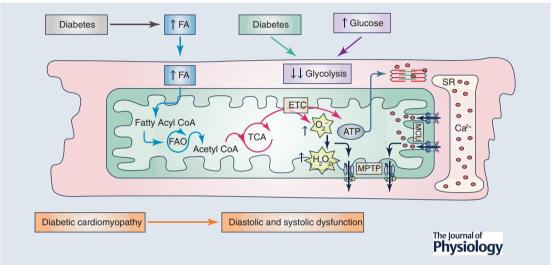
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SYMPOSIUM REVIEW

The role of mitochondria in metabolic disease: a special emphasis on heart dysfunction

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Abstract Metabolic diseases (MetDs) embrace a series of pathologies characterized by abnormal body glucose usage. The known diseases included in this group are metabolic syndrome, prediabetes and diabetes mellitus types 1 and 2. All of them are chronic pathologies that present metabolic disturbances and are classified as multi-organ diseases. Cardiomyopathy has been extensively described in diabetic patients without overt macrovascular complications. The heart

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This review was presented at the joint *Australian Physiological Society* and *Australian Society for Biophysics* Meeting symposium 'Unravelling the mysteries of mitochondria in health and disease' organised by Livia Hool (University of WA), which took place at the Australian National University, Acton Campus, Canberra on 2 December 2019.

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is severely damaged during the progression of the disease; in fact, diabetic cardiomyopathies are the main cause of death in MetDs. Insulin resistance, hyperglycaemia and increased free fatty acid metabolism promote cardiac damage through mitochondria. These organelles supply most of the energy that the heart needs to beat and to control essential cellular functions, including Ca²⁺ signalling modulation, reactive oxygen species production and apoptotic cell death regulation. Several aspects of common mitochondrial functions have been described as being altered in diabetic cardiomyopathies, including impaired energy metabolism, compromised mitochondrial dynamics, deficiencies in Ca²⁺ handling, increases in reactive oxygen species production, and a higher probability of mitochondrial permeability transition pore opening. Therefore, the mitochondrial role in MetD-mediated heart dysfunction has been studied extensively to identify potential therapeutic targets for improving cardiac performance. Herein we review the cardiac pathology in metabolic syndrome, prediabetes and diabetes mellitus, focusing on the role of mitochondrial dysfunctions.

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Abstract figure legend Cardiac mitochondrial function in metabolic disease. Metabolic disease is characterized by decreased glycolysis due to insulin resistance and increased free fatty acid (FA) uptake that promotes FA oxidation (FAO) for ATP generation. Excessive FA accumulation leads to increases in superoxide anion (O_2^-) and hydrogen peroxide (H_2O_2) production over a threshold limit. High levels of reactive oxygen species (ROS) lead to uncoupling of the mitochondria electron transport chain (ETC), which reduces mitochondrial ATP production. In addition, the influx of Ca^{2+} through mitochondrial Ca^{2+} uniporter (MCU) increases excessively. These increases in ROS and Ca^{2+} eventually trigger mitochondrial permeability transition pore (mPTP) opening, leading to cardiomyocyte death. All these alterations promote diastolic and systolic dysfunction, which leads to diabetic cardiomyopathy.

Introduction

Metabolic diseases (MetDs), which result from disrupted normal glucose usage, have increased in incidence in recent years (World Health Organization, 2020). They are divided into three types – prediabetes, metabolic syndrome (MetS) and diabetes mellitus (DM) – according to the organ compromised and/or the severity of the disease itself.

MetDs affect several organs across the human body and raise the risk for multiple conditions including cardiovascular disease (CVD). In patients with DM, metabolism-mediated heart damage can affect heart structure and function, leading to diabetic cardiomyopathy (DCM) (Rubler et al. 1972), without the need for other associated co-morbidities. DCM manifests as persistent cardiac dysfunction that frequently leads to heart failure (HF), the principal cause of death in DM (Boonman-de Winter et al. 2012; Vasiliadis et al. 2014; Lee & Kim, 2017).

Among the factors that affect MetD aetiology, mitochondrial dysfunction has been shown to play a critical role. It is essential to elucidate the mitochondrial processes that lead to MetD progression, from the early stages to the most severe conditions. Improved understanding may guide the identification of potential therapeutic targets and eventually develops strategies to

mitigate or even revert the DCM. The purpose of this review is to summarize the current knowledge about the mitochondrial role within several MetDs, including MetS, prediabetes, and DM, with a focus on the mechanisms of cardiac dysfunction.

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Metabolic diseases

Prediabetes. Impaired glucose tolerance and impaired fasting glycaemia are conditions that define prediabetes. Without changes in their diet and exercise habits, half of the patients with prediabetes will develop type 2 DM (T2DM) (American Diabetes Association, 2019). Diagnosis for prediabetes can be made using the same tests as for T2DM (i.e. fasting glucose, glycated haemoglobin test and/or oral glucose tolerance test) but with a different cut-off (for prediabetes diagnosis: 100 mg/dL \leq fasting glucose < 126 mg/dL, $5.7\% \leq$ glycated haemoglobin < 6.4%, and/or 140 mg/dL \leq glucose after 2 h tolerance test < 200 mg/dL). However, because prediabetes is clinically silent and its detection is usually random, the chances that the patient evolves to develop the more severe T2DM are high.

To study prediabetes, researchers use animal models in which glycaemia is altered without other relevant risk factors (such as obesity and hypertension). Mouse and

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rat fed with a fructose-rich diet are proven models of prediabetes (Alzugaray *et al.* 2009; Mellor *et al.* 2011; Sommese *et al.* 2016; Federico *et al.* 2017; Szűcs *et al.* 2019), as well as fructose-rich diet + streptozotocin (STZ; to destroy pancreatic β -cells) (Koncsos *et al.* 2016), or a single dose of STZ (Mali *et al.* 2016).

Metabolic syndrome. According to the American Heart Association, MetS is diagnosed when an individual shows at least three of the following risk factors: hyperglycaemia, increased blood pressure, dyslipidaemia and abdominal obesity (Grundy *et al.* 2004; American Heart Association, 2016; Dommermuth & Ewing, 2018). In the USA the prevalence of MetS is around 35% (Moore *et al.* 2017), and the worldwide incidence is linearly associated with the degree of obesity and overweight (Saklayen, 2018).

