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Pathological implications of cellular stress in cardiovascular diseases

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Abstract

Cellular stress has been a key factor in the development of cardiovascular diseases. Major types of cellular stress such as mitochondrial stress, endoplasmic reticulum stress, hypoxia, and replicative stress have been implicated in clinical complications of cardiac patients. The heart is the central regulator of the body by supplying oxygenated blood throughout the system. Impairment of cellular function could lead to heart failure, myocardial infarction, ischemia, and even stroke. Understanding the effect of these distinct types of cellular stress on cardiac function is crucial for the scientific community to understand and develop novel therapeutic approaches. This review will comprehensively explain the different mechanisms of cellular stress and the most recent findings related to stress-induced cardiac dysfunction.

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1. Introduction

Cell degeneration and dysfunction are among the primary causes of numerous cardiovascular diseases, leading to tissue and cumulative organ collapse and decline. Such a phenomenon is even more prominent as we age. Cardiovascular diseases (CVDs) are a common co-morbidity of ageing-associated diseases (Suzman et al., 2015). The heart is the central regulator of the body, which must pump constantly to meet daily needs. In pathological conditions, the heart faces multiple cellular stresses such as mitochondrial stress, endoplasmic reticulum stress, replicative stress, and hypoxia. But the defence system undertakes countermeasures to neutralize the stress and restore the balance. However, at a certain point, excessive stress contributes to cardiac dysfunction. Knowledge of cellular stress is imperative for the successful development of a drug specific to the disease condition. Considering the importance of stress dynamics in pathology, this review focus on the mechanism of action of different organelle molecular stress response. There are unique molecular mechanisms in each organelle, but all these mechanisms interlink with one another to maintain body homeostasis. The mitochondria provide a vital source of cellular energy: adenosine triphosphate (ATP), nicotinamide adenine dinucleotide phosphate (NADPH), and NADP (Morales et al., 2020), meeting the cell's daily demands. But impairment of mitochondria function causes an imbalance in reactive oxygen species (ROS) which results in premature apoptosis and activates other cellular responses. One of the active responses is endoplasmic reticular (ER) stress, which leads to the accumulation of misfolded and unfolded protein, leading to the activation of the unfolded protein response (UPR) pathway and autophagy, impairing cardiac contraction and relaxation. Cells undergo a spectrum of stress and are exposed to a multitude of stress-inducing elements which cause alterations in cellular functioning. In response to stress, cells generate countermeasures to maintain cellular balance. For example, when quality control mechanisms, like autophagy, are activated, damaged organelles (such as mitochondria) are cleared and new organelles are synthesized (Fulda et al., 2010). However, prolonged stress impairs the repair mechanisms of the cell and leads to the activation of cell death mechanisms (such as apoptosis, necrosis, etc.) (Jurivich and Zhou, 2007). Similarly, cells also face pathological stress conditions such as a lack of oxygen. Oxygen is essential for the heart to function properly, a decrease in normal oxygen supply (normoxia) is known as hypoxia. Under hypoxic conditions, the heart is kept under constant pressure to maintain the normal body environment, which further increases cellular stress in cardiac cells. All these processes lead to cell senescence or the development of tumorigenic properties. A cell's fate is also determined by the crosstalk between stress response pathways.

2. Mitochondrial stress

Mitochondria is the powerhouse of the cell: it is capable of migrating to other organelles, with compatible bioenergetics and morphology to subsidize the target organ (Adaniya et al., 2019). Mitochondria are regulated by fusion and fission. Fusion is an event where different mitochondrial compositions are mixed, thereby alleviating the mitochondrial damage, whereas, fission is the fragmentation of mitochondria to distribute the mitochondria contents evenly (Losón et al., 2013). As the heart is a continuous pumping organ, it requires huge energy demand, relying on mitochondrial bioenergetics. They cover one-third of the total cell volume and contribute to the 6–7 kg ATP/day (Morales et al., 2020). Cardiac mitochondria are segregated into three main types based on their subcellular locations: perinuclear mitochondria, subsarcolemmal mitochondria, and intermyofibrillar mitochondria (Jhun et al., 2018). The mitochondrial dynamics are maintained by multiple cellular factors, fission, for example, is regulated by dynamin-related protein-1 (Drp-1), mitochondrial fission protein (Fis1), mitochondrial fission factor (Mff), and dynamins proteins 49 and 51 (MiD49 and MiD51). Meanwhile, fusion is regulated mainly by mitofusin: Mfn1 and Mfn2, and optic atrophy 1 (Opa1) (Losón et al., 2013). Impairment of fusion and fission is known to induce cardiac dysfunctions such as heart failure, ischemia, and myocardial infarction (MI). Recently, it was identified that Mfn-2 and AMP-activated protein kinase (AMPK) are key regulators of autophagy in response to mitochondrial stress [9]. Mitochondrial stress triggers a cascade of responses such as mitochondrial fission, autophagy, and more importantly, accumulation of mitochondrial-associated ER membrane (MAM). The latter is essential for the regulation of autophagy and mitochondrial division because it triggers the translocation of AMPK from the cytosol to the MAM and the mitochondrion where it interacts directly with Mfn2 [9] (Figure 1).

2.1. Drp-1 as a key mediator of mitochondrial fission

Drp-1 has been shown to play a critical role in mitochondrial fission. A recent study found that Drp-1 deficient HeLa cells expressed altered respiratory function and changes in mitochondrial nucleoid morphology which suggests that mitochondrial fission is required to maintain proper respiratory activity and morphology of mitochondrial nucleoids in human cells (Ota et al., 2020). Drp-1 recruitment is modulated by MiD49, MiD51, Mff, and Fis1 [7]. Recently, it was found that Drp1/Fis1 interaction mediates mitochondrial dysfunction in septic cardiomyopathy (Haileselassie et al., 2019; Losón et al., 2013). Additionally, Drp-1 is regulated by several post-translational modifications: ubiquitination, phosphorylation, SUMOylation, palmitoylation, S-nitrosylation, and O-GlcNAcylation; these modifications play an important role in mitochondrial dynamics and are linked to cardiovascular disease pathogenesis (Jin et al., 2021). Ubiquitination of Drp-1 by mitochondrial ubiquitin ligase MITOL/MARCH5 or by Parkin targets the damaged mitochondria for proteasomal degradation; this process, for example, plays an important role in mitochondrial transport and interaction with ER (Nagashima et al., 2014; Qi et al., 2019). Deficiencies of these regulating factors are associated with increased activity of Drp-1, leading to ROS imbalance, and resulting in cardiovascular pathological conditions (Nagashima et al., 2014). Drp-1 knockout models have upregulated IL-1, IFN- γ , and TNF- α resulting in defective efferocytosis leading to atherosclerosis (Hu et al., 2020).

2.2. Mitophagy

Mitophagy is vital for the proper functioning of the cell, it is a quality control mechanism that eliminates defective mitochondria after damage or stress through the autophagosome-lysosome pathway (Onishi et al., 2021). Mitophagy is specific to defective mitochondria groups, thereby eliminating only detrimental units. Failure of the mitochondria to cope with the structural instability will activate certain autophagy-related factors such as proteases, chaperones, and ubiquitin-proteasomes to reinstate homeostasis (Braun and Westermann, 2017). Furthermore, the accumulation of unfolded proteins in mitochondria triggers the transcriptional activation of mitochondrial proteases and chaperones. There are two mechanisms by which mitophagy occurs, one dependent and another independent of autophagic factors. The autophagic-independent mechanism is modulated mainly through an outer mitochondrial membrane (OMM)-localized mitophagy receptors and proteolysis (mediated by ubiquitin ligases such as Parkin and MARCH5). In OMM receptor-mediated mitophagy, the presence of transmembrane receptors such as NIX, BNIP3, and FUNDC1 results in the formation of a bridge between the LC3-interaction region (LIR) motif of these receptors and the LC3 ligand present on the OMM. A recent study found that dysregulation of FUNDC1 destabilized cardiomyocytes during high-fat consumption (Pei et al., 2021). An example of indirect mitophagy regulation is BMAL1, a cardiac rhythm gene involved in monitoring the cardiac cycle. It regulates BNIP3 by binding to its promoter region, thereby indirectly controlling mitophagy (Li et al., 2020). On the other hand, proteolysis-mediated mitophagy is activated by the accumulation of PINK1 (PTEN-induced putative kinase protein 1), which is known to activate E3 ubiquitin ligase Parkin. Parkin targets OMM-related proteins using PINK1-generated phosphoubiquitin, which is feedbacked as a substrate for PINK1. The long non-coding RNA H19 prevents superfluous mitophagy by downregulating PINK1. H19-deficient cells showed low PINK1 expression, causing dysfunctional cardiomyocytes via excess mitophagy (Wang, S.H. et al., 2021). Drp1 also plays a crucial role in regulating mitophagy by interrupting the PINK1 pathway and inducing apoptosis in senescent cells (Wei et al., 2021). Alternatively, mitophagy can be regulated independently of autophagic factors. Though this pathway is not well explored, it was reported that mitochondria can be eliminated by lysosomes through early Rab5+ve endosomes. In obesity-induced cardiac failure, overexpression of Rab9 protected the heart from high-fat consumption by promoting mitophagy (Tong et al., 2021). Additionally, the inactivation of mitophagy was reported to cause diabetic cardiomyopathy. One of the main results of doxorubicin (DOX)-induced cardiotoxicity is the fragmentation of mitochondria and impaired mitophagy. Mitophagy also poses a promising target for DOX-induced cardiomyopathy, as mice treated with DOX, showed reduced expression of Rubicon, a negative regulator of autophagy (Liu, X. et al., 2019).

