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## The role of Ca<sup>2+</sup> signaling in the coordination of mitochondrial ATP production with cardiac work

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### Abstract

The heart is capable of balancing the rate of mitochondrial ATP production with utilization continuously over a wide range of activity. This results in a constant phosphorylation potential despite a large change in metabolite turnover. The molecular mechanisms responsible for generating this energy homeostasis are poorly understood. The best candidate for a cytosolic signaling molecule reflecting ATP hydrolysis is Ca<sup>2+</sup>. Since Ca<sup>2+</sup> initiates and powers muscle contraction as well as serves as the primary substrate for SERCA, Ca<sup>2+</sup> is an ideal feed-forward signal for priming ATP production. With the sarcoplasmic reticulum to cytosolic Ca<sup>2+</sup> gradient near equilibrium with the free energy of ATP, cytosolic Ca<sup>2+</sup> release is exquisitely sensitive to the cellular energy state providing a feedback signal. Thus, Ca<sup>2+</sup> can serve as a feed-forward and feedback regulator of ATP production. Consistent with this notion is the correlation of cytosolic and mitochondrial Ca<sup>2+</sup> with work in numerous preparations as well as the localization of mitochondria near Ca<sup>2+</sup> release sites. How cytosolic Ca<sup>2+</sup> signaling might regulate oxidative phosphorylation is a focus of this review. The relevant Ca<sup>2+</sup> sensitive sites include several dehydrogenases and substrate transporters together with a post-translational modification of F1-FO-ATPase and cytochrome oxidase. Thus, Ca<sup>2+</sup> apparently activates both the generation of the mitochondrial membrane potential as well as utilization to produce ATP. This balanced activation extends the energy homeostasis observed in the cytosol into the mitochondria matrix in the never resting heart.

### Keywords

Dehydrogenase; F1-FO-ATPase; Membrane Potential; Oxidative Phosphorylation; NADH; Oxygen Consumption; Sarcoplasmic Reticulum; Starling Effect; Energy Homeostasis; Aralar; Citrin

### Introduction

The requirement to continuously pump blood to the body makes the heart one of the most active tissues in the body when integrated over any significant amount of time. This continuous work requirement results in an energy conversion system that is capable of supporting this activity with little or no mismatch between energy conversion and utilization, or the system will fail. To get some perspective in this process, the entire ATP pool in the canine heart is turned over in ~1 minute at “rest” (~5 μmol/gram ATP [127],

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respiratory rate  $\sim 5\mu\text{mol}/\text{gram}/\text{min}$ [64]) and less than 10 sec at maximum workloads[64,76]. Thus, even a small mis-match between ATP production and utilization would rapidly lead to energy failure in the heart. This requirement likely generates a cytosolic energy conversion control network that is not only accurate, but has several parallel/backup systems to prevent a sustained mismatch between energy conversion and utilization for work.

The major source of cardiac energy conversion in the steady state is ATP generated by oxidative phosphorylation. This was appreciated many years ago when the rate of respiration was found to be linear with the level of work[76,118,139]. Glycolysis may play a role during burst activity[36,50], providing additional ATP during transition phases helping to maintain the energy homeostasis as well as provide pyruvate as a substrate for oxidative phosphorylation. However, in the steady state oxidative phosphorylation is clearly the major source of ATP that must be balanced with the rate of hydrolysis by the myosin ATPase for contraction and active ion transport in the sarcoplasmic reticulum used to control the contraction process.

In addition to maintaining the balance of ATP production with utilization the heart is also capable of supporting large changes in ATP turnover without altering the effective free energy of ATP hydrolysis (for recent review see[13]. That is, the hydrolysis products of ATP, ADP and Pi, are essentially held constant over most physiological workloads resulting in a near constant free energy of hydrolysis independent of the workload. Thus, the heart is able to balance the rate of ATP production with the rate of utilization while maintaining the energy generating capacity of ATP hydrolysis by not having [ATP] decrease or [ADP] and [Pi] increase during increases in workload [17,24,67,73,84,101,111,120,141]. An example of this phenomenon is presented in Figure 1 in a canine heart *in vivo*[61]. In this example an NMR coil was placed directly on the heart and the  $^{31}\text{P}$  NMR spectra of ATP, creatine phosphate (CrP), and inorganic phosphate (Pi) were collected under controlled and paced up conditions. The pace up roughly increased the rate pressure product by a factor of 2. As seen in the different spectra between these conditions, no significant change in the high energy phosphates occurred despite the fact that the turnover of these molecules doubled under these conditions.

What is the cytosolic control network that orchestrates the complex ATP hydrolysis at the filaments and sarcoplasmic reticulum (SR) with ATP production at the mitochondrion? The earliest model of the regulation of oxidative phosphorylation with work was a simple feedback of the ATP hydrolysis products ADP and Pi back to the mitochondrion[33,66]. That is, as ATP hydrolysis increases the concentration of ADP and Pi in the cytosol increases driving oxidative phosphorylation faster via simple enzyme kinetic driving forces. This has often been coupled to a facilitated diffusion or shuttle mechanism associated with the compartmentation of different isoforms of creatine kinase[20,21,117,137]. The feedback of ADP and Pi or creatine back to the mitochondrion clearly does play a role in the regulation of oxidative phosphorylation under a variety of different specialized conditions[13,14]. However, as discussed above (Figure 1), over the last two decades evidence has been building that the concentrations of ATP, ADP, Pi and CrP are maintained in the myocardium in the face of physiological challenges, *in vivo*. Thus, other cytoplasmic regulatory mechanisms have been looked at to supplement or modify the simple metabolite feedback mechanism of respiratory control. The two major, non-exclusive, models currently being investigated include a metabolite compartmentation model that relies on small pools of ADP at the interface of the mitochondria and cytosolic elements (for example see[1]). This is usually supplemented by the distribution of creatine kinase isoforms in the different compartments of the cell, relying on the diffusion of creatine in the free cytosol [21,137]. Compartmentation or “channeling” of ADP at the sarcoplasmic reticulum/mitochondria interface has also been proposed[5,71], much like demonstrated for  $\text{Ca}^{2+}$  signaling[92,114].