In earlier studies of MetS, researchers used a transgenic mouse model, ob/ob (Ingalls et~al.~1950; Enser, 1972), which shows hyperinsulinaemia, hyperglycaemia, obesity and associated cardiac complications. Currently, additional models are available to mimic MetS, including mice with deficient leptin receptor (db/db) (Hummel et~al.~1966), transgenic mice that overexpress 11β -hydroxysteroid dehydrogenase type 1 to develop increased visceral obesity (Masuzaki et~al.~2001), and mice fed with a high-sucrose plus high-fat diet (HFD) (Surwit et~al.~1995) among others (for full review see Kennedy et~al.~2010; Panchal & Brown, 2011; Fellmann et~al.~2013).

Diabetes mellitus. DM is a well-studied chronic disease that is classified into three different types: type 1 diabetes mellitus (T1DM), T2DM and gestational diabetes. DM is characterized by elevated levels of blood glucose, which occur when the body becomes resistant to insulin or doesn't make enough insulin' (World Health Organization, 2020). T1DM can be an idiopathic disease or an autoimmune disease in which islet autoantibodies are produced against the pancreatic β -cells and therefore insulin production is defective. T2DM results from ineffective use of insulin and is often associated with modifiable factors like obesity and sedentarism (World Health Organization, 2020). An increase in blood pressure due to the impact of the underlying insulin resistance on the vasculature and kidney is also usually related to T2DM (Ferrannini & Cushman, 2012). Gestational diabetes is diabetes diagnosed for the first time during pregnancy, and it leads to an increased risk of developing DM in the future for both the mother and the child. Additionally, pregnancy and delivery complications are higher in individuals with gestational diabetes than in non-diabetic people (Alberti & Zimmet, 1998; American Diabetes Association, 2019; World Health Organization, 2020). The DM diagnosis can be made by measuring fasting glucose (fasting glucose > 126 mg/dL), by using the glycated haemoglobin test (>6.4%), and/or by using the oral glucose tolerance test (glucose after 2 h tolerance test >200 mg/dL).

Prevalence of DM has been increasing in recent years and is currently 8.6% on average worldwide, although it varies widely by country (World Health Organization, 2019). Several non-biological factors (e.g. socioeconomic, demographics, environmental), as well as the increase in human population age and obesity (Unwin & International Diabetes Federation, 2009; International Diabetes Federation, 2019), contribute substantially to the increasing prevalence. The most frequent type of DM is T2DM, which is *per se* a risk for heart disease and can run with other vascular co-morbidities such as increased blood pressure, microangiopathy or kidney disease (among others), enhancing a vicious cycle to increase the risk for heart damage (Boonman-de Winter *et al.* 2012; Shah *et al.* 2012; Chen *et al.* 2018).

To study DM, several models are available. For T1DM, the most widely used is the induction of pancreatic β -cell destruction by STZ injection (McNeill, 2018). However, the potential of STZ to cause non-specific effects has been a major criticism of this model. Other animal models are based on genetic manipulation, such as the diabetic BB rat (Mordes et al. 2005), non-obese diabetic mice (Li et al. 2008), and the Otsuka Long-Evans Tokushima fatty rat (Karakikes et al. 2009; for review see Yorek, 2016). Distinguishing DM, MetS and prediabetes can be difficult since MetS and prediabetes are closely related to DM as the common endpoint of the disease progression. For T2DM, several researchers adopt *ob/ob* and *db/db* mice since they present hyperinsulinaemia and hyperglycaemia (Han et al. 2017; Lee et al. 2018), but both models present hyperlipidaemia and obesity, worsening the cardiovascular risk. Another widespread model of T2DM is based on a HFD (Surwit et al. 1988; Namekawa et al. 2017; Li et al. 2020) in which animals are obese and develop T2DM. Recently, a HFD plus low doses of STZ have been used to mimic T2DM (Guo et al. 2018).

The genetic models of T2DM have an advantage in that they can be used at an early age, but the HFD models are more representative of the human disease. The decision of which model to use for experiments should be made carefully, taking into account that T2DM and MetS present different features that could interfere with the interpretation of the results.

Cardiac pathology in metabolic diseases

Heart disease is a major concern in MetD because it is the primary cause of death in these patients. An extensive study in patients from the Netherlands with T2DM showed that the prevalence of unknown HF was 27.7%, which was higher than in patients with increased body mass index and patients treated for arterial

hypertension (Boonman-de Winter *et al.* 2012). The presence of prediabetes or MetS also enhances the probability of developing T2DM and its progression to DCM and HF (Grundy *et al.* 2004).

The triggers that lead to DCM include hyperglycaemia, hyperlipidaemia and hyperinsulinemia, but the molecular mechanisms are not completely understood (Battiprolu et al. 2010). Several harmful processes occur together in DCM, including left ventricular hypertrophy, interstitial fibrosis, cell death, diastolic and systolic dysfunction, impaired contractility, changes in Ca²⁺ homeostasis, altered substrate utilization, myocardial lipotoxicity and increased reactive oxygen species (ROS) production, and several of these are consequences of mitochondrial dysfunction (Battiprolu et al. 2010). Not all of these deleterious alterations develop at the same time and some of them are the cause or consequence of another. Indeed, to study the MetD model, it is critical to consider not only the election of the model but also the time course of disease progression for conducting the research. In normal conditions, cardiac mitochondria use fatty acids (FAs) to generate approximately 70% of the ATP required by the working heart. In DCM, decreases in glucose transporter type 4 (GLUT4) cause excessive mitochondrial FA uptake, which enhances ROS generation to toxic levels leading to subsequent oxidative stress damage (Boudina & Abel, 2010). The cellular redox environment is one of the major post-translational modulators of protein activity, such as that of the Ca²⁺ handling proteins responsible for excitation-contraction coupling. Sarcoplasmic reticulum (SR) Ca²⁺ uptake and release proteins are subject to oxidative modulations (for review see Federico et al. 2020). For instance, oxidative conditions generally increase the ryanodine receptor 2 (RyR2) open probability, which can lead to cardiac arrhythmias and HF (Xu et al. 1998; Sun et al. 2008). Moreover, the kinases and phosphatases are also subject to oxidation. Lastly, the decreased rate of glycolysis generates glucose accumulation and advanced glycation end products (AGEs). AGE complexes can compromise several enzyme activities, altering cardiac contraction (Shao & Tian, 2015).

