



Myocardial metabolism in heart failure: Purinergic signalling and other metabolic concepts



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ABSTRACT

Despite significant therapeutic advances in heart failure (HF) therapy, the morbidity and mortality associated with this disease remains unacceptably high. The concept of metabolic dysfunction as an important underlying mechanism in HF is well established.

Cardiac function is inextricably linked to metabolism, with dysregulation of cardiac metabolism pathways implicated in a range of cardiac complications, including HF. Modulation of cardiac metabolism has therefore become an attractive clinical target. Cardiac metabolism is based on the integration of adenosine triphosphate (ATP) production and utilization pathways. ATP itself impacts the heart not only by providing energy, but also represents a central element in the purinergic signaling pathway, which has received considerable attention in recent years. Furthermore, novel drugs that have received interest in HF include angiotensin receptor blocker-neprilysin inhibitor (ARNi) and sodium glucose cotransporter 2 (SGLT-2) inhibitors, whose favorable cardiovascular profile has been at least partly attributed to their effects on metabolism.

This review, describes the major metabolic pathways and concepts of the healthy heart (including fatty acid oxidation, glycolysis, Krebs cycle, Randle cycle, and purinergic signaling) and their dysregulation in the progression to HF (including ketone and amino acid metabolism). The cardiac implications of HF comorbidities, including metabolic syndrome, diabetes mellitus and cachexia are also discussed. Finally, the impact of current HF and diabetes therapies on cardiac metabolism pathways and the relevance of this knowledge for current clinical practice is discussed. Targeting cardiac metabolism may have utility for the future treatment of patients with HF, complementing current approaches.

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Contents

1. Introduction	133
2. Cardiac metabolism in health and disease.	133
3. Current therapies and their effects on cardiac metabolism	135
4. Relevance for clinical practice – targeting dysregulated metabolic pathways in heart failure	139
5. Conclusion.	140

Abbreviations: ADHF, acute decompensated heart failure; ANP, atrial natriuretic peptide; ARNi, angiotensin receptor blocker-neprilysin inhibitor; ATP, adenosine triphosphate; BCAA, branched chain amino acid; hCPT-1, carnitine palmitoyltransferase-1; CHF, chronic heart failure; CV, cardiovascular; DM, diabetes mellitus; HF, heart failure; HFrEF, HF with reduced ejection fraction; FAO, fatty acid oxidation; FA, fatty acids; FFA, free fatty acid; GLP-1RA, glucagon-like peptide-1 receptor agonist; IR, insulin resistance; LVEF, left ventricular ejection fraction; MetS, metabolic syndrome; MI, myocardial infarction; NPs, natriuretic peptides; NYHA, New York Heart Association; PDH, pyruvate dehydrogenase; PFOx, partial fatty-acid oxidation; PPARs, peroxisome proliferator-activated receptor agonists; RAAS, renin-angiotensin-aldosterone system; SGLT-2, sodium glucose cotransporter-2; TCA, tricarboxylic acid; TZDs, thiazolidinediones; TMZ, trimetazidine.

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Conflicts of interest statement: financial interests unrelated to primary employment and conflicts of interest	141
Acknowledgements	141
References	141

1. Introduction

Heart failure (HF) is associated with a significant health burden with an estimated prevalence of 62 million patients worldwide (Benjamin et al., 2017). Despite recent advances in HF therapies, the 5-year mortality rate continues to increase (Benjamin et al., 2017). Current therapeutic approaches for HF target the neurohumoral systems and include the renin-angiotensin-aldosterone system and/or the β -adrenergic receptor signaling pathway, mineralocorticoid receptor antagonists, inotropes, diuretics, and mechanical devices (Ponikowski et al., 2016). However, they do not sufficiently address the ‘metabolic nature’ of the heart.

Metabolic failure is considered to play a central role in the pathogenesis of HF (Neubauer, 2007). There is growing evidence that patients with HF exhibit disturbances in myocardial energy substrate metabolism, resulting in the progression and worsening of disease (Bertero & Maack, 2018; Stanley, Recchia, & Lopaschuk, 2005). Moreover, the role of adenosine triphosphate (ATP) as an extracellular signaling molecule in cardiovascular (CV) pathophysiology and its therapeutic potential in cardiac diseases have invoked significant interest recently and are discussed in a number of detailed reviews (Burnstock, 2006, 2007a, 2017).

Novel metabolic therapies to target cardiac metabolism have the potential to improve patient outcomes (Greene et al., 2016; Wende, Brahma, McGinnis, & Young, 2017). This review aims to discuss the pivotal role of cardiac metabolism at all stages of HF (early, mid and advanced), the role of purine nucleosides and nucleotides as extracellular signaling molecules in the disease, and the effects of therapies approved for the treatment of HF (or associated co-morbidities) on cardiac metabolism, including its relevance for clinical practice. Finally, the concept of ‘resetting’ metabolic pathways as an important therapeutic option in HF is discussed.

2. Cardiac metabolism in health and disease

2.1. Metabolic pathways in the healthy heart

The normal adult heart obtains 60–100% of its ATP supply from fatty acid oxidation (FAO) (Stanley, Lopaschuk, Hall, & McCormack, 1997; Wisneski, Stanley, Neese, & Gertz, 1990). Mitochondrial oxidation of fatty acids (FAs) consumes more O_2 per molecule of ATP produced than most other sources of fuel, making FAs the less efficient substrate for energy production (Lopaschuk, Ussher, Folmes, Jaswal, & Stanley, 2010). Glucose metabolism exhibits a greater fuel efficiency, providing 40% more ATP per O_2 molecule. FAs are thus the dominant substrates for energy production in the unstressed heart, while glucose may become the favorable substrate in high-energy demand conditions (Depre, Vanoverschelde, & Taegtmeyer, 1999; Rosano, Fini, Caminiti, & Barbaro, 2008; Stanley et al., 2005; Witteles & Fowler, 2008).

While glucose metabolism has a greater capacity to generate ATP, glycolysis accounts for just 5% of the ATP produced in the normal oxygenated heart (Abozguia, Shivu, Ahmed, Phan, & Frenneaux, 2009). *In vitro* and *in vivo* studies have demonstrated that glucose metabolism is inhibited by FAO and is dependent on the dietary state and physical activity of the body (Randle, Garland, Hales, & Newsholme, 1963; Randle, Newsholme, & Garland, 1964). This reciprocal relationship between FAs and glucose for oxidative metabolism was originally described by Randle et al. in 1963 (Randle et al., 1963).

The common end product, acetyl coenzyme A (acetyl-CoA), produced from FAO or from the glycolytic pathway, is transferred into the

citric acid cycle (also known as the tricarboxylic acid [TCA] cycle or the Krebs cycle) (Kantor, Lopaschuk, & Opie, 2001). Acetyl-CoA in the Krebs cycle generates one molecule of ATP via substrate phosphorylation and the formation of reducing equivalents – three molecules of nicotinamide adenine dinucleotide (NADH) and one molecule of FADH₂ (Berg, Tymoczko, & Stryer, 2002, Chap. 17).

The metabolic flexibility of the heart is demonstrated by its ability to utilize energy substrates based on their availability and complex regulatory mechanisms (Kolwicz Jr., Purohit, & Tian, 2013).

