking. However, a couple of studies have proposed that tethering of two OMMs occurs through the oligomerization of the GTPase domains of MFNs, and GTP hydrolysis is required for this oligomerization (16, 17). Upon GTP binding and hydrolysis, a conformational change occurring in the GTPase domains leads to their oligomerization, facilitating the docking of the two mitochondria at the two outer membranes and their subsequent fusion (Figure 3a).

Based on the new MFNs topology suggesting only one transmembrane domain in human MFNs, another mechanism of the oligomerization of MFN molecules, critical for outer membrane fusion, has evolved (Figure 3b). Mattie et al. demonstrated that two cysteine residues located in the HR2 domains (which reside in the intermembrane space) can be oxidized by increased oxidized glutathione levels leading to the formation of disulfide bonds between MFN molecules and their oligomerization (15). They also showed that the addition of GSH to preformed GSSG-induced oligomers of MFN2 led to a reversal of MFN2 oligomer formation. This new mechanism indicates that redox signaling plays a vital role in OMM fusion. Further studies are needed to clarify the mechanistic basis of mitochondrial fusion and better understand the effects of aberrant redox signaling on fusion.

The activity of MFN 1 is regulated by phosphorylation, ubiquitination, and deacetylation. Phosphorylation of Mfn1 in the HR1 domain by the extracellular-signal-regulated kinase (ERK) inhibits mitochondrial fusion and promotes apoptosis (18). On the other hand, deacetylation of Mfn1 by histone deacetylase 6 (HDAC6) leads to its activation and promotion of fusion in conditions of glucose deprivation (19). In response to cellular stress, JNK phosphorylates MFN 2, leading to the recruitment of E3 ubiquitin ligase, which ubiquitinates MFN2 causing its proteasomal degradation. This degradation of MFN2 results in mitochondrial fragmentation and enhanced apoptotic cell death (20). Mfn2 can also be phosphorylated by PINK1, leading to its ubiquitination by Parkin and eventual mitophagy (21).

Inner mitochondrial membrane fusion: role of Optic atrophy protein 1 and Cardiolipin

Inner mitochondrial membrane (IMM) fusion is mediated by OPA1 and specific IMM lipid components, for example- cardiolipin (22). OPA1 is a complex protein that localizes to the inner mitochondrial membrane (Figure 3). It consists of eight isoforms which are products of alternative splicing and are characterized by different combinations of three small exons (4,4b and 5b) located in the N-terminal part of the molecule (23). One to three sites of proteolytic cleavage can be formed in different isoforms. The formation of these cleavage sites depends on the set of exons (24). These sites are usually termed S1, S2, and S3. Site S1 is present in all eight isoforms, whereas each S2 and S3 sites are present in four isoforms (24). All isoforms encode for a polypeptide containing an N-terminal mitochondrial targeting sequence (MTS) (Figure 2). The MTS is removed by the matrix processing protease during the import of the N-terminus into the matrix (4). The cleavage of the S1 site is mediated by OMA1. If the S1 site is left intact, the resulting long-form of OPA1 (L-OPA1) is anchored to the inner membrane, with most of the protein facing the intermembrane space (4). On the other hand, if the S1 site is cleaved by OMA1, a short form of Opa1 (S-OPA1) is produced. Cleavage at the S2 and S3 sites occurs constitutively, and this cleavage is mediated by YME1L (25, 26), while the cleavage of OPA1 isoforms at the S1 site occurs only under certain conditions associated with stress (27).

Currently, the precise mechanism of IMM fusion is not yet fully understood. A study by Song et al. revealed that a combination of S-OPA1 and L-OPA1 is required for IMM fusion to occur (26). Similarly, Ge et al. showed that L-OPA1 and S-OPA1 work together to stimulate fusion activity leading to efficient and fast membrane pore opening in liposomes (28). In contrast, some other studies have shown that only L-OPA1 is sufficient to promote IMM fusion (8, 29). Therefore, further studies are needed to confirm if S-OPA1 is dispensable for IMM fusion.

Cardiolipin (CL), a phospholipid and component of the inner mitochondrial membrane, is vital for IMM fusion. Ban et al. showed that the incubation of recombinant L-OPA1 with reconstituted CL-containing liposomes led to an interaction between L-OPA1 and CL, resulting in IMM fusion. Findings also revealed that when cardiolipin was removed from the liposomes, no membrane fusion was observed even in the presence of L-OPA1 on both sides of the membranes (30). They further demonstrated that GTP hydrolysis was needed for OPA1-mediated fusion and that fusion activity was absent in liposomes containing an OPA1 mutant lacking GTP hydrolysis activity. (30). These findings indicate that the binding of Cardiolipin to OPA1 and GTP hydrolysis of OPA-1 are crucial for IMM fusion. Additional studies are required to decipher the precise roles of cardiolipin in IMM fusion and delineating the underlying molecular mechanisms.

Apart from the proteolytic processing of Opa1, which is mediated by YME1L and OMA1, NAD-dependent deacetylase sirtuin-3 (SIRT3) deacetylates OPA1 at its GTPase effector domain (Lys926 and Lys931), elevating its GTPase activity and enhancing mitochondrial fusion (31).