Taken together, the metabolic imbalance between FA oxidation and glycolysis is critical in the pathogenesis of MetD-mediated cardiac pathology (Wang *et al.* 2006). The disproportionate mitochondrial FA uptake subsequently leads to disturbances in mitochondrial functions that have a direct impact on cardiac performance.

Mitochondrial role in MetD-mediated cardiac dysfunction

The heart obtains most of its energy from FA oxidation (FAO) and switches to the glycolysis pathway under pathological conditions (Stanley *et al.* 2005; Shao & Tian,

2015). In MetD, the heart is forced to use FAs almost exclusively for generating ATP and this overburdens mitochondria and subjects them to oxidative stresses and injury (Christoffersen *et al.* 2003; Hall *et al.* 2014). On the contrary, it has also been shown that FA can regulate mitochondrial biogenesis by modulating the activity of the peroxisome proliferator-activated receptor- γ (PPAR γ) and PPAR γ -coactivator 1 α (PGC1 α) (Lehman *et al.* 2000; Finck *et al.* 2002; Arany *et al.* 2005).

The morphology of mitochondria is directly related to their functions including ATP and ROS production. It has been described that there are subpopulations of mitochondria defined by their spatial location: subsarcolemmal mitochondria, located immediately beneath the plasma membrane, perinuclear mitochondria, surrounding the nucleus, and intermyofibrillar (IMF) mitochondria, embedded within the myofibrillar networks and making up the most abundant population (Palmer & Hoppel, 1977). The IMF mitochondria in the adult heart are densely compacted between sarcomeres, but their morphology can be changed by the fission-fusion process (Kane & Youle, 2010) and tunnelling connection (Lavorato et al. 2017). Although mitochondrial fission-fusion processes in adult cardiomyocytes are infrequent in physiological conditions, it has been described in pathological situations such as MetDs (Galloway & Yoon, 2015). Furthermore, mitochondrial distribution is altered in MetS and prediabetes (Federico et al. 2017; Yuan et al. 2018) affecting SR-mitochondrial communication, impairing mitochondrial Ca²⁺ and ADP exchange. Therefore, not only is mitochondrial distribution important for the adequate traffic of molecules from and to the SR, but also the expression of several key proteins that tether both organelles and maintain the optimal distance to ensure privileged signal transduction (e.g. Ca²⁺) between them (Seidlmayer et al. 2019). Since three enzymes (2-oxoglutarate dehydrogenase, pyruvate dehydrogenase, and NAD⁺-isocitrate dehydrogenase) of the tricarboxylic acid (TCA) cycle are regulated by Ca2+ in the mitochondrial matrix, it is important to maintain proper Ca²⁺ communication between these two organelles to have an efficient excitation-contraction-bioenergetic coupling (Brookes et al. 2004).

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Taken together, there are multifaceted changes in mitochondrial energy metabolism, shape, Ca²⁺ signalling, connections to SR, ROS generation and quality control that can contribute to the pathogenesis of MetD-mediated heart dysfunction.

Mitochondrial energy metabolism in MetD-mediated heart dysfunction. To carry out blood-pumping activities, the human heart requires 6 kg of ATP per day (Neubauer, 2007). To meet this high energy demand, the

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cardiomyocytes possess a higher number of mitochondria when compared to other cell types. ATP production is coupled to the $\rm O_2$ consumption at the electron transport chain (ETC). H⁺ is pumped into the intermembrane space during the electron transfer process, which generates an inwardly directed proton motive force that will be used later on by the ATP synthase to produce ATP (Mitchell, 1972).

The alterations in O₂ consumption and ATP production rate of MetD hearts remain controversial and may depend on the degree of disease progression. Pham et al. have demonstrated that in the rat STZ model, the decrease in O₂ consumption is associated with a decrease in ATP production, either stimulating complex I with glutamate/malate/pyruvate or complex II with succinate. The authors conclude that diabetic hearts have an overall depression of respiration capacity and ATP production with a significantly decreased P/O ratio (ATP production per O₂ consumed) (Pham et al. 2014). As mentioned above, mitochondria can be divided into different subpopulations according to their location. In patients with T2DM, the O₂ consumption was decreased in states 3 and 4 in subsarcolemmal mitochondria either with glutamate/malate or FA/malate as substrates, without changes in IMF mitochondria.

Additional experiments showed a decrease in ATP production rate in rat models with one dose of STZ (Bombicino *et al.* 2017) or HFD+STZ (Fang *et al.* 2018). Mitochondrial oxidative phosphorylation (OXPHOS) alterations were also studied by measuring the activity of enzymatic complexes from the ETC, TCA cycle enzyme activity and proteomics. The analysed data showed that several of the essential proteins required for a normal mitochondrial function, such as PGC1 α , complex I, II, III and IV, among others, were downregulated in MetD (Yan *et al.* 2013; Szűcs *et al.* 2019; Wang *et al.* 2020).

However, How et al. showed increased O_2 consumption in isolated mitochondria from db/db mice in state 3 when the substrate was palmitoyl-carnitine and detected no changes when pyruvate was used, suggesting an enhanced FAO and a decreased glucose oxidation. The increased O_2 consumption did not translate into an enhancement of cardiac output, indicating inefficiency in cardiac performance, and this may contribute to contractile dysfunction in the diabetic heart (How et al. 2006).