2.3. The Mitochondrial unfolded protein response (mtUPR) pathway

Under stress conditions, mitochondrial unfolded protein response (mtUPR) acts as a last resort to neutralize the affecters and reinstate the homeostasis of the system. Additionally, mtUPR is tightly regulated and helps prevent any aberrant misregulation by directing the activation of autophagy/mitophagy to eliminate the dysfunctional mitochondria. However, prolonged activation of mtUPR has detrimental effects on cellular metabolism. Furthermore, mtUPR activation has been implicated in various pathological conditions such as heart

failure, neurological diseases, and cancer. Initially, mtUPR was discovered in mammalian cells and it was reported that when mitochondria face certain specific stressors, mtUPR promotes the upregulation of mitochondrial chaperones; this up regulation does not affect the other organelles' functions. Later, Zhao et al. (2002) displayed the same effects by inducing the accumulation of the misfolded proteins in the mitochondria, which lead to the confirmation of mtUPR existence in mitochondria. mtUPR is activated under various stress conditions which include deletions in mtDNA, and overexpression of misfolded protein via activation of transcriptional activation of nucleus DNA to the expression of mitochondrial chaperones. This activation of nucleus-localized DNA occurs by retrograde mode of transport of transcriptional factors from the mitochondria to the nucleus. The accumulation of truncated proteins is the most effective mode of mtUPR activation, which triggers the expression of mitochondrial chaperones such as DNAJ, Hsp60, and Hsp10. Failure of these chaperones will disrupt the protein trafficking and produces powerful mtUPR responses. For example, the inhibition of the oxidative phosphorylation pathway (OXPHOS) by rotenone causes significant increases in UPR activation, which in turn dysregulate the OXPHOS transcriptional factors.

2.3.1. Regulation of mtUPR—The mechanism underlying mtUPR stress response is densely regulated. mtDNA deletion causes upregulation of mitochondrial chaperones such as hsp60, and hsp10. In addition, the C/EBP homologous protein (CHOP) further activates DNAJ, ClpP, and LonP1 within the UPR cascade. Moreover, activation transcription factor 5 (ATF5) modulates the mtUR cascade which carries two factors, the mitochondrial targeting sequence (MTS) and the nuclear localization sequence (NLS). Under healthy conditions, ATF5 is localized in mitochondria; in stress conditions, ATF5 translocates to the nucleus to regulate the proteases and chaperone transcription levels. In addition to the above-mentioned factors, ATF4 is also implicated in mtUPR activation. Compared with ER stress factors, activation of all CHOP, ATF4, and ATF5, requires recruitment of ISR (integrated stress response). ISR is an evolutionarily conserved pathway, activated by eIF2 α kinases namely PRKR-like endoplasmic reticulum kinase (PERK), double-stranded RNA-dependent protein kinase PKR, General Control Nonderepressible 2 (GCN2), and heme-regulated eukaryotic translation initiation factor 2 α kinase (HRI) (Wek et al., 2006). The eIF2 α kinase can significantly reduce global protein synthesis while enhancing the generation of selective genes such as ATF4, assisting in cell recovery. However, the severity of the cell stress leads to the induction of cell death. The dephosphorylation of eIF2 α kinase can abort the ISR and return to normal protein synthesis. In addition, kinase response varies based on the stress stimulus such as amino acid depletion (Pakos-Zebrucka et al., 2016). Though various stress elements activate eIF2 α phosphorylation, the outcome varies based on the context. The decisive result of ISR depends on the duration and severity of stress, other than its nature of it. As such prolonged ISR is considered to culminate in cell death whereas, short-term ISR are meant to establish a pro-survival response and reinstate homeostasis (Dey et al., 2010). Various studies have reported on how ISR is diversely regulated by CHOP, ATF4, and ATF5 (Michel et al., 2015; Sasaki et al., 2020). For instance, altered expression of mtDNA causes reduced expression of ISR-responsive genes which depend on the transcriptional regulator ATF4 (Michel et al., 2015). However, further studies are required to establish strong relationships between ISR, mtUPR, and mitochondrial stress.

2.3.2. The connection between mtUPR and mitophagy—Mitophagy and mtUPR are two damage responses that balance homeostasis in the mitochondria. The process of activation for both responses shares common factors that are essential in expressing the downstream target. For example, perturbations in ROS level, accumulation of misfolded/unfolded proteins, and mutations in the mtDNA trigger both mtUPR and mitophagy (Smyrniak, 2021). Although some studies state the independence of mitophagy and other mitochondrial stress responses (Chen et al., 2021), some of the signaling is common to both pathways, for instance, excess mitophagy activates mtUPR in HNC cells (Kang et al., 2021). Remarkably, inhibition of mtUPR partially distorted the mitophagy response; it has been shown that mitophagy regulates myocardial stress via mtUPR responses (Wang, Y. et al., 2021). One primary example of a shared factor for activation of both mitophagy and mtUPR especially the SKN-1 gene, which senses an imbalance in ROS levels. SKN-1 activates mitophagy in a retrospective manner (Palikaras et al., 2015), whereas, it has also been shown to interact with ATF5 (ATFS-1, *C.elegans* homologue), thereby inducing the mtUPR pathway (Nargund et al., 2012).

2.3.3. Clinical significance of mtUPR in cardiac dysfunction—Mitochondria is the main provider of the daily energy requirements for heart contraction and relaxation. These organelles are the main source of ROS production, which act as signaling molecules, and control systemic communication. However, an imbalance in ROS causes impairment of normalcy, which triggers the homeostasis mechanism (Dietl and Maack, 2017). In cardiomyocytes, activation of mtUPR is reported to have beneficial effects by alleviating the deteriorating effects of mitochondrial dysfunction and improving contractile failure (Smyrniak et al., 2019). Furthermore, mtUPR is also activated by hemodynamic overload and neurohumoral stress, which protect against cardiac dysfunction (Smyrniak et al., 2019). ATF5 is a key mammalian modulator of mtUPR, which has been proved to enable cardioprotection (Wang, Y.T. et al., 2019). Most of the treatments available for cardiac diseases act by blocking neurohumoral hyperactivation (such as angiotensin-receptors blockers, and angiotensin-converting enzyme inhibitors) to alleviate cardiac stress. Examining the activation of mtUPR under neurohumoral overload inhibitors will help to understand its systemic regulation of cardiac stress (Bozi et al., 2019). LonP1 protease is a multi-functional enzyme that regulates mitochondrial proteostasis and prevents cellular stress. Under hypoxic conditions, LonP1 protease regulates ROS levels, providing cardioprotection (Kuo et al., 2015). Furthermore, LonP1 mitigates cardiac injury by adjusting the mitochondrial bioenergetics and it adapts to maintain homeostasis by reducing the complex one composition and activity (Venkatesh et al., 2019). Interestingly, LonP1 is also indirectly involved in controlling ferroptosis (Wang et al., 2020). Being ubiquitous in mitochondria, oxidative post-translational modifications impair the electron transport chain, mitochondrial respiration, and left ventricular dysfunction (Hoshino et al., 2014). Mitochondrial dysfunction has also been linked to ER stress; however, the main mechanism of interaction has not yet been elucidated. For example, mtDNA damage induced eIF2 α phosphorylation, which activated integrated stress response (ISR) genes, implicating activation of ISR by ATF4 rather than by mtUPR induction (Sasaki et al., 2020). Mitochondrial dysfunction activates the ISR arm of UPR focusing mainly on ATF4. The interaction of ATF4 with CHOP is a well-studied interplay in the UPR pathway

which results in negative regulation of ATF4-dependent genes (Su and Kilberg, 2008). Activation of ATF4 upregulates several genes involved in autophagy: *Atg3*, *Atg5*, *Atg7*, *Atg10*, *Atg12*, *Atg16*, *Becn1*, *Gabarap*, *Gabarap12*, *Map1lc3b* and *Sqstm1* upon amino acid deprivation (B'Chir et al., 2013). The regulation of autophagy genes depends on the ATF4 and CHOP signaling, which is decided by the ratio of CHOP and ATF4 bound to specific promoter *cis*-elements. Therefore, ATF4 acts as a fine tuner of autophagic response based on cellular requirements (B'Chir et al., 2013). A study by Kaspar et al. (2021) group showed that ATF4 acts as an attenuator diminish prolonged ISR signaling, where CHOP-C/EBP β interaction modulates the ATF4 expression. Thus, prevention of overactivation of ATF4 during mitochondrial stress delays cardiomyopathy. Moreover, the upstream targets of ATF4 also affect stress responses such as HRI which plays vital in the OMA1-DELE1-HRI pathway. Repression of OMA1 is proved *in vivo* to be protective against heart failure conditions under mitochondrial dysfunction which is essential in the cleavage of DELE1 which modulates HRI kinase activity (Guo et al., 2020). Blockage of OMA1-DELE1-HRI is beneficial in certain stress conditions, on the other hand detrimental. Inhibition of this pathway also repressed cytosolic Hsp70 and displayed a protective effect under mitochondrial stress. Furthermore, a similar correlation was confirmed by the absence of mitochondrial protease and chaperone alteration (such as Hsp60 and LonP1) (Evinova et al., 2022). Contrastingly, the loss of other mitochondrial protease CLPP ameliorates cardiac injury by inducing the mtUPR pathway (Seiferling et al., 2016). Similarly, upregulation of Hsp60 results in cardiomyocyte cell death (Lin et al., 2007). Surprisingly, mtProhibitin depletion activates mtUPR, through lipid modulation and autophagy instead of mitophagy resulting in extending the lifespan of mammals (de la Cruz-Ruiz et al., 2021). Choline improved the cardiac condition by promoting mtUPR via the AMPK-SIRT3 pathway (Xu et al., 2019). Thus, mtUPR acts as a promising therapeutic target for treating CVD.

