



Stress Response Signaling Pathways May Lead to Mitochondrial Biogenesis



Diabetes 2014;63:1831–1832 | DOI: 10.2337/db14-0373

Diabetes, a worldwide epidemic, represents a major public health problem and the vast majority of the patients with diabetes presents with insulin resistance, a fundamental manifestation of this disease. Insulin resistance impairs glucose uptake into skeletal muscle, which takes up about 80% of postprandial glucose in healthy individuals (1). Thus, skeletal muscle plays an indispensable role in maintaining glucose homeostasis. However, the mechanisms underlying the development of insulin resistance remains poorly understood, which perhaps accounts for the lack of effective therapies.

Mitochondria, where low levels of superoxide radicals are constitutively generated as a by-product of electron transport, serve as the powerhouse and are also considered a main source for overproduction of reactive oxygen species (ROS) triggered by diabetes (2,3). Oxidative stress is a key pathological signal leading to diabetes complications (4,5). It has been disappointing that broad-spectrum antioxidant therapies have not been effective in improving outcomes in high-risk patients, including patients with diabetes (6), when used as primary prevention, suggesting that detailed knowledge of oxidative injury mechanisms is necessary to develop effective antioxidant therapies that target specific pathogenic mechanisms while sparing physiologically important ROS-dependent pathways. Oxidative stress causes mitochondrial dysfunction and contributes to mitochondrial uncoupling and impaired energetics in the diabetic heart (7–9). Overexpression of ROS-detoxifying proteins, including superoxide dismutase, metallothionein, and catalase, reverses mitochondrial dysfunction induced by diabetes (10–12). These results suggest that mitochondria are a key source of oxidative stress in patients with diabetes and an important target for ROS-mediated damage.

In this issue, Jain et al. (13) reveal a role of mitochondrial-generated ROS in causing mitochondrial biogenesis via a mechanism dependent on calcium/calmodulin protein

kinase II (CaMKII). They use an obesity model of high-fat feeding in both rats and mice to demonstrate that the increase in fat intake triggers signaling cascades, ultimately activating CaMKII and AMP-activated protein kinase (AMPK) and stimulating mitochondrial biogenesis. The increase in mitochondria was measured at both the mitochondrial DNA and protein levels (specifically, electron transport chain constituents were measured) following high-fat feeding. CaMKII can be activated by modification of a number of residues in the activation domain (14), and two of these amino acid sites were tested (13). CaMKII activation by phosphorylation occurred following high-fat feeding and was reversed by inhibiting mitochondrial ROS emissions. Surprisingly, CaMKII was not activated via oxidation, indicating a different mode of CaMKII activation than reported for the streptozotocin diabetic model of CaMKII activation (15). In the streptozotocin diabetic mouse model, activation of CaMKII occurs by both phosphorylation (16) and oxidation (15) (Fig. 1). Uncovering the different mechanisms of CaMKII activation under various pathologic conditions is paramount for a thorough understanding of mitochondrial function.

AMPK, a main regulator of cellular energy, preserves an optimal AMP/ATP ratio and is activated by mitochondrial ROS. However, the AMPK activation that is found with high-fat feeding likely occurs by a signaling pathway other than ROS because, unlike CaMKII activation, inhibition of mitochondrial ROS further increased AMPK activation (13). This is consistent with the possible alternate modes of activation for this energy regulator (17). An increase in cytosolic calcium from the ryanodine receptor (RyR) can activate CaMKII (18). Jain et al. (13) report that an increase in S-nitrosylation by ROS activates the RyR but did not test this in the presence of an antioxidant; however, the authors do show that CaMKII phosphorylation depends on opening of the RyR. High-fat feeding conceivably activates several signaling pathways,

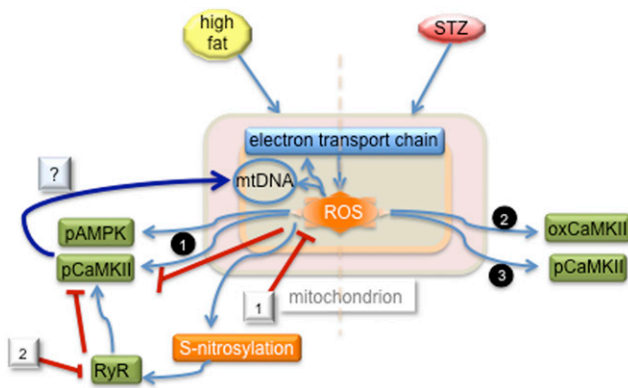


Figure 1—Consequences of chronic high-fat feeding. High-fat feeding (*left* side of mitochondrion) leads to increased mitochondrial ROS production causing a number of signaling changes, including increased phosphorylated (p)CaMKII (black circle 1 [13]) and pAMPK and S-nitrosylation of the RyR. These changes either directly or indirectly result in mitochondrial biogenesis, as measured by increased mitochondrial DNA (mtDNA) and protein complexes. Streptozotocin (STZ) treatment (*right* side of mitochondrion) leads to increased CaMKII activation by both oxidation (ox) (black circle 2 [15]) and phosphorylation (black circle 3 [16]) with downstream outcomes not shown. Blocking excess mitochondrial ROS generation reduces CaMKII activation, but not AMPK activation (red line 1), and blocking RyR calcium current will reduce CaMKII activation (red line 2). The key to this signaling cascade will be to show whether inhibiting CaMKII activity under these conditions prevents mitochondrial biogenesis (blue arrow ?).

as components of one signal transduction pathway may affect another because of shared constituents.

Jain et al. (13) suggest that the function of mitochondrial biogenesis under the stress of high fat may be to promote fatty acid oxidative phosphorylation and to decrease mitochondrial ROS production. However, mitochondrial ROS production did not decrease in the time frame of this study. Interestingly, a considerably longer-term study of a high-fat diet showed increase in ROS per unit respiration for liver and heart tissue mitochondria (19). In a study to identify whether activated CaMKII is upstream of mitochondrial biogenesis following high-fat feeding, it would be useful to show whether inhibiting CaMKII activity reverses the mitochondrial biogenesis observed in Jain et al., as has been suggested by others (20). Furthermore, it remains to be determined whether mitochondrial biogenesis or dysfunction is a cause or consequence of insulin resistance.

Duality of Interest. No potential conflicts of interest relevant to this article were reported.

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