These changes in energy metabolism observed in diabetic animal models are also found in humans. It has been shown that mitochondria in atrial tissue of T2DM patients show a decrease in respiration with glutamate and FA as substrates. Furthermore, the atrial tissue from diabetic patients shows increased mitochondrial $\rm H_2O_2$ emission and decreased glutathione (GSH) levels. These data support the role of mitochondrial dysfunction and oxidative stress in the pathogenesis of HF in diabetic patients (Anderson *et al.* 2009). Another study also

showed decreases in complex I and IV activity in mitochondria isolated from right atrial appendages of diabetic patients compared to non-diabetic (Croston *et al.* 2014). Finally, Montaigne *et al.* reported that heart tissue from patients with T2DM has reduced complex II and III activity, and decreased state 3 respiration, supported by FA, pyruvate or succinate. In contrast, heart tissue from obese patients, associated with less pronounced contractile dysfunction than T2DM, did not show any significant perturbation of mitochondrial function or oxidative stress (Montaigne *et al.* 2014). From these results it can be concluded that the worsening intrinsic myocardial contraction in the transition from obesity to DM is likely related to the impairment of cardiac mitochondrial function (Montaigne *et al.* 2014).

Therefore, using different models of MetD, the majority of studies show an altered O_2 consumption (Table 1) suggesting the importance of mitochondrial energy metabolism in the pathogenesis of MetD-mediated heart dysfunction. Results obtained from human heart tissues (Anderson *et al.* 2009; Montaigne *et al.* 2014) were similar to those from animal models (Yan *et al.* 2013; Wang *et al.* 2020), endorsing the translation of animal studies to humans.

Mitochondrial dynamics in MetD-mediated heart **dysfunction**. Mitochondrial dynamics encompasses fusion, fission, selective degradation and transport processes (Chan, 2020). Fission and fusion are in balance in physiological conditions and maintain normal mitochondrial mass, shape, network, biogenesis and turnover. The fusion process generates a bigger mitochondrion from two smaller ones, merging the contents of both original mitochondria, which helps to mitigate the mitochondrial damage in addition to establishing a mitochondrial network. On the opposite side, fission creates two new mitochondria from a single one, contributing to mitochondrial turnover and facilitating apoptosis during high levels of cellular stress (Kane & Youle, 2010).

Fission and fusion are also related to mitochondrial OXPHOS. Stressed mitochondria or defective OXPHOS promotes mitochondrial fragmentation (Sauvanet *et al.* 2010). The fission process is regulated by several proteins, including dynamin-related protein 1 (DRP1) (Herskovits *et al.* 1993), Fis-1, which connects DRP1 to the outer mitochondrial membrane, and other described adaptors such as MFF, MiD49 and MiD51 (Yoon *et al.* 2003; Otera *et al.* 2010; Palmer *et al.* 2011). Mitochondrial fusion is controlled by two major proteins: optic atrophy protein (OPA1), located in the inner mitochondrial membrane, and mitofusin 1 and 2 (Mfn1/2), located in the outer mitochondrial membrane (Cipolat *et al.* 2004, 2006). The balance between mitochondrial fusion and

Table 1. O ₂ consumption rate in different model	Table 1. C	2 consump	tion rate in	different models
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O ₂ Consumption	Substrate	Model	Disease	Reference
	FA/malate	Human	Diabetic patients (right atrial appendages)	Croston et al. (2014)
↑	FA	db/db	Genetic model of T2DM	How et al. (2006)
\leftrightarrow	Pyruvate	db/db	Genetic model of T2DM	
$\downarrow\downarrow$	FA/glutamate	Human	Diabetic patients (right atrial appendages)	Anderson et al. (2009)
$\downarrow\downarrow$	FA/pyruvate/succinate	Human	Diabetic patients (right atrial appendages)	Montaigne et al. (2014)
$\downarrow \downarrow$	Pyruvate/malate	OVE26	Genetic model of T1DM	Shen et al. (2004)
\leftrightarrow	Glutamate/malate/succinate	HFD	Dietary model of T2DM	Koncsos et al. (2016)

FA, fatty acids; HFD, high-fat diet; T1DM, type 1 diabetes mellitus; T2DM, type 2 diabetes mellitus. Note, the references mentioned in this table are cited in the main text.

fission is essential in mammals, and even mild defects in mitochondrial dynamics are associated with disease aetiology. In general, a tip of the balance toward fission is usually associated with deleterious processes and toward fusion is associated with compensatory mechanisms (Chen *et al.* 2003; Ishihara *et al.* 2009).

In the adult myocardium, fission events are challenging to detect in part due to the abundance and immobility of mitochondria, and therefore the data available related to the mitochondrial dynamics in MetD-mediated heart dysfunction are limited. Transmission electron microscopy images of the heart tissue have shown that in the early stages of cardiac MetD pathogenesis, such as prediabetes induced by a fructose-rich diet, mitochondria are smaller and more spherical in shape compared with control animals (Federico et al. 2017), indicating that fission processes might occur. Koncsos et al. similarly described a decrease in area, perimeter and sphericity of mitochondria in the prediabetic rat model with HFD and STZ treatments (Koncsos et al. 2016). Flow cytometry showed that mitochondrial size and cristae complexity were decreased in diabetic IMF mitochondria in mouse models with one dose of STZ (Williamson et al. 2010). In another paper, the same research group reported that cardiac mitochondrial density was increased and mitochondrial area was decreased, showing unbalanced mitochondrial dynamics towards the fission processes in this diabetic model (Dabkowski et al. 2010).

Montaigne et al. explore the role of impaired mitochondrial dynamics in myocardial contractile dysfunction in patients with T2DM without obesity. The mitochondria of the heart tissues from these patients, harvested during cardiopulmonary bypass, showed no difference in density but a significant decrease in size. The authors also analysed the amounts of proteins related to the mitochondrial dynamics such as Mfn2, Mfn1, OPA1, DRP1 and Fis1. They only found a large decrease in the expression of the mitochondrial fusion related protein Mfn1, which may account for mitochondrial fragmentation. These changes in mitochondrial morphology were associated with impaired

complex I, II and III activity, decreased respiratory control ratio and increased oxidative stress, further confirming the close relationship between mitochondrial shape and function (Montaigne *et al.* 2014).