Mitochondrial fission and the molecular insight

Mitochondrial fission is the process whereby a mitochondrion divides into two mitochondria (Figure 4). It plays different roles, including inheritance and partitioning of organelles during cell division, proper distribution of mitochondria, and cytochrome C release during apoptosis (32, 33, 34). Fission is also crucial for removing damaged organelles by mitophagy, and its loss results in an increase in the number of elongated mitochondria due to unbalanced fusion (35). On the other hand, disruption in the fusion process results in more fragmented mitochondria (36, 37). Although the precise reason for this is unknown, this could happen because of the need to maintain ATP supply in the cells. Fission in mammals is coordinated by a large dynamin-like GTPase, known as Dynamin-related protein 1 (DRP1, a.k.a. DNM1L, human chromosome 12p11). Other proteins involved in the fission process include Dynamin 2 (DNM2, a.k.a. DYN2, human chromosome 19p13.2), human mitochondrial dynamics proteins 49 (MID49, a.k.a. MIEF2, human chromosome 17p11) and 51 (MID51, a.k.a. MIEF1, human chromosome 22q13), mitochondrial fission 1 protein (FIS1, a.k.a. TTC11, human chromosome 7q22) and mitochondrial fission factor (MFF, a.k.a. C2orf33, human chromosome 2q36.3) (22, 35, 38, 39). DRP1 is a cytosolic protein recruited to the mitochondria by its adaptors present on the OMM, including MFF, MID49, MID51, and FIS1. DRP1 consists of four domains, an N-terminal GTPase domain followed by the middle domain, variable domain (or B-insert), and the GED in C-terminal (Figure 2).

The initial step of mitochondrial division occurs at positions where the endoplasmic reticulum (ER) tubules contact the mitochondria to mediate constriction before Drp1 recruitment (40) (Figure 4). This ER-mediated mitochondrial constriction is required to decrease the average mitochondrial diameter from approximately 300–500 nm to around 150 nm to allow Drp1-oligomeric ring formation (40). At the ER-mitochondria contact sites, the ER-bound inverted-formin 2 (INF2) cooperates with mitochondria anchored formin-binding Spire1C to regulate the actin assembly required for mitochondrial constriction before Drp1 recruitment and oligomerization (41, 42). Studies have shown that some proteins involved in regulating the actin cytoskeleton, for example, Arp2/3, cofilin, and cortactin, are also involved in mitochondrial fission (43, 44). Therefore, ER and actin are essential in the process and regulation of mitochondria division. However, it is not fully understood how the ER recognizes the sites for mitochondrial constriction requiring more investigations to better understand the underlying mechanisms.

After DRP1 is recruited to the OMM by MFF, MID 49, MID 51, and FIS1, it forms a ring-like structure around the mitochondrion, enhancing the pre-existing constriction of the mitochondrion (38). GTP hydrolysis of DRP1 then occurs, followed by the recruitment of DNM2 to the mitochondrion-constricted site, where it assembles and completes the division process (Figure 4). In contrast, another study has revealed that DNM2 is dispensable for mitochondrial fission and that DRP1 has constricting and severing abilities, which enables it to complete the fission process even in the absence of DNM2 (45). Further studies would help determine if complete mitochondrial fission can occur without DNM2.

Inner mitochondrial membrane (IMM) constriction is Ca^{2+} -dependent and occurs at mitochondria–ER contact sites (46). The calcium release from the ER into the mitochondria

leads to the constriction of the inner membrane compartment, resulting in IMM division before the recruitment of DRP1. Apart from playing a role in mitochondrial fusion, Cardiolipin (CL) also interacts with DRP1. This interaction drives the oligomerization of DRP1 and stimulation of its GTPase activity, which increases the constriction of liposome membranes (47, 48). Future investigations are needed to reveal how cardiolipin balances mitochondrial fusion and fission and what triggers its differential actions.

DRP1 is phosphorylated by cdk1/cyclin B kinase on serine (Ser) 585 during the process of mitosis, leading to its oligomerization and promotion of mitochondrial fission (49). Mitogen-activated protein kinase I (MAPK1) also plays a vital role in DRP-1 phosphorylation. MAPK1, also known as ERK2, phosphorylates DRP1 at Ser 616 to cause its activation, promoting mitochondrial fission (50). In contrast, protein kinase A phosphorylates DRP1 at Ser 637, leading to its retention in the cytoplasm, thereby inhibiting fission and sparing mitochondria from autophagic degradation during nutrient deprivation and cell death (10,51). Phosphorylation at Ser 637 is abrogated by calcineurin through dephosphorylation leading to its translocation to the mitochondria and mitochondrial fission (52).

SUMOylation, S-nitrosylation, O-GlcNAcylation, and Ubiquitination, can also regulate DRP1 activity. SUMOylation of DRP1 by mitochondrial -associated protein ligase (MAPL) is triggered by the activation of apoptosis. After the SUMOylation of DRP1 by MAPL, DRP1 stabilizes ER- mitochondrial contact sites, calcium flux, cristae remodeling, and cytochrome c release (53). O-GlcNAcylation and S-nitrosylation of DRP1 increase its fission activity. O-GlcNAc transferase induces the translocation of Drp1 from the cytoplasm to mitochondria, enhancing fission (54). Comparably, S-nitrosylation of DRP1 by nitric oxide increases the GTPase activity of DRP1, inducing mitochondrial fission (55). Ubiquitination of DRP1 by Parkin results in its degradation by the proteasome-dependent pathway (56).