2.2. Shift of metabolic pathways in the progression of heart failure

Altered energetics plays a key role in the pathophysiology of the failing heart, which switches from FA utilization to oxygen-sparing carbohydrate metabolism for energy production (Bedi Jr. et al., 2016) (Fig. 1). Chronic HF (CHF) is associated with abnormalities in skeletal muscle metabolism that affect exercise capacity and contributes to insulin resistance (IR) (Jordan et al., 2017). The metabolic alterations in cardiomyocytes depends on the stages of HF (early, mid or advanced) (Chandler et al., 2004). Most studies show that FAO is unchanged or only slightly elevated in the early stages of HF (Chandler et al., 2004; Stanley et al., 2005). However, in advanced- or end-stage decompensated HF, there is a down-regulation in FAO enzyme expression, and FA utilization is decreased (Chandler et al., 2004; Stanley et al., 2005). Glucose utilization is typically increased in the early stages of HF (in the hypertrophied heart) and is mainly characterized by an increase in glucose uptake and glycolysis as a result of reduced oxidative metabolism (Allard, Schonekess, Henning, English, & Lopaschuk, 1994; Nascimben et al., 2004). This increase in glucose metabolism could be due to alterations in the regulation of carbohydrate utilization pathways secondary to FAO suppression and/or upregulation of the anaplerotic pathway (Pound et al., 2009; Sorokina et al., 2007). In contrast, in advanced HF or HF with type 2 diabetes, IR develops in the myocardium, resulting in decreased glucose metabolism (Kalsi et al., 1999; Razeghi et al., 2001; Taylor et al., 2001). This shift from FAO to glucose metabolism is considered to be part of the ‘foetal reprogramming’ hallmark of cardiac hypertrophy and HF (Razeghi et al., 2001). Gene expression profiling demonstrated early and sustained down-regulation of metabolic gene classes in HF (Rowell, Koitabashi, Kass, & Barth, 2014). A number of studies have demonstrated that the failing heart exhibits decreased expression and activity of enzymes involved in mitochondrial FAO (Iemitsu et al., 2002; Osorio et al., 2002). The reduced glucose oxidation seen in advanced HF is attributed, at least in part, to mitochondrial dysfunction. Functional blockade of the pyruvate dehydrogenase (PDH) complex, the rate-limiting step in glucose oxidation, is also thought to play a major role in this process (Doehner, Frenneaux, & Anker, 2014).

In addition to myocardial metabolism of glucose and fatty acids, the heart is also capable of oxidising a range of other substrates including ketone bodies, lactate and amino acids (Kolwicz Jr., Airhart, & Tian, 2016). Ketone bodies compete with other substrates in the heart, especially FA, to be used as fuel. This is particularly significant in the hypertrophied and failing heart, wherein there is down-regulation of FAO gene expression (Tian & Barger, 2006) and increased blood ketone bodies (Lommi et al., 1996). The increase in ketone bodies is proportionate to the level of cardiac dysfunction and neurohumoral activation (Lommi et al., 1996). IR and cardiac cachexia are common features of advanced HF, which also increases the likelihood of ketone production and cardiac ketone utilisation (Schugar et al., 2014).

Metabolic remodelling and the development of heart failure

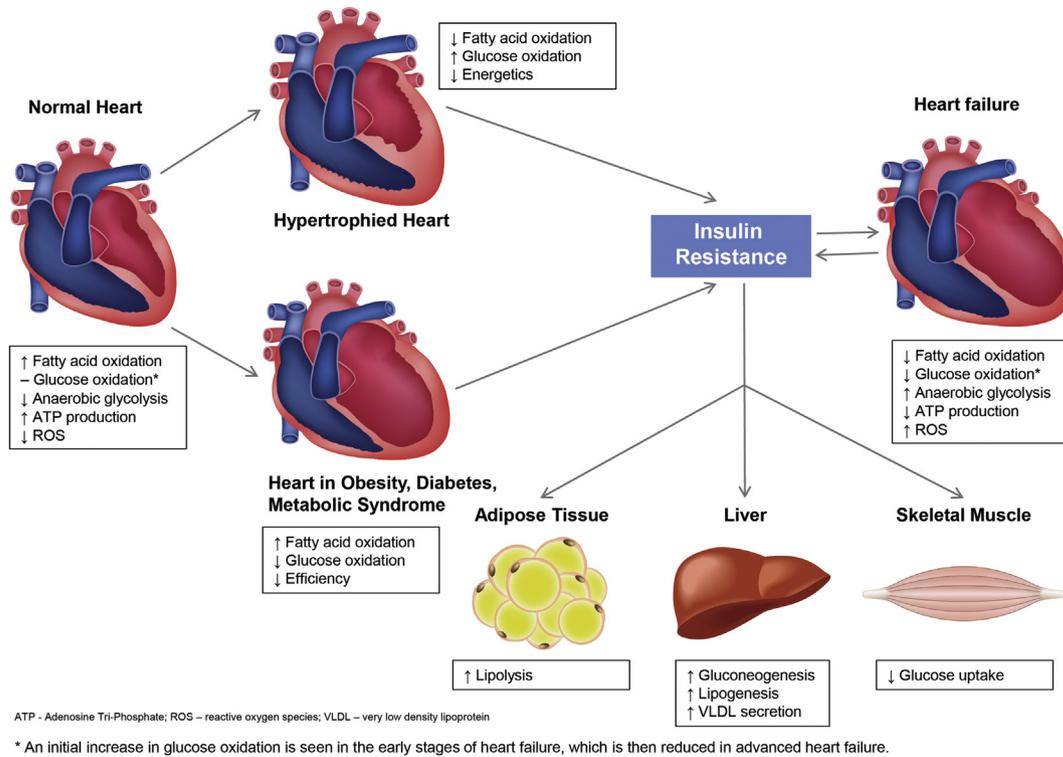


Fig. 1. Pathological changes in the healthy heart leading to insulin resistance (IR) and the development of heart failure. Mechanical dysfunction and other associated co-morbidities (obesity, diabetes, and metabolic syndrome) can lead to IR. Increased insulin levels lead to metabolic disturbances in adipose tissue, liver, and skeletal muscle. Metabolic perturbations in these systems can subsequently promote the progression to heart failure.

The shift of energy metabolism to ketone body metabolism has been shown to be an efficient alternative avenue for oxidative ATP production (Aubert et al., 2016). Ketone bodies, especially the principal ketone body D- β -hydroxybutyrate, have been proposed to act as a “superfuel”, producing more energy than FA or glucose (Aubert et al., 2016; Cahill Jr. & Veech, 2003; Ferrannini, Mark, & Mayoux, 2016; Mudaliar, Aljojo, & Henry, 2016; Sato et al., 1995). This shift to ketone body metabolism is supported by a further case-control study, that evaluated the metabolic signature in the human non-diabetic failing heart (Bedi Jr. et al., 2016). This study showed that the metabolic and genetic profile characteristic of ketone oxidation was present in failing hearts only, suggesting that ketone utilization is a late event in HF. It has been suggested that the failing heart relies on ketone metabolism when other substrate metabolism pathways begin to shut down (Bedi Jr. et al., 2016; Taegtmeier et al., 2016). These observations are supported by studies in advanced HF patients, which demonstrated that the use of circulating ketones was reduced by 50% in skeletal muscle, but was preserved in cardiac tissue (Janardhan, Chen, & Crawford, 2011). In contrast, a more recent animal study reported that increased levels of ketone bodies impairs α -ketoglutarate dehydrogenase activity and blocks the Krebs cycle, subsequently resulting in contractile dysfunction (Karlstaedt et al., 2016). In cardiomyocytes, ketone bodies cause concurrent inhibition of glucose and FAO metabolism, thereby impairing myocardial energy supply (Taegtmeier, 1994). Furthermore, the O_2 consumed for ATP production during ketone metabolism is more efficient than FA, but less than that of glucose. However, more energy is derived from β -hydroxybutyrate versus glucose due to β -hydroxybutyrate being more reduced (Mudaliar et al., 2016). Interestingly, when β -hydroxybutyrate is infused in healthy volunteers to reach very high physiological levels, it is oxidized at the expense of glucose. Moreover, myocardial blood flow and heart rate also increase with the infusion of β -hydroxybutyrate, (Gormsen et al., 2017), a phenomenon previously also observed for the kidney, brain and forearm (Fioretto et al., 1987; Hasselbalch et al., 1996; Walker, Fulcher, Marsiaj, Orskov, & Alberti, 1991).