Mitochondrial calcium signalling in MetD-mediated heart dysfunction. The mitochondria are juxtaposed with the SR in the cardiomyocytes and participate in taking up a fraction of the Ca²⁺ during each heart-beat (Beutner et al. 2005). Localized Ca²⁺ released from the SR creates a high Ca²⁺ microdomain in the SR mitochondria contact sites to stimulate mitochondrial Ca²⁺ uptake. The mitochondrial calcium uniporter (MCU) at the inner mitochondrial membrane, a highly Ca²⁺-selective ion channel (Kirichok et al. 2004), is responsible for the bulk of Ca²⁺ uptake from microdomains to the mitochondrial matrix (Csordás et al. 2006; de Brito & Scorrano, 2008). In addition to the MCU, other mitochondrial Ca2+ influx mechanisms such as mitochondrial ryanodine receptor 1 (Beutner et al. 2005) and the rapid mode of Ca²⁺ uptake (RaM) (Buntinas et al. 2001) have also been identified. The extrusion of Ca²⁺ from the matrix to the cytosol is carried out by the Na⁺/Ca²⁺/Li⁺ exchanger (NCLX) (Li et al. 1992) and the Ca²⁺/H⁺ exchanger (Gunter et al. 1991).

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The kinetics of mitochondrial Ca2+ uptake and extrusion in the beating adult cardiomyocytes is still under debate (De la Fuente & Sheu, 2019). Some authors describe that the amount of Ca²⁺ taken up by mitochondria in each heartbeat is modest and the Ca2+ gradually accumulates inside the mitochondrial matrix throughout the heartbeat until a new steady state is reached, in which the uptake and extrusion are balanced (Miyata et al. 1991). Other authors propose that mitochondria can follow the cytosolic Ca²⁺ oscillations and take up and release Ca²⁺ on a beat-to-beat basis (Murgia et al. 2009; Andrienko et al. 2009). It has been proposed that mitochondria may function as a Ca²⁺ buffer due to their capacity in taking up a large amount of Ca²⁺ through the MCU, and as such they can modulate the amplitude of cytosolic Ca²⁺ transients (Drago et al. 2012). This will require that mitochondria can take up

Ca²⁺ on a beat-to-beat basis, which is still unclear at present. The most accepted role for the mitochondrial Ca²⁺ in cardiomyocytes is associated with the regulation of cardiac energy production. The mitochondrial Ca²⁺ regulates the activity of the TCA cycle, as mentioned above (Duchen, 1992; Kohlhaas et al. 2017; De la Fuente & Sheu, 2019). Interestingly, this function has been recently challenged due to the lack of energetic phenotype in the normal beating heart of a germline MCU-knockout mouse model (Pan et al. 2013). However, under intense β -adrenergic stimulation, it was reported that Ca²⁺ influx through the MCU is a requisition for the fight or flight response (Wu et al. 2015).

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In pathological conditions, the mitochondrial Ca²⁺ uptake and overload have detrimental consequences for energy production and possibly promote DCM complications (Federico et al. 2017; Wu et al. 2019). Several studies have attempted to monitor Ca²⁺ signalling in isolated cardiomyocytes from different models of MetD. In cardiomyocytes isolated from 5-week STZ-induced diabetic rats, diastolic Ca2+ concentration and Ca2+ spark frequency significantly increased in comparison to age-matched control rats. The amplitude of Ca²⁺ transients was significantly decreased and the duration was prolonged (Yaras et al. 2005). In cardiomyocytes isolated from a prediabetic model, increased spontaneous Ca²⁺ oscillations in the cytosol were associated with spontaneous contractions, which were prevented by KN-93, a Ca²⁺-calmodulin kinase II (CaMKII) inhibitor, or the addition of Tempol, a ROS scavenger, in the diet (Sommese et al. 2016). The increases in Ca²⁺ spark frequency and spontaneous Ca2+ transients indicate that these animals are prone to cardiac arrhythmias. In another study, the increment in the frequency of sparks, which also depends on ROS and CaMKII, promoted apoptosis that was linked to increased mitochondrial swelling and decreased mitochondrial membrane potential (Federico et al. 2017).

A small number of studies have measured mitochondrial Ca²⁺ regulation in the cardiomyocytes of MetD animal models. Suarez et al. observed decreased MCU expression, low glucose usage and high FAO in the heart of an STZ mouse model, which led to a decrease in respiratory control ratio, ATP production and mitochondrial membrane depolarization (Suarez et al. 2018). The mitochondrial Ca2+ concentration was monitored with a mitochondria-targeted Ca²⁺ probe, pericam, and was found to be decreased in diabetic heart. Moreover, when the MCU was restored by AVV9-MCU injection, mitochondrial metabolism recovered to normal levels (Suarez et al. 2018). Also, mitochondrial Ca²⁺ was found to be decreased in neonatal cardiomyocytes (Suarez et al. 2008) and adult cardiomyocytes exposed to high glucose (HG) (Diaz-Juarez et al. 2016). Besides, Diaz-Juarez et al. showed decreased expression of MCU

in the HG condition, and recovered MCU expression improved mitochondrial Ca²⁺ handling (Diaz-Juarez et al. 2016), proving that optimal MCU expression reverts the mitochondrial metabolic and functional changes in

Despite the importance of mitochondrial Ca²⁺ in regulating heart function, very few studies have monitored mitochondrial Ca²⁺ dynamics in MetD hearts (Yaras et al. 2005; Sommese et al. 2016; Federico et al. 2017; Suarez et al. 2018). Several additional mitochondria-targeted Ca²⁺ probes are currently available, such as genetically expressed CEPIA and MitoCam (Lu Xiyuan et al. 2013; Kanemaru et al. 2020), and chemical dyes such as Rhod-2AM (Chen Chen et al. 2012; Fernandez-Sanz et al. 2014), for measuring spatiotemporal aspects of the mitochondrial Ca²⁺ signalling in the heart of MetD models. These measurements will help in our understanding of the role of mitochondrial Ca²⁺ dynamics in MetD-mediated heart dysfunction.