The second, again non-exclusive, model relies on a feed forward or parallel activation scheme using  $\text{Ca}^{2+}$  in many of the same compartments proposed for metabolite compartmentation. It is important to note that these models are not exclusive. That is it is likely that elements of both models, compartmentalized metabolic substrate feedback and  $\text{Ca}^{2+}$  feed-forward and feedback, are likely important under different conditions in the heart. The role of  $\text{Ca}^{2+}$  in the orchestration of oxidative phosphorylation with cytosolic ATP hydrolysis will be evaluated in this review. A special focus will be applied to the putative control sites for  $\text{Ca}^{2+}$  regulating oxidative phosphorylation in the mitochondrial matrix.

## **$\text{Ca}^{2+}$ as a Feed-Forward and Feed Back Signaling Molecule for the rate of ATP hydrolysis**

$\text{Ca}^{2+}$  is very unique as a signaling molecule in that it can serve as a feed-forward or a feed-back signaling molecule reflecting the rate of ATP hydrolysis. A feed-forward signaling molecule for ATP hydrolysis provides information about this process either in parallel or before the change in rate occurs. Since  $\text{Ca}^{2+}$  is the primary signaling molecule driving ATP hydrolysis in muscle contraction and ion transport, it is ideally suited as a feed-forward signaling molecule for ATP hydrolysis. Duncker and Bache [45] recently reviewed the major sources of cardiac work with exercise as with regard to rate, contractility and ventricular work (Starling). These effects are summarized in a normalized fashion in Figure 2. The black bars represent the rate and contractility terms that are controlled by  $\text{Ca}^{2+}$  or reflected by the integrated level of cytoplasmic  $\text{Ca}^{2+}$ . The contractility improvement associated with heart rate, *trappe*, is incorporated into the contractility term. Heart rate is the major driver of the overall metabolic load during exercise in the heart, supporting the earlier analysis of using pacing as a work transition in the  $^{31}\text{P}$  NMR analysis as presented in Figure 1 [17,61]. From this analysis, 80 percent of the exercise work transition is clearly dependent on integrated increases in cytosolic  $\text{Ca}^{2+}$ , supporting the notion that  $\text{Ca}^{2+}$  is an excellent feed forward signal.

The relatively small contribution of the Starling effect, or change in end-diastolic volume, to the cardiac work associated with exercise has been appreciated for years. Though the Starling phenomenon itself has been well characterized *in vitro* as an increase in  $\text{Ca}^{2+}$  sensitivity of the contractile apparatus with stretch [83] and is thus not dependent on an increase in cytosolic  $\text{Ca}^{2+}$ , the large majority of studies in dogs [136] and man [35,62,102,112,125] find little or no change in end diastolic volume with exercise even using the latest MRI techniques. Thus, as suggested by Duncker and Bache, the Starling phenomenon apparently plays a small role in the overall stimulation of cardiac output with exercise.

The “grey” area represents the Starling component of the increase in work that is generally believed to be initially independent of cytosolic  $\text{Ca}^{2+}$  as described by Allen and Kurihara in the isolated rat and cat heart papillary muscles and trabeculae [3]. However, in a subsequent study in the ferret Allen et al found a strong correlation of fiber length with resting  $\text{Ca}^{2+}$  concluding: “*We suggest that muscle length influences resting  $[\text{Ca}^{2+}]_i$  and this in turn affects the  $\text{Ca}^{2+}$  transients and developed tension.*” [4]. A minority of subsequent studies have found an increase in resting  $\text{Ca}^{2+}$  with stretch [86] [82] using sensitive optical methods for detecting diastolic  $\text{Ca}^{2+}$  levels, while most only detect increases in the “slow response” to stretch [74]. The relationship between stretch and  $\text{Ca}^{2+}$  was reviewed by Calaghan and White [32]. As mentioned above, it is generally accepted that increases in muscle stretch enhances the sensitivity of the muscle fibers to  $\text{Ca}^{2+}$  [83]. Without a coordinated increase in  $\text{Ca}^{2+}$  sensitivity of ATP production with stretch an unraveling of the metabolic homeostasis would occur if it only depended on changes in cytosolic calcium. It is interesting to note that some increases in the end-diastolic volume occurs in canines near maximum exercise [136]

where the metabolic homeostasis has been shown to breakdown[73] independent of oxygen tension [146]. Possibly, the Starling effect resulting from an increase in  $\text{Ca}^{2+}$  sensitivity of the myofilaments may be contributing to imbalance of ATP production with utilization at high workloads resulting in a requirement for the free energy of ATP to decrease. However, it is still unclear whether the slow component of  $\text{Ca}^{2+}$  increase seen with muscle stretch in most preparations could also influence the overall metabolic network. Thus, intracellular  $\text{Ca}^{2+}$  may also play a direct role in the smaller Starling component of exercise induced increases in cardiac work through the slow component of  $\text{Ca}^{2+}$  increase, a few beats after the change in stretch.