While these studies point to an important role of ketone bodies in cardiac metabolism and HF, it remains unclear whether ketone body metabolism is adaptive or maladaptive in heart failure. Targeted deletion of succinyl CoA-3-oxoacid CoA transferase (an enzyme essential for terminal oxidation of ketone bodies) in cardiomyocytes of mouse models of HF suggests that inability to oxidize ketones may predispose the heart to metabolic reprogramming contributing to pathological remodeling following pressure overload (Schugar et al., 2014). It has been suggested that myocardial ketone oxidation is a metabolic adaptation in the failing heart (Bedi Jr. et al., 2016). Preference of ketone bodies over FA and glucose for oxidation to provide energy may not only improve cardiac function but also enhance cardiac efficiency (Ferrannini et al., 2016). Although it would appear that ketone bodies have a positive effect on cardiac function, further studies are needed to clarify the long-term effects of ketone metabolism in patients with HF.

Perturbations in amino acid availability and metabolism have also been observed in HF (Wende et al., 2017). Accumulation of branched chain aminoacids (BCAA; including isoleucine, valine and the ketogenic aminoacid leucine) and their corresponding branched chain α -keto acid (BCKA) derivatives due to defective catabolism has emerged as one of the hallmark signatures of the metabolic changes in failing heart (Sun et al., 2016; Wang et al., 2016; Wende et al., 2017). Elevated levels of BCKA may have a detrimental effect on cardiomyocytes due to cytotoxicity resulting from mitochondrial dysfunction and oxidative stress (Sun et al., 2016). The accumulation of BCKAs has been attributed to transcriptional repression of subunits of the BCKA dehydrogenase, a key enzyme involved in subsequent catabolism of BCKAs. These findings are further supported by the observation that pharmacological activation of BCKA dehydrogenase prevents BCKA accumulation and improves cardiac function (Sun et al., 2016). In addition to being potential sources of energy, BCAAs are also essential for de novo protein synthesis and function as signaling molecules in various metabolic and growth pathways.

For example, by activating mTOR, BCAAs (especially lysine) may regulate diverse cellular processes like protein synthesis, autophagy and insulin signalling thereby affecting glucose and FA metabolism, and muscle anabolism (Sun et al., 2016; Wende et al., 2017).

2.3. Purinergic signaling in HF

Purinergic signaling (ATP acting as extracellular signaling molecule) is mediated by purine receptors that are expressed in all cells of the heart and blood vessels including erythrocytes, leukocytes, and platelets (Burnstock, 2017; Burnstock & Knight, 2004; Burnstock & Pelleg, 2015). There are four subtypes of P1 G protein-coupled receptors (GPCR) (A_1 , A_{2A} , A_{2B} , and A_3), seven P2X ($1-7$) subtypes of ion channel receptors and eight subtypes P2Y GPCRs (P2Y $_{1/2/4/6/11/12/13/14}$) (Burnstock, 2007b; Ralevic & Burnstock, 1998). They mediate actions on the heart which are described in original publications (Burnstock & Ralevic, 2014; Givertz, 2009). The heart is controlled by the sympathetic, parasympathetic, and sensory nervous systems, which utilize ATP as a co-transmitter. Cardiac expression of purine receptors is increased in CHF patients (Hou et al., 1999), with a resultant accumulation of adenosine in plasma (Funaya et al., 1997). Furthermore, adenosine therapy has demonstrated cardioprotective effects in CHF patients, which are mediated through A_1 and A_3 receptors (Dougherty, Barucha, Schofield, Jacobson, & Liang, 1998; Liang & Jacobson, 1998).

Accumulating evidence supports the role of purinergic signaling in cardiac pathophysiology. An up-regulation of P2X $_1$ and P2Y $_2$ receptor mRNA was reported in the heart of a rat model of congestive HF (Hou et al., 1999). Increased expression of P2X $_1$ receptors has similarly been reported in the atria of patients suffering from dilated cardiomyopathy (Berry, Barden, Balcar, Keogh, & dos Remedios, 1999). Early *in-vivo* studies have shown that regulated over-expression of A_1 receptors leads to adverse ventricular remodeling. (Funakoshi et al., 2006). This finding is in contrast to more recent data, indicating that adenosine accumulation may be cardioprotective in heart failure. Adenosine A_1 receptor activation attenuated cardiac hypertrophy in rat neonatal cardiac myocytes (Chuo et al., 2016). Partial adenosine A_1 agonism has demonstrated promise as a treatment for heart failure, with the potential to enhance cardiac metabolism, calcium homeostasis, cardiac structure and function, and patient outcomes, when combined with standard therapies (Greene et al., 2016).

An association of purinergic signalling with cardiac energy metabolism has also been demonstrated, with animal studies showing that adenosine (an A_1 receptor agonist) altered glucose metabolism and tended to decrease acidosis and calcium overload, exerting a cardioprotective effect. (Finegan, Lopaschuk, Coulson, & Clanachan, 1993; Fraser, Lopaschuk, & Clanachan, 1999; Puhl et al., 2016). Adenosine inhibits adenyl cyclase and reduces intracellular levels of cyclic adenosine monophosphate (cAMP) (Akbar, Okajima, Tomura, Shimegi, & Kondo, 1994; Fredholm, AP, Jacobson, Klotz, & Linden, 2001; Wang & Belardinelli, 1994), subsequently leading to reduced sympathetic nervous system activation and increased release of atrial natriuretic peptide (ANP) (Schutte, Burgdorf, Richardt, & Kurz, 2006; Yuan, Cao, Han, Kim, & Kim, 2005). Under hypoxic conditions, adenosine activates protein kinase C and improves mitochondrial function, by modulating mitochondrial sensitive potassium (mKATP) channels (Xiang et al., 2010).

HF is characterized by volume overload, a condition that is particularly relevant for the effect of adenosine on the renal systems. Renal dysfunction is a major co-morbidity of HF, with about half of patients with CHF and two-thirds of patients with acute HF (AHF) presenting with associated cardiorenal syndrome (CRS) (Ronco, Haapio, House, Anavekar, & Bellomo, 2008). Adenosine has multiple, complex effects on the kidney, including vasoconstriction of afferent renal arterioles, sodium reabsorption in the proximal tubules and enhanced tubuloglomerular feedback (TGF) in the macula densa (Vallon, Muhlbauer, & Osswald, 2006). CHF is characterized by an increased accumulation of endogenous adenosine in plasma (Funaya et al., 1997;

Vallon, Miracle, & Thomson, 2008). In the kidney, adenosine can induce both vasoconstriction via the A_1 receptor (in the outer cortex) and vasodilation via the A_2 receptor (in the deep cortex and medulla) (Vallon et al., 2008). The effect of adenosine on TGF plays a key role in the progression of the disease (Burnstock & Pelleg, 2015; Givertz, 2009). Increased renal adenosine levels mediate A_1 receptor activation and causes fluid retention by stimulating NaCl and fluid reabsorption in the proximal tubule (Vallon et al., 2008). The net effect of these is fluid overload and decreased glomerular filtration rate (GFR).

