Heart failure (HF) is a clinical syndrome in which myocardial pump function is inadequate for maintaining and supporting an individual’s physiological requirements. The clinical presentation is characterized by pulmonary congestion, dyspnea, and fatigue. Historically, HF was suspected when systolic function was impaired. Stages of cardiac hypertrophy without systolic dysfunction have mostly been called compensated hypertrophy. More recently, it has become clear that HF symptoms can also exist despite relatively preserved systolic function. This condition is caused mostly by diastolic...
dysfunction, which may even be present in conditions historically called compensated hypertrophy. Thus, moving forward, metabolic research will need to take this aspect into account. It is possible that distinct changes in cardiac metabolism may mediate these 2 forms of cardiac dysfunction. For the sake of simplicity and because most studies on cardiac metabolism in HF did not investigate diastolic function, we use the term compensated hypertrophy for all conditions associated with normal systolic function and the term HF to indicate the presence of systolic dysfunction. Metabolic changes that specifically affect or contribute to diastolic dysfunction will be addressed if information is available.

In this review, we focus primarily on metabolic adaptations in chronic HF. Acute changes such as those that develop after myocardial stunning or ischemia/reperfusion have been addressed elsewhere. To understand metabolic alterations in HF, an overview of basic metabolic processes in the healthy heart is necessary.

Metabolism in the Normal Heart
Under normoxic conditions, >95% of ATP generated in the heart is derived from oxidative phosphorylation in the mitochondria. The remaining 5% comes mainly from glycolysis and to a lesser extent from the citric acid cycle (Krebs cycle). The heart uses ≈60% to 70% of generated ATP to fuel contraction and the remaining 30% to 40% for various ion pumps, especially the Ca2+-ATPase in the sarcoplasmic reticulum. The energy pool of the heart includes ATP (≈5 µmol/g wet weight) and phosphocreatine (PCr; ≈8 µmol/g wet weight), with the latter serving as an ATP transport and buffer system. In the mitochondria, the high-energy phosphate bond in ATP can be transferred to creatine by mitochondrial creatine kinase to form PCr. With a smaller molecular weight than ATP, PCr can easily diffuse through the mitochondrial membrane into the cytosol. Here, it can be used to generate ATP from ADP through reactions catalyzed by the cytosolic creatine kinase. Because of its continuous mechanical work, the heart has a high rate of ATP hydrolysis (≈0.5 µmol/g wet weight per second). Accordingly, the high-energy phosphate pool in the heart is relatively small and can be exhausted within a few seconds. Therefore, cardiac work depends strongly on ATP generation, and impairments in this process can rapidly induce contractile dysfunction. Approximately 70% to 90% of cardiac ATP is produced by the oxidation of fatty acids (FAs). The remaining 10% to 30% comes from the oxidation of glucose and lactate, as well as small amounts of ketone bodies and certain amino acids. However, it is also important to note that cardiac substrate selection in human studies has been assessed mostly in the fasted state. In the fed state, when plasma levels of glucose and insulin rise, the contribution of glucose use to cardiac ATP production increases.

FA Use
FA use can be divided into 3 steps: uptake into the cytosol, transportation across the mitochondrial membrane, and oxidation within the mitochondria. Although FAs can traverse the plasma membrane (flip flop), their uptake is facilitated by transport proteins including FA translocase (CD36) and the plasma membrane FA-binding protein. In the cytosol, free FAs are esterified to fatty acyl-coenzyme A (CoA), which is either esterified to triglyceride or converted to long-chain acylcarnitine by carnitine palmitoyltransferase (CPT I) located in the outer mitochondrial membrane before entering the mitochondria. The turnover of the myocardial triglyceride pool is high and represents an important source of fatty acyl-CoA that subsequently is metabolized by the mitochondria. Long-chain acylcarnitine is then transported into the mitochondrial matrix and converted back to long-chain acyl-CoA by CPT II. Acyl-CoA then enters β-oxidation, generating acetyl-CoA and the reducing equivalents reduced nicotinamide adenine dinucleotide (NADH) and reduced flavin adenine dinucleotide.

Fatty acyl-CoA, particularly palmitoyl-CoA, can be used for de novo synthesis of ceramides, which has pleiotropic effects on cellular physiology. Incomplete FA oxidation, particularly in skeletal muscle, may result in release of acylcarnitines from mitochondria into the cytosol and subsequently into the circulation. These acylcarnitines have been implicated in the pathophysiology of insulin resistance.

The reaction catalyzed by CPT I represents a critical regulatory node that determines FA oxidation rates. In the normal adult heart, the muscle isoform (CPT Iβ) is predominant. In contrast, the expression of the liver isoform (CPT Iα), which is expressed abundantly in the fetal heart, has been shown to increase in the hypertrophied heart. The activity of CPT I is inhibited by malonyl-CoA, which is generated by carboxylation of cytosolic acetyl-CoA by the enzyme acetyl-CoA carboxylase. Malonyl-CoA is converted back to acetyl-CoA by malonyl-CoA decarboxylase (Figure 1). Although this pathway has been evaluated as a therapeutic target in the setting of ischemic heart disease, recent evidence has also...
suggested that CPT I activity may be regulated via mechanisms that are independent of changes in malonyl-CoA.24

Glucose Use
Glucose that is used by the heart either comes from uptake of exogenous glucose or is derived from glycogen stores. The heart has a relatively small glycogen pool (≈30 µmol/g wet weight, which is 20% that of skeletal muscle), but rates of glycogen turnover are high. In the heart, glycogen-derived glucose may contribute ≤40% of glucose-mediated ATP production in rats.25 Glucose is transported into the cytosol by glucose transporters (GLUTs), including GLUT1 and GLUT4. Although GLUT1 is the major glucose transporter in the fetal heart and contributes to constitutive glucose uptake, in the adult heart, GLUT4 is the predominant isoform and mediates the bulk of basal myocardial glucose uptake.26,27

After uptake, free glucose is rapidly phosphorylated to glucose 6-phosphate (G6P), which subsequently enters many metabolic pathways. Glycolysis represents the major pathway in glucose use. Glycolysis generates pyruvate, NADH, and a small amount of substrate-level ATP. This glycolytic ATP seems to be important for Ca2+ uptake into the sarcoplasmic reticulum and diastolic relaxation.28,29 In the cytosol, pyruvate can be converted to lactate. If transported into the mitochondrial matrix, pyruvate undergoes oxidation to acetyl-CoA or carboxylation to form oxaloacetate or malate. Pyruvate oxidation is catalyzed by the multienzyme complex pyruvate dehydrogenase (PDH), the activity of which is highly regulated by its products (acetyl-CoA, NADH) and by phosphorylation of its E1 subunit.30 The carboxylation of pyruvate is a major anaplerotic pathway (see below).

Accessory Pathways of Glucose Metabolism
Beside glycolysis, G6P may also be channeled into glycogen synthesis or the pentose phosphate pathway (PPP). The PPP is an important source of reduced nicotinamide adenine dinucleotide (NADPH), which plays a critical role in regulating cellular oxidative stress and is required for lipid synthesis and anaplerosis (see below). The key oxidative enzyme of the PPP is G6P dehydrogenase, which catalyzes the first reaction of the pathway to generate NADPH. In addition to the PPP, a small amount of G6P can enter the hexosamine biosynthetic pathway (HBP), leading to the formation of UDP–N-acetylglucosamine (GlcNAc), a monosaccharide donor for O-GlcNAcylation of various proteins.12 Because the HBP requires not only glucose but also acetyl-CoA and glutamine, it may serve as a metabolic sensor linking metabolic status to several cellular processes. Although flux through the PPP and HBP in the normal heart is relatively small, recent evidence has suggested a role for these pathways in the pathophysiology of heart disease (see below).

The Krebs Cycle and Anaplerosis
Acetyl-CoA, the common end product of glucose and FA oxidation, enters the citric acid cycle (also known as tricarboxylic acid cycle or Krebs cycle) to generate ATP (or GTP), CO2, and reducing equivalents NADH.32 Because Krebs cycle intermediates can be used for many biosynthetic pathways (eg, amino
and nucleic acids), they are constantly removed from the cycle and therefore need to be replaced. The replenishment of the Krebs cycle intermediate pool through pathways independent of acetyl-CoA is called anaplerosis.\textsuperscript{32,33} The carboxylation of pyruvate to malate is an important anaplerotic reaction. This requires NADPH and therefore links anaplerosis to processes that generate (PPP) or consume (lipogenesis, antioxidative defense) NADPH. Anaplerosis is a crucial process in the heart, where impairment rapidly causes contractile dysfunction.\textsuperscript{34} Changes in anaplerotic pathways have recently been implicated in heart disease (see below).

**Oxidative Phosphorylation and the Generation of Reactive Oxygen Species**

The reducing equivalents (NADH\textsubscript{2} and FADH\textsubscript{2}) enter the electron transport chain (ETC) for oxidative phosphorylation. A byproduct of this process is the generation of reactive oxygen species (ROS) arising mainly from complexes I and III.\textsuperscript{35} Mitochondrial ROS production has been implicated in a wide variety of cellular processes, ranging from protective mechanisms such as preconditioning to detrimental mechanisms such as oxidative damage and activation of adverse ventricular remodeling.\textsuperscript{36,37}

**Short-term Regulation of Cardiac Substrate Use**

FA and glucose use is tightly linked and coregulated. Use of 1 substrate may directly inhibit the use of the other (the Randle cycle).\textsuperscript{37} Complete metabolism of glucose is more oxygen efficient than that of FAs.\textsuperscript{38} Therefore, substrate selection and the interaction between glucose and FA use in the heart have been considered highly relevant in cardiac disease.\textsuperscript{39} Substrate use and selection in the heart are also modulated by hormones such as insulin, glucagon-like peptides (GLPs), and catecholamines. Although important, these regulatory mechanisms lie outside of the scope of this review.

**Long-term Regulation of Cardiac Metabolism**

Expression levels of metabolic enzymes and their posttranslational modifications may strongly affect cardiac metabolic activity. Peroxisome proliferator–activated receptor (PPAR) nuclear receptors are important transcriptional regulators of FA use. Although PPAR\textsubscript{\alpha} is the predominant isoform in the heart, PPAR\textsubscript{\beta} and PPAR\textsubscript{\gamma} may also modulate FA metabolism.\textsuperscript{11} Cardiac FA use is also regulated by the estrogen-related receptor (ERR)\textsubscript{\alpha}. In addition to sharing common targets with PPAR\textsubscript{\alpha}, ERR\textsubscript{\alpha} stimulates the transcription of genes involved in glucose metabolism and oxidative phosphorylation.\textsuperscript{40,41}

The transcriptional activities of PPARs and ERRs are potentially induced by interacting with members of the PPAR\textsubscript{\gamma} coactivator-1 (PGC-1) family. PGC-1\textsubscript{\alpha} binds to and coactivates PPARs and ERRs, leading to increased capacity of FA uptake and oxidation.\textsuperscript{42} Although less extensively studied, PGC-1\textsubscript{\beta} may also play an important role in the regulation of cardiac energy metabolism.\textsuperscript{43} PGC-1 proteins are powerful activators of mitochondrial biogenesis. This is mediated in part by induction of the nuclear respiratory factor 1 and the mitochondrial transcription factor A.\textsuperscript{44} The activity of PGC-1\textsubscript{\alpha} is highly regulated by both its expression levels and posttranslational modifications such as phosphorylation, acetylation, or methylation.\textsuperscript{42}

AMP-activated protein kinase (AMPK) is another important mediator of metabolic adaptation that promotes increased ATP production and inhibition of energy-consuming biosynthetic pathways under conditions of hemodynamic stress or ischemia. AMPK boosts ATP production by acutely stimulating both FA oxidation and glycolysis while slowing down ATP-consuming processes such as lipid and protein synthesis. Furthermore, AMPK may also improve cardiac energetics in a long-term manner by activating PGC-1\textsubscript{\alpha}, leading to increased mitochondrial biogenesis and oxidative capacity.\textsuperscript{45}

**Metabolism Beyond ATP Production**

Metabolic intermediates may act as regulators of many pathways not directly related to ATP production. Table 1 summarizes classic metabolites that have been recognized as signal transducers. Although much of our discussion so far has focused on substrate oxidation and ATP production in the heart, it is equally important to consider that cardiac metabolism also involves anabolic processes that are essential for maintaining cellular activities and promoting cell growth and proliferation.\textsuperscript{46,47} The development of HF is characterized by profound changes in cardiac structure and function. Given the fundamental role of metabolism in all of these processes, it is reasonable to assume that cardiac metabolism occupies a central position in the pathophysiology of HF.

### Table 1. Classic Metabolic Intermediates That Have Been Recognized as Signal Transducers

<table>
<thead>
<tr>
<th>Metabolic Intermediates</th>
<th>Regulatory Effects</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fatty acids</td>
<td>Activation of PPARs,\textsuperscript{40} modulation of ion channels by palmitoylation\textsuperscript{49}</td>
</tr>
<tr>
<td>Acylcarnitines</td>
<td>Activation of Ca\textsuperscript{2+} channels,\textsuperscript{34} induction of insulin resistance\textsuperscript{15}</td>
</tr>
<tr>
<td>Ceramides</td>
<td>Activation of P2PA, PKC\textsubscript{\zeta} \textrightarrow inhibition of insulin signaling,\textsuperscript{44} induction of mitochondrial and ER stress and apoptosis\textsuperscript{51}</td>
</tr>
<tr>
<td>Pyruvate</td>
<td>Stimulation of mitochondrial biogenesis,\textsuperscript{52} regulation of PGC-1\textsubscript{\alpha} expression\textsuperscript{53}</td>
</tr>
<tr>
<td>Acetyl-CoA</td>
<td>Induction of cell growth and proliferation by promoting the acetylation of histones\textsuperscript{54}</td>
</tr>
<tr>
<td>Hexosamine</td>
<td>Multiple cellular effects via O-GlcNAcylation of regulatory proteins\textsuperscript{55}</td>
</tr>
<tr>
<td>NAD(P)\textsubscript{+}/NAD(P)H</td>
<td>Modulation of activity of metabolic enzymes, numerous additional effects via regulation of redox state and sirtuins\textsuperscript{37,38}</td>
</tr>
<tr>
<td>ROS</td>
<td>Regulation of redox state, enzyme activity; high levels induce apoptosis, hypertrophy, inflammation\textsuperscript{56,57}</td>
</tr>
<tr>
<td>AMP</td>
<td>Diverse effects on metabolism and cell growth through activation of AMPK\textsuperscript{46}</td>
</tr>
<tr>
<td>BCAA</td>
<td>Stimulation of protein synthesis\textsuperscript{47} and various additional effects via activation of mTOR and inhibition of autophagy\textsuperscript{48}</td>
</tr>
</tbody>
</table>

\textsuperscript{AMPK} indicates AMP-activated protein kinase; BCAA, branched-chain amino acids; CoA, coenzyme A; ER, endoplasmic reticulum; GlcNA, N-acetylglucosamine; mTOR, mechanistic target of rapamycin; PGC-1, peroxisome proliferator–activated receptor \textgamma coactivator-1; PKC, protein kinase C; PPAR, peroxisome proliferator–activated receptor; P2PA, protein phosphatase; and ROS, reactive oxygen species.
Cardiac Metabolism in HF

There are 2 major points that should be considered in the interpretation of study results on metabolic alterations in HF. First, metabolic phenotypes and their mechanisms differ between HF of different pathogeneses. Second, because the progression to HF is often long and complex, the time point of assessment (ie, compensated hypertrophy with or without diastolic dysfunction versus manifest systolic dysfunction) influences the metabolic adaptations that are observed. Despite these caveats, findings in humans and animal models provide clear evidence indicating severe metabolic alterations in the failing heart. Table 2 summarizes reported changes in substrate use and energy production in various models of HF.

FA Use in HF

Most studies reveal reduced cardiac FA use. FA uptake is reduced in concert with high-salt diet–induced HF65 and by rapid pacing.71 In agreement with these findings, studies in other models of HF also observed a reduction in mRNA and protein expression of FA transporters when systolic dysfunction was present.59,63,64,70 We found that FA oxidation rate and the expression of FA oxidation enzymes were already decreased in early (compensated) stages of left ventricular hypertrophy.59 These results are also consistent with findings in spontaneously hypertensive rats66,72 and in rats with abdominal aortic constriction63,64 but not with those in Dahl salt-sensitive rats65 and in rats with myocardial infarction.66 However, by the time that systolic dysfunction manifests, there is clear evidence from studies in animal models and human subjects that myocardial FA oxidation is decreased. Figure 2A summarizes the fate of FAs in HF and how these changes may lead to decreased ATP production.

Glucose Use in HF

In contrast to FA use, data on cardiac glucose use are less consistent (Table 2). In the presence of systolic dysfunction, cardiac glucose uptake was found to be decreased in mice after aortic constriction,84 unchanged in rats with myocardial infarction,79 and increased in Dahl salt-sensitive rats.61 In compensated hypertrophy, induced by abdominal aortic constriction, glycolysis was modestly increased without changes in glucose oxidation.62,63 By assessing substrate oxidation at various time points after aortic constriction in rats, we observed that cardiac glucose oxidation tended to increase initially but was unchanged relative to controls in the phase of compensated hypertrophy and ultimately decreased when systolic dysfunction occurred.59 The impaired glucose oxidation that parallels systolic dysfunction might be attributable in part to mitochondrial dysfunction, reduced expression of genes involved in glycolysis and glucose oxidation, or decreased abundance of the PDH complex.65,74 However, in infarcted rat hearts, we observed no change in glucose oxidation rate despite manifest systolic dysfunction.69 Interestingly, spontaneously hypertensive rats, at the cardiac hypertrophy stage and before HF, were found to have higher glucose oxidation rates64 or increased flux through the PDH complex67 relative to control rats. In addition, Osorio et al73 showed increased glucose oxidation rates in failing dog hearts induced by rapid pacing, and Dávila-Román et al73 demonstrated higher total rates of glucose use in patients with idiopathic dilated cardiomyopathy. It is unlikely that these differences can be explained by methodological differences. We therefore suggest that in contrast to changes in FA oxidation, glucose oxidation does not correlate with contractile function in HF but that changes in glucose oxidation may depend on both the stage and the pathogenesis of HF.

Anaplerosis in HF

Another factor that may influence the interpretation of glucose oxidation results is the fact that pyruvate may be channeled into anaplerotic pathways (Figure 2B). In hypertrophied rat hearts induced by aortic constriction, Sorokina et al77 showed that glucose oxidation by PDH is unchanged despite increased glycolysis. More important, they identified an increase in anaplerotic flux into the Krebs cycle probably via pyruvate carboxylation by malic enzyme.17 The increase in this alternative pathway of pyruvate use may account for the mismatch between glycolysis and glucose oxidation that is commonly seen in models of pressure overload–induced cardiac hypertrophy. This hypertrophy-associated anaplerotic change has also been confirmed in mice with aortic constriction73 and in hyperthyroid rats.78 Thus, induction of anaplerotic pathways seems to be a hallmark of metabolic remodeling in cardiac hypertrophy. Considering that hypertrophic growth requires increased supply of amino acids and nucleic acids derived from precursors in the Krebs cycle, activation of anaplerotic pathways may be required to maintain Krebs cycle function. However, this compensatory mechanism might also have unfavorable consequences (Figures 2B and 3 for illustration). For example, increased flux of pyruvate through anaplerotic pathways reduces its availability for oxidation by the PDH complex. As a result, pyruvate oxidation might not sufficiently compensate for the impaired FA oxidation, leading to energetic inefficiency of the Krebs cycle.77 Furthermore, increased flux through malic enzyme may also affect cardiac function by consuming NADPH,77 which is required for triglyceride synthesis and for defending against oxidative stress. Therefore, the role of anaplerotic changes, particularly in relation to the nature of cardiac hypertrophy, remains incompletely understood. This knowledge gap is attributable in part to the technical challenges inherent in measuring anaplerosis.

Mitochondrial Biogenesis and Function in HF

The above-described alterations in substrate oxidation and anaplerosis occur at the level of mitochondria. It is therefore not surprising that many studies have described significant mitochondrial changes in HF (Table 2). In rat hearts with systolic dysfunction induced by aortic constriction, we identified abnormal mitochondrial morphology, reduced mitochondrial volume density, and altered levels of most ETC proteins, with the majority being decreased.60 Mitochondrial proteomic remodeling in HF has also been demonstrated in mice with pressure overload, which is characterized primarily by altered abundance of proteins involved in ETC and substrate metabolism.74 These results suggest that perturbed mitochondrial biogenesis is an important feature of pressure overload–induced HF. Consistent with this notion, expression of PGC-1α is decreased in systolic HF, as has been shown by us62,66 and others.78,79 There is limited evidence of mitochondrial alterations...
Table 2. Changes in Substrate Oxidation and Mitochondrial Function in Various Models of Cardiac Hypertrophy and Failure

<table>
<thead>
<tr>
<th>Models of Heart Disease</th>
<th>Morphological and Functional Characteristics</th>
<th>FA Metabolism</th>
<th>Glucose Metabolism</th>
<th>Mitochondrial Changes and Energy Status</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aortic constriction in rats</td>
<td>Compensated hypertrophy without/diastolic dysfunction; systolic dysfunction</td>
<td>FAO and mRNA expression of genes regulating FAO decreased in compensated hypertrophy and systolic dysfunction</td>
<td>GO decreased in systolic dysfunction</td>
<td>State-3 respiration initially increased but decreased in systolic dysfunction</td>
<td>59</td>
</tr>
<tr>
<td>Aortic constriction in rats</td>
<td>Hypertrophy with diastolic and systolic dysfunction</td>
<td>FAO, mRNA, and protein expression of FAO enzymes decreased</td>
<td>GO decreased, protein expression of PDH complex increased</td>
<td>Disorganized mitochondrial cristae, mitochondrial volume density, and levels of most ETC proteins decreased, state-3 respiration decreased</td>
<td>60</td>
</tr>
<tr>
<td>Aortic constriction in mice</td>
<td>Hypertrophy with systolic dysfunction</td>
<td>FAO unchanged</td>
<td>Glycolysis and GO increased</td>
<td>Mitochondrial dysfunction, decreased respiration and ATP content</td>
<td>43</td>
</tr>
<tr>
<td>Aortic constriction in mice</td>
<td>Hypertrophy with diastolic and systolic dysfunction</td>
<td>FAO unchanged</td>
<td>GU, glycogen synthesis, glucose, and lactate oxidation decreased</td>
<td></td>
<td>61</td>
</tr>
<tr>
<td>Abdominal aortic constriction in rats</td>
<td>Mild, compensated hypertrophy</td>
<td>FAO and mRNA expression of genes regulating FAO unchanged</td>
<td>Glycolysis increased modestly</td>
<td></td>
<td>62</td>
</tr>
<tr>
<td>Abdominal aortic constriction in rats</td>
<td>Mild, compensated hypertrophy</td>
<td>FAO and mRNA expression of genes regulating FAO decreased</td>
<td>GO unchanged</td>
<td></td>
<td>63</td>
</tr>
<tr>
<td>Abdominal aortic constriction in rats</td>
<td>Hypertrophy, heart function ex vivo unchanged</td>
<td>FAO decreased</td>
<td>Glycolysis increased, GO unchanged</td>
<td></td>
<td>64</td>
</tr>
<tr>
<td>Dahl salt-sensitive rats</td>
<td>Compensated hypertrophy; systolic dysfunction</td>
<td>FA uptake and mRNA expression of genes regulating FAO use decreased in systolic dysfunction</td>
<td>GU increased, mRNA expression of genes regulating glycolysis and GO decreased; pentose phosphate pathway flux increased in systolic dysfunction</td>
<td>mRNA and protein expression of genes regulating mitochondrial biogenesis increased in systolic dysfunction; PCr/ATP ratio decreased</td>
<td>65</td>
</tr>
<tr>
<td>SHRs (Sprague-Dawley rats as controls)</td>
<td>Hypertrophy, heart function ex vivo unchanged</td>
<td>FAO lower (note that some strains of SHRs have a mutation in CD36, which could independently modulate FAO)</td>
<td>GO higher</td>
<td></td>
<td>66</td>
</tr>
<tr>
<td>Spontaneously hypertensive rats (Wistar rats as controls)</td>
<td>Hypertrophy, minor differences in diastolic and systolic functions</td>
<td>Flux through PDH higher</td>
<td></td>
<td>PCR/ATP ratio not different</td>
<td>67</td>
</tr>
<tr>
<td>Myocardial infarction in rats</td>
<td>Compensated hypertrophy; systolic dysfunction</td>
<td>mRNA expression of genes regulating FAO decreased</td>
<td>mRNA and protein expression of GLUT1 increased in systolic dysfunction</td>
<td></td>
<td>68</td>
</tr>
<tr>
<td>Myocardial infarction in rats</td>
<td>No hypertrophy, left ventricular dilatation, systolic dysfunction</td>
<td>FAO and mRNA expression of genes regulating FAO decreased</td>
<td>GU and GO unchanged</td>
<td>mRNA expression of genes regulating mitochondrial biogenesis decreased</td>
<td>69</td>
</tr>
<tr>
<td>Myocardial infarction in rats</td>
<td>Mild hypertrophy, systolic dysfunction</td>
<td>FA use decreased, protein expression of fatty acid transporters decreased</td>
<td></td>
<td></td>
<td>70</td>
</tr>
<tr>
<td>Pacing-induced HF in dogs</td>
<td>No hypertrophy, left ventricular dilatation, systolic dysfunction</td>
<td>FA uptake and oxidation, activity of CPT I, and MCAD decreased</td>
<td>GO increased</td>
<td></td>
<td>71</td>
</tr>
<tr>
<td>Patients with HF with IDCM or ischemic heart disease</td>
<td>Systolic dysfunction</td>
<td>mRNA expression of MCAD, LCAD lower</td>
<td></td>
<td></td>
<td>72</td>
</tr>
<tr>
<td>Patients with HF with IDCM</td>
<td>Hypertrophy, systolic dysfunction</td>
<td>FA use lower</td>
<td>Glucose use higher</td>
<td></td>
<td>73</td>
</tr>
<tr>
<td>Patients with HHD, AS, or DCM</td>
<td>Hypertrophy with normal systolic function in patients with HHD and AS; left ventricular dilatation and systolic dysfunction in patients with DCM</td>
<td></td>
<td></td>
<td>PCR/ATP ratio not different among groups; PCr content lower in AS and DCM; ATP content lower in DCM</td>
<td>5</td>
</tr>
</tbody>
</table>

AS indicates aortic stenosis; CPT, carnitine palmitoyltransferase; DCM, dilated cardiomyopathy; ETC, electron transport chain; FA, fatty acid; FAO, fatty acid oxidation; GLUT, glucose transporter; GO, glucose oxidation; GU, glucose uptake; HF, heart failure; HHD, hypertensive heart disease; IDCM, idiopathic dilated cardiomyopathy; LCAD, long-chain acyl-CoA dehydrogenase; MCAD, medium-chain acyl-CoA dehydrogenase; PCr, phosphocreatine; PDH, pyruvate dehydrogenase; and SHR, spontaneously hypertensive rat.
in other models of HF. In failing rat hearts caused by myocardial infarction, we found normal mRNA expression of PGC-1α. However, the expression of p38 mitogen–activated protein kinase, which could modulate PGC-1α activity, was reduced.69 In patients with HF of diverse pathogeneses, Karamanlidis et al80 observed decreased mitochondrial DNA content accompanied by reductions in mitochondrial DNA–encoded proteins. Of note, these changes were associated with increased abundance of PGC-1α protein but decreased expression of ERRα and mitochondrial transcription factor A at both the mRNA and protein levels.80 These findings suggest that mitochondrial biogenesis signaling is depressed in advanced HF and that posttranslational modulation of PGC-1α may play a role.

Little is known about the regulation of mitochondrial biogenesis in compensated hypertrophy. We found a significant decline in mRNA expression of PGC-1α, ERRα, and mitochondrial transcription factor A at both the mRNA and protein levels.80 These findings suggest that mitochondrial biogenesis signaling is depressed in advanced HF and that posttranslational modulation of PGC-1α may play a role.

Mitochondrial dysfunction as evidenced by decreased mitochondrial respiration and reduced ATP production is consistently observed when systolic dysfunction occurs in various models of HF.59,82,83 Interestingly, we and others found that mitochondrial respiration in pressure-overloaded hearts initially increased and did not decrease until systolic dysfunction developed.59 Considering that mitochondrial damage is probably an early event in the progression to HF, this biphasic response of mitochondrial respiratory capacity might reflect unknown compensatory mechanisms that can sustain oxidative phosphorylation during the stage of compensated hypertrophy but are lost as cardiac dysfunction develops.

Cardiac Energetics in HF
Mitochondrial dysfunction in advanced HF has been linked to impaired myocardial energetics. Studies in animal models and humans have reported a decrease in the PCR/ATP ratio, ATP content, and the ATP flux through creatine kinase in advanced HF with reduced ejection fraction. Given that sufficient ATP supply is essential for normal cardiac function, this change has been suggested to be responsible for the transition to systolic dysfunction.6,84 If this were true, it would be reasonable to hypothesize that ATP depletion should be detectable in compensated

Figure 2. Alterations in substrate metabolism and mitochondria during the development of heart failure (HF). Bold lines indicate pathways reported to be activated. Thin lines represent pathways reported decreased. The question marks imply unknown changes or inconsistent observations. A, Fatty acid oxidation is impaired in cardiac hypertrophy and failure, leading to reduced ATP production. B, Most evidence suggests that glucose oxidation is unchanged in compensated hypertrophy and decreased in HF, but discrepancies exist. In contrast, several non–ATP-generating pathways of glucose metabolism (HBP, PPP, anaplerosis) are induced. C, Increased generation of mitochondrial reactive oxygen species (ROS; perhaps because of changes in the electron transport chain) causes direct mitochondrial damage, which may further increase mitochondrial ROS production to create a vicious cycle. Mitochondrial damage results in ATP deficiency. Mitochondrial ROS may also cause oxidative damage to other cellular components and may contribute to adverse structural remodeling. BCAA indicates branched-chain amino acid; CoA, coenzyme A; CPT, carnitine palmitoyltransferase; FAT, fatty acid transporter; G6P, glucose 6-phosphate; GLUT, glucose transporter; HBP, hexosamine biosynthetic pathway; IMS, mitochondrial intermembrane space; PPP, pentose phosphate pathway; and TG, triglyceride. Illustration Credit: Ben Smith.
hypertrophy just before the onset of systolic dysfunction. Kato et al. showed a 12% decrease in the PCr/ATP ratio in compensated hypertrophy in Dahl salt-sensitive rats. In contrast, Dodd et al. found that both absolute content of high-energy phosphate metabolites and the PCr/ATP ratio were normal in the hypertrophied heart of spontaneously hypertensive rats. In hearts of patients with hypertensive heart disease with normal ejection fraction, the PCr/ATP ratio was found to be decreased, but the absolute content of ATP and PCr has been shown to be preserved. Thus, data in hypertrophied hearts with normal systolic function do not support a model in which impaired ATP-producing capacity might be an antecedent to the transition to decompensated HF. It is possible that the lack of a clear conclusion could be attributable in part to methodological limitations in using PCr/ATP ratios to quantify myocardial energetics. However, an alternative conclusion is that decreased levels of high-energy phosphates do not cause HF per se but represent an adaptation to decreased pump function.

In advanced HF, there is consistent evidence of decreased myocardial ATP availability, but it remains unclear whether the reduction in ATP abundance contributes to contractile dysfunction. Approaches that would directly enhance myocardial ATP abundance in the failing heart are required to address this question. In a recent study, the xanthine oxidase inhibitor allopurinol was shown to acutely improve the relative and absolute concentrations of myocardial high-energy phosphates and ATP flux through creatine kinase in the failing human heart. Nevertheless, whether cardiac function changed in response to this energetic improvement was unknown. Furthermore, in a retrospective study in a large cohort of patients with HF, Struthers et al. found no beneficial effects of long-term allopurinol treatment on cardiovascular mortality. Of note, because allopurinol may exert complex systemic effects, these negative results can neither confirm nor refute a potential role of energetic impairment in HF pathogenesis. Although the correlation between cardiac energy status and survival in patients with HF is striking, this correlation could also represent the worsening mitochondrial function that occurs in concert with progression of HF severity. Although this alternative hypothesis remains to be disproved, studies on cardiac energetics in HF are attractive because they may provide not only mechanistic insights and potential new therapeutic strategies but also valuable prognostic information.

Normal cardiac function requires the coordinated regulation and interaction of several physiological and signaling systems in addition to energy supply. In rats developing HF attributable to pressure overload, we calculated the ATP amount generated from substrate oxidation and found that the ratio of cardiac power to ATP was consistently reduced as soon as cardiac hypertrophy developed. This result provides indirect evidence for inefficient transduction from ATP into mechanical power. Before the onset of systolic dysfunction, the heart undergoes severe structural changes (eg, hypertrophy, fibrosis, dilatation). It is therefore likely that such profound remodeling of the contractile apparatus may involve mechanisms that significantly affect cardiac function independently of ATP supply. Potential mechanisms range from changes in the extracellular matrix (myocardial fibrosis, inflammation) to impaired calcium handling or modification of sarcomeric proteins, which have all been reviewed by others.

Mitochondrial ROS and Its Link to Cardiac Metabolism in HF

Although metabolic and structural alterations in the failing heart have been increasingly well characterized, little is known about the mechanisms that drive the remodeling process in HF. Increased cardiac ROS levels have been implicated in HF, but the role of ROS in the pathogenesis of HF was questioned as a result of disappointing outcomes of antioxidant interventions in human studies. However, in a recent animal study, Dai et al. demonstrated that angiotensin II increased mitochondrial ROS, leading to mitochondrial damage, activation of mitogen-activated protein kinases, and finally cardiac hypertrophy and fibrosis. Another study by the same group also showed that mitochrondria-targeted antioxidant treatment but not nontargeted ROS scavenging with N-acetyl cysteine ameliorated cardiomyopathy induced by chronic angiotensin II infusion. Of note, mouse hearts in this model of pressure overload presented mild diastolic dysfunction without changes in left ventricular ejection fraction, indicating an early stage of compensated hypertrophy. These results suggest that increased mitochondrial ROS could be an early event triggering structural remodeling and mitochondrial defects in hypertensive heart disease. Figure 2C illustrates the generation of mitochondrial ROS and its potential impact on energy metabolism and other pathological processes.

The regulation of cellular ROS homeostasis is complex and is only partially understood. In the mitochondria, ROS are produced mainly from the ETC particularly from complexes I and III. Therefore, changes in the ETC may favor electron leakage and consequently ROS formation. The elevation in ROS production may further affect the function of the ETC, leading to a vicious cycle (Figures 2C and 3). Studies in various tissues have linked FA use to increased ROS levels. In diabetic cardiomyopathy, ROS have also been associated with myocardial lipid accumulation, lipotoxicity, and decreased cardiac efficiency on the basis of mitochondrial uncoupling. The failing heart is believed to be subjected to higher levels of free FAs, probably as a result of increased lipolysis. In addition, models of HF have been associated with myocardial lipid accumulation. As a result, FA use has been considered unfavorable for the stressed heart because of increasing ROS production. However, in animal models with a cardiac-specific loss of acetyl-CoA carboxylase-2, increased myocardial FA use did not adversely affect left ventricular remodeling after pressure overload. This might represent a scenario of complete substrate oxidation without increased generation of mitochondrial ROS. Furthermore, cardiac FA oxidation is depressed during HF progression, and there is little direct evidence in HF models that FA use may increase ROS production. Thus, the causes of increased mitochondrial ROS in the progression to HF remain unclear and warrant further investigation.

Changes in the PPP in HF

The regulation of the cellular redox environment is tightly linked to substrate metabolism via the PPP as an important source of NADPH. NADPH is required for the generation of
cytosolic ROS, which, at low levels, are involved in proliferation and survival signaling. Conversely, NADPH also maintains the pool of reduced antioxidants such as glutathione that are crucial defenses against oxidative stress. Hence, the PPP may play a dual role in the regulation of redox homeostasis. Although much effort has been made to characterize glycolysis and glucose oxidation, little is known about the regulation of the PPP in HF. In dogs subjected to pacing-induced HF, increased superoxide levels were attributed to increased activity of G6P dehydrogenase, the key oxidative enzyme of the PPP. If the effects of superoxide are indeed damaging, this activation of the PPP in the failing heart could be considered detrimental. However, G6P dehydrogenase-deficient mice developed higher oxidative stress and worsened contractile function after myocardial infarction or aortic constriction. In Dahl salt-sensitive rats, Kato et al also found that the flux through the PPP progressively increased during the development of HF. Importantly, they demonstrated that treatment with dichloroacetate (DCA) further increased this flux, which was associated with improved cardiac function. Taken together, the PPP is activated in HF models. Although superoxide production may consequently increase, currently available data support the notion that higher flux through the PPP in HF may represent a compensatory mechanism whose further activation could be of therapeutic relevance.

Changes in the HBP in HF

The HBP, which is linked to metabolism of glucose, FAs, and amino acids, has been implicated in various models of heart disease. The HBP and HBP-dependent O-GlcNAcylation are induced in the diabetic heart, which may result in increased apoptosis, mitochondrial dysfunction, and impaired Ca$^{2+}$ cycling. Recently, the role of the HBP in HF has also received special interest. By using various models of HF, including aortic constriction, myocardial infarction, and hypertensive rats, Lunde et al demonstrated that global O-GlcNAcylation was increased by ≥40% in hypertrophied and failing hearts. They also confirmed these findings in patients with aortic stenosis. In endothelial cells, increased flux through the HBP has been attributed to overproduction of mitochondrial superoxide. Considering that mitochondrial ROS formation also increases in cardiac hypertrophy, mitochondrial ROS might represent a potential mechanism for activation of the HBP in the heart.

Whereas the induction of O-GlcNAcylation in the progression of HF is well described, less is known about the functional relevance of these changes. In a cardiomyocyte model of hypertrophy, Facundo et al found that increased flux through the HBP and the resulting increase in O-GlcNAcylation were responsible for hypertrophic growth via activation of the nuclear factor of activated T cells. This finding is highly relevant because it indicates that induction of the HBP is an early event that triggers myocardial remodeling. Because nuclear factor of activated T cells signaling has been associated with pathological hypertrophy, one might consider this activation of the HBP to be detrimental. However, reducing O-GlcNAcylation in mice with myocardial infarction exacerbated ventricular dysfunction. Thus, although the HBP activates signaling pathways that initiate cardiac remodeling, additional signaling pathways linked to the HBP may also promote favorable effects. Further studies are therefore needed that focus on the characterization and targeted modulation of intracellular signaling pathways that are regulated by HBP, in the context of clinical and experimental models of HF.

Autophagy and Its Link to Cardiac Metabolism in HF

Metabolic remodeling in HF is also associated with changes in autophagy. Autophagy is a highly conserved process by which organelles and large cellular components are degraded. The products of autophagy (amino acids, FAs, sugars, and nucleosides) may then be channeled into both energy-generating and -biosynthesis pathways. Under normal conditions, basal autophagy is crucial by eliminating damaged organelles and misfolded proteins. In states of nutrient deprivation such as starvation or ischemia, autophagic activity is increased, which may support cell function by mobilizing endogenous nutritional sources. In models of HF including pressure overload and myocardial infarction, autophagy has also been shown to be induced. Mechanisms for the activation of autophagy in HF are less clear. A number of changes observed in the hypertrophied and failing heart such as energy depletion, AMPK activation, mitochondrial ROS overproduction, and damaged mitochondria are strong mediators of autophagy in various settings. However, the potential contribution of these events to autophagic activation in HF remains to be verified.

Autophagy has also been implicated in ventricular remodeling. In an elegant study, Cao et al provided evidence indicating that the activation of autophagy, although degradative in nature, is essential for cardiac hypertrophy. Because cell growth requires stimulation of biosynthesis pathways, these data may seem paradoxical at first glance. However, they are supported by earlier studies showing that blunting of protein degradation mediated by the ubiquitin-proteasome system may attenuate cardiac hypertrophy. Together, these data indicate that cardiac hypertrophy and remodeling are dynamic reconstructive processes in which degradation of certain cellular components by autophagy and the ubiquitin-proteasome system is an important antecedent that might stimulate the biosynthesis of new structures.

Because of the essential role of autophagy in ventricular remodeling, one might expect that inhibiting autophagy may prevent cardiac hypertrophy and failure. However, studies in knockout models with suppressed autophagy have delivered inconsistent results. Given the highly complex regulation of autophagy, it is reasonable to assume that specific changes in the induction or targeting of autophagy but not the autophagic flux itself may affect functional outcome. For example, Oka et al recently demonstrated in mice with aortic constriction that mitochondrial DNA that escapes from autophagy causes cardiac inflammation and failure. Therefore, the regulation and the role of autophagy in HF remain to be fully elucidated. Because both the induction of autophagy and the processing of autophagic products are linked to metabolism, the relationship between metabolic remodeling in HF and the regulation of autophagy is an attractive target for future studies.
Figure 3 schematically illustrates the interaction between metabolic and structural remodeling of the heart in the progression to heart failure (HF). Metabolic pathways are blue. Bold lines indicate pathways/processes that are increased or dominant. Thin lines represent pathways/processes that are decreased. The question marks imply unknown causes/effects. In general, metabolic remodeling in cardiac hypertrophy and failure is characterized by a shift away from energy production to activation of biosynthetic pathways required for structural remodeling processes such as ventricular hypertrophy and fibrosis. Particularly, fatty acid oxidation is decreased and may not be sufficiently compensated given the lack of increase in glucose oxidation. These alterations and further mitochondrial defects result in ATP depletion. Instead of being oxidized, pyruvate may be preferentially used for anaplerosis to maintain Krebs cycle moieties, which might be increasingly channeled into protein synthesis. Hypertrophic mediators such as mitogen-activated protein kinases (MAPKs) and nuclear factor of activated T cell (NFAT) are activated as a result of increased mitochondrial reactive oxygen species (ROS) and flux through the hexosamine biosynthetic pathway (HBP), respectively. Overproduction of mitochondrial ROS causes oxidative damage. Although the flux through the pentose phosphate pathway (PPP) is increased, antioxidative defense might be inadequate, attributable to the consumption of NADPH by the anaplerotic malic enzyme. Mitochondrial damage and ATP depletion may stimulate autophagy. Increased activity of autophagy and the ubiquitin-proteasome system (UPS) may contribute to hypertrophy by providing amino acids and other metabolites. Increase in mitophagy may trigger myocardial inflammation by releasing mitochondrial DNA. A indicates anaplerosis; CoA, coenzyme A; ETC, electron transport chain; G, glycolysis; H, HBP; O, oxidation; and P, PPP.

Potential Metabolic Therapy for HF

Modulation of Cardiac FA Metabolism

Modulation of cardiac FA use has been a target of metabolic therapy in HF for the past decade. The failing heart has been suggested to be in a state of FA overload, suffering from increased oxygen wastage and oxidative stress or from accumulation of cardiotoxic lipid derivatives. Consequently, many pharmacological approaches sought to reduce cardiac FA use, and some studies revealed beneficial effects. However, the concept of inhibiting FA use has now been challenged by contradictory results of studies in animal models of HF subjected to high-fat diets. For example, Raher et al. showed that high-fat diet in mice induced myocardial insulin resistance and exacerbated left ventricular remodeling caused by aortic constriction. In contrast, Okere et al. reported decreased cardiac hypertrophy and improved contractile function after treatment with high-fat diet in hypertensive Dahl salt-sensitive rats. In addition, a cute inhibition of FA oxidation in a population of patients with end-stage HF led to significant worsening of left ventricular function. The plethora of studies on the modulation of cardiac FA use and its effects on contractile function has been extensively reviewed and discussed elsewhere. Although a mechanistic link between cardiac FA metabolism and contractile function remains controversial because some therapeutic strategies targeting cardiac FA use have suggested functional consequences of manipulating this pathway, additional investigation of therapies that modulate FA metabolism in the failing heart is warranted.
Modulation of Cardiac Glucose Metabolism

A small number of studies suggest that direct modulation of glucose use could also be beneficial. In mice subjected to pressure overload, life long cardiac-specific overexpression of GLUT1 increased glucose uptake and glycolysis and improved cardiac energetics and function. Although the enhanced ATP production may account for the improved functional outcome in these mice, possible changes in accessory pathways of glucose metabolism such as the PPP and the HBP could also play a role but were not evaluated. Because the increase in glucose uptake in this model preceded the induction of pressure overload, it remains to be determined whether increasing glucose uptake after the onset of pressure overload or before the transition to HF will have any effect.

Among the limited pharmacological strategies to stimulate glucose use directly in HF, DCA has been the most widely studied compound. DCA indirectly activates the PDH complex and thus glucose oxidation, which is considered the mechanism of cardioprotection in ischemia/reperfusion models. The use of DCA to treat HF has been tested in some animal models and humans. In patients with advanced HF, Bersin et al. showed that a 30-minute infusion of DCA stimulated myocardial lactate consumption, which was accompanied by decreased oxygen consumption and increased cardiac work. However, not all human studies have demonstrated short-term benefit, and long-term clinical trials have never been performed in HF, perhaps in part because neuropathy has been reported when DCA was used long term in cases of inherited mitochondrial disorders.

In Dahl salt-sensitive rats with hypertension, DCA treatment reduced ventricular hypertrophy and improved cardiac function and survival, which was associated with increased myocardial glucose uptake and energy reserves. Of note, treatment with DCA also enhanced flux through the PPP, which was shown to be the mechanism by which DCA reduced oxidative damage and apoptosis in cardiomyocytes. Interestingly, long-term DCA treatment also increased flux through PDH and reduced cardiac hypertrophy in rats with hyperthyroidism. Collectively, these results suggest that augmenting cardiac glucose use could represent a potential strategy to treat HF, which not only may improve cardiac energetics but also may attenuate oxidative stress and structural remodeling. However, additional studies with less toxic agents are required.
Modulation of Cardiac Anaplerosis

As described above, anaplerotic flux through pyruvate carboxylation is elevated in compensated hypertrophy, which may affect cardiac lipogenesis and antioxidant defense mechanisms by consuming NADPH. In hypertrophied rat hearts, Pound et al. demonstrated that acute activation of PDH by DCA competed for pyruvate and partially reduced its flux through malic enzyme, which led to normalization of the myocardial triglyceride pool and improved contractile function. These results may suggest therapeutic relevance of inhibiting pyruvate carboxylation in cardiac hypertrophy. Furthermore, they provide an additional protective mechanism beyond the energetic aspect of improving cardiac glucose oxidation. However, the role of long-term inhibition of anaplerotic pathways in cardiac hypertrophy and failure remains to be elucidated.

Cardiac function may also be enhanced by targeting other anaplerotic routes. If the induction of anaplerosis through pyruvate carboxylation is a compensatory mechanism to maintain Krebs cycle moieties, early supplementation with an anaplerotic substrate may allow pyruvate to be oxidized by PDH. We found that feeding aortic-constricted rats with triheptanoin-enriched diets, which may exert anaplerotic effects by providing the Krebs cycle with propionyl-CoA, attenuated ventricular hypertrophy and diastolic dysfunction. Importantly, these effects were accompanied by increased cardiac glucose oxidation. Although the mechanistic role of anaplerosis in these treatments remains to be substantiated, the results again point to anaplerotic pathways as a potential therapeutic target that may modulate metabolic and structural remodeling in HF.

AMPK Activation

Cardiac hypertrophy and failure are associated with increased activity of AMPK, which may be attributable to increased AMP/ATP ratio, ROS, or Ca2+ load. Pharmacological interventions that further increase AMPK activity in HF models have resulted in reduced ventricular remodeling and improved cardiac function. These findings suggest that the activation of AMPK in HF may be adaptive and amenable to pharmacological manipulation. Activation of AMPK induces a wide range of effects that coordinate the improvement of cardiac energetics and counteract ventricular remodeling. For example, AMPK activation may acutely stimulate both glucose and FA oxidation, thereby enhancing energy production. This mechanism has been shown to exist in normal hearts or after ischemia and reperfusion and may apply to HF. Activation of AMPK could also increase energy metabolism by increasing PGC-1α activity, which would induce genes of FA use. Furthermore, a PGC-1α–mediated increase in mitochondrial biogenesis could potentially compensate for mitochondrial damage and loss in HF. This potential mechanism has been suggested in mice with myocardial infarction, but further studies in other models of HF are warranted.

Activation of AMPK also alleviates ventricular remodeling in terms of hypertrophy, myocardial fibrosis, and inflammation. Various potential mechanisms may account for these beneficial effects. AMPK reduces ROS-related oxidative stress in endothelial cells by inducing the antioxidant thioredoxin. Because ROS can lead to mitochondrial damage and cardiac structural remodeling, inhibition of ROS signaling by AMPK could potentially attenuate these pathological processes. Similarly, AMPK plays an important role in the regulation of autophagy, which has been implicated in ventricular hypertrophy and inflammation. Given that ventricular remodeling may occur early in the development of HF, studies examining the impact of early AMPK activation on pathological remodeling are therefore warranted.

AMPK can be activated by a number of drugs. A long-used agonist is 5-aminoimidazole-4-carboxamide 1-β-D-ribofuranoside which activates AMPK in various tissues, including the heart, by forming the AMP-mimetic ZMP (5-aminoimidazole-4-carboxamide 1-β-D-ribofuranoside monophosphate). Although 5-aminoimidazole-4-carboxamide 1-β-D-ribofuranoside has been used extensively in animal studies, its role in humans is still unclear. The anti-diabetic drug metformin has also been shown to activate AMPK in the heart. Although metformin was initially contraindicated in advanced HF attributable to the risk of lactic acidosis, recent studies have shown beneficial effects of early administration of metformin in models of HF. Metformin is believed to activate AMPK by inhibiting complex I, leading to increased cellular AMP levels. However, complex I–independent mechanisms have also been proposed. Because metformin may also act independently of AMPK, caution is warranted when attributing treatment effects of metformin to AMPK activation.

Activation of Cardiac GLP-1 Receptors

GLP-1 is an incretin hormone that is secreted by neuroendocrine cells in the gut in response to feeding. Once secreted, GLP-1 is rapidly degraded by the enzyme dipeptidyl peptidase-4. Dipeptidyl peptidase-4 inhibitors and GLP-1 agonists are now commonly used to treat diabetes mellitus because increased GLP-1 or activation of its receptors in the β cell or gastrointestinal tract stimulates insulin secretion and delays gastric emptying, thereby improving metabolic homeostasis.

GLP-1 receptors are expressed in the heart. Activating cardiac GLP-1 receptors in models of ischemia/reperfusion have consistently shown beneficial effects in terms of reduced infarct size and improved contractile function. In pacing-induced HF in dogs, Nikolaidis et al. found a significant improvement in ventricular function after a 48-hour infusion of GLP-1, which was associated with increased cardiac glucose uptake and insulin sensitivity. In spontaneously hypertensive rats receiving a long-term infusion of GLP-1, Poornima et al. also reported improved survival and cardiac function. Because GLP-1 treatment increased insulin secretion in these rats, it is unclear whether GLP-1 or insulin accounted for these effects. In contrast, in our rat model of pressure overload, we also observed improved functional outcome and preserved cardiac glucose oxidation without changes in insulin levels, which suggest insulin-independent effects of GLP-1. There is also evidence that GLP-1 might mediate cardiovascular effects via GLP-1 receptor independent mechanisms.
underlying molecular mechanisms. In HF models, the protective effects of GLP-1 are mostly associated with improved glucose use. However, the mechanisms by which GLP-1 influences glucose metabolism and the relationship between changes in glucose metabolism and cardiac function in this context are incompletely understood.

Conclusions

HF is associated with profound changes in cardiac metabolism. Metabolic remodeling in HF is characterized by the decreased cardiac energy production that may result from progressive impairments in substrate use and mitochondrial biogenesis and function. In addition to ATP deficiency, metabolic remodeling involves changes in metabolic pathways that regulate essential, non–ATP-generating cellular processes such as growth, redox homeostasis, and autophagy. Therefore, modulating cardiac metabolism may also affect these critical processes and improve cardiac function by mechanisms beyond ATP production. Nevertheless, the exact mechanisms linking metabolic changes to other pathological processes in HF are still poorly understood. Future mechanistic investigations are therefore needed to decipher this complex network and to improve the effectiveness of metabolic therapies for HF.

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Disclosures

None.

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