Feedback implies that the  $\text{Ca}^{2+}$  levels can increase after an increase in ATPase activity. The  $\text{Ca}^{2+}$  gradient generated by the sarcoplasmic reticulum  $\text{Ca}^{2+}$  pump (SERCA) is one of the largest potential energies in the cell[34] from 70% to 90% of the theoretical thermodynamic limits as defined by  $\Delta G_{\text{ATP}+\text{nRT}}\ln([\text{Ca}^{2+}]_{\text{out}}/[\text{Ca}^{2+}]_{\text{in}})$ [80,133] Being so close to its thermodynamic limits, it is not surprising the alterations in the  $\Delta G_{\text{ATP}}$  due to a mismatch between ATP production and utilization either locally or across the entire cell would result in an increase in diastolic  $\text{Ca}^{2+}$  [48,133]. This sensing of the  $\Delta G_{\text{ATP}}$  can also occur just in the region of the sarcoplasmic reticulum providing a compartmentalized signal of ATP depletion [71] if such gradients exist. Thus, under conditions where  $\Delta G_{\text{ATP}}$  decreases with large increases in workload[73,145] or compromised substrate oxidation, cytoplasmic  $\text{Ca}^{2+}$  levels would predictably increase providing a signal that oxidative phosphorylation is not keeping up with ATP hydrolysis, a classical feedback indicator. This mechanism could be applicable to the whole cytosol or regional variations in  $\Delta G_{\text{ATP}}$  at the SR.

Direct experimental evidence that cytosolic  $\text{Ca}^{2+}$  follows the work level of the heart has been provided by many investigators in the intact heart[27,28,49,81,87,128,142] and cells or trabeculae[27,28,51,94] [2,12,44]. An example of the correlation of intracellular  $\text{Ca}^{2+}$  and oxygen consumption in the perfused rat heart treated with different catecholamines is presented in Figure 3 adapted from Wu et al [142]. As predicted by the mechanisms of action of  $\text{Ca}^{2+}$ , there is a tight correlation between oxygen consumption and free intracellular  $\text{Ca}^{2+}$  determined by fluorescent probes in the cytosol. Thus, there is significant evidence, from molecular mechanisms to whole heart and cellular measurements, that cytosolic  $[\text{Ca}^{2+}]$  correlates with myocardial workload and would make an excellent element in a metabolic control network regulating energy conversion with utilization.

Are changes in cytosolic  $\text{Ca}^{2+}$  reflected in the mitochondrial matrix? This has been a controversial topic over the years since the kinetics for  $\text{Ca}^{2+}$  uptake and more importantly efflux were believed to be much too slow at physiological concentrations to account for reasonable tracking of matrix  $\text{Ca}^{2+}$  with cytosolic transients. Even if the matrix did not track transients in the cytosol, it is clear that the matrix could integrate both systolic and diastolic  $\text{Ca}^{2+}$  levels even without rapid transport systems[90]. However, recently evidence has been gaining that more rapid mitochondrial transport mechanisms are present. Gunter and Sheu[53] recently reviewed the potential fast mechanisms for  $\text{Ca}^{2+}$  import including the  $\text{Ca}^{2+}$  uniporter, RaM and a ryanodine sensitive transporter. However the export mechanism is still limited to rather slow  $\text{Na}/\text{Ca}^{2+}$  exchange and some poorly defined  $\text{Na}$  independent mechanisms. Again, a rapid export mechanism against the substantial electrochemical potential for  $\text{Ca}^{2+}$  is still one of the unsolved problems in this field along with the lack of definitive identification of the  $\text{Ca}^{2+}$  uniporter.

One of the major advances in this field was the realization that the systolic local  $\text{Ca}^{2+}$  concentration around the intrafibrillar mitochondria may be much higher than the average cytosolic concentration, resulting in a sufficient high  $\text{Ca}^{2+}$  concentration that the conventional uniporter kinetics could result in rapid  $\text{Ca}^{2+}$  mitochondrial uptake. In a clever

set of experiments by Rizzuto and Pozzan [108,109] these local gradients in  $\text{Ca}^{2+}$  were visualized and correlated with mitochondrial  $\text{Ca}^{2+}$  levels as well as activation of PDH [114]. The local release of  $\text{Ca}^{2+}$  from the SR associated with the mitochondria in the intrafibrillar mitochondria is a reasonable mechanism for the observed close coupling of cytosolic and mitochondrial  $\text{Ca}^{2+}$  observed by numerous investigators using both genetically inserted as well as extrinsic optical probes [104,110,114,134]. However the compartmentation of  $\text{Ca}^{2+}$  at the mitochondria still does not resolve the mechanism for rapid  $\text{Ca}^{2+}$  efflux since it is unclear how a compartment could be used to enhance this process, significantly. Thus, the  $\text{Ca}^{2+}$  efflux pathway remains a nagging unresolved question.

Supporting the notion that mitochondrial  $[\text{Ca}^{2+}]$  tracks the pacemaker cytosolic  $[\text{Ca}^{2+}]$  are numerous less direct experiments demonstrating that the altering the mitochondrial transport of  $\text{Ca}^{2+}$  with ruthenium red and similar molecules severely alters the metabolic homeostasis associated with increases in cardiac work in the intact heart [72,96,135] and isolated preparations [91]. Furthermore, a surrogate marker of matrix  $\text{Ca}^{2+}$  is the activation of PDH (see below). Numerous studies have confirmed that an activation of PDH mirrors cardiac work [30,79,96] supporting the notion that the matrix is tracking cytosolic  $\text{Ca}^{2+}$  levels. Both of these classes of experiments support the hypothesis that matrix  $\text{Ca}^{2+}$  tracks cytosolic  $\text{Ca}^{2+}$  and is partially responsible for the metabolic homeostasis observed.