2.4. Cardiac implications of co-morbidities

2.4.1. Metabolic syndrome

Metabolic syndrome (MetS) refers to a cluster of risk factors that can lead to heart disease, including obesity, dyslipidemia, elevated blood pressure and glucose intolerance/IR (American Heart Association, 2016; Hanefeld, Pistrosch, Bornstein, & Birkenfeld, 2016). Alterations in substrate availability/utilization and impairment in transcriptional regulation of oxidation pathways is often noted in MetS (Ilkun & Boudina, 2013). IR-mediated impairment of glucose transport leads to enhanced long-chain FA uptake through relocation of the FA transporter CD36 to the sarcolemma (Ouwens et al., 2007) and increased mitochondrial carnitine palmitoyltransferase-1 (CPT-1) activity (Menard et al., 2010).

There is mounting evidence to support the role for increased FA levels (as seen in MetS and diabetes mellitus [DM]) in mitochondrial oxidative dysfunction. The mechanism promotes cardiac lipotoxicity, myocardial damage, myocyte apoptosis, reduced contractility, and subsequent myocardial dysfunction (Lehrke & Marx, 2017; Schulze, Drosatos, & Goldberg, 2016; Seferovic et al., 2018). Early studies in patients with obesity noted the accumulation of lipids around the epicardium, (Carpenter, 1962) a phenotype that was associated with cardiac dysfunction (Alpert, 2001; Carpenter, 1962). The link between lipid accumulation and heart failure is summarised in a recent review in the area (Schulze et al., 2016). An improvement in cardiac metabolism and function in response to reduction in toxic lipids has been reported (Goldberg, Trent, & Schulze, 2012). Key evidence for this effect is summarised in the following sections.

2.4.2. Diabetes mellitus

Patients with type 2 DM (T2DM) have a two to three times increased risk of CV mortality compared to those without T2DM (The Emerging Risk Factors Collaboration et al., 2015). CV mortality accounts for approximately 80% of deaths in patients with T2DM (M. Abdul-Ghani, Del Prato, Chilton, & DeFronzo, 2016). Data suggest that HF may lead to IR and DM (Amato et al., 1997; Swan et al., 1997). DM and IR impairs the ability of the heart to adjust to changing energy demands by reducing the ability of the heart to use glucose and increasing the delivery of FA to the heart, thereby shifting cardiac metabolism towards a greater reliance on FA for energy (Bayeva, Sawicki, & Ardehali, 2013). In support of this observation, IR was found to be associated with myocardial triglyceride accumulation, cardiac remodeling and impaired diastolic function in overweight and obese women (Utz et al., 2011). Greater dependence of the diabetic heart on FAO results in increased mitochondrial oxygen consumption in addition to increased cellular stress from elevated reactive oxygen species (ROS) production, and mitochondrial dysfunction (Dietl & Maack, 2017; Feuvray, 2010). These changes in myocardial metabolism may contribute to structural and functional alterations in the heart that can lead to progression of HF (Carley & Severson, 2005; Stanley et al., 2005).

3. Current therapies and their effects on cardiac metabolism

Current treatments for HF, aim at blocking neurohormonal signaling. However, more recently these therapies have been proposed to affect cardiac metabolism and associated energetics (Neubauer, 2007)

(Figs. 2A and 2B). The cardiac metabolic effects of some of the major HF therapies are described in the following sections.

3.1. β -blockers

β -adrenergic blockers are one of the main therapies that improve patient survival in HF. In these patients, long-term upregulation of catecholamines results in IR by antagonizing insulin, increasing lipolysis and raising free FA (FFA) levels (Nonogaki, 2000; Witteles & Fowler, 2008). Adrenergic blockade with carvedilol and metoprolol helps to improve myocardial function and survival in patients with HF through several mechanisms, including an energy-sparing effect, possibly by favouring altered myocardial substrate utilization from FFA to glucose oxidation (Bayeva et al., 2013; Eichhorn et al., 1994; Wallhaus et al., 2001). However, it is important to note the differences in the pharmacological effects of various β -blockers on metabolism (Bayeva et al., 2013).

3.2. Renin-angiotensin-aldosterone system (RAAS) inhibitors

The failing heart is associated with increased renin-angiotensin-aldosterone system (RAAS) activity (Mizuno et al., 2001; Nakamura et al., 2004; Yoshimura et al., 2002). Prolonged activation of the RAAS system contributes to altered insulin/insulin-like growth factor 1 (IGF-1) signaling pathways and ROS formation, resulting in endothelial dysfunction and IR (Cooper et al., 2007). Unlike β -blockers, ACEIs have been shown to increase FA uptake and improve myocardial energetics in HF. Studies in animal models with obesity and IR have shown that ACEIs can improve insulin responsiveness in the heart (Kadkhodayan, Coggan, & Peterson, 2013; Tabbi-Anneni, Buchanan, Cooksey, & Abel, 2008). Chronic ACE inhibition causes inactivation of bradykinin, which in turn has favorable effects on glucose uptake, glucose oxidation and glycolysis (Mori, Zhang, Oudit, & Lopaschuk, 2013). Furthermore, trials comparing the effects of ACEIs or ARBs with anti-hypertensive medicines have also demonstrated that RAAS blockade significantly improves insulin sensitivity (Grassi et al., 2003; Jin & Pan, 2007; Olsen et al., 2005). In-vitro studies with human adipocytes suggests that some ARBs can activate PPAR- γ target genes and induce adipogenesis (Janke et al., 2006). As seen with ACEIs and ARBs, mineralocorticoid receptor antagonists can also increase glucose metabolism and restore

insulin sensitivity (Pfeffer et al., 2003; Yusuf et al., 2000; Vecchiola, Lagos, Carvajal, Baudrand, & Fardella, 2016).

3.3. Angiotensin receptor blocker-nepriylsin inhibitors (ARNi)

Sacubitril/valsartan (ARNi), acts by simultaneously blocking the RAAS and neprilysin (Ruilope et al., 2010). Neprilysin degrades the peptides that have the potential to modulate lipid and glucose metabolism, such as natriuretic peptides (NPs), bradykinin, endothelin-1, and glucagon-like peptide 1 (GLP-1) (Standeven et al., 2011). Neprilysin inhibition with sacubitril/valsartan increases the activity of NPs, bradykinin, GLP-1 and skeletal muscle cGMP, but decreases dipeptidyl peptidase 4 (DPP4) activity. Treatment with sacubitril/valsartan in normoglycemic patients with obesity and hypertension resulted in increased insulin sensitivity (Jordan et al., 2017). A more recent study that compared the effects of sacubitril/valsartan with a comparator, amlodipine, demonstrated that sacubitril/valsartan did not elicit any clinically relevant changes in exercise-induced lipolysis or substrate oxidation in these patients with obesity and hypertension, suggesting that the cardiovascular benefits of sacubitril/valsartan are not attributable to changes in lipid metabolism during exercise (Engeli et al., 2018).