Pathobiological implications of the imbalance in mitochondrial fusion and fission

The processes of fusion and fission are critical for normal mitochondrial functioning, energetics, and movement. Reduction or excess of any of these processes results in an imbalance affecting mitochondrial function, ultimately resulting in various diseases, including neurodegenerative disorders, cardiovascular diseases, and cancer (Table 1), as discussed below:

Charcot-Marie-Tooth Disease Type 2A (CMT2A)

CMT2A is an autosomal dominant peripheral neuropathy characterized by sensory and motor loss in the distal limbs (57, 58). This disease occurs as a result of heterozygous mutations in MFN2. In contrast to demyelinating forms of CMT, CMT2A is an axonopathy, and in most cases, there is no change or a slight decrease in nerve conduction velocity (5). The disease is primarily characterized by muscle weakness, hyporeflexia, sensory loss in the lower limbs, and gait defects. These symptoms usually appear before the age of 10 in most patients (59, 60).

Most of the MFN2 mutations are missense mutations distributed throughout the entire ORF sequence with some enrichment in functional domains (60, 61, 62). The overexpression of T105M (63, 64) or R94W mutation (65) in transgenic mice resulted in various neurological phenotypes associated with clumping of mitochondria in neurons and sparsity of mitochondria in axons due to defective trafficking. The mitochondrial defects result in mitochondrial aggregation, dysmotility, fragmentation, and depolarization. Under normal conditions, MFN1 and MFN2 interact with Miro and Milton proteins that form the molecular complex linking MFN2 to kinesin motors. In CMT2A, the mutation in MFN2 affects this interaction leading to impairment in axonal mitochondrial transport. Some MFN2 mutations are also associated with optic atrophy, thereby overlapping with Dominant optic atrophy (DOA) and, in severe cases, resembling the DOA plus syndrome. These findings indicate MFN2 is crucial for proper neuronal functioning.

Dominant Optic Atrophy

Dominant Optic Atrophy (DOA) is the most common inherited optic neuropathy, with most cases caused by mutations in the optic atrophy 1 gene (*OPA1*). The disease is usually diagnosed in early childhood and characterized by a progressive bilateral loss of visual acuity, blue-yellow dyschromatopsia or generalized color vision deficits, variable centrocecal, central or paracentral visual field defects, and temporal or diffuse optic nerve pallor with optic disc excavation (66). DOA shows variable expression, both between and within families, ranging from an asymptomatic state to blindness (67). Different *OPA1* mutations have been reported, including missense, frameshift, nonsense, and deletion mutations. Of which missense mutations have the highest frequency (26%) (68). Although the main feature of DOA is optic nerve degeneration, some patients with *OPA1* mutations also develop additional extra-ocular neurological features called DOA plus syndrome, which entails deafness, ataxia, peripheral neuropathy, myopathy, and progressive external ophthalmoplegia.

Mutations in the *OPA1* gene lead to mitochondrial morphology and function impairments, leading to increased autophagy or apoptosis. A study by Ban et al. revealed that the expression of seven *Opa1* pathogenic mutants associated with DOA or DOA plus in *Opa1*-null mouse embryonic fibroblasts (MEFs) did not restore tubular mitochondrial morphology, indicating a loss of mitochondrial fusion activity (69). Davies et al. also reported that fibroblasts taken from adult heterozygous *Opa1* mutant mice had alterations in mitochondrial morphology, along with an increase in mitochondrial fission and fragmentation (70). Another study using mouse models of DOA revealed that retinal ganglion cells from adult heterozygous *Opa1* mutant mice showed an increased number of autophagosomes than the *Opa1* wild-type mice (71). These studies show that mutations in the *OPA1* gene lead to defective mitochondrial fusion and aberrant mitochondrial functioning.

Parkinson's disease

Parkinson's disease (PD) is one of the most common neurodegenerative disorders, with most cases being sporadic while about 10–15% of patients having a family history. Clinical features include tremors, akinesia or bradykinesia, progressive rigidity, and postural

instability. One of the significant neuropathological findings in Parkinson's disease is the loss of pigmented dopaminergic neurons of the substantia nigra pars compacta, which occurs due to dopamine deficit in the striatum. The dopaminergic neurons from the substantia nigra are vulnerable to changes in mitochondrial dynamics. One reason for this is that these neurons have lower basal mitochondrial content than other midbrain neurons (72). Imbalance in mitochondrial dynamics and mitochondrial dysfunction resulting from mtDNA defects are associated with PD (73, 74, 75, 76). Sporadic Parkinson's disease (sPD) cybrid cells exhibit dysfunctional mitochondria due to mtDNA defects, abnormal mitochondrial localization, and an increased fragmentation pattern (77, 78, 79). Similarly, increased mitochondrial fragmentation has been linked to Huntington's disease (80). Santos et al. revealed that the increase in mitochondrial fission in sPD was due to OPA1 long isoform cleavage and increased mitochondrial DRP1 phosphorylation levels, which led to mitochondrial fragmentation (81). The knockdown of DRP1 in sPD cybrid cells led to increased mitochondrial interconnectivity, elongation, and membrane potential, while ROS production was decreased, indicating that DRP1 inhibition could alleviate mitochondrial deficits in sporadic cases of Parkinson disease (81).