These data, direct observation of mitochondrial  $\text{Ca}^{2+}$  tracking cytosolic  $\text{Ca}^{2+}$  and the correlation with other surrogate markers of matrix  $\text{Ca}^{2+}$ , support the notion that the matrix  $\text{Ca}^{2+}$  tracks the pacemaker cytosolic  $\text{Ca}^{2+}$ . However, the molecular mechanisms associated with this process are not fully described. The remainder of this discussion will focus on the effects of  $\text{Ca}^{2+}$  on oxidative phosphorylation.

## **$\text{Ca}^{2+}$ modulation of oxidative phosphorylation**

To regulate oxidative phosphorylation in a feed forward or feedback mode  $\text{Ca}^{2+}$  must have the appropriate sites within the mitochondria to properly alter the rate of ATP synthesis. The regulation of oxidative phosphorylation by  $\text{Ca}^{2+}$  is extremely complex and has been an area of study for many years. The different areas of interaction sites can be grouped as dehydrogenase activity, substrate transport, F<sub>1</sub>-FO-ATPase and cytochrome oxidase. Other mechanism associated with  $\text{Ca}^{2+}$  activation of liver mitochondria include modifications of volume and pyrophosphate levels (for review see [97]). However, neither of these mechanisms seem to play a role in the heart based on the work of Griffiths and Halestrap [52] and will not be discussed in this review.

## **$\text{Ca}^{2+}$ Modulated Mitochondria Substrate Transport**

Some aspects of substrate exchange and import into the mitochondria is regulated by  $\text{Ca}^{2+}$  regulated mitochondrial carriers (CaMC) [39,119]. These pathways are particularly interesting since cytosolic  $\text{Ca}^{2+}$  could alter mitochondrial metabolism without entering the matrix via the uniporter, which has been a controversial topic in past. Both citrin and aralar are present in the heart [38,68] with more aralar present in the atria than the ventricles. Aralar and citrin are aspartate/glutamate carriers involved in the malate-aspartate NADH shuttle across the inner membrane possibly capable of equilibrating the NAD/NADH ratio from the cytosol to the matrix across the inner membrane. The activation of these transporters occurs at physiological levels of  $\text{Ca}^{2+}$  on the order of 300 nM [38]. Based on these substrate transport mechanisms, and subsequent metabolism, the cytosolic  $\text{Ca}^{2+}$  activation citrin and aralar could result in the transfer of cytosolic reducing equivalents into the mitochondria matrix to increase the capacity for ATP production. However, the capacity of this pathway is limited, Williams et al estimated the maximum flux on the order of 3  $\mu\text{mol}$  NADH/min/gm wt [140], while the maximum exercise NADH consumption of the heart

approaches 50  $\mu\text{mol NADH}/\text{min}/\text{gm wt}$  [100]. In addition, no evidence of the cytosolic NADH/NAD ratio on the mitochondrial NADH/NAD ratio has been demonstrated in the heart[122]. Thus, the direct support of oxidative phosphorylation by this shuttle is likely minimal. However, the shuttle removing cytosolic NADH may improve the oxidation of lactate and glucose in the cytosol improving the delivery of pyruvate for oxidation[116] which could be very important in burst activity [37,50]. Thus, it is more likely that the activation of the NADH shuttle system by  $\text{Ca}^{2+}$  is likely related to keeping pyruvate entering the TCA cycle rather than being “wasted” to lactate via lactate dehydrogenase regeneration of NAD.

Based on the original work by Aprille et al [8] the ATP-Mg/Pi (APC) carrier is a method of modifying the net adenosine pool in the matrix. The ATP-Mg/Pi carrier is electroneutral exchanging divalent phosphate with divalent ATP and in some situations divalent ADP. This transport mechanism is sensitive to extra-mitochondrial Ca in the  $\mu\text{M}$  range increasing the affinity for ATP[60,103]. In the APC2 and AP3 isoforms of the carrier are present in the heart[47], but at a rather low activity and likely only plays a significant role in long term regulation of matrix adenosine pools[123].

Mitochondrial glycerol phosphate dehydrogenase (GPDH) is an inner membrane protein that responds to physiological levels of cytosolic  $\text{Ca}^{2+}$  by lowering its  $K_m$  for reactants which increased the delivery of reducing equivalents to Coenzyme Q via FADH[29,46,93]. However the content [68,106] and activity[116] of this enzyme is very low in the heart. Thus, it is unlikely that this pathway significantly contributes as a source of reducing equivalents to oxidative phosphorylation in the heart.

## **Ca<sup>2+</sup> Modulated Dehydrogenases**

Since the early experiments in Randle's lab [42,107] on pyruvate dehydrogenase (PDH), it has been appreciated that the citric acid cycle dehydrogenases are extremely sensitive to  $\text{Ca}^{2+}$ . Subsequently  $\text{Ca}^{2+}$  activation of isocitrate dehydrogenase (ICDH) and  $\alpha$ -ketoglutarate dehydrogenase (KDH) was demonstrated[43,95,97] and reviewed by McCormack and Denton[97]. The mechanism of action of  $\text{Ca}^{2+}$  is surprisingly different for each of the dehydrogenase systems. PDH is deactivated by phosphorylation by PDH kinases and activated by the dephosphorylation via  $\text{Ca}^{2+}$  sensitive phosphatase [41,42,59,75]. The activation of PDH seems to be primarily an alteration in  $V_{\text{max}}$  of the enzyme. In contrast to PDH,  $\text{Ca}^{2+}$  apparently binds directly to ICDH and KDH[115] resulting in alterations in the kinetics of both substrates and inhibitory metabolites[85]. In the heart it has been proposed that the KDH reaction is the most significant  $\text{Ca}^{2+}$  activated dehydrogenase under physiological conditions[138]. This is consistent with the observations by Hansford and Castro[55] as well as our experience since we find that the oxidation of  $\alpha$ -ketoglutarate is nearly obligatorily linked to the presence of  $\text{Ca}^{2+}$  in porcine heart mitochondria. It is interesting that all three of these dehydrogenases are activated through different mechanisms suggesting that the origins of the activation are very different or the specific mechanisms required are very dissimilar.