3.4. Natriuretic peptides (NPs)

NPs can favorably affect human lipid metabolism by increasing lipolysis and insulin sensitization, while leptin release is suppressed (Birkenfeld et al., 2005; Birkenfeld et al., 2008; Birkenfeld et al., 2012; Kerkela, Ulvila, & Magga, 2015; Moro, 2016; Schlueter et al., 2014). NPs have been shown to improve energy production by enhancing mitochondrial biogenesis and oxidative capacity in skeletal muscle and adipose tissue (Bordicchia et al., 2012; Engeli et al., 2012; Kerkela et al., 2015). In skeletal muscle, NPs can increase mitochondrial oxidative metabolism and lipid oxidation, thereby augmenting energy metabolism (Engeli et al., 2012). ANP and BNP are potent mediators of lipolysis as compared with CNP that has a minor lipolytic effect (Sengenès, Berlan, De Gliszinski, Lafontan, & Galitzky, 2000). In mice, transgenic BNP over-expression attenuates high-fat feeding-induced adiposity and IR (Miyashita et al., 2009). Obesity and T2DM are associated with NP deficiency, thus suggesting a possible role of NPs in the

Metabolic modulators and their targets

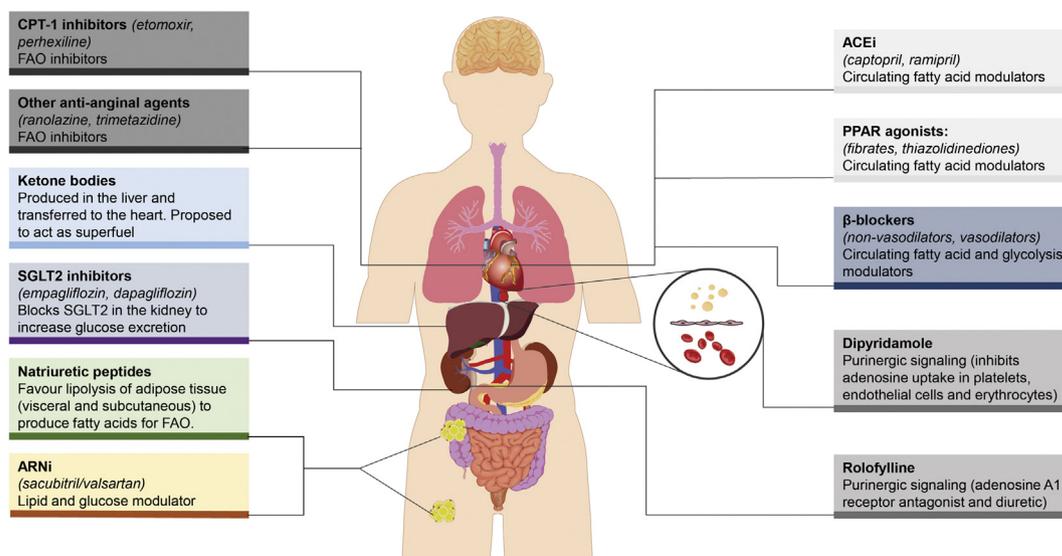


Fig. 2A. Overview of major targets of metabolic modulators. Several metabolic modulators exert their effects on cardiac metabolism indirectly through effects on other organs and cell types (adipose tissue, platelets, endothelial cells, or erythrocytes).

Lipolysis, Ketones and Cardiac Metabolism

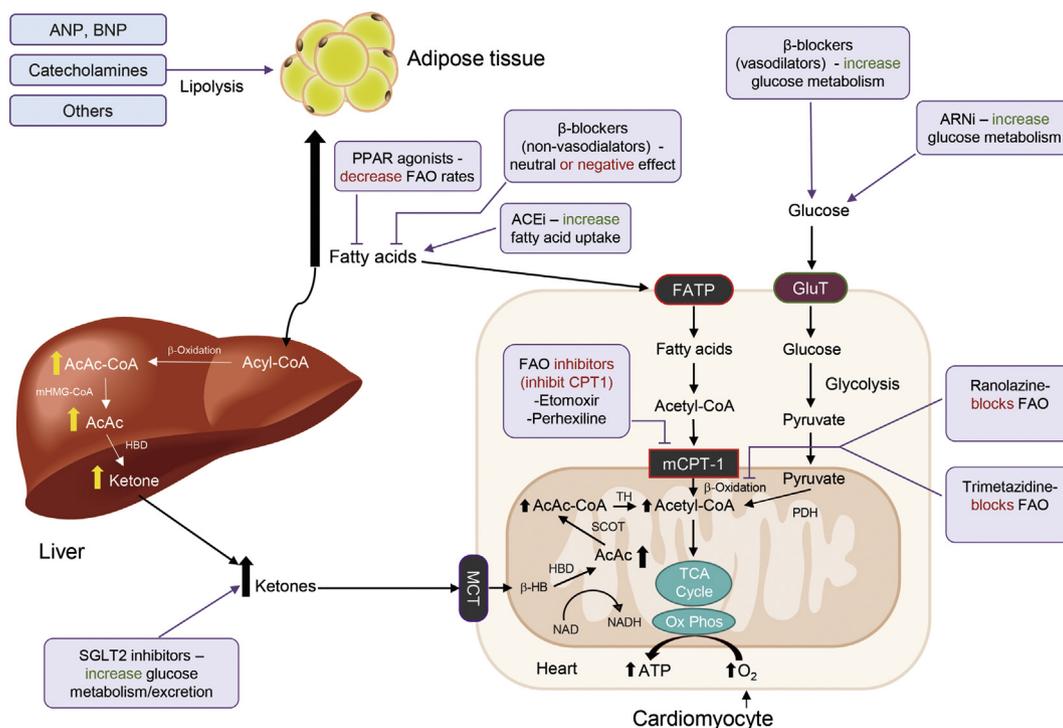


Fig. 2B. Summary of metabolic pathways and therapies that modulate cardiac metabolism. Natriuretic peptides (ANP and BNP) favor lipolysis and result in an increase in free fatty acids. Fatty acids are taken up by the liver and undergo β -oxidation to form ketone bodies (acetoacetate and β -hydroxybutyrate). The ketones are transferred to the heart via the bloodstream. In the cardiomyocyte, the ketone bodies enter the Krebs cycle and undergo oxidative phosphorylation. In cardiomyocytes, acetyl-CoA formed from the ketones limits additional production of acetyl-CoA from the pyruvate and β -oxidation pathways (dotted arrows).

pathophysiology of these diseases (Schlueter et al., 2014). Finally, polymorphisms in the genes encoding atrial natriuretic peptide (ANP) and BNP contribute to the variability in the risk for T2DM (Jujic et al., 2014; Meirhaeghe et al., 2007). Previous studies have shown that ANP promotes adipose tissue lipolysis and hepatic ketogenesis (Birkenfeld et al., 2008). The NP system in adipose tissue is not desensitized in CHF. The lipolytic response to ANP is therefore preserved, ensuring that cardiac metabolism is maintained (Birkenfeld, Adams, Schroeder, Engeli, & Jordan, 2011).

NPs are degraded either through enzymatic degradation by neprilysin or via cellular uptake through the NP-C receptor. Evidence from various non-clinical and clinical studies has established the role of neprilysin inhibition in augmentation of the NP system (Doenst et al., 2010; Jordan et al., 2017; Kobalava et al., 2016; Kuhn, 2016).

Recombinant ANP (carperitide) and BNP (nesiritide) were approved in 1995 and 2001 respectively for treatment of congestive HF. However, nesiritide was shown to be ineffective in reducing HF rehospitalization or death from any cause in the Acute Study of Clinical Effectiveness of Nesiritide in Decompensated Heart Failure Trial (ASCEND-HF) (O'Connor et al., 2011). Cenderitide, a chimeric peptide that activates natriuretic peptide receptor (NPR) A and NPRB, is being tested for preservation of left ventricular (LV) function in post-MI patients (Kerkela et al., 2015).

3.5. Sodium glucose cotransporter (SGLT) inhibitors

SGLT inhibitors belong to a class of drugs that inhibit glucose reabsorption in the kidney, thereby increasing urinary glucose excretion and providing an important therapeutic strategy for the treatment of T2DM (Abdul-Ghani, Norton, & Defronzo, 2011). Among the two most well known SGLTs, 90% of glucose reabsorption is via SGLT-2 and the remaining 10% is via SGLT-1 (Hediger & Rhoads, 1994). Dapagliflozin (List,

Woo, Morales, Tang, & Fiedorek, 2009), empagliflozin (Grempler et al., 2012) and canagliflozin (Neal et al., 2017) are recently developed selective SGLT-2 inhibitors that have been investigated for the treatment of T2DM.