Atherosclerosis

Atherosclerosis is a chronic and progressive vascular disease characterized by narrowing of an artery due to the formation of a plaque containing inflammatory cells, oxidized- LDL, and myofibroblasts (82). One of the factors promoting the development of this disease is the activation of the vascular smooth muscle cells (VSMCs). The activation of VSMCs by Platelet-derived growth factors (PDGF) is associated with decreased MFN2 levels and mitochondrial fragmentation. Conversely, inhibition of fission with Mitochondrial division inhibitor 1 (Mdivi-1) has also been associated with decreased PDGF- induced mitochondrial fragmentation and reduction of VSMCs proliferation (83). Similarly, the inhibition of Drp1 has been shown to reduce endothelial dysfunction and atherosclerosis in apolipoprotein E (ApoE) knockout diabetic mice (84). These findings indicate that maintaining the balance between fusion and fission is vital in preventing atherosclerosis progression.

Left ventricular hypertrophy

Left ventricular (LV) hypertrophy is a condition characterized by either enlargement of the left ventricular cavity or thickening of the heart's left ventricular wall or both. LV hypertrophy can lead to an increased risk of arrhythmias and heart failure. A study by Javadov et al. showed that in a cell model of phenylephrine-induced cardiomyocyte hypertrophy, the expression of Drp1 was increased while Mfn2 levels were reduced (85). Using a pressure overload animal model, the inhibition of mitochondrial fission by Mdivi-1 led to abnormal cardiac mitophagy inhibition, induced angiogenesis by increasing expression of CD31 and VEGF, and decreased the expression of anti-angiogenic factors, preventing collagen deposition. These effects of Mdivi-1 led to the amelioration of left ventricular dysfunction (86), suggesting that increased mitochondrial fragmentation and mitophagy might be associated with LV hypertrophy development.

Carcinogenesis

The imbalance in mitochondrial dynamics contributes significantly to cancer development and metastatic progression. Most studies investigating mitochondrial morphology in tumor cells have reported that increased fission promotes tumorigenesis (13, 50, 87, 88). Several cancer cell lines, which have been transformed with oncogenes, have more fragmented mitochondria than their non-transformed control lines (13, 50, 87). One pathway associated with mitochondrial fission in cancer is the MAPK pathway, activated in cancer cells by excess signaling from growth factors or oncogenic mutations like BRAF^{V600E} or RAS^{G12V}. MAPK activation causes the phosphorylation of DRP1 at Ser 616, leading to its activation and subsequent increase in mitochondrial fission. The inhibition of DRP1 or promotion of fusion reduces cancer cell growth by inducing cell death (13, 50, 87, 88). A study from our laboratory has demonstrated that increased fusion led to the growth suppression of breast cancer cells. Overexpression of SH3GL2, an SH3 domain-containing cytosolic protein, upon translocation to the mitochondria, led to increased MFN2 expression and reduced proliferation and invasion of breast cancer cells (89).

Since fission is critical during mitosis to assure equal segregation of mitochondrial contents between daughter cells (90), its loss possibly induces cell death and cellular dysfunction due to replicative stress and mitotic defects affecting genomic integrity (91). A recent study proposed that increased mitophagy due to increased fusion might be another mechanism of reduced cancer growth. Yu et al. revealed that inhibition of fission in pancreatic cancer cells led to increased fusion, which resulted in increased mitophagy, reduced mitochondrial mass, and decreased mitochondrial respiration, leading to a reduction in ATP production and a decrease in tumor growth (13).

Increased mitochondrial fusion has also been reported to promote cancer growth (92, 93). According to Humphries et al., treatment of breast cancer cells with leflunomide, a potent activator of mitochondrial fusion proteins, overcame inhibitory effects of fission on migration, signaling, and metastasis (93). Similarly, mining existing datasets for breast cancer showed increased expression of genes associated with mitochondrial fission, which correlated with improved survival in human breast cancer (93). Since increased mitochondrial fusion and fission have been reported to drive tumor growth and vice versa, more mechanistic studies are needed to have a comprehensive understanding of how an imbalance in mitochondrial dynamics causes cancer development and progression.