Some evidence that  $\text{Ca}^{2+}$  may be involved in other oxidative pathways. Malstrom and Carafoli [77] found the oxidation of  $\beta$ -hydroxybutyrate, even under uncoupled conditions, was critically dependent on  $\text{Ca}^{2+}$ , but no mechanism has been subsequently generated. This is particularly interesting since the ketones are the preferred substrate of the heart, *in vivo* [77]. Otto and Ontko [105] found an activation of fatty acid oxidation to  $\beta$ -hydroxybutyrate, not oxidation to  $\text{CO}_2$  by Krebs cycle, was doubled by the addition of  $\text{Ca}^{2+}$  to liver mitochondria. This was accompanied with an increase in mitochondrial NADH, again

consistent with the increased oxidation of fatty acids. The specific mechanisms involved in these rather fascinating results are also still unknown.

No evidence is currently available on the role of  $\text{Ca}^{2+}$  at complex 1 where the reducing equivalents enter the cytochrome chain and is a potent source of reactive oxygen species[18]. Thus, it is apparent that the control of the delivery of NADH, via the dehydrogenase regulation, is the major mechanism of  $\text{Ca}^{2+}$  regulation. This notion is consistent with the direct measurement of NADH formation on Complex 1 using the photo-oxidation of NADH to monitor the rate of re-reduction using ED-FRAP[70] relying on the assumption that most of the fluorescently enhanced matrix NADH is within Complex 1[22]. These studies reveal that the rate of reduction or binding of NADH to Complex 1 essentially matches the rate of electron flow through the cytochrome chain, implying this reaction is far from equilibrium and dependent on the generation of NADH by the dehydrogenases. The advantage of this approach is that electrons are not permitted into the ROS generating Complex 1, or the cytochrome chain, during periods of low flux, reducing the potential for damaging oxygen free radical generation[18]. These observations underscore the importance of the  $\text{Ca}^{2+}$  regulation of dehydrogenases in the regulation of oxidative phosphorylation as reviewed by Denton, McCormack, Hansford and Halestrap in several reviews[40,54,56,97].

It is also important to note that there is no evidence that  $\text{Ca}^{2+}$  alters the resistance or ability to convert the Complex 1 NADH/NAD redox potential into membrane potential via the cytochrome chain as demonstrated for inorganic phosphate[26]. Even though a strong binding site for  $\text{Ca}^{2+}$  has been identified in Complex 4, no functional correlation has been made[78]. Also  $\text{Ca}^{2+}$  has been shown not to alter the proton leak across the mitochondrial membrane at physiological levels[98]. These observations suggest the effects of  $\text{Ca}^{2+}$  are limited to the dehydrogenases and F1-FO-ATPase, but given the complexity of the interaction and difficulty of the experimental methods available, this author would not be surprised to see an even more distributed interaction of  $\text{Ca}^{2+}$  on oxidative phosphorylation with continuing discovery.

Since the mitochondria is essentially dependent on cytosolic sources of carbon substrates to oxidize in the form of pyruvate, fats, amino acids or ketones. The regulation the supply of these substrates from the cytosol by  $\text{Ca}^{2+}$  should not be ignored. One of the classical regulatory sites of  $\text{Ca}^{2+}$  in the cytosol is the activation of glycogen phosphorylase kinase that subsequently phosphorylates and activates glycogen phosphorylase increasing the delivery of glucose to glycolysis. In addition,  $\text{Ca}^{2+}$  has also been linked to GLUT-4 mobilization via a calmodulin dependent protein kinase and AMPK (for review see[113]). Like GLUT-4 the fatty acid transporter FAT/CD36 is also mobilized to the plasma membrane [25] and modulated by AMPK (for review see [69]) however, no direct link between FAT/CD36 translocation and cytosolic  $\text{Ca}^{2+}$  has yet been made. Thus,  $\text{Ca}^{2+}$  activity in the cytosol is also linked to the transport and metabolism of metabolic substrates to support oxidative phosphorylation.

## F1-FO-ATPase

The first suggestion that the F1-FO-ATPase may be directly affected by matrix  $\text{Ca}^{2+}$  came from the studies of Das and Harris [57] that demonstrated  $\text{Ca}^{2+}$  activated the ATP hydrolytic activity in extracted F1-FO-ATPase from pretreated heart cells. This was reproduced in serial biopsy samples from dobutamine treated canine hearts, *in vivo*[121]. Thus, changes in cytosolic  $\text{Ca}^{2+}$  apparently generated a post-translational modification of the F1-FO-ATPase that persisted as an alteration in ATP hydrolytic activity, *in vitro*. It is important to note that the addition of  $\text{Ca}^{2+}$  directly to isolated F1-FO-ATPase does not affect activity, thus the effect is more than a direct association of  $\text{Ca}^{2+}$  with the enzyme[65]. We have also