An earlier study that evaluated the efficacy and safety of dapagliflozin in patients with T2DM who were at high risk for future CVD events, showed that dapagliflozin significantly reduced haemoglobin A_{1c} (HbA_{1c}) (-0.38% [-4.2 mmol/mol]), body weight and systolic blood pressure without adversely affecting CV safety relative to placebo (Cefalu et al., 2015). Another recent study, the Empagliflozin Cardiovascular Outcome Event Trial in Type 2 Diabetes Mellitus Patients study (EMPA-REG OUTCOME), has shown that treatment with SGLT-2 inhibitor empagliflozin has beneficial cardiometabolic effects in patients with T2DM and established CVD. A 14% reduction in primary major adverse cardiac events was observed in addition to a 35% relative reduction in HF hospitalizations (Zinman et al., 2015).

The results of the EMPA-REG trial have been validated from the CANVAS program (Neal et al., 2017). CANVAS indicated that canagliflozin reduces CV events by 14%, in addition to a 33% relative reduction in HF hospitalizations, although at an increased risk of lower-limb amputation and bone fractures. Clinical practice guidelines have already begun to reflect the efficacy of SGLT-2 inhibitors patients with T2DM and will impact on clinical decision making in cardiologists (Association American Diabetes, 2018; Ponikowski et al., 2016; Tanaka & Node, 2017).

Finally, SGLT-2 inhibitors increase ketone body availability by increasing FAO in the liver via β -oxidation. Indeed, a recent untargeted metabolomic study showed an increase in the levels of ketone bodies as well as BCAAs in patients with T2DM and CV disease treated with empagliflozin (Kappel et al., 2017). Ketone bodies (acetoacetate and β -hydroxybutyrate) are then exported from the liver into blood stream

Table 1
Clinical studies using metabolic modulators.

Metabolic modulator	Metabolic mechanism affected by modulator	Study type (pre-clinical studies, POC studies, pilot studies and clinical trials) ^a
β-blockers		
Non-vasodilators	↓ insulin sensitivity ↑ glucose levels Neutral/negative effect on lipid metabolism	Prospective study; ARIC (n = 12,550) (Gress, Nieto, Shahar, Wofford, & Brancati, 2000) Double-blind, prospective, parallel-group study; LIFE (n = 8300) (Dahlof et al., 2002) Prospective, randomized, open-blinded study; INVEST (n = 22,576) (Pepine et al., 2003) Prospective, randomized, open-blinded study; ASCOT-BLA (n = 19,257) (Gupta et al., 2008)
Vasodilators		
Carvedilol Carvedilol/metoprolol	↓ FFA metabolism	Pilot study (n = 9) (Wallhaus et al., 2001) Double-blind, randomized study (n = 72) (Jacob et al., 1996)
Talinolol/atenolol		Double-blind, randomized study; TALIP (n = 198) (Sourgens, Schmidt, & Derendorf, 2003)
Carvedilol/bisoprolol	↑ glucose metabolism	Randomized study (n = 26) (Podbregar & Voga, 2002)
ACE inhibitors		
Captopril	↑ insulin sensitivity	<i>In vivo</i> study in ob/ob mice (Tabbi-Anneni et al., 2008) Double-blind, randomized Heart Outcomes Prevention Evaluation study (n = 9297) (Yusuf et al., 2000)
Ramipril	↑ reduced incidence of diabetes	
ARBs		
Candesartan	↑ glucose metabolism	Parallel, randomized, double-blind, controlled trials; CHARM-Overall program (n = 7601) (Pfeffer et al., 2003)
SGLT-2 inhibitors		
Canagliflozin	↑ glucose metabolism/excretion	Randomized, double-blind, placebo-controlled trials; CANVAS program (n = 10,142) (Neal et al., 2017)
Empagliflozin	↑ glucose metabolism/excretion	Randomized, double-blind, placebo-controlled trial (EMPA-REG; n = 7020) (Zinman et al., 2015)
Dapagliflozin	↑ glucose metabolism/excretion	Randomized, placebo-controlled, double-blind trial (n = 75) (Lambers Heerspink et al., 2013)
GLP-1receptor agonists		
Lixisenatide	Inhibit glucagon secretion ↑ insulin secretion	Randomized, double-blind, placebo-controlled trial (ELIXA; n = 6068) (Pfeffer et al., 2015)
Liraglutide	Inhibit glucagon secretion ↑ insulin secretion	Randomized, double-blind, placebo-controlled trial (LEADER; n = 9340) (Marso, Daniels, et al., 2016)
Semaglutide	Inhibit glucagon secretion ↑ insulin secretion	Randomized, double-blind, placebo-controlled trial (SUSTAIN-6; n = 3297) (Marso, Bain, et al., 2016)
CPT-1 inhibitors		
Etomoxir	↓ FFA metabolism	<i>In-vivo</i> rat model (Zarain-Herzberg et al., 1996) Randomized, double-blind study; ERGO (n = 350) (Holubarsch et al., 2007)
Perhexiline	↓ FFA metabolism	<i>In-vivo</i> rat model (Rupp & Vetter, 2000) Randomized, double-blind, placebo-controlled, parallel-group study (n = 50) (Beadle et al., 2015) Randomized, double-blind study (n = 56) (Lee et al., 2005) Randomized, double-blind, placebo-controlled study (n = 72) (Singh et al., 2014)
Other anti-anginal agents		
Trimetazidine	↓ FFA metabolism	<i>Ex vivo</i> rat model (Gambert et al., 2006) <i>In vivo</i> rat model (L. Zhang et al., 2016) Randomized open-label study (n = 55) (Fragasso et al., 2006) Randomized, double-blind, crossover study (n = 16) (Fragasso et al., 2003) Double-blind parallel group study (n = 149) (Detry et al., 1994)
Ranolazine	↑ glucose metabolism	<i>Ex vivo</i> rat model (McCormack et al., 1996) <i>Ex vivo</i> explant model (n = 14) (Sossalla et al., 2008) Double-blind, placebo-controlled, randomized study, (MERLIN)-TIMI 36 (n = 6560) (Morrow et al., 2007) Randomized, double-blind, placebo-controlled POC study; RALI-DHF (n = 20) (Maier et al., 2013)
PPAR agonists		
Fibrates	↓ triglycerides	Systemic review & meta-analysis (Jun et al., 2010) ^a
Thiazolidinediones	↑ insulin sensitivity	Systemic review & meta-analysis (Loke et al., 2011) ^a
Pioglitazone		Randomized controlled trial (n = 802) (R. B. Goldberg et al., 2005) Randomized, double-blind, double-dummy with active comparator, intervention; PIRAMID (n = 78) (van der Meer et al., 2009)
ARNi		
Sacubitril/valsartan	↑ insulin sensitivity ↑ abdominal adipose lipolysis (NS) No change in whole body lipolysis and in exercise induced lipolysis	Randomized, double-blind, double-dummy, active-controlled, and parallel-group (n = 98) (Engeli et al., 2018; Jordan et al., 2017)
Natriuretic peptides	↑ fatty acids ↑ lipolysis ↑ postprandial energy expenditure ↑ adiponectin ↑ adiponectin ↓ ghrelin (induced by BNP)	Human physiological study (n = 14) (Birkenfeld et al., 2005) Cross-over study (n = 10) (Birkenfeld et al., 2006) Randomized, double-blind, cross-over study (n = 12) (Birkenfeld et al., 2008) Human physiological study (n = 12) (Birkenfeld et al., 2012) Human physiological study (n = 47) (Yamaji et al., 2009) Randomized, placebo-controlled, crossover, single-blinded study (n = 10)

Table 1 (continued)