MetD-mediated dysfunction. The ROS heart mitochondrion is the principal organelle involved in ROS production (Jensen, 1966). ROS are free radical oxidants, such as superoxide (O_2^-) and the hydroxyl radical (${}^{\bullet}OH$), and non-radical oxidants, such as singlet oxygen (${}^{1}O_{2}$) and hydrogen peroxide (H₂O₂). ROS generation is tightly related to ATP production, O2 consumption and mitochondrial Ca²⁺ signalling (Brookes et al. 2004). A sustained net increase of ROS will eventually damage the cell (Wang et al. 2008; Zorov et al. 2014; Nickel et al. 2014; Korge et al. 2017) and therefore both ROS generating and eliminating systems exist in cells. Under physiological conditions, mitochondria produce O₂⁻ from O₂ oxidation by complex I or complex III, which is dismutated to H₂O₂ by manganese-dependent superoxide dismutase (MnSOD). The H₂O₂ will be further eliminated in the mitochondrial matrix by antioxidant systems, glutathione peroxidase and peroxiredoxin. These systems are coupled with NADPH production. Thus, increased cytosolic ROS can be a cause of increased production and/or decreased elimination (Nickel et al. 2014). Zorov et al. described a process named ROS-induce ROS-release in which the ROS produced by a single mitochondrion can be transferred to an adjacent mitochondrion, leading to a chain reaction in which many consecutive mitochondria produce a massive amount of ROS, which causes subsequent cell injury (Zorov et al. 2000, 2014).

In the early stages of MetD, such as prediabetes and hyperglycaemia, morphological and functional changes in mitochondria have been associated with an increase in oxidative stress. Koncsos et al. (2016) showed an increased H₂O₂ and nitrotyrosine production in DCM. As mentioned above, excessive Ca²⁺ traffic from SR/ER to the mitochondria can cause mitochondrial Ca²⁺ overload that

results in ETC uncoupling and excessive ROS production. Koncsos et al. attributed the increase in ROS production to an enhanced SR/ER-mitochondria connection through Mfn2 due to their reported overexpression of the Mfn2 without any changes in other fusion proteins (Koncsos et al. 2016). In a prediabetic model, we found an increase of ROS as well as lipid peroxidation in cardiac homogenates, which promoted CaMKII-mediated arrhythmias and apoptosis. These effects could be prevented either by ROS scavenging or by CaMKII inhibition (Sommese et al. 2016; Federico et al. 2017). Phosphorylation of RyR2 by CaMKII enhances the open probability of the channel, increasing SR Ca²⁺ leak. Therefore, preventing RyR2 activation by CaMKII avoids not only mitochondrial swelling but also mitochondrial membrane depolarization induced by prediabetes. We also reported a decreased distance between SR and mitochondria in the prediabetic heart, which would further augment ROS-mediated CaMKII activation (Federico et al. 2017).

Additionally, in advanced stages of MetD, an increase in ROS, malondialdehyde or 4-hydroxy-2-nonenal has been reported, as well as changes in O_2 consumption, MnSOD activity and/or NADPH oxidase activity (Santos *et al.* 2003; Csont *et al.* 2007; Rajesh *et al.* 2010; Suzuki *et al.* 2015). Furthermore, increases in mitochondrial superoxide flashes and ROS generation have been described in the STZ model (Ni *et al.* 2016b).

Either increased production or decreased antioxidant capacity can cause net increased ROS levels. Anderson *et al.* showed human atrial tissue from T2DM had enhanced H₂O₂ production and decreased GSH/GSSG ratio (Ghosh *et al.* 2005; Anderson *et al.* 2009). Dabkowski *et al.* showed the *ob/ob* model had increased malondialdehyde and 4-hydroxyalkenal (both products of oxidation of polyunsaturated FAs), coupled with decreased peroxiredoxin-V (Dabkowski *et al.* 2010). Accordingly, Shen *et al.* showed that intensifying the ROS scavenger systems, such as overexpression of MnSOD, was beneficial in preventing DCM (Shen *et al.* 2006).

Taken together, ROS imbalance appears to be one of the most damaging factors in cardiometabolic pathologies (Shen et al. 2006; Suzuki et al. 2015). Therefore, antioxidant treatments could be a reasonable approach to deter the harmful ROS effects on the heart (Qin et al. 2012; Fang et al. 2018). Mito-TEMPO, a scavenger of mitochondrial ROS, has been shown to prevent mitochondrial ROS-mediated damage and to mitigate the diastolic dysfunction in DCM (Ni et al. 2016a). The search for effective candidates, including SOD mimetics and ROS scavengers among others, to relieve oxidative stress in MetD is ongoing (see Kiyuna et al. 2018). However, only limited studies have proven the benefits of the antioxidant approach in humans. Coenzyme Q10 (CoQ10) has been reported to improve cardiac function in patients with DM and HF (Mortensen et al. 2014). CoQ10 is a component of the ETC, mediating the electron transport from complexes I and II to complex III. Ubiquinol is a reduced form of CoQ10 that acts as an antioxidant inside mitochondria (Kelso *et al.* 2001). Since optimal ROS concentrations are critical in carrying out physiological signalling, future studies will be needed to identify compounds that will lessen the pathological oxidative stresses while preserving physiological redox signalling.