confirmed that  $\text{Ca}^{2+}$  does not directly activate F1-FO-ATPase complex activity in blue native gels or from immune captured complexes from porcine heart mitochondria (Phillips and Balaban, unpublished data). Thus it is likely that  $\text{Ca}^{2+}$  regulates a post-translational process that occurs in the mitochondrial matrix in combination with others proteins or enzymes. What is the evidence that this post-translational modification that alters ATPase activity *in vitro* affects normal ATP production by this enzyme in the intact mitochondria? Territo et al in a series of studies [15,130-132] demonstrated that  $\text{Ca}^{2+}$  can rapidly increase the velocity of ATP production by the F1-FO-ATPase at a given driving force (i.e. membrane potential). Similar conclusions were reached by Mildaziene using control theory analysis during  $\text{Ca}^{2+}$  additions [98]. These studies show that the addition of  $\text{Ca}^{2+}$  essentially reduced the resistance of the F1-FOATPase to form ATP using the membrane potential. Thus,  $\text{Ca}^{2+}$  is capable of increasing the capacity of ATP production by the F1-FO-ATPase at a given driving force simultaneously with the increase delivery of reducing equivalents to the cytochrome chain via the several  $\text{Ca}^{2+}$  sensitive dehydrogenases discussed above.

An example of this “balanced” activation by  $\text{Ca}^{2+}$  in intact mitochondria is given by experiments where  $\text{Ca}^{2+}$  was added to mixtures of mitochondria and purified SR vesicles from the same heart [16].  $\text{Ca}^{2+}$  was added to activate the dehydrogenases, F1-FO-ATPase and SERCA ATP hydrolytic activity simultaneously to establish whether a potential energy homeostasis could be simulated in under these reconstituted conditions.  $\text{Ca}^{2+}$  additions increased ATP turnover by activating SERCA while the mitochondrial NADH and membrane potential was shown to be held constant or slightly increase with the addition of  $\text{Ca}^{2+}$ . The addition of  $\text{Ca}^{2+}$  in this system was contrasted with the graded addition of a non- $\text{Ca}^{2+}$  sensitive ATPase directly generation ADP and Pi alone. Not only did NADH become more oxidized and the membrane potential depolarize with increasing ATP turnover, but the overall maximum rate of ATP production was reduced due to the lack of activation of the dehydrogenases and F1-FO-ATPase by  $\text{Ca}^{2+}$ . This rather simple reconstitution illustrates that extramitochondria  $\text{Ca}^{2+}$  driving the SERCA and activating dehydrogenases and the F1-FO-ATPase can result in the required balanced activation to create the potential energy homeostasis during large, 5 fold, increases in ATP production.

What is still yet to be resolved is the molecular mechanism associated with the activation of the F1-FO-ATPase by  $\text{Ca}^{2+}$ . Since this effect apparently persists in the purified protein extracted from mitochondria or cells activated with  $\text{Ca}^{2+}$  it is likely that some type of post-translational modification is responsible for this action. There are several published post-translational modifications of the F1-FO-ATPase that might be responsible for the  $\text{Ca}^{2+}$  induced change. These include s-nitrosylation [126], phosphorylation [10,11,124], oxidation [99,129] and glycosylation [6]. Aponte et al [7] have recently demonstrated dynamic  $^{32}\text{P}$  association with several of the F1-FO-ATPase sub-units in the intact mitochondria including,  $\alpha$ ,  $\beta$ ,  $\gamma$ , OSCP and d. Hopper et al [63] showed that the  $\gamma$  subunit phosphorylation was sensitive to mitochondrial  $\text{Ca}^{2+}$  levels, however, a definitive link between  $\gamma$  subunit phosphorylation and the function of the enzyme has yet to be established.

Another post-translational modification of the F1-FO-ATPase is the association of regulatory peptides [58]. The F1 inhibitory protein is the classic example of a regulatory protein on the F1-FO-ATPase [31] but its association has not been linked to  $\text{Ca}^{2+}$  levels. Yamada et al [143,144] described a protein that associates with the F1-FO-ATPase that inhibits activity and that reversed by  $\text{Ca}^{2+}$ . While Boerries et al described a protein, S100A1, that has a  $\text{Ca}^{2+}$  dependent association with the F1-FO-ATPase improving ATP production capacity [23]. The role of both of these proteins in normal work transitions in the heart has not been investigated, but both proteins *in vitro* seem to have the proper dynamic range and  $\text{Ca}^{2+}$  sensitivity to regulate the F1-FO-ATPase.



## Cytochrome Oxidase

Bender and Kadenbach [19,88] demonstrated a  $\text{Ca}^{2+}$  dependent dephosphorylation of cytochrome oxidase (COX) in intact bovine heart mitochondria that they suggested removed the inhibition of ATP increasing net ATP production. This COX phosphorylation site was also shown to be cAMP dependent. Lee et al [89] demonstrated a cAMP dependent tyrosine phosphorylation site in liver COX subunit I that decreased the  $V_{\max}$  as well as the affinity for cytochrome c. In the original studies,  $\text{Ca}^{2+}$  only dephosphorylated COX in intact mitochondria and did not dephosphorylate purified samples. However, the  $\text{Ca}^{2+}$  doses used in these studies were excessive at 1 mM [19] and 100  $\mu\text{M}$  [88] where the ATP content of the matrix could have been severely depleted via uncoupling and damage. Thus, some of the effects observed may be due to depleted ATP rather than specific effects of  $\text{Ca}^{2+}$ . To my knowledge, a dose dependent  $\text{Ca}^{2+}$  study on COX dephosphorylation has not been conducted, thus it is difficult to establish its physiological role. Though a phosphorylation of COX has been detected in mitochondria phosphorylation screens [7,63]. A  $\text{Ca}^{2+}$  dependent dephosphorylation of COX was not detected [63], however this screening study did not focus on subunit I let alone COX. A  $\text{Ca}^{2+}$  activation of COX would provide another downstream activation of oxidative phosphorylation by cytoplasmic  $\text{Ca}^{2+}$  aiding to a balanced activation of ATP production. It would potentially help explain the redox homeostasis of the cytochrome chain through cytochrome c with alterations of work as observed by Arai et al [9]. Based on the important role of COX in oxidative phosphorylation further study on this interaction with  $\text{Ca}^{2+}$  is likely warranted.