2.4. Correlation between mitochondrial stress and cardiac dysfunction

Mitochondria are overly sensitive organelles; they could be easily damaged by a lack of nutrients or oxygen supply. However, their adaptation mechanisms allow them to eliminate the damaged mitochondria to maintain proper mitochondrial function in the cell. Proper mitochondrial function is vital for many organs of high energy consumption such as the heart. When the mitochondrial function is impaired in cardiac cells, there is enhanced production of reactive oxygen species, uncoupling of the electron transport chain, depletion of cell ATP stock, and many other disruptions that eventually lead to extensive cell damage and apoptosis. Usually, mitophagy will restore normal cell function but when this process is dysfunctional, the cardiomyocytes cannot withstand the increased oxidative stress derived from mitophagy dysfunction and this will lead to apoptosis. Altered mitochondrial function and clearance will lead to cardiovascular disease due to enhanced ROS formation and decreased ATP levels in cardiomyocytes. Below, we will discuss other ways mitochondrial dysfunction can lead to cardiovascular disease (Figure 2).

2.4.1 Proteolytic processing of OPA1—The proteolytic processing of dynamin-like GTPase OPA1, in the inner mitochondrial membrane, is a pivotal step in the regulation of mitochondrial dynamics. There are two mitochondrial proteases, YMEL1 and OMA1, that mediate the cleavage of OPA1 from long (L-OPA10) to the short form (OPA1-S)

which is essential for mitochondrial fission. Under cellular stress, OPA1 is cleaved to S-OPA1, inhibiting fusion, and causing mitochondrial fragmentation, resulting in dilated cardiomyopathy and heart failure (Wai et al., 2015). Contrastingly, mtUPR induces fusion, instead of fission and upregulates mitochondrial biogenesis elements. Furthermore, FUNDC1-mediated mitophagy induces mtDNA fragmentation and induces mtUPR during myocardial ischemic injury (Ji et al., 2022). Several studies are required to delineate the coupling of mitophagy and mtUPR to design highly specific targeted therapy.

2.4.2. Lipid peroxidation—Lipid oxidation-mediated cardiac dysfunction has not been well investigated. Lipid overload is a primary cause of heart-related diseases, inhibiting glucose utilization and resulting in lipotoxicity (Wende and Abel, 2010). Increased fatty acid utilization causes metabolic inflexibility through the Randle cycle and suppresses glucose oxidation (Goodpaster and Sparks, 2017). Lipid oxidation is the main commodity for cardiac functioning. At the prenatal stage, the heart relies on maternal lactate and glucose supply as the main source of energy. However, during perinatal development, cardiomyocytes shift to lipid oxidation as a central energy source (Makinde et al., 1998). During this process, mitochondria undergo dire conformational change, both shape and volume, accompanied by a change in cellular enzyme composition (LCAD, MCAD, CPT1, and ACSL1) to adapt to energy requirements (Lopaschuk et al., 1994). Post-translational modification of Drp-1 plays an essential role in cardiac maturation after birth. Extended exposure to lipids causes enhanced ROS production, morphological changes, increased mitochondrial respiration and promotes mitochondrial fission (Tsushima et al., 2018). Furthermore, the accumulation of ceramide caused the upregulation of mitochondrial dynamic factors such as OPA1, MFF, and mitophagic factors such as PINK1. In addition, insulin dependent Akt regulation is limited in cells with ceramide accumulation, triggering protein phosphatase 2A (PP2A) activation (Bekhite et al., 2021).

2.4.3. Doxorubicin cardiotoxicity—Cancer treatment is associated with multiple layers of chemotherapeutic treatment to eliminate tumor growth. However, chemotherapy has been associated with damage to several organs. Doxorubicin (dox), an anthracycline agent, is a primary anti-cancer drug for a spectrum of cancer diseases: breast, ovarian, gastric, acute lymphoblastic leukaemia, neuroblastoma, small cell lung, bladder, thyroid, osteogenic bone tumors, Wilm's tumor, Hodgkin's and cutaneous T cell lymphoma (Sritharan and Sivalingam, 2021). However, doxorubicin-mediated anti-cancer therapy is associated with increased heart failure because of upregulated ROS environment (Varricchi et al., 2018). DOX-mediated cardiotoxicity is caused because of the accumulation of DOX in mitochondria. It forms an iron complex, which causes increased ROS production (Ichikawa et al., 2014). Furthermore, downregulated glutathione peroxidase 4 and increased expression of lipid oxidation via the Dox-Fe²⁺ reaction culminate in the condition of toxicity (Tadokoro et al., 2020). Loss of ubiquitin E3 ligase TRIM21, which negatively regulates the p62-Keap1-Nrf2 - antioxidant pathway, improved the mortality of mice and protected against DOX-induced cardiotoxicity (Hou et al., 2021). Dox treatment caused non-heme deposition through heme breakdown by Nrf-2 mediated pathway (Fang et al., 2019). Supportively, Ferrostatin and iron chelation have alleviated heart failure (Fang et al., 2019; Tadokoro et al., 2020).

3. ENDOPLASMIC RETICULUM STRESS

Post-translational modification of protein takes place in the endoplasmic reticulum (ER), where proteins are folded into the proper three-dimensional structure and destined for different cellular locations. The ER is the main server of the cell organization and takes part in the secretory pathway, cellular storage of Ca^{2+} , cellular communication, protein folding, and translocation (Sun et al., 2021). Interruptions in ER functioning activate the unfolded protein response (UPR) and ER-associated degradation (ERAD) pathway, which neutralizes the cause of ER stress to promote homeostasis. Inefficacy of these mechanisms leads to activation of cell death, and apoptosis, eliminating the cell (Hwang and Qi, 2018). The heart being the constant worker of the body requires a constant flow of energy; impairment in the cardiac function such as ischemia, cardiomyopathy, heart failure, or atherosclerosis will impose increased demand on the ER protein folding unity, which induces ER stress. The induction of ER stress has been a negative regulator of pathological conditions in the heart, which increases the chance of heart failure (Zhou et al., 2021).

3.1. Crosstalk between ERAD and other signaling pathways

The ER is an oxidative environment, stocked with enzymes like protein disulfide isomerase (PDI), which enhances the formation of a disulfide bond, thereby folding into proper protein structure (Trevelin and Lopes, 2015). Any disruptions in the folding will cause the retention of misfolded and unfolded proteins in the ER, which will activate ER stress, resulting in apoptosis (Delbrel et al., 2018). ERAD is a checkpoint mechanism, that monitors protein folding in the ER, and maintains homeostasis, for example, ERAD can sense alterations in lipid biogenesis, which can either upregulate/downregulate the expression of enzymes involved in the process (Lemberg and Strisovsky, 2021). The misfolded/unfolded protein sensing mechanism of ERAD involves multiple stages: detection, translocation, and elimination (Lemberg and Strisovsky, 2021). Briefly, ERAD detects any unfolded proteins by N-glycans motif in the misfolded proteins with the help of EDEM (ER degradation-enhancing α -mannosidase-like protein) and lectin chaperones. Later, the misfolded proteins are translocated to the cytosol by the Hrd1-Sel1-ERAD axis for proteasomal degradation (Li et al., 2010).