Mitochondrial permeability transition pore in MetD-mediated heart dysfunction. The mitochondrial permeability transition pore (mPTP) is a non-selective pore in the mitochondrial membrane that allows any solute up to 1.5 kDa to pass through (Hunter & Haworth, 1979). The mPTP has multi-conductance that suggests the molecular nature is a multi-subunit complex oligomerizing to varying degrees (Hunter et al. 1976). The molecular identity of the mPTP has been studied for years and is still a matter of debate. One of the first models proposed that the mPTP is composed of Bcl-2 associated-X-protein (Bax), voltage-dependent anion channel (VDAC), the peripheral benzodiazepine receptor (translocator protein, TSPO) and hexokinase II (HKII) in the outer mitochondrial membrane; mitochondrial creatine kinase (mtCK) in the inter-membrane space; adenine nucleotide transporter (ANT) in the inner mitochondrial membrane; and mitochondrial cyclophilin D (CypD) bound to ANT in the matrix (Halestrap & Davidson, 1990; Kinnally et al. 1993; Beutner et al. 1997; Marzo et al. 1998). The phosphate carrier model proposed the following composition of mPTP: Bax, VDAC, TSPO, HKII, mtCK, ANT and CypD, bound to the phosphate inorganic carrier (PiC) (Kokoszka et al. 2004). Recent studies have provided new insights about several potential candidates for the molecular identity of the mPTP, which include multiple subtypes of ANT (Bround et al. 2020), F-ATP synthase c-subunit (Mnatsakanyan & Jonas, 2020), and the dimer (tetramer) of F-ATP synthase (Carraro et al. 2020). The idea that more than one protein may act as mPTPs offers a rational clarification for current disagreements in the field. Intriguingly, these candidate proteins are already well-known for their role in catalysing ATP generation. Therefore, mPTPs appear to have two opposite functions: controlling cell life and death through their participation in energy metabolism and apoptosis/necrosis. The mPTP can be regulated or inhibited by different compounds. The most well-known is cyclosporin A, which blocks CypD (Fournier et al. 1987). Other inhibitors include Mg²⁺ and Mn²⁺ (by competing with Ca²⁺ to bind), adenine nucleotides, and matrix acidic pH. The primary activator of the mPTP is mitochondrial Ca²⁺ overload (Baumgartner et al. 2009); nevertheless, ROS (Seidlmayer et al. 2015), reactive nitrogen species, mitochondrial morphology and

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inorganic phosphate can also modulate its activity (Hurst *et al.* 2017).

The transient opening of the mPTP may have a physiological role by serving as a releasing valve for Ca^{2+} efflux to prevent mitochondrial Ca^{2+} overload. Under pathological situations, the pore is opened more sustainably, which leads to the dissipation of proton force, loss of metabolites, mitochondrial swelling, and cytochrome c release. All of these processes will eventually lead to cell death (Halestrap, 2009a,b).

Studies using the STZ model have reported that Ca²⁺ retention capacity is decreased, which is a sign of increased propensity for mPTP opening, coupled to a decreased O2 consumption (Oliveira et al. 2003; Ma et al. 2016). Similar results were found when the cardiac myoblast cell line H9c2 was exposed to HG (Diao et al. 2019). The mPTP opening can also be determined by Ca²⁺-induced swelling of isolated cardiac mitochondria. Some studies have shown increased mitochondrial swelling in mitochondria isolated from prediabetic or diabetic animals, demonstrating susceptibility to the Ca²⁺ overload (Federico et al. 2017; Guo et al. 2018). Finally, when Anderson et al. tested the mPTP opening by Ca²⁺ retention capacity assays in human atrial fibres, they found, once more, an increase in mPTP opening sensitivity. The authors noted that during prolonged metabolic changes and oxidative stress (as happens in DM), the components that can activate the mPTP opening, such as CypD, may be overexpressed (Anderson et al. 2011).

Mitochondrial biogenesis in MetD-mediated **dysfunction**. Mitochondrial biogenesis been described as a process that includes mitochondrial division and growth. The mitochondrion has its own DNA (mtDNA) which encodes 13 subunits of ETC proteins (Robin & Wong, 1988; Dorn et al. 2015). Initially, the nDNA controls mtDNA quality and biogenesis by regulating mtDNA replication. The critical regulator of mitochondrial biogenesis is PGC1α (Wu et al. 1999; Ventura-Clapier et al. 2008). PGC1α can regulate nuclear factors 1 and 2, as well as transcription factor A mitochondrial (TFAM) (Wu et al. 1999). It has been described that when the PGC1 α level is reduced, there is a loss of mtDNA, and when it is overexpressed, there is an increase in mitochondrial biogenesis, OXPHOS, FAO and glycolysis (Lehman et al. 2000; Arany et al. 2005; Lin et al. 2004). In organs that require high energy for their functional performance, such as skeletal or heart muscle, the PGC1 α level is higher in comparison with other tissues (Garnier et al. 2003). Multiple mechanisms regulate PGC1 α , including epigenetic regulation, post-transcriptional modifications and post-translational modifications (Duncan et al. 2007; Oka et al. 2020).

When mitochondrial biogenesis declines, heart function is eventually compromised. Bombicino *et al.* showed in an STZ-diabetic rat model that there was an enhancement in PGC1 α expression. The authors proposed that the H_2O_2 and nitric oxide are responsible for the PGC1 α activation (Bombicino *et al.* 2017). Similar results were shown previously by Finck *et al.*, where PPAR γ and PGC1 α were increased in an STZ model (Finck *et al.* 2002). In contrast, Yan *et al.* described decreased PGC1 α function in the heart in the *ob/ob* model, due to acetylation by AMP-activated protein kinase, which is activated by dephosphorylation for adiponectin activity (Yan *et al.* 2013).

In an OVE26 mouse model of T1DM, mRNA levels of TFAM and two mitochondrially encoded proteins were increased, suggesting that mitochondrial biogenesis was augmented (Shen *et al.* 2004). Using HFD as a model of T2DM, it was found that mtDNA, PGC1 α expression and nuclear factor expression were all decreased (Fang *et al.* 2018). The same result was confirmed by Duncan *et al.* (2007) in an insulin-resistance model.

Even though several studies have measured the amount of PGC1 α in the MetD mouse models, the data obtained are still controversial. The different MetD models used may underlie these discrepancies, where some studies detect a decrease in PGC1 α while others see an increase. The expression of PGC1 α has never been correlated with the PPAR γ expression and mtDNA changes in MetD. Therefore, divergent outcomes from these studies show that the regulation of the expression or PGC1 α activity is multifaceted. Further studies would be required to fully understand the whole process of mitochondrial biogenesis in MetD (Nisoli *et al.* 2007; Ren *et al.* 2010).

Conclusions

The prevalence of MetDs has been increasing in recent years. Several research groups around the world have focused on determining the mechanisms of disease pathogenesis with a common goal to prevent, delay or revert MetD. The impact of MetDs on the heart is highly relevant to human health due to their propensity to cause life-threatening cardiac arrhythmias and HF.

