

## Forum Review

# Zinc Dynamics in the Myocardial Redox Signaling Network

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### ABSTRACT

**Zinc plays a vital role in various cellular functions. Zinc deprivation is associated with severe disorders related to growth, maturation, and stress responses. In the heart, zinc affects differentiation and regeneration of cardiac muscle, cardiac conductance, acute stress responses, and recovery of heart transplants. Recent discoveries of the molecular players in zinc homeostasis revealed that the amount of intracellular free zinc is tightly controlled on the level of uptake, intracellular sequestration, redistribution, storage, and elimination, consequently creating a narrow window of optimal zinc concentration in the cells. Most of intracellular zinc is bound to numerous structural and regulatory proteins, with metabolically active, labile zinc present in pico- to nanomolar concentrations. The central position of zinc in the redox signaling network is built on its unique chemical nature. The redox inert zinc creates a redox active environment when it binds to a sulfur ligand. The reversible oxidation of the sulfur ligand is coupled to the reversible zinc release from the protein, thereby executing the task of so-called protein “redox zinc switch.” Clearly, the impairment of zinc homeostasis will have far reaching physiological consequences. *Antioxid. Redox Signal.* 8, 1707–1721.**

### INTRODUCTION

**Z**INC IS ONE OF THE MOST ABUNDANT TRANSITION metals in the human body, second only to iron, and it is responsible for a wide range of biological functions. Approximately 10% of the United States population ingests <50% of the recommended daily allowance for zinc. Nutritional studies of trace elements demonstrated the necessity of the proper intake profile of microelements with an emphasis on the zinc-to-copper ratio. They also linked an imbalance of these elements to the development of cardiovascular disorders (95). Zinc affects cardiac differentiation (2), the regeneration of cardiac muscle, lipid peroxidation in cardiac tissue (16), and the outcome of surgical procedures on an open heart (93). In general, dietary zinc deprivation is lethal in mice, and in humans it is associated with severe disorders related to growth, maturation, and immunity. The complexity of zinc-dependent functions is further demonstrated by the fact that an excess of zinc is also associated with a number of abnormalities, the

best illustrated in neuronal tissue (9, 42–44). Diabetic cardiomyopathy is associated with serum zinc deficiency (26), contradicting elevated intracellular zinc in cardiomyocytes (5). However, zinc supplementation via induction of cardiac metallothionein (MT) prevents development of diabetic cardiomyopathy in a rat model (110).

Zinc is critical for the structural integrity of the cells, since it influences membrane stability and cytoskeletal organization. Intracellular zinc homeostasis is challenged by oxidative stress, acidosis, and possibly by the signaling network, and it is an essential regulator of apoptosis. A specific protective role for a labile zinc pool against apoptosis has emerged within the last two decades (106). The limited regenerative potential of adult cardiac myocytes, along with the exciting possibilities of regeneration of cardiac muscle with cardiac progenitor cells, recognizes the necessity for new strategies. New knowledge would allow suppressing undesirable cell death in patients with ischemic heart disease, heart failure, myocarditis, arrhythmogenic right ventricular dysplasia, and immune rejection after

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cardiac transplantation (myocardial apoptosis has been recently reviewed in Refs. 1, 52, and 94).

The dynamic properties of zinc can be traced back in evolution to single cell organisms. Hence, under the conditions of nutritional imbalance, exchangeable zinc ions transiently accumulate in the vesicular compartment of the yeast *Saccharomyces cerevisiae* (21). A pool of cellular available zinc participates in phosphorylation/dephosphorylation cascades in mammalian cells, suggesting the existence of a signaling system based on zinc as second messenger. As a result, intracellular free zinc levels are strictly regulated by a complex system that includes transporters, storage vesicles, and buffering zinc-binding proteins, metallothioneins.

Zinc signals are often compared to the calcium signaling system, and even courageously  $\text{Zn}^{2+}$  was named "Calcium of the 21st century." Indeed, zinc and calcium are ubiquitous intracellular metals. Both are vital for cellular function. Both require tight control of their homeostasis. Similar to calcium, there is a mechanism for zinc sequestration into the storage compartment. It can be disputed whether a specific  $\text{Ca}^{2+}$ -sensing protein calmodulin is comparable to metallothionein. Although molecular mechanisms of metal regulation by the two proteins are different, the functional outcome is the same, specifically where the transfer of information from the ion to the effector protein is concerned. Yet, the principle of zinc signaling is based on different and unique chemical properties of interaction of zinc ions with redox reactive sulfur ligands.

Ironically, many of the tools that were originally designed for monitoring Ca signals can be used effectively for  $\text{Zn}^{2+}$  determination. Thus, the first report of intracellular  $\text{Zn}^{2+}$  concentration in cardiomyocytes is based on fura-2 measurements performed in the presence of a  $\text{Zn}^{2+}$  chelator (5). Ayaz and Turan estimated resting  $\text{Zn}^{2+}$  in cardiomyocytes to be  $0.52 \pm 0.06 \text{ nM}$ . Remarkably, this level is nearly double in diabetic cardiomyocytes.

Since fura-2 or Mag-fura-2 initially used for  $\text{Zn}^{2+}$  determination were lacking specificity, making it difficult to separate zinc signals from calcium signals, the need for the development of zinc-specific probes has been growing with the expansion of zinc signals research. The number of newly developed  $\text{Zn}^{2+}$ -specific probes has been increasing exponentially since the late 1990s. These probes differ in their chemical properties and physical characteristics, and provide different benefits depending on experimental goals. For example, the Zinquin, the zinc probe that has a nanomolar affinity for zinc, overestimates the level of  $\text{Zn}^{2+}$  due to some degree of repartitioning of weakly bound zinc, the so-called labile zinc. On the other hand, the pool of labile zinc is possibly the most physiologically relevant and can be readily exchanged with an altered cellular state.

Whereas the total zinc concentration in eukaryotic cells is quite high (approximately  $200 \mu\text{M}$ ), cytoplasmic free zinc concentrations are in the range of hundreds of picomolars. Thirty to 40% of the cellular zinc is localized in the nucleus, 50% in the cytosol and organelles, and the remainder is associated with membranes (107). Under physiological conditions, the majority of zinc within the cells is complexed by proteins. It took some time to realize that zinc indeed is not only a structural component of the proteins, but also an important regulatory ion. Intracellular zinc is tightly regulated and fluctuates dynamically.

An intense interest of the researchers to zinc has been stimulated by the discovery of a new regulatory function of reactive oxygen species (ROS), which can function as intracellular second messengers (19). Reactive oxygen species have been implicated in diverse cellular processes, including growth factor signal transduction, gene expression, and apoptosis. ROS are produced as a part of physiological signaling by hormones, lymphokines, and growth factors (20, 39, 114). There is growing evidence that many proteins are regulated by a redox environment through the reversible oxidation of their cysteine residues. The amino acid cysteine combines catalytic activity with an extensive redox chemistry and unique metal binding properties. Biologically zinc ions can act both as antioxidants and pro-oxidants. Both zinc deficiency and zinc overload elicit oxidative stress.