The ER also regulates the flow of Ca^{2+} in the cytoplasm, ER, and extracellular matrix. The Ca^{2+} required for the contraction and relaxation of cardiac muscle regulates the opening and closing of the ER membrane. In addition, sarcoplasmic/ER Ca^{2+} ATPase 2a (SERCA2a) also controls the Ca^{2+} balance that is required for proper heart functioning (Saheki and De Camilli, 2017). The misaligned nature of Ca^{2+} circulation in CVD promotes the activation of proteases, lipases, and nucleases. Stromal interaction molecule 1 (STIM1) is a molecular Ca^{2+} detector that regulates cardiac metabolism. A previous study showed that knockout of STIM1 causes abrogated mitochondria, erratic lipid accumulation, and dilated cardiomyopathy (Collins et al., 2019). Overall, ER is involved in regulating protein, lipid, and Ca^{2+} balance in cardiac tissues. Additionally, junctions between ER and other organelles have been crucial for effective cellular communication. For instance, the lack of Golgi membrane tethering protein, At CASP which is responsible for forming a junction between ER and Golgi to eliminate ceramide, will cause an accumulation of toxic lipids in

ER (Gillingham and Munro, 2016; Osterrieder et al., 2017). Furthermore, ER trafficking is also associated with mitochondria, by the presence of MAM (Mitochondrial associated ER Membrane), which regulates the signaling molecule Ca^{2+} , as well as the translocation of lipid molecules vital for promoting cell survival (Sasi et al., 2020). In post-mitotic cells like cardiomyocytes, it is essential to monitor calcium overloading (Whelan et al., 2010). A study by Beretta et al. (2020) displayed the pro-survival mechanism involved in the generation of ROS-generating protein Nox4. Under stress conditions, Nox4 is recruited at the MAM site and amplifies Akt-mediated phosphorylation of InsP_3R (which is a major channel for calcium release from ER), preventing calcium flux and thereby inhibiting necrosis. Heart exposed to ischemia-reperfusion condition activates Nox4 mediated mechanism to reduce the infarct size. Various proteins carry the MAM domain, such as the FUN14 domain-containing protein 1, which interacts with the IP_3 receptor, modulating the Ca^{2+} signaling in diabetic heart conditions (Wu et al., 2019). Accumulation of Ca^{2+} has a two-edged effect on the system: Excess Ca^{2+} promotes autophagy (Wang and Kaufman, 2016) and parallelly it also blocks autophagy by inducing calpain during ischemic reperfusion (IR) injury (Lu et al., 2020). A study showed that blocking the transposon has potential therapeutic benefits to restore cardiac performance, diastolic Ca^{2+} flow, and recovery of contraction ability in myocardium-stunned hearts (Mariángelo et al., 2022). Furthermore, in IR injury, ferroptosis seems to augment the effect of ER stress; overexpression of miR-133a and H_2S treatment attenuated ER stress-mediated cell death and cardiomyocyte motility (Ren et al., 2019). Chen et al. (2020) reported circDLGAP4, a circular RNA, to be a mediator of ER stress, which regulates the expression of HECT domain E3 ubiquitin-protein ligase 1 (HECTD1) and mediates IR injury.

3.2. Unfolded protein response (UPR) pathway

The unfolded protein response maintains the cellular proteins in a balanced state. It functions in either two ways: increasing or limiting the protein folding capacity of ER (Wang and Kaufman, 2012). Three vital signaling components are involved in this mechanism: IRE1 α (inositol-requiring enzyme 1 α), ATF6(activating transcription factor 6), and PERK (pancreatic endoplasmic reticulum kinase), which help ER to propagate its actions (Ron and Walter, 2007). The common element between all three of the signaling components is the ER luminal domain, which can sense the critical concentration of misfolded protein in the ER. When the protein requirement is high, UPR tries to increase the folding machinery by increasing ER capacity, transcription of ER chaperones, and biogenesis of ER components. Each UPR sensor has a unique mechanism to execute its response. IRE1 α has two enzymatic actions at the cytoplasmic tail: The serine/threonine kinase domain and the endoribonuclease domain (RNase) (Tirasophon et al., 1998; Wang et al., 1998). In presence of unfolded proteins, IRE1 α is trans-auto phosphorylated and gains RNase activity, which leads to the splicing of XBP1(X-box protein1) mRNA (Calton et al., 2002; Korennykh and Walter, 2012). Then, the active XBP1 translocates to the nucleus and upregulates the proteins associated with increasing ER size and function like MANF (Mesencephalic astrocyte-derived neurotrophic factor) to protect from ER stress (Wang et al., 2018; Yoshida et al., 2001). Additionally, ATF6 collaborates with XBP1 by translocating to the Golgi and gains active form by cleaving at site-1 and site-2 proteases, increasing the ER size (Yamamoto et al., 2007). After cardiac arrest, during recovery, the

UPR pathway is activated in various organs to restore the damage. Activation of ATF6 arms improved neuronal function and triggered protein removal pathways. This showed the prosurvival capabilities of UPR-mediated ATF6 activation after cardiac arrest (Shen et al., 2021). Contrastingly, PERK slows protein translation by inactivating eukaryotic translation initiation factor 2 α (eIF2 α) to clear the unfolded proteins (Bertolotti et al., 2000; Harding et al., 1999). However, this stalling is detrimental: hyperactivation of PERK upregulates CHOP (C/EBP-homologous protein) which inhibits the Bcl2 expression, resulting in cell death (Marciniak et al., 2004; McCullough et al., 2001). Extended ER stress results in pressure overload in cardiomyocytes triggering CHOP signaling, deletion of CHOP, improved cardiomyocyte resistance to cardiac remodeling, and cardiac dysfunction. Recently, Al-Yacoub et al. (2021) reported the existence of CHOP-mediated non-canonical pathways in FBXO32-associated cardiovascular diseases. FBXO32 is a muscle-specific E3 ubiquitin ligase, which regulates Akt and calcineurin A dependent cardiac hypertrophy mice model (Li et al., 2004; Li et al., 2007). Likewise, exposure to chronic ER stress enables IRE1 α to gain off-target RNA substrate by oligomerization, resulting in the degradation of ER elements (Han et al., 2009; Hollien and Weissman, 2006). Furthermore, the aberrant splicing of IRE1 α limits some microRNAs, which leads to the upregulation of proapoptotic factors such as TXNIP (thioredoxin-interacting protein), which promotes Caspase1 mediated cell death (Lerner et al., 2012) (Figure 3).

The ER stress response also protects against cardiac dysfunction, for example, cardiac-specific kinase, Pak2 is a stress-responsive protein that protects from apoptosis. Pak2 is localized near the ER membrane; it is activated by PI3K (phosphatidylinositol 3 kinases)-Akt, AMPK, and PERK-ERK1-ERK2(extracellular signal-regulated kinase 1) to inhibit cell death (Binder et al., 2019). However, in ischemic reperfusion conditions, PAK2 is downregulated, inducing ROS generation, Ca²⁺ overload, and activation of caspase 12 resulting in apoptosis, implicating the protective role of PAK2 in cardiac disease conditions (Wang, S. et al., 2019). Furthermore, Pak2 also regulates Nrf2 in a stressed heart; deletion of Pak2 upregulated Nrf2 expression. Pak2 attenuates the ER-mediated Nrf2 activation by inducing the XBP1-Hrd1 axis (Binder et al., 2022). The UPR pathway interlinks with mitochondria-mediated cell death. Lowering of the mitochondrial permeability transition pore (mPTP) causes the release of cytochrome C, which activates the caspase cascade, leading to intrinsic apoptosis. The mPTP is regulated by the distribution ratio of proapoptotic (such as Bax, Bak) to antiapoptotic factors (bcl2, mcl1, Bcl-xl) (Shi et al., 2021). The terminal UPR has been shown to interact with at least six BH3-only proteins (Bim, Bik, Bid, Bad, Noxa, and Puma) (Arystarkhova et al., 2021; Li et al., 2006; López et al., 2017; Puthalakath et al., 2007; Rodriguez et al., 2012; Upton et al., 2008). In addition, UPR is correlated with the biogenesis of mitochondria, it is involved in the control of mitophagy and mitochondrial integrity. For instance, IRE1 α has a scaffolding role for Ca²⁺ transport into the mitochondria through its non-canonical path in MAM (Malli and Graier, 2019). Furthermore, UPR also monitors the major elements of mitochondrial biogenesis such as PGC1 α , Nrf1, TFAM, citrate synthetase, and TFEB (Transcription factor EB), altered expression of these genes leads to heart failure (He et al., 2020; Pan et al., 2022; Prola et al., 2019; Xu et al., 2020; Zhang et al., 2021).

3.3. ER stress and autophagy

Autophagy is another adaptive measure in ER to remove the surplus accumulation of misfolded/unfolded protein, termed reticulophagy. Precisely, uncontrolled deposition of proteins, activates auto-ubiquitination of E3 ubiquitin ligase, TRIM13 (tripartite motif-containing protein 13), which binds with p62 (or sequestosome1), autophagy regulator (Ji et al., 2019). Simultaneously, the arginine transferase enzyme attaches arginine residues to the N terminal of ER chaperones, causing destabilization of ER-resident chaperones such as Bip (Ji et al., 2019). This unstable N-terminal, known as N-degron, binds with p62, forms an oligomer of TRIM13 and p62, and causes induction of autophagy by recruiting an LC3B autophagy adaptor (Ji et al., 2020). In ER stress, induction of autophagy exerts cytoprotective effects, for example, PERK signaling during ER stress, recruits autophagy-related protein 12 (ATG12) and activates the ATG12-ATG16-ATG5 axis, which converts LC3-I to LC3-II form, and promotes cardioprotection (Hsieh et al., 2020; Kouroku et al., 2007). Autophagy is a double-edged sword, as ER stress prolongs, it activates the apoptotic pathway, instead of recovering the ER. In some pathological cases, ER stress impairs autophagy, disrupts the clearance of protein accumulation, and promotes the disease condition (Rashid et al., 2015).