Metabolic modulator	Metabolic mechanism affected by modulator	Study type (pre-clinical studies, POC studies, pilot studies and clinical trials) ^a
Ketone bodies	↑ β-hydroxybutyrate dehydrogenase-1 causing increased delivery and uptake of ketone bodies	(Vila et al., 2012)
		<i>In vivo</i> mouse model (Aubert et al., 2016) <i>Ex vivo</i> explant model (n = 35) (Bedi Jr. et al., 2016)
Purinergic signaling <i>Dipyridamole</i>	↓ adenosine uptake and ↑ diuretic responsiveness	Pilot study (n = 6) (Akhtar et al., 2007)
<i>Rolofylline</i>	Adenosine A1 receptor antagonist. ↑ diuretic responsiveness	Prospective, open, randomized, controlled trial (n = 28) (Sanada et al., 2007)
		Randomized, double-blind, placebo-controlled, POC (n = 146) (Givertz et al., 2007)
		Randomized, double-blind, placebo-controlled, two-way crossover study (n = 32) (Givertz et al., 2007)
		Pilot: PROTECT—randomized, placebo-controlled, dose-finding study (n = 301) (Cotter et al., 2008)
		Double-blind, placebo-controlled study (n = 2033) (Massie et al., 2010)
<i>Adenosine</i>		REACH UP study— randomized, double-blind, placebo-controlled (n = 76) (Gottlieb et al., 2011)
		Prospective, open-label, placebo controlled, randomized study; AMISTAD (n = 236) (Mahaffey et al., 1999)
		Double-blind, placebo-controlled, randomized study; AMISTAD-II (n = 2118) (Ross et al., 2005)
L-carnitine	↑ glucose metabolism	<i>Ex vivo</i> rat model (Broderick, Quinney, Barker, & Lopaschuk, 1993)

Abbreviations: ACEi, angiotensin converting enzyme inhibitors; AMISTAD, Acute Myocardial Infarction Study of Adenosine; ARB, angiotensin II receptor blockers; ARIC, Atherosclerosis Risk In Communities; ARNI, angiotensin receptor blocker–neprilysin inhibitor; ASCOT-BPLA, Anglo-Scandinavian Cardiac Outcomes Trial – Blood Pressure Lowering Arm; BNP, B-type natriuretic peptide; CANVAS Program, The Canagliflozin Cardiovascular Assessment Study and CANVAS-Renal; CHARM, Candesartan in Heart Failure-Assessment of Reduction in Mortality and Morbidity; EMPA-REG, Empagliflozin, Cardiovascular Outcomes, and Mortality in Type 2 Diabetes trial; ERGO, etomoxir for the recovery of glucose oxidation; FFA, free fatty acid; INVEST, International Verapamil-Trandolapril Study; LIFE, Losartan Intervention for Endpoint Reduction; MERLIN-TIMI 36, Metabolic Efficiency With Ranolazine for Less Ischemia in Non-ST-Elevation Acute Coronary Syndromes; PIRAMID, Influence on tRiglyceride Accumulation in the Myocardium in Diabetes; POC, proof of concept; PPAR, Peroxisome proliferator-activated receptor; PROTECT, Placebo-Controlled Randomized Study of the Selective A(1) Adenosine Receptor Antagonist Rolofylline for Patients Hospitalized With Acute Decompensated Heart Failure and Volume Overload to Assess Treatment Effect on Congestion and Renal Function; SGLTi, sodium glucose cotransporter inhibitors.

^a Systematic review and meta-analysis.

and are utilized by the heart in preference to FA, resulting in more efficient oxidation and increase ATP hydrolysis to produce energy (Ferrannini et al., 2016). Moreover, treatment with SGLT-2 inhibitors also increases haematocrit and erythropoietin, possibly improving oxygen delivery to tissues and organs (Ferrannini et al., 2016; Ferrannini et al., 2017; Lambers Heerspink, de Zeeuw, Wie, Leslie, & List, 2013).

3.6. Glucagon-like peptide-1 (GLP-1) receptor agonists

GLP-1 receptors are expressed in the endothelium and cardiac and vascular myocytes. GLP-1 administration in isolated mouse heart showed cardioprotective effects by increasing glucose uptake, cAMP and cGMP release, left ventricular developed pressure, and coronary flow (Ban et al., 2008). Lixisenatide, a GLP-1 receptor agonist was shown to be safe in patients with diabetes and acute coronary syndrome (ACS) in ELIXA trial (Pfeffer et al., 2015). The long-acting liraglutide and very-long-acting semaglutide demonstrated superiority over placebo in reducing the occurrence of CV events in high-risk patients with diabetes in LEADER and SUSTAIN-6 trials, respectively (Marso et al., 2016; Marso et al., 2016). Furthermore, a non-significant reduction in HF hospitalizations was observed in liraglutide treatment (Margulies et al., 2016). However, liraglutide treatment did not improve clinical outcomes in HFrEF patients with or without diabetes (Jorsal et al., 2017).

4. Relevance for clinical practice – targeting dysregulated metabolic pathways in heart failure

4.1. Optimizing myocardial substrate utilization – glycolysis and FA metabolism

Several therapeutic strategies to optimize myocardial substrate utilization in HF have been investigated suggesting that metabolic therapy may be an important therapeutic option (Rosano, Vitale, & Spoletini, 2015). Table 1 summarizes the studies of cardiac metabolism modulators and their clinical benefits.

4.1.1. Fatty acid oxidation inhibitors

Reversal of the metabolic ‘foetal reprogramming’ that is characteristic of HF would aim to metabolise substrates as quickly as possible using the available oxygen. However, it is not desirable to depend on FAO under HF conditions in which oxygen demands are increased and supply limited. There is a risk of lipotoxicity and the oxidative capacity of the cardiomyocytes is also limited (due to reduced mitochondrial mass). An alternative approach would be to block FAO to stimulate the heart to switch to glucose oxidation (Heggermont, Papageorgiou, Heymans, & van Bilsen, 2016). In support of this approach, postinfarction HF was associated with upregulation of the glucose transporter, GLUT-1 in rats, while GLUT-1 overexpression prevented the development of HF in a mouse model (Liao et al., 2002; Rosenblatt-Velin, Montessuit, Papageorgiou, Terrand, & Lerch, 2001). Etomoxir and perhexiline are inhibitors of CPT-1, which also block FAO. They decrease the activity of this rate-limiting enzyme in FAO pathway, while favoring glucose oxidation (via the Randle Cycle) (Lam & Lopaschuk, 2007). Studies with etomoxir have shown that it can improve cardiac function by enhancing sarcoplasmic Ca²⁺ handling and increasing sarco/endoplasmic reticulum Ca²⁺-ATPase (SERCA)2A (Rupp & Vetter, 2000; Zarain-Herzberg, Rupp, Elimban, & Dhalla, 1996). However, its association with serious side effects (including hepatotoxicity caused by increased liver transaminase levels) means that etomoxir is not considered a suitable therapy for use in HF patients (Holubarsch et al., 2007).

Perhexiline is an anti-anginal drug that inhibits the cardiac, but not hepatic isoform of CPT-1 and is associated with improved exercise capacity and left ventricular ejection fraction (LVEF) in patients with HF (Lee et al., 2005). Trimetazidine (TMZ) is a second anti-anginal agent, which has been approved world-wide (in many European countries) (Beadle & Frenneaux, 2010). It has anti-ischemic actions without causing central hemodynamic effects. TMZ belongs to a group of inhibitors known as ‘partial fatty-acid oxidation’ (PFox) inhibitors (Fragasso et al., 2006). It exerts its effects by causing a shift in cardiac energy metabolism to glucose metabolism. The response results in a greater production of high-energy phosphates (increase in cardiac

phosphocreatinine: ATP ratio by 33%) (Fragasso et al., 2006) and causes an anti-ischemic effect. In addition, TMZ is known to cause an improvement in endothelial function, a reduction in calcium overload and free radical-induced injury (improved reperfusion mechanical function), (Fragasso et al., 2003; Gamber et al., 2006) and an inhibition of cell apoptosis and cardiac fibrosis (L. Zhang et al., 2016). There is a growing evidence to support the efficacy of TMZ in improving LV function, cardiac volume, contractility, inflammation, endothelial function and fasting glucose levels (Rosano et al., 2015).

Ranolazine is an inhibitor that is similar in structure and function to TMZ (also a PFOX inhibitor). It acts by blocking FAO to enhance glucose oxidation, thus indirectly increasing PDH complex activity, and resulting in increased ATP production (McCormack, Barr, Wolff, & Lopaschuk, 1996). It is currently approved as an anti-anginal agent in Europe and the USA. It has been shown to inhibit the late sodium current and normalize Ca^{2+} elimination in cardiac myocytes in end-stage HF, thus improving myocardial diastolic function and reducing diastolic wall tension (Sossalla et al., 2008). Furthermore, ranolazine has been shown to significantly increase LVEF in patients with systolic and diastolic HF (Horvath & Bers, 2014).

The RANOLAZINE for the Treatment of Diastolic Heart Failure study (RALI-DHF) was a randomized, prospective, placebo-controlled study in diastolic HF patients (ranolazine = 12; placebo = 8) with ejection fraction (EF) $\geq 45\%$. The study concluded that ranolazine improves haemodynamic measurements (reduction in LV end-diastolic pressure and pulmonary capillary wedge pressure) in patients with HF. However, no significant effects on relaxation parameters or BNP concentrations were observed (Maier et al., 2013).

4.1.2. Peroxisome proliferator-activated receptor agonists (PPARs)

PPARs play a role in the modulation of glucose homeostasis, IR and lipid metabolism (Desvergne & Wahli, 1999; Willson, Lambert, & Kliewer, 2001). PPAR α agonists, such as fibrates, mediate hypolipidaemic actions while the PPAR γ agonists, such as thiazolidinediones (TZDs), improve insulin sensitivity by shifting lipids from ectopic sources back to adipose tissue (Barbier et al., 2002). PPARs decrease the circulating FFA supply to the heart, resulting in reduced cardiac FAO rates (Lopaschuk et al., 2010). A systematic review concluded that fibrates lower the risk of major CV and coronary events compared with placebo, but do not affect the risk of CV or all-cause mortality or prevent the development of HF (Jun et al., 2010). PPAR γ agonists, TZDs (rosiglitazone and pioglitazone), are used to treat patients with T2DM. A systematic study analysed the CV outcomes in patients with T2DM using TZDs, concluded that rosiglitazone is associated with a higher risk of congestive HF, myocardial infarction (MI), and death than pioglitazone (Loke, Kwok, & Singh, 2011). Furthermore, rosiglitazone, exhibited a more powerful renal PPAR γ agonistic effect, leading to more fluid retention, a worsening of HF, and an increased in HF-associated hospitalizations (Loke et al., 2011; H. Zhang et al., 2005).

4.2. Ketone bodies

Ketone bodies are an alternative and glucose-sparing fuel source, which are oxidized in the heart and skeletal muscle. Studies in both animal models (Aubert et al., 2016) and humans (Bedi Jr. et al., 2016), have demonstrated that ketone utilization is increased in HF. These are in contrast to the more recent observation that increased levels of ketone bodies may lead to contractile dysfunction (Taegtmeyer, 2017). Ferrannini et al. pointed to the hypothesis that β -hydroxybutyrate is freely taken up by the heart during persistent, but mild hyperketonemia (such as that seen during treatment with SGLT-2 inhibitors) and utilized in preference to FAs. (Ferrannini et al., 2016). Such a mechanism may provide some explanation for the cardioprotection observed in the EMPA-REG study (Zinman et al., 2015). While these studies have already been discussed in detail in the section on ketone metabolism

(Section 2.2), they suggest an ongoing debate surrounding the role of ketone bodies in HF. Recent studies suggest that ketone oxidation may be a key metabolic adaptation in human HF, implying that reducing ketone utilization may be a valuable therapeutic approach (Kappel et al., 2017; Wende et al., 2017). However, further studies are required to fully uncover the effect of chronic ketone utilization on cardiac metabolism and function.

4.3. Purinergic signaling

Several studies have assessed the effects of modulators of purinergic signaling on cardiac metabolism. Dipyridamole (DIP) is an adenosine uptake blocker that causes increased adenosine levels (Stea et al., 2016). Small observational studies in patients with HF have shown that DIP improves LV function, symptoms (New York Heart Association [NYHA] class) and exercise capacity (Akhtar, Ordovas, Martin, Higgins, & Michaels, 2007; Sanada et al., 2007). Rolofylline is an adenosine A₁ receptor antagonist that increased diuresis in patients with AHF (Givertz et al., 2007) and significantly increased GFR and renal plasma flow in CHF (Givertz et al., 2007). This suggests that rolofylline may have potential for the clinical treatment of renal dysfunction in HF.

In a dose-ranging pilot study in 301 patients with AHF, rolofylline demonstrated short and medium-term clinical benefits in association with renal protection (Cotter et al., 2008). However, the results from the pivotal study, PROTECT (A Placebo-controlled Randomized Study of the Selective A₁ Adenosine Receptor Antagonist Rolofylline for Patients Hospitalized With Acute Decompensated Heart Failure and Volume Overload to Assess Treatment Effect on Congestion and Renal Function) did not demonstrate a renal-protective effect in 2033 patients admitted with acute decompensated heart failure (ADHF) and renal dysfunction, despite similarities in study design, inclusion criteria, and dose of rolofylline in the pilot study (Massie et al., 2010). The authors concluded that the inconsistency in study results could be due to the complexity and heterogeneity of AHF and suggested that new therapeutic approaches are needed. Similar to PROTECT, the REACH UP study did not demonstrate any CV benefit with rolofylline in patients with acute decompensated HF and worsening renal function (Gottlieb et al., 2011).

The Acute Myocardial Infarction Study of Adenosine (AMISTAD) trial (Mahaffey et al., 1999) and AMISTAD II (Ross et al., 2005) studied the effect of adenosine on infarct size in MI patients. While a significant reduction in infarct size was reported following adenosine treatment in AMISTAD (patients within 6 h of an onset of MI), this effect could not be replicated in AMISTAD II, in which infarct size was assessed in ST-segment elevation in MI patients undergoing reperfusion therapy. The authors noted that infarct size was reduced in patients receiving a higher concentration of adenosine (70- μ g/kg/min infusion), suggesting that a larger study at the 70- μ g/kg/min dose is warranted.

AICA-riboside, otherwise known as acadesine, acts by increasing the adenosine bioavailability. By activating the 5' adenosine monophosphate pathway, it increases the ATP production. However, development of acadesine was terminated after an analysis that suggested the drug had a low probability of reducing cardiovascular events in patients who underwent coronary artery bypass surgery (CABG) (NCT00872001, 2018).

5. Conclusion

Shifting myocardial energetics from FAO to favor more energy-efficient metabolic pathways have the potential to improve cardiac function and prognosis in HF. Furthermore, the use of insulin-sensitizing agents may promote the ability of glucose to be utilized as a preferred metabolic substrate in HF. Given that current HF therapies and concepts, including purinergic signaling, are known to have effects on metabolic pathways, agents that leverage more efficient myocardial energetics should be further investigated.

In the future, it is hoped that HF patients will not only be stratified according to their LVEF and any associated co-morbidities, but also according to their individual metabolic status allowing personalized metabolic treatment for each patient that is tailored to their specific metabolic needs.

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