## Summary

$\text{Ca}^{2+}$  is an excellent candidate as a feed-forward and feedback cytosolic signaling molecule for the rate of ATP hydrolysis. Indeed, the positioning of the mitochondria within the cytosol intertwined with the  $\text{Ca}^{2+}$  activation machinery may enhance the coupling of the cytosolic signals with the mitochondria. Within the mitochondria  $\text{Ca}^{2+}$  exerts a complex activation of mitochondrial oxidative phosphorylation by simultaneously activating several dehydrogenases and the F1-FO-ATPase. The six major  $\text{Ca}^{2+}$  sensitive sites in the mitochondria matrix are outlined in Figure 4. Note that most of the sites generating NADH are either directly or indirectly regulated by  $\text{Ca}^{2+}$ , with the exception of MDH. The glutamate dehydrogenase (GDH) is indirectly regulated by the delivery of glutamate via citrin/Aralar. The mechanisms of activating the dehydrogenases are rather well defined while the precise molecular mechanisms involved in the activation of the F1-FO-ATPase are yet to be resolved. This balanced activation of oxidative phosphorylation by  $\text{Ca}^{2+}$ , along with other regulatory mechanisms, likely plays a significant role in the balancing the rate of ATP production with utilization in the constantly working heart.

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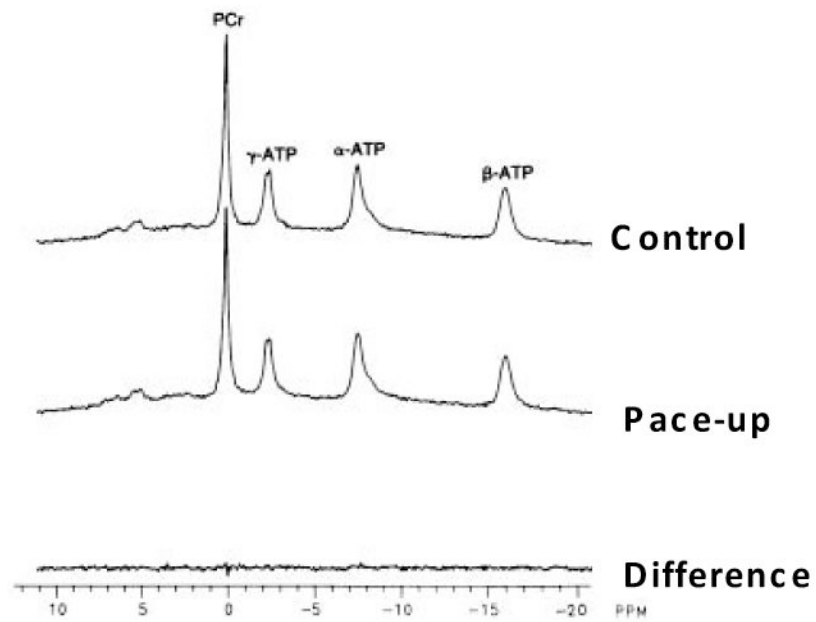
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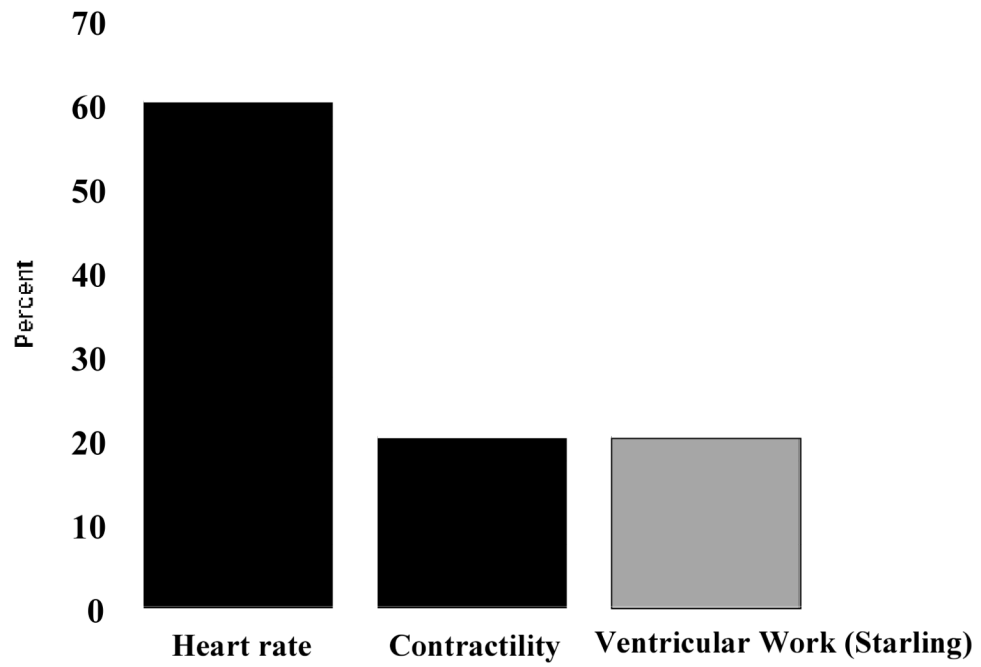
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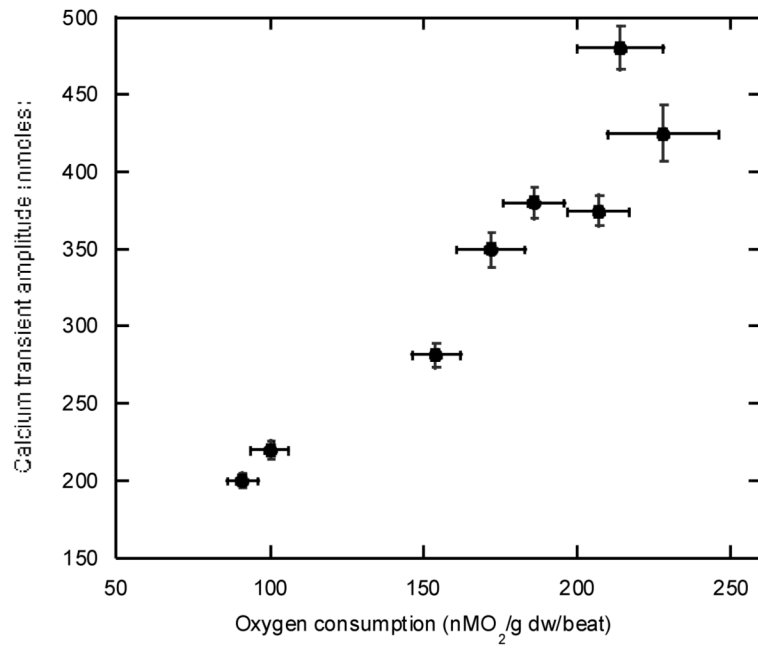