Increased DRP1 levels also promote metastasis. Zhao et al. showed that invasive breast cancer cell lines have more fragmented mitochondria, higher total and phosphorylated DRP1^{S616}, and lower MFN1 levels in comparison with a non-metastatic cell line (87). Increased mitochondrial fragmentation via activated DRP1 or MFN silencing also resulted in metabolic repositioning to the peripheral cytoskeleton's lamellipodia, providing a concentrated energy source to power tumor cell motility and invasion (87). Another factor that stimulates migration and invasion in cancer cells is hypoxia. Wan et al. showed that hypoxia led to increased DRP1 expression and mitochondrial fission in glioblastoma U251 cells. They also showed that exogenously expressed GFP-DRP1 enhanced hypoxia-induced migration of U251 cells and mitochondrial division inhibitor-1 (Mdivi-1), a selective dynamin-related protein 1 (DRP1) inhibitor, efficiently attenuated hypoxia-induced

migration of U251 cells (88). These studies strongly suggest that increased fission facilitates cancer metastasis.

High-mobility group box 1 (HMGB1) is a cellular response signaling protein released by immune cells following cell death or injury. It is also released into the tumor microenvironment following cell stress or necrosis. Increased HMGB1 levels stimulate pancreatic tumor cell proliferation and ATP production, and its inhibition led to a decrease in tumor growth (94). HMGB1 binds to the receptor for advanced glycation end products (RAGE), a transmembrane receptor overexpressed in cancer. The binding of HMGB1 to RAGE led to the activation of RAGE and increased phosphorylation of Erk1/2, leading to increased mitochondrial ATP production (94). A recent study revealed that HMGB1 protein led to the activation of Erk1/2, which led to the phosphorylation of DRP1, thereby leading to increased tumor growth (95). HMGB1 has also been associated with high glucose levels. Huang et al. showed that culturing human umbilical vein endothelial cells (HUVECs) under high glucose conditions led to increased secretion of HMGB1 (96). Since diabetes is associated with an increased risk of malignancies, HMGB1 may play a role in driving tumor growth and metastasis due to its effects on Erk1/2 activation and DRP-1 phosphorylation. More studies are required to investigate the link between hyperglycemia and imbalance in mitochondrial dynamics as a contributor to tumor growth.

Conclusion and Future perspectives

It appears from the above discussion that mitochondrial fusion and fission play an indispensable role in determining cell fate by maintaining the functional homeostasis of mitochondria. Fission is essential for maintaining the mitochondrial number and proper distribution in the daughter cells, while fusion ensures optimal mitochondrial activity by allowing the exchange of contents between fusing mitochondria. Imbalance in mitochondrial dynamics results in alteration of the mitochondrial number, morphology, and functioning, leading to the development of various diseases, including cancer. At present, the knowledge of molecular events involved in mitochondrial fusion and fission is premature, and more in-depth mechanistic studies are required. Studies are also warranted to better understand how fusion and fission processes are linked to mitophagy, a crucial phenomenon associated with various mitochondrial disorders and human cancers. In addition, it is also important to enhance our knowledge on the crosstalk between various oncogenic signaling and mitochondrial dynamics regulatory pathways. Considering the emerging role of mitochondrial dynamics in determining cellular fate, mitochondria hold great promise in developing novel treatment strategies and biomarkers for disease diagnosis and treatment. Next-generation sequencing of genome, transcriptome, or proteome can identify molecular heterogeneity and relevant pathways associated with the changes in the mitochondrial dynamics in a patient-specific manner. Functional characterization of these alterations utilizing appropriate humanized model systems and clinical validation may open up new avenues for therapeutic interventions.

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Abbreviations

TOMM	Translocase of the outer mitochondrial membrane
SAM	Sorting and assembly machinery complex
MFN1	Mitofusin 1
MFN2	Mitofusin 2
OPA1	Optic atrophy protein 1
DRP1	Dynamin related protein 1
Fzo	Fuzzy onions
HR	Helical repeat
MTS	Mitochondrial targeting sequence
DNM2	Dynamin 2
MID49	Mitochondrial dynamics protein 49
MID51	Mitochondrial dynamics protein 51
FIS1	Mitochondrial fission 1 protein
MFF	Mitochondrial fission factor
INF2	Inverted formin 2
CMT2A	Charcot- Marie-Tooth Disease Type 2A
DOA	Dominant optic atrophy
sPD	Sporadic Parkinson Disease
HMGB1	High mobility group box 1
RAGE	Receptor for advanced glycation end products

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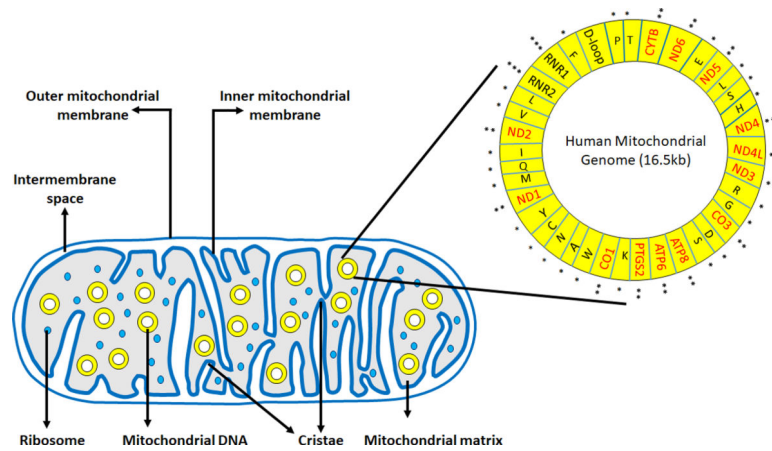


Figure 1. Structure of a mitochondrion showing the outer mitochondrial membrane, inner mitochondrial membrane, intermembrane space and the mitochondrial matrix. Mitochondrial genome residing in the mitochondrial matrix has 37 genes coding for 13 OXPHOS proteins (in red, **), 2 ribosomal RNAs (12s rRNA, 16s rRNA, *), 22 tRNAs (***) and a regulatory D loop region.