4. Hypoxia

Hypoxia is a condition of low oxygen in the body or a region of the body. Hypoxia-inducing factor (HIF) is the fundamental factor in promoting hypoxia during oxygen deprivation (Wang and Semenza, 1995). In normoxia, HIF is prevented from translocating to the nucleus by proteasomal degradation. HIF is highly regulated by prolyl-4-hydroxylases (PHDs), which hydroxylate the proline residues in HIF-1 α ; asparagine residues are hydroxylated by Factors Inhibiting Hypoxia (FIH) (Majmundar et al., 2010). These hydroxylated residues are recognized by Von Hippel–Lindau protein (pVHL), an E3 ubiquitin ligase, a signaling enzyme for proteasomal degradation (Ivan et al., 2001). However, under hypoxia conditions, pVHL and FIH expressions are repressed, promoting HIF-1 α translocation. In the nucleus, HIF-1 α binds with HIF-1 β forming a complex and interacting with Hypoxia Responsive Elements (HRE), thereby promoting hypoxia (Jaakkola et al., 2001). Apart from HIF-1, there are HIF-2 α and HIF-3 α . Similar to HIF-1 α , HIF-2 α is also stabilized during hypoxia by forming a dimer with ART(aryl hydrocarbon receptor nuclear translocator), transactivating the VEGF (Vascular endothelial growth factor) and erythropoietin promoter, implicating a vital role in promoting vascular development (Ozaki, 2007). The exact role of HIF-3 α during hypoxia is still unknown, however, it dimerizes with HIF-1 β despite its lack of the c-terminal transactivation domain, thereby negatively regulating the transcription of HIF-1 α and HIF-2 α (Knutson et al., 2021) (Figure 4).

4.1. Metabolic switch alternation in hypoxia

The human body mainly relies on two major sources of energy, glucose, and fatty acids. Around 96% percent of ATP production depends on fatty acids and glucose, but, oxidation of fatty acids produces the highest ATP yield (Su et al., 2021). However, the utilization of minimal oxygen, which is required for glucose oxidation, yields a prominent amount of ATP compared to fatty acids (Su et al., 2021). This variation in energy dependence

correlates with the geographical location of ethnic groups such as Tibetans, Sherpas in Nepal, and the Andeans (Holden et al., 1995). People located at higher altitudes rely on glucose as their main source of energy and tend to suffer from severe cardiovascular disease, due to the presence of a constant hypoxia environment. Compared to the highlanders, lowlanders showed increased utilization of fatty acids as their metabolic fuel (Holden et al., 1995). Two chief regulators that are associated with modulating the hypoxic environment are peroxisome proliferator-activated receptor- α (PPAR- α) and peroxisome proliferator-activated receptor- γ coactivator-1 α (PGC-1 α); both are downregulated under hypoxic conditions (Cole et al., 2016). High altitude residents: Tibetans and Sherpas have shown PPAR- α lacking genetic variants among the population (Ge et al., 2012). PPAR- α is found to be downregulated by the elevated expression of HIF1 α . Additionally, PPAR- α regulates PDK2 and PDK4 factors that are involved in glucose oxidation (Cole et al., 2016; Mansor et al., 2016). Furthermore, PPAR- δ , an isoform of PPAR also regulates HIF-1 α , by restoring vascular homogenesis during post-ischemia in a ligand-dependent manner (Wu et al., 2022). PGC-1 α is a regulator of PPAR- α , it is involved in mitochondrial biogenesis, and seems to function erratically in the left and right ventricles in the heart during hypoxic conditions (Dorn et al., 2015). For instance, 3-week hypoxia-exposed both the left and right ventricle in a rat model showed downregulated PGC-1 α (Ramjiawan et al., 2013). However, in a 4-week hypoxia model, the left ventricle displayed no notable difference, but in the right ventricle, PGC-1 α expression was downregulated, and PGC-1 β was upregulated with increased mitochondrial respiration (Ferri et al., 2018). Under a hypoxic environment, the energy consumption by either of the ventricles (left and right) varies; the muscles respond differently to the same hypoxic exposure. For example, in a study of rats exposed to 10% oxygen, the left ventricle relied on pyruvate for maximum energy utilization and its maximal mass-specific respiration and mitochondrial-specific respiration were significantly increased after hypoxia exposure when compared to normal conditions. On the other hand, the right ventricle's maximal mass-specific and mitochondrial-specific respiration did not show any significant differences between hypoxia and normal conditions (Ferri et al., 2018). This study demonstrated the energy reliance of the heart on glucose-dependent oxidation under hypoxic conditions and it also demonstrated that muscles respond differently to hypoxia. The changes were correlated with the alterations in the electron transport chain (ETC) complex: I, II, IV (Heather et al., 2012). Coenzyme Q (CoQ) is an important structural component of ETC has been associated with potential antioxidant capabilities and acts as a vital electron carrier (Zozina et al., 2018). In hypoxia, the mRNA stabilization which is associated with the CoQ is interfered with, causing reduced ATP synthesis, increased cell death and leading heart failure (Liu, Y. et al., 2019). Supplementation of CoQ, improved antioxidant properties in high altitude inhabitants (Biuomy et al., 2020).

A study by Cho et al. (2013) led to the finding of PGC-1 and ERR-induced Regulator in Muscle 1 (PERM1), a novel effector of PGC-1 and ERR, enriched in skeletal muscle and cardiomyocytes. Perm1 regulates the mitochondrial biogenesis in cardiomyocytes, thereby monitoring the energy metabolism required for the heart. PERM1 protected the cardiomyocytes against hypoxic conditions and promoted mitochondrial biogenesis (Cho et al., 2021). Insulin resistance development in diabetic hearts, impairs HIF-1 α mediated signaling, disabling the metabolic switch from fatty acid to glucose, resulting in cardiac

dysfunction (Su et al., 2021). Factors such as obesity and hyperglycemia, are notably associated with CVD in highlanders (Zheng et al., 2019). The development of insulin resistance is a common characteristic observed in intermittent hypoxia and congenital heart disease (Ip et al., 2002; Niwa, 2019). In addition to glucose and fatty acids, ketone poses another prime source of energy; energy generation from ketone is comparable to glucose and fatty acid utilization (Zozina et al., 2018). A recent study showed that elevated levels of β -OHB, the main constituent of ketone bodies, are harmful to cardiomyocytes exposed to hypoxic/ischemic conditions, however, inhibition of HIF-1 α by Roxadustat administration alleviated the effects of β -OHB by inducing a metabolic shift toward glycolysis (Ma et al., 2021). Their results suggest that increased ketone body supply in cardiomyocytes under hypoxic conditions exacerbates cardiac dysfunction.

4.2. Induction of mitophagy in Hypoxia

The heart is more sensitive to oxygen-deprived conditions like hypoxia. Most of the high energy demand of the heart is supplemented by mitochondrial OXPHOS. In heart failure, excess demand for energy will compromise the OXPHOS activity causing depletion of ATP synthesis and augmenting the cardiac injury. Under ischemia, a low oxygen-deficient condition that causes cardiac damage, the Ca^{2+} flux and the electrochemical gradient are impaired. Excessive autophagy in the ischemia-reperfusion models reflects the degradation of vital organelles that are complementing the energy supply. Hypoxia also induces receptor-mediated-mitophagy. For instance, FUNDC1 is known to cause mitophagy in response to hypoxia, by dephosphorylation of PGAM5. This circuit is blocked by the Bcl2L1/Bcl-xL binding to PGAM5, inhibiting the dephosphorylation. Polo-like kinase 1 (PLK1) is known to cause mitophagy; it suppresses ischemia-induced cardiac injury by FUNDC1-dependent pathway resulting in mitophagy activation. In a PLK1 overexpression model, upregulated mitophagy and attenuated hypoxia were observed (Mao et al., 2021). Conditions like ischemia and starvation trigger a phenomenon known as autophagy, a cell death process mediated by ion channels, characterized by increased formation of autophagosomes (Liu et al., 2013).

4.3. Hypoxia in CVD

Ischemia occurs due to the narrowing of the coronary artery or ruptures of plaques. This leads to an impoverished oxygen supply causing irregular ATP synthesis, increased ROS generation, and cardiac dysfunction. Ischemia injury occurs during heart transplantation, surgery, or angioplasty (Lee et al., 2019). The two critical causes of ischemia-reperfusion injury are Ca^{2+} overloading and subsequent ROS accumulation, lowering the mitochondrial permeability transition pore (mPTP). Low mPTP will result in the release of cytochrome C into the cytoplasm leading to cell death by activation of the caspase cascade (Abdelwahid et al., 2017). Interestingly, periodical exposure to hypoxia such as Chronic Continuous Normobaric Hypoxia (CNH) and short-term intermittent hypoxia (IH) causes acclimatization, developing resistance toward hypoxia (Chang et al., 2019; Prokudina et al., 2019). In a recent study, rat hearts under CNH conditions showed reduced infarct size in response to ischemia and reperfusion (Lishmanov et al., 2017; Maslov et al., 2013; Neckar et al., 2003). This cardiac protection was characterized by developing mPTP resistance

towards Ca^{2+} loading, however, blockage of opioid receptors completely terminates the MPTP resistance effects (Lishmanov et al., 2017).