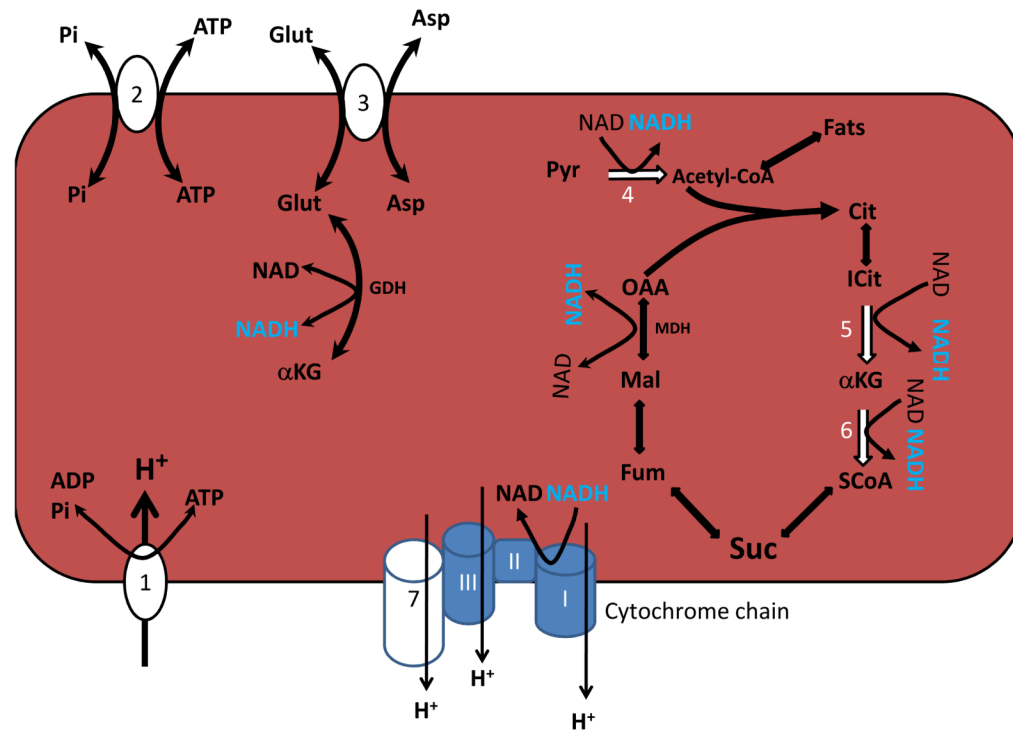
**Figure 1.** Effect of pacing workload on the  $^{31}\text{P}$  NMR detected high energy phosphates in the canine heart *in vivo*. The post spectrum was collected after a pacing that increased the rate pressure product by  $\sim 2$  fold. Data adapted from Heineman and Balaban [61]



**Figure 2.** Estimated relative contributions of heart rate, contractility and Starling relationship to the overall increase in myocardial oxygen consumption associated with exercise. Data adapted from [45].



**Figure 3.** Correlation of peak systolic Ca<sup>2+</sup> levels and oxygen consumption in the perfused rat heart. Heart work was increased using a combination of inotropic agents. Data adapted from [142].



**Figure 4.**

Summary of the six  $\text{Ca}^{2+}$  regulatory sites in the heart mitochondria. The seven sites, outlined in white, are 1) F1-FO-ATPase, 2) APC, 3) Aralar/Citrin, 4) PDH, 5) ICDH, 6)  $\alpha$ KDH and 7) COX. Of these sites COX is the least studied. Cit: Citrate. ICit: Isocitrate. OAA: Oxaloacetate. MDH Malate dehydrogenase. Succ: Succinate. ASP: Aspartate SCoA: Succinyl-CoA Fum: Fumarate. MAL: Malate. Other abbreviations are in the Text.