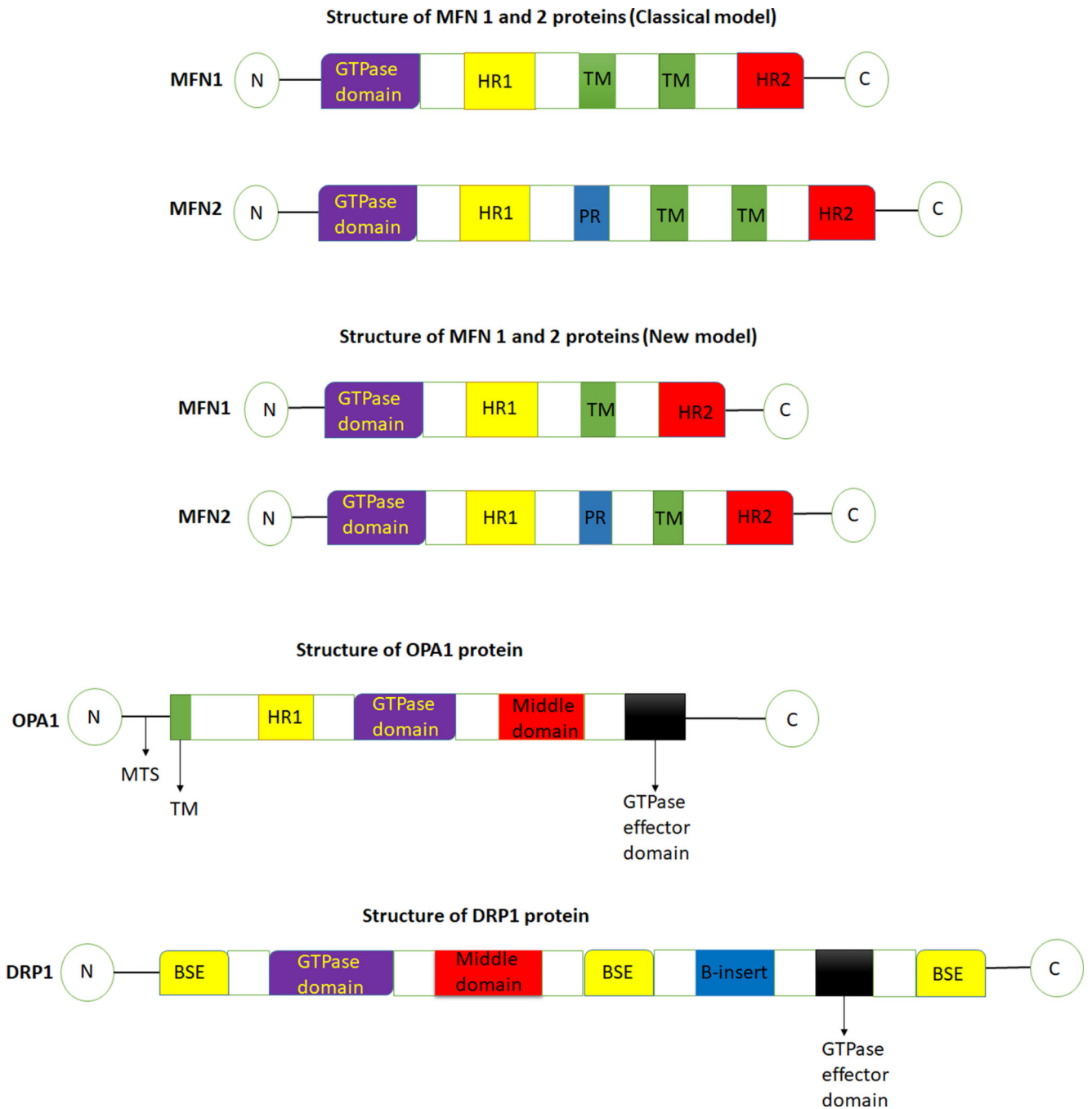


Figure 2. Schematic diagram of the structure of fusion (MFN1, MFN2, OPA1) and fission (DRP1) regulators. MFN1- Mitofusin 1, MFN2- Mitofusin 2, OPA1- Optic atrophy protein 1, DRP1- Dynamin related protein 1, TM- transmembrane, PR- proline rich, HR1- helical repeat 1, HR2- helical repeat 2, N- N terminal, C- C terminal, MTS- mitochondrial targeting sequence, BSE- bundle signaling element.