The heart has extremely high energy demands. Heart mitochondria consume glucose and FAs to produce the necessary ATP (Fig. 1, left), but since the usage of glucose is reduced in MetD, FAO by mitochondria is increased. This leads to a shift in the balance of mitochondrial energy metabolism favouring cardiac dysfunction.

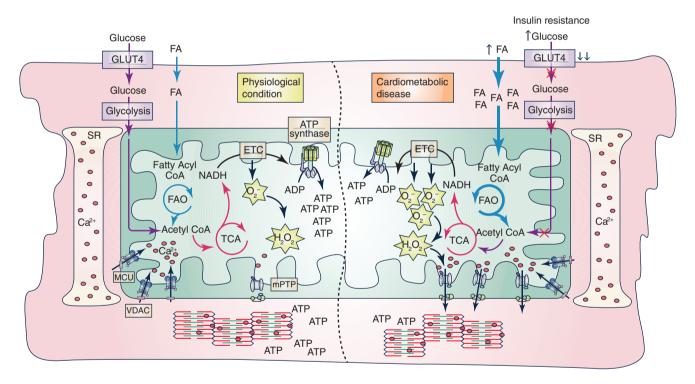
In this review, we have summarized what is known about the mitochondrial changes occurring in heart tissue during the progression of MetD. We have described the mechanisms by which metabolic stress causes mitochondrial dysfunction, including disturbances

in energetics, changes in dynamics, Ca²⁺ signalling impairment, increased oxidative stress, mPTP opening and mitochondrial biogenesis (Fig. 1, right). The mitochondrial alterations described are not exclusive for MetD and DCM. Similar phenotypes have been also seen in the pathogenesis of other heart diseases like hypertension, coronary artery disease and hypertrophy. As in MetD these mitochondrial alterations can also lead to heart failure in many cases (Graham et al. 2009; Ardanaz et al. 2010; Bhatt et al. 2011; Hollander et al. 2014; Ait-Aissa et al. 2019). However, the origin of mitochondria dysfunction is different and pivotal in designing therapeutic strategies, i.e. for MetD the fuel for ATP production is the initial mitochondrial signal disturbing its function. A confluence point in several heart pathologies in which mitochondria are compromised is increased ROS generation, the most important component of mitochondrial dysfunction. As brief examples, Graham *et al.* (2009) showed that inhibition of ROS production by mitoQ prevents hypertension development. Similarly, the use of resveratrol avoids NO generation and hypertension (Bhatt *et al.* 2011). Finally, in coronary arterial disease, altered mitochondrial dynamics due to alteration in DRP1 levels as well as alterations in ETC complex activity have been reported. Thereby general mitochondrial function and metabolism are affected in coronary arterial disease (Ait-Aissa *et al.* 2019).

There are still many questions and challenges that need to be addressed to further understand the role of mitochondria in MetD-mediated heart dysfunction. For instance, there is a lack of reliable direct measurements of mitochondrial functional parameters such as ATP, fission and fusion events, Ca²⁺ and ROS concentrations in live cardiomyocytes isolated from the DCM heart to elucidate the dynamics and specific role of these parameters in the

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Figure 1. Mitochondrial metabolism in the physiological condition vs. metabolic disease In the physiological condition (left), the cardiomyocytes fuel up mainly with free fatty acid (FA) but also supplement this from glycolysis. FA oxidation (FAO), the tricarboxylic acid (TCA) cycle, the electron transport chain (ETC), and ATP synthase produce the ATP required for muscle contraction. The ATP production is coupled with O_2 consumption and superoxide anion (O_2) and hydrogen peroxide (H_2O_2) production in healthy amounts. Metabolic disease (right) presents elevated free FA and insulin resistance. Therefore, decreased expression of GLUT4 favours FA uptake and oxidation. FAO requires higher levels of O_2 than glucose to produce an equal amount of ATP, decreasing the efficiency of energy production. Under this condition, reactive oxygen species (ROS) production increases up to pathological levels, triggering mitochondrial permeability transition pore (mPTP) opening and oxidation of other proteins for normal cell function. The whole process decreases the cardiomyocyte's performance and favours the pathogenesis of diabetic cardiomyopathy that finally leads to heart failure.

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pathogenesis of MetD-mediated heart dysfunction. These measurements will also provide information about the mechanisms of crosstalk signalling among these interconnected functions such as the role of mitochondrial Ca²⁺ signalling in the regulation of mitochondrial energy metabolism and ROS homeostasis. Future advances in experimental technology and theoretical concepts will help to resolve these challenges. One such progress is the recent discovery of multiple molecular identities in the formation of the mPTP complex, which provides a new opportunity for using genetic approaches to decipher the role mPTP opening in MetD-linked cell injury and death.

All of the MetD animal models and heart samples from MetD patients show increased ROS production. Thus, ROS appear to be key players in the development of the MetD-mediated heart dysfunction, although the mechanisms of ROS-mediated downstream effects are still to be elucidated. It is plausible that the ROS-mediated signalling pathways are potential drug targets for the treatment of MetD-mediated heart dysfunction.

Findings of MetD-related changes in heart mitochondrial biogenesis are still contradictory. While some studies show an increase in PGC1 α , others show no changes in this protein. Furthermore, other components involved in mitochondrial biogenesis have been barely studied in DCM. Therefore, additional experiments are required to elucidate the specific role of other mitochondrial biogenesis regulators in MetD.

Finally, the comparative studies between animal models and heart samples from human patients (including induced pluripotent stem cells differentiated into cardiomyocytes) will be useful for translating basic mechanisms into clinical practice. Collectively, this new knowledge will be useful for the development of new and effective therapeutic interventions for treating these devastating disorders.

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Additional information

Competing interests

None.

Author contributions

M.F. and S.D.la.F. wrote the first draft, J.P. and S.-S.S. reviewed and revised the manuscript. All authors have read and approved the final version of this manuscript and agree to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. All persons designated as authors qualify for authorship, and all those who qualify for authorship are listed.

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