Similarly, IH also known as cyclic hypoxia involves the exposure of cells to cycles of hypoxia/reoxygenation. These short cycles of hypoxia are sufficient for the occurrence of the metabolic switch and non-oxidative energy consumption. One of the consequences of transient normoxia in hypoxic cells is the accumulation of ROS, due to the inability of mitochondria to activate the ROS-scavenging pathway. Furthermore, restored oxygen availability will lead to rapid HIF- α degradation and the hypoxic stress response necessary for survival will be compromised exposing the cells to oxidative stress (Guan et al., 2019). IH leads to obstructive sleep apnea, which is associated with intermittent loss of airflow in sleep. Several studies point out that IH is characterized by hypertension, stroke, and MI (Marin et al., 2005). Contrastingly, IH also improves cardioprotection by regulating the vital signaling molecule, ROS. This perpetual exposure is enabling cardioprotection, however, the mechanism underlying this protection is yet to be explored. This cardioprotection is attained by upregulating -antioxidant factors, mainly superoxide dismutase (SOD) and glutathione peroxidase (GPx) and preventing the mPTP opening (Aguilar et al., 2018). Furthermore, this protection is enabled by maintaining Ca^{2+} homeostasis. This adaptation is associated with the elevation of the O-linked N-acetylglucosamine protein, activating the glucose-6-phosphate dehydrogenase (G6PDH). The activation of G6PDH results in homeostasis by regulating NADPH/NADP⁺ and GSH/GSS implicating control of anti-oxidant properties (Ou et al., 2021). HIF1 α exerts its protective effect by generating adenosine molecules and promoting adenosine receptors which are proven to display anti-inflammatory effects (Eltzschig et al., 2003; Kong et al., 2006). Consequently, hypoxia upregulates HIF2 α , an isoform of HIF that promote cardioprotection by inducing its target site amphiregulin (AREG) (Koeppen et al., 2018). Lee, et. Al., (Lee et al., 2020) reported that HIF2 α protects from myocardial ischemia by induction of epidermal growth signaling receptor ERBB1. Furthermore, deletion of HIF2 α resulted in increased infarct size, implicating the HIF2 α 's role in ensuring cardio-specific protection. HIF2 α shows cardioprotective action by regulating IL6 through PI3K/Akt axis and STAT3 pathway (Wu et al., 2021).

Recently, Hif3 α was found to regulate hypoxia tolerance; knockout of HIF3 α significantly reduced the hypoxia tolerance. The mechanism undermining this kind of characteristic is erythropoiesis via GATA4 (Cai et al., 2020). Alternative splicing of HIF3 α results in the generation of different HIF3 α variants hypothesized to have a spectrum of regulatory functions. Furthermore, HIF3 α 2 can directly regulate the erythropoietin (EPO) gene, by binding at the HRE element situated at the promoter of EPO (Tolonen et al., 2020). Surprisingly, HIF3 α 2 can also induce apoptosis by accumulating at the later stages of hypoxia. Surfeit deposition of the HIF3 α 2 isoform can induce the expression of DNA damage-inducible transcript 4 (*DDIT4*); as a consequence, caspase 3-mediated apoptosis will be activated, resulting in cell death (Jaskiewicz et al., 2022). The effects of differential expression of hypoxia isoform in cardiac disorder are summarized in Table 1 (Chen et al., 2022; Eubank et al., 2011; Ghosh et al., 2021; Hickey et al., 2010; Hnatiuk et al., 2016; Menendez-Montes et al., 2021; Sun et al., 2015; Tolonen et al., 2020).

Future perspectives and conclusion

Response to cell stress is a vital element in deciding cell fate. For temporal stress, a systemic response will try to eliminate the damaged organelles and reinstate them to their original form. However, protracted stress often leads to either cell death or senescence. Because stress pathways are dynamic, understanding their mutual crosstalk will aid in understanding the molecular mechanisms underlying them. Nonetheless, despite the emergence of new findings demonstrating their dynamic nature, several interconnections between these stress pathways remain largely unknown. Furthermore, research in this area has been restricted to in-vitro culture-based systems. Novel approaches to developing complex model systems involving 3D culture systems such as endothelial cells and CMCs should be initiated (Bartoszewska and Collawn, 2020; Bartoszewska et al., 2022). Understanding the mechanism triggering these responses will lay a stronger foundation to develop potential therapeutics for the existing pathophysiology. Another limitation in this field is that the results do not account for the pathways' genome-wide consequences, as activation of PERK and IRE1 leads to transcription and translation of multiple genes. This is possible by incorporating next-generation sequencing and single-cell sequencing. Although challenging, incorporating this will significantly improve our understanding of the crosstalk.

A large portion of hypoxia-related research has concentrated on exposure for a specific amount of time. However, because physiological oxygen demands vary with each cell in our body, our experiments should be tailored to account for IH. Another issue is the use of hypoxia mimics, which merely degrade FIH. Such compounds do not shed light on the molecular complexities of these pathways. So, the results obtained should be substantiated by limited oxygen availability (Bartoszewska and Collawn, 2020; Bartoszewska et al., 2022). Since mitochondria are the central source of energy, it is highly regulated. However, several regulatory mechanisms are still unknown or not explored. For instance, the LC3-independent mode of mitophagy is still not completely resolved, though it contributes to the lysosomal way of mitochondrial removal. Abnormal stress responses are frequently reported in most disease conditions, they exacerbate the patient's state of condition and diminish their lifespan. Therefore, considerable studies are required to clear out the perplexity of the underlying stress mechanism to obtain a lucid view of these stress elements.

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ABBREVIATIONS

MI Myocardial infraction

| | |
|---------------|--|
| Drp-1 | Dynamin related protein-1 |
| Dox | Doxorubicin |
| mtUPR | Mitochondrial unfolded protein response |
| HGPS | Hutchinson-Gilford progeria syndrome |
| ER | Endoplasmic reticulum |
| ERAD | Endoplasmic reticulum associated degradation |
| UPR- | Unfolded protein response |
| CVDs | Cardiovascular diseases |
| ROS | Reactive oxygen species |
| iCM | Inner cell mass |
| VEGF | Vascular endothelial growth factor |
| iNOS | Induced nitric oxide synthetase |
| IL | Interleukin |
| DNA | Deoxyribonucleic acid |
| RNA | Ribonucleic Acid |
| LncRNA | Long non-coding RNA |
| MALAT1 | Metastasis associated lung adenocarcinoma transcript 1 |
| PI3K | Phosphoinositide 3-kinases |
| Akt | Ak strain transforming/Protein kinase B |
| FUS1 | Fused in sarcoma |
| Mff | Mitochondrial <i>fission factor</i> |
| MiD | Mitochondrial dynamics protein |
| OPA1 | Optic atrophy-1 |
| Mfn | Mitofusin |
| MAM | Mitochondrial associated membrane |
| AMP | Adenosine monophosphate |
| AMPK | AMP-activated protein kinase |
| SUMO | Small ubiquitin-like Modifier |
| OMM | Outer <i>mitochondrial</i> membrane |

| | |
|--------------------------------|---|
| IFN-γ | Interferon-gamma |
| FGF | Fibroblast growth factor |
| TNF-α | Tumor necrosis factor-alpha |
| LCAD | <i>Long</i> -chain acyl-CoA dehydrogenase |
| MCAD | <i>Medium</i> -chain acyl-CoA dehydrogenase |
| CPT-1 | Carnitine palmitoyltransferase 1 |
| ACSL-1 | Acyl-CoA synthetase-1 |
| PTEN | Phosphatase and tensin homolog |
| PINK1 | PTEN-induced kinase 1 |
| PP2A | Protein <i>phosphatase</i> 2A |
| TRIM21 | Tripartite motif containing-2 |
| p62k | protein 62 kinase |
| KEAP1 | Kelch like ECH associated protein 1 |
| Nrf-2 | Nuclear respiratory factor 2 |
| BNIP3 | BCL2 interacting protein 3 |
| LC3 | Microtubule-associated protein light chain 3 |
| OXPHOS | Oxidative phosphorylation |
| CHOP | CCAAT-enhancer-binding protein homologous protein |
| CLPP | Caseinolytic mitochondrial matrix peptidase proteolytic subunit |
| LONP1 | Lon protease-1 |
| ATFS-1 | Activating transcription factor associated with stress—1 |
| MTS | mitochondrial targeting sequence |
| NLS | Nuclear localization signals |
| ISR | Integrated stress response |
| PERK | RNA-dependent protein kinase (PKR)-like ER kinase |
| PKR | Protein kinase RNA |
| GCN2 | General controlled nonrepressed-2 |
| HRI | Heme-regulated inhibitor |
| eIF2α | Eukaryotic initiation factor-2 α |

| | |
|---------------------------------|---|
| mt | Mitochondria |
| SIRT | Sirtuin |
| SKN-1 | Skinhead-1 |
| PDI | Protein disulfide isomerase |
| EDEM | ERAD-enhancing α -mannosidase-like proteins |
| SERCA | Sarco/endoplasmic reticulum Ca^{2+} -ATPase |
| STIM1 | Stromal interaction molecule 1 |
| IR | Ischemic- reperfusion |
| XBP-1 | X-box binding protein-1 |
| MANF | Mesencephalic Astrocyte-Derived Neurotrophic Factor |
| Bcl2 | B-cell lymphoma 2 |
| TXNIP | <i>Thioredoxin-interacting protein</i> |
| Pak2 | p21-activated kinase-2 |
| ERK | Extracellular signal-regulated kinase |
| mPTP | Mitochondrial permeability transition pore |
| TFEB | Transcription factor EB |
| PGC-1α | Peroxisome proliferator-activated receptor-gamma coactivator-1 α |
| Bip | Binding immunoglobulin protein |
| FIH | Factor inhibiting HIF |
| HIF | Hypoxia inducing factor |
| PHD | Prolyl-4-hydroxylases |
| pVHL | Von Hippel–Lindau protein |
| ART | Aryl hydrocarbon receptor nuclear translocator |
| ATP | Adenosine triphosphate |
| CoQ | Coenzyme Q |
| ETC | electron transport chain |
| PPARα | Peroxisome proliferator activated receptor- α |
| PERM1 | PGC-1 and ERR-induced Regulator in Muscle 1 |
| ERR | Estrogen related receptor |

| | |
|--------------|---------------------------------------|
| CNH | Chronic Continuous Normobaric Hypoxia |
| IH | Short-term intermittent hypoxia |
| SOD | Superoxide dismutase |
| GPx- | Glutathione peroxidase |
| G6PDH | Glucose-6-phosphate dehydrogenase |
| AREG | Amphiregulin |
| EPO | Erythropoietin |
| DDIT4 | DNA damage-inducible transcript 3 |

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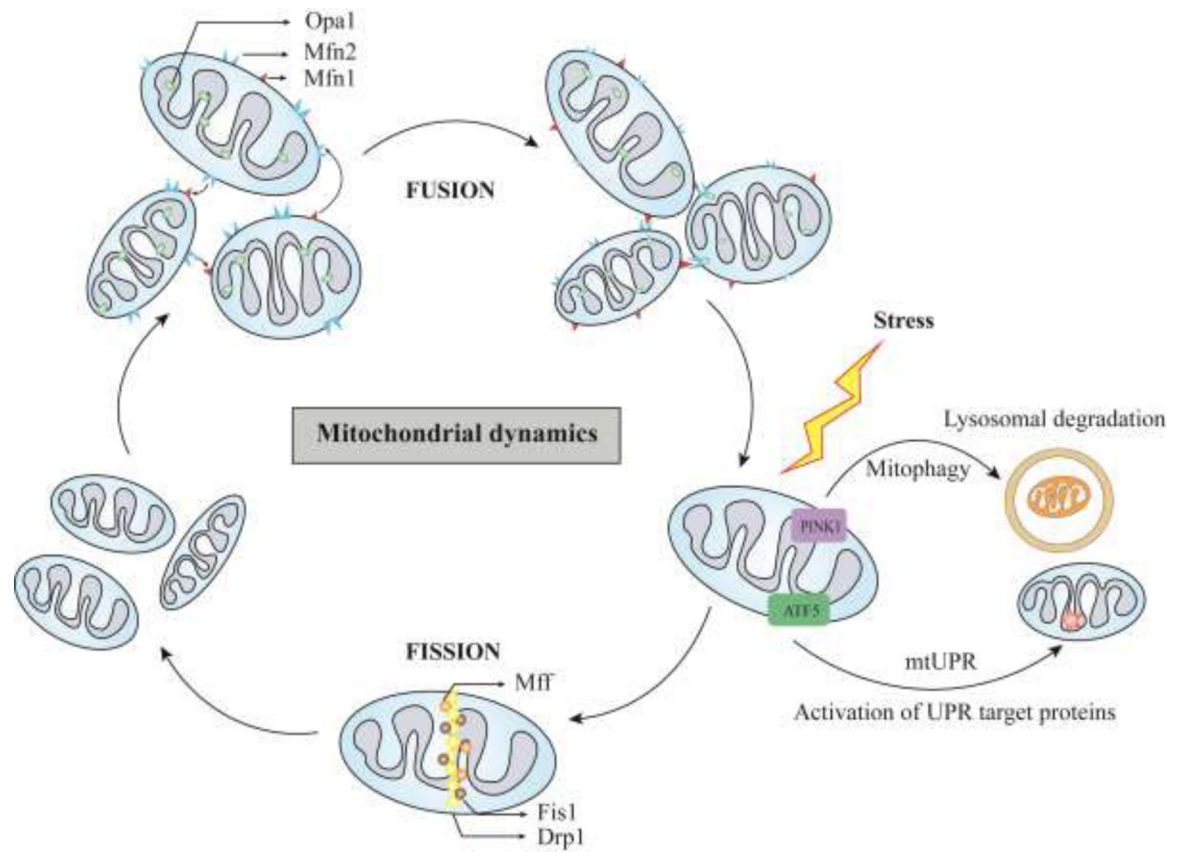


Figure 1. Mitochondrial dynamics and stress response

Mitochondria dynamics is regulated by balanced fusion and fission. Fusion is regulated by Mfn1, Mfn2 and Opa1. Fission is regulated by Drp1, Fis1, and Mff. Imbalance in this homeostasis results in induction of mtUPR and mitophagy. Mfn1- Mitofusin-1; Mfn2- Mitofusin-2; Opa1- Optic atrophy type 1; Drp1- Dynamin-related Protein 1; Fis1-Fission-1; Mff-Mitochondrial Fission Factor; mtUPR- Mitochondrial Unfolded protein response

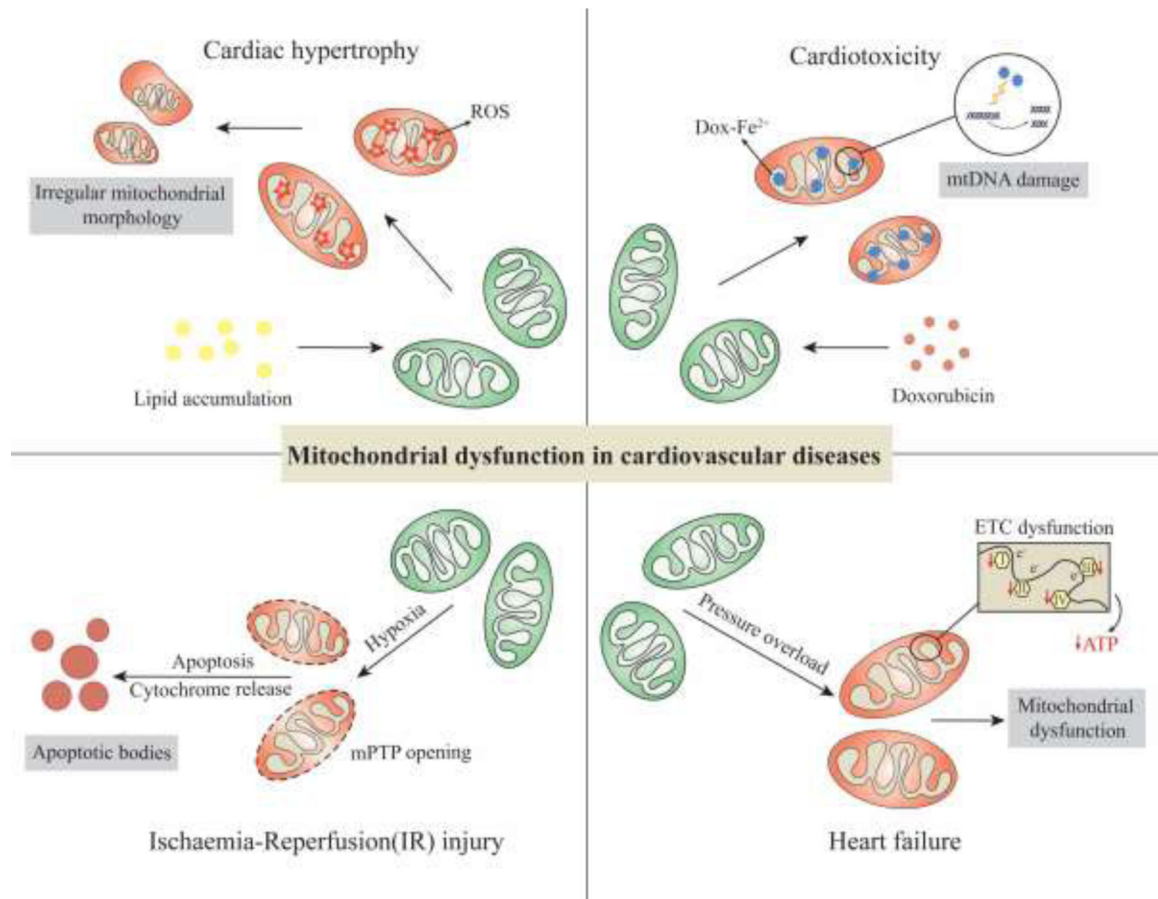


Figure 2. Summary of mitochondria mediated cardiovascular pathologies

Any interruptions in mitochondrial network causes imbalance in homeostasis. In cardiac hypertrophy, increased lipid accumulation causes, accumulation of ROS in the mitochondria, disrupting mitochondrial morphology. In Cardiotoxicity, formation of damages Doxorubicin- Fe^{2+} the mtDNA. Under low oxygen condition, it causes release of cytochrome C and results in apoptosis. In heart failure condition, pressure overload induces ETC impairment and results in mitochondrial dysfunction.

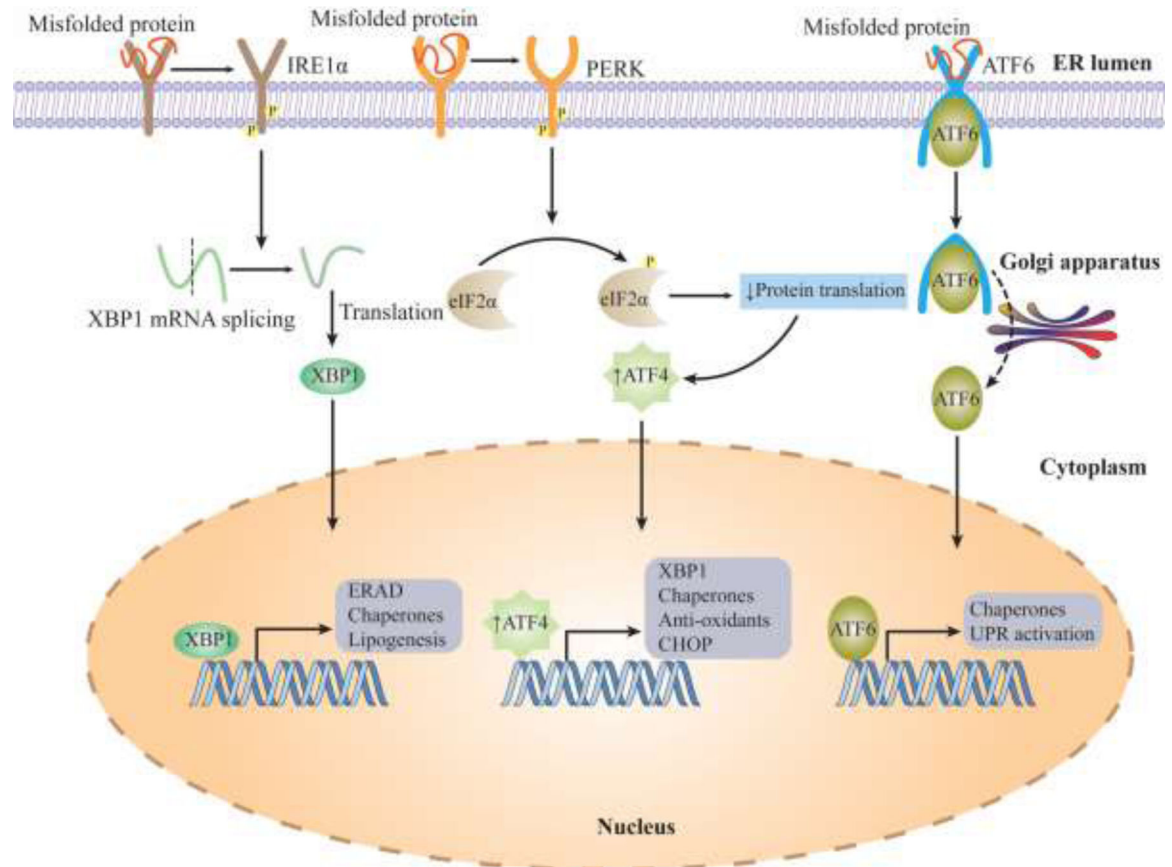


Figure 3. ER stress mechanism

Unfolded Protein Response (UPR) maintains the cellular homeostasis. When misfolded proteins accumulate, they activate three major mechanisms: IRE1 α , PERK, ATF6. These proteins translocate to the nucleus and upregulate the proteins responsible for increased functioning in the ER. Failure to eliminate the accumulation of misfolded proteins, triggers apoptosis.

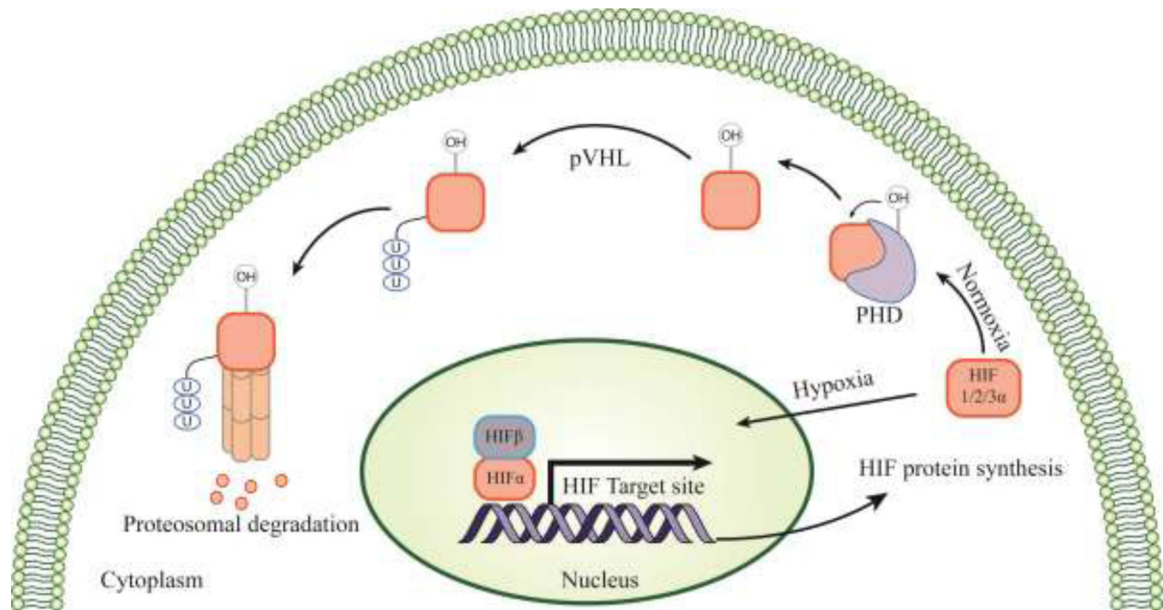


Figure 4. Pictorial representation of Hypoxia mechanism.

Under Normoxia, Hif protein is eliminated by proteasomal mechanism with the help of PHD and pVHL enzymes. However, depletion of oxygen leads to downregulation of PHD and pVHL, results in translocation of Hif to nucleus and forms complex with Hif1 β . This complex promotes the transcription of Hif protein. pVHL- Von Hippel-Lindau protein; PHD- Prolyl-4-hydroxylases

Table-1:

Effect of differential expression of HIF isoforms

| Isoforms | Alterations | Cell line/Model/Organism | Mode of mechanism | Ref |
|------------------|----------------|--|---|--|
| Hif1 α | Overexpression | peri-infarct of sheep (n=6) undergoing coronary occlusion | Reduced infarct size and improved LV systolic performance increased neovascularization | Chen et al., 2022 |
| | | Hif1 α null mouse model | Increased HIF2A Increased mitochondrial number Impaired embryonic glycolysis Activation of amino acid catabolism | Eubank et al., 2011 |
| | Knockdown | H9c2 cells exposed to high glucose | Downregulated angiopoietin-like protein 2, alleviating the hypoxia injury by promoting nrf2 and HO-1 expression | Ghosh et al., 2021 |
| Hif2 α | Overexpression | 46C ESC cell line | Promotes cardiomyogenesis by wnt/ β -catenin pathway | Hickey et al., 2010 |
| | Knockdown | VHLR200W (Chuvash Polycythemia) mouse model | Normalized erythropoietin and endothelin level suppressed both the polycythemia and pulmonary hypertension partial protection against vascular remodeling, haemorrhage, and edema | Hnatiuk et al., 2016 Menendez-Montes et al., 2021 |
| | | HIF-1 α ^{flox/flox} /LysMcre knockout mice | Inhibited soluble form of the VEGF receptor-1 (sVEGFR-1) production in a hypoxic condition Production of VEGF was unaffected | Sun et al., 2015 |
| Hif3 α | Overexpression | - | - | - |
| | Knockdown | Hep3B hepatoma cells | Downregulation of EPO gene | Tolonen et al., 2020 |
| Hif3 α .2 | Overexpression | Hep3B hepatoma cells SK-N-AS cells | Promotes expression of erythropoietin gene (EPO), BMP6, PTX3 | Tolonen et al., 2020 |
| | Knockdown | - | - | - |