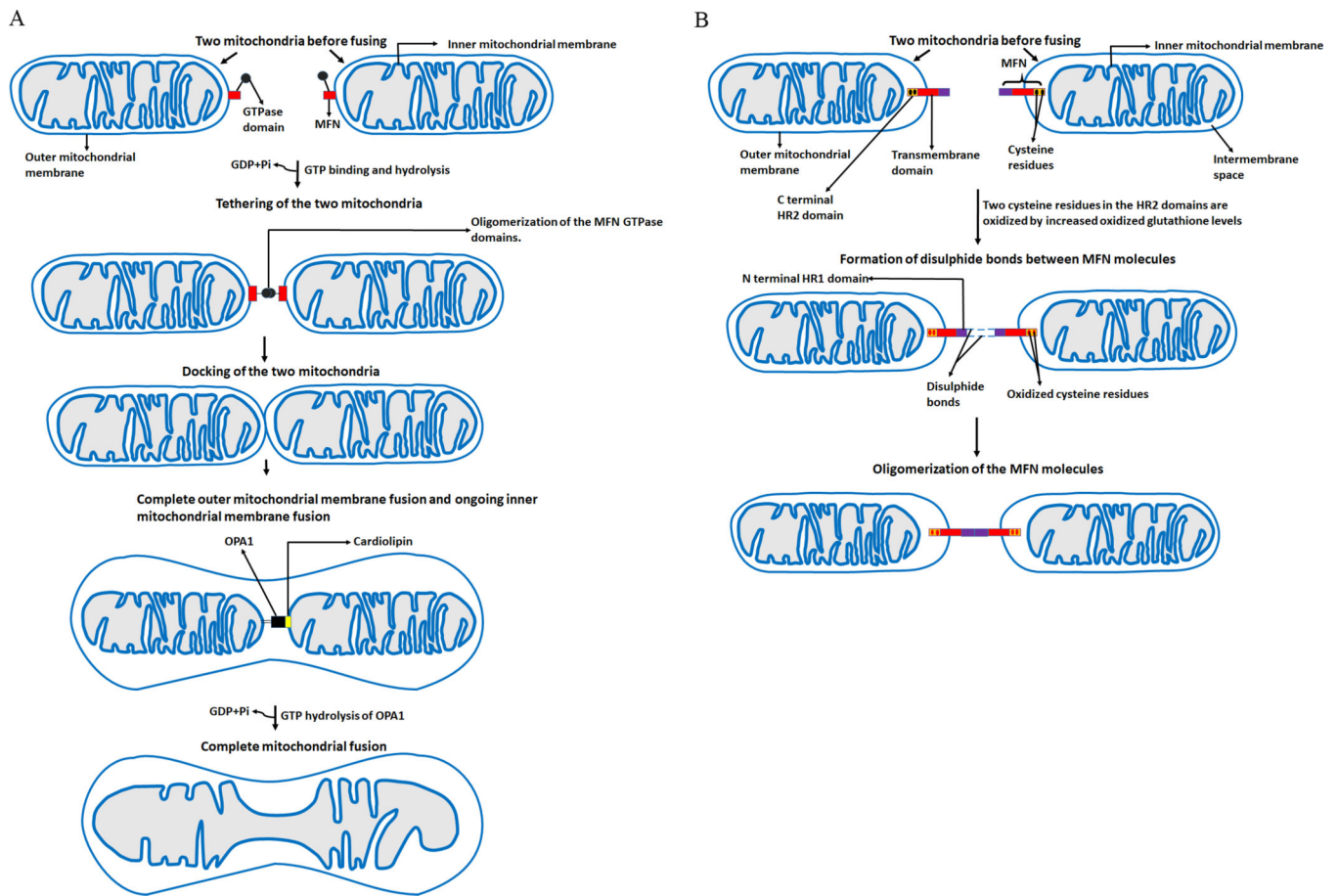


Figure 3.

The fusion paradigm. Depiction of various steps involved in mitochondrial fusion. (a) GTP binding and hydrolysis leads to a conformational change in the GTPase domains of MFNs resulting in their oligomerization. The oligomerization of the GTPase domains brings about the tethering of the two mitochondria, which facilitates their docking and fusion. (b) A new mechanism of the oligomerization of MFN molecules. Increased oxidized glutathione levels oxidizes two cysteine residues located in the HR2 domains of MFN molecules. This leads to the formation of disulphide bonds between MFN molecules and their oligomerization. MFNs- Mitofusins, OPA1- Optic atrophy protein 1, GTP- Guanosine triphosphate, GDP- Guanosine diphosphate, Pi- inorganic phosphate, HR2- helical repeat 2.

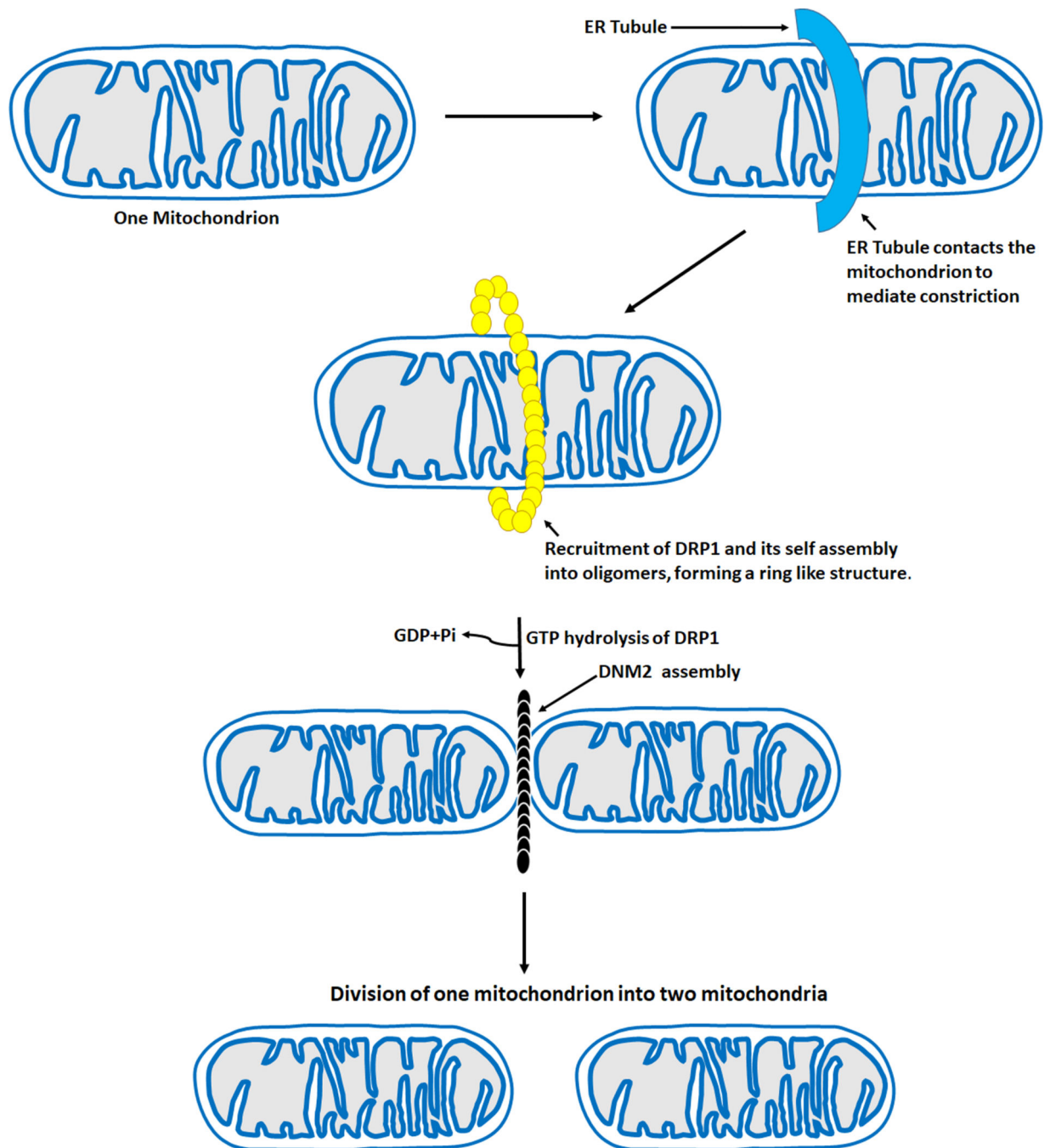


Figure 4. Mitochondrial fission machinery. The steps involved in mitochondrial fission are as follows- ER tubules contact the mitochondria to mediate constriction before the recruitment of DRP1. After the recruitment of DRP1 to the OMM, it forms a ring like structure, GTP hydrolysis of DRP1 then occurs followed by the recruitment of DNM2 to the mitochondrion-constricted site, where it assembles and completes the division process leading to two daughter mitochondria. ER- Endoplasmic reticulum, DRP1- Dynamin related protein 1, DNM2-

Dynamin 2, GTP- Guanosine triphosphate, GDP- Guanosine diphosphate, Pi- inorganic phosphate, OMM- Outer mitochondria membrane.

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Table 1–

A list of fusion and fission associated genes, their functions, reported alterations and associated diseases.

Gene Name	Yeast Orthologue	Functions	Alterations	Diseases
MFN1	Fzo1	Outer mitochondrial membrane fusion	Mfn1 downregulation	Hepatocellular carcinoma (97, 98), Triple negative breast cancer (99)
MFN2	Fzo1	Outer mitochondrial membrane fusion	Heterozygous mutations in Mfn 2 Mfn2 downregulation	Charcot Marie Tooth Disease type 2A (4) Breast cancer (100)
OPA1	Mgm1	Inner mitochondrial membrane fusion	Mutations (mostly missense)	Dominant optic atrophy (68).
DRP1	Dnm1	Mitochondrial fission	Increased Drp1 phosphorylation levels.	Sporadic Parkinson's disease (81) Diseases
DRP1	Dnm1	Mitochondrial fission	Increased phosphorylation of Drp1 at serine 616 Increased expression levels of Drp1 Increased Drp1 mRNA expression and protein levels Drp1 upregulation	Pancreatic ductal adenocarcinoma (50), Glioblastoma (101). Left ventricular hypertrophy (85), Lung adenocarcinomas (102). Hepatocellular carcinoma (97). Triple negative breast cancer (99)