On the Control of Metabolic Remodeling in Mitochondria of the Failing Heart

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The metabolic phenotype of the failing heart may be defined as follows.1 Metabolism remodels in the failing heart, leading to a loss in energy reserve and the inability to increase ATP supply. Ultimately, this metabolic rigidity leads to a fall in ATP. The likely time line is decreased energy reserve via the phosphotransferase reactions (creatine kinase [CK] and adenylate kinase) leading to increases in ADP and AMP, triggering an increase in glycolysis. Although the contribution of glycolysis to overall ATP synthesis increases at least in the hypertrophied heart, glycolytic reserve is limited. Importantly, as heart failure evolves, ATP synthesis from oxidation of both endogenous and exogenous fatty acids by mitochondria, the major source of ATP in the heart, falls.2

Remodeling of the failing myocardium is controlled by energy sensors such as AMP that lead to changes in phosphorylation state (as well as other chemical modifications) of many proteins for short-term preservation of ATP and by activation of transcription factors that coordinately control long-term remodeling of entire ATP synthesis and utilizing pathways.

Given that the requirement for ATP for all metabolic processes and for cell viability is absolute, a renewed interest in metabolism has led to identification of the molecular links between physiological and metabolic stimuli and the regulation of gene expression in the heart. We not only have identified the metabolic targets of specific nuclear receptors and DNA-binding transcriptional activators but also are beginning to learn how their signals are amplified and sustained to remodel metabolism.

Transcription is activated when transcriptional activators, including peroxisome proliferator-activated receptors, estrogen receptors, retinoid receptors, nuclear respiratory factors, and myocyte-enhancing factor-2 (MEF-2) form protein-protein complexes with the peroxisome proliferator-activated receptor-γ coactivators, namely PGC-1α and β, tethering PGC-1s to DNA (Figure). When complexed with the transcription activators, PGC-1s activate genes encoding proteins comprising entire metabolic pathways that control ATP synthesis in mitochondria (fatty acid uptake, β-oxidation, oxidative phosphorylation, the Krebs cycle, and electron transport chain), phosphoryl transfer (sarcomeric mitochondrial CK and adenine nucleotide transporter), glucose uptake and utilization, and ATP-utilizing proteins (Figure). The different transcription factors confer specificity of PGC-1s for its genomic targets. Substantial overlap exists, and there is much to learn about the full range of targets. Because of its central role in transcriptional control of metabolism, PGC-1α is referred to as a master regulator.

PGC-1α is itself regulated. For example, the cyclin-dependent kinases Cdk9 and Cdk7 target PGC-1α, thereby conferring additional specificity for the transcriptional control of ATP synthesizing and utilizing reactions. Other known regulators of PGC-1α in striated muscle include p38 mitogen-activated protein kinase, calcineurin A/calmodulin-dependent protein kinase II (CaMKII), possibly AMP-activated protein kinase (AMPK), and humoral factors.3 Evidence suggests that PGC-1α may be regulated differently in different tissues.3 Given its important role in regulating metabolism, knowing how the level of PGC-1α changes in the failing heart and how it is regulated are crucial for our understanding of metabolic control at a basic level and also how to develop new metabolic-based therapies for the failing heart. The article entitled “Control by Circulating Factors of Mitochondrial Function and Transcription Cascade in Heart Failure: A Role for Endothelin-1 and Angiotensin-II” by Garnier et al4 in this issue makes substantial contributions to our understanding of the control of mitochondrial function in the failing heart, a major step in this process.

The overall hypotheses tested in this article are that angiotensin-converting enzyme inhibition (ACEi) protects against reduced oxidative capacity in the failing myocardium and that this may be mediated by circulating hormones. The rationale is based on 2 observations: circulating hormones such as endothelin-1 (ET-1) are hyperactivated in heart failure patients5 and, as shown in previous work by this group, ACEi treatment was found to correct mitochondrial defects in skeletal muscle of heart failure patients.6 The specific hypotheses tested were (1) myocardial mitochondrial oxidative capacity is lower in ACEi-treated heart failure patients, (2) ACEi therapy protects myocardial mitochondrial function by activating PGC-1α expression, and (3) hormonal signals induce the PGC-1α transcription cascade. Three sets of experiments were performed.

Human Myocardium

Biopsy specimens from myocardium from 20 patients with end-stage heart failure (caused either by coronary artery disease or by nonischemic cardiomyopathy) who underwent
transplantation, from nonfailing myocardium obtained from brain-dead accident victims, and from open-heart surgery patients (total n=17) were analyzed for PGC-1α content, mitochondrial oxidative capacity, and activities of key mitochondrial enzymes, namely citrate synthase (CS) in the Krebs cycle and cyclooxygenase IV in the respiratory chain as well as CK isozymes located both in the cytosol and the mitochondrial oxidative capacity, or enzyme activity changes, recapitulating the human heart failure phenotype. The trends, however, are close to full protection for the enzyme activities measured. Because perindopril was supplied early after ligation, whether ACEi therapy reverses or prevents defects in mitochondrial oxidative capacity remains to be fully tested.

Rat Ventricular Myocytes
The next step taken was to define the effects of humoral factors known to be involved in heart failure on transcriptional control of mitochondrial protein expression and the PGC-1α transcription cascade in isolated adult rat ventricular cells. ET-1, angiotensin II, phenylephrine, aldosterone, and isoprenaline were tested. Exposing cells to ET-1 recapitulated the heart failure phenotype with regard to lower cyclooxygenase IV activity and lower expression of the transcriptional regulators PGC-1α, nuclear respiratory factor-2α, and mito-
Mitochondrial Dysfunction in Failing Heart

An important lesson made by the study by Garnier et al. 4 is that ET-1 downregulates mRNA expression and protein levels of the sarcoplasmic reticulum calcium ATPase. Possibly, PGC-1α gene expression was upregulated by aldosterone (by ~60%) and downregulated by angiotensin II (by approximately ~20%). These results show how important it is to consider hormonal regulation of transcription cascade in the failing heart. They also may be useful in designing new markers for end-stage heart failure and new strategies for therapy.

What Do We Have to Look Forward to?
As rich as this study is, there is much more to learn. For example, most of the subjects were men, and responses to hormones can be gender-specific; the subjects were also relatively young (~55 years old). Because metabolism remodels with age, age-dependent effects should also be examined. The patients studied here have ejection fractions of ~24%; it is possible that the phenotype reported here is even worse with worse contractile function. There is also much to learn with regard to the basic biology of transcription cascade. What happens to PGC-1α? This study focused on mitochondria, but we now know that the PGC-1α transcription cascade and hormones have targets in other organelles as well. Notable in this regard is the recent article by Dillman and coworkers, 13 reporting that ET-1 downregulates mRNA expression and protein levels of the sarcoplasmic reticulum calcium ATPase. Possible impact on sarcomere remodeling may also be determined. An important lesson made by the study by Garnier et al. 4 is how important it is to take an integrated multilevel approach to understand the heart failure phenotype. This report used skinned fibers, mRNA levels, protein amounts, and cell cultures to study a central issue in heart failure phenotype, namely mitochondrial function, setting an exemplary standard for future research in this area.

Disclosures
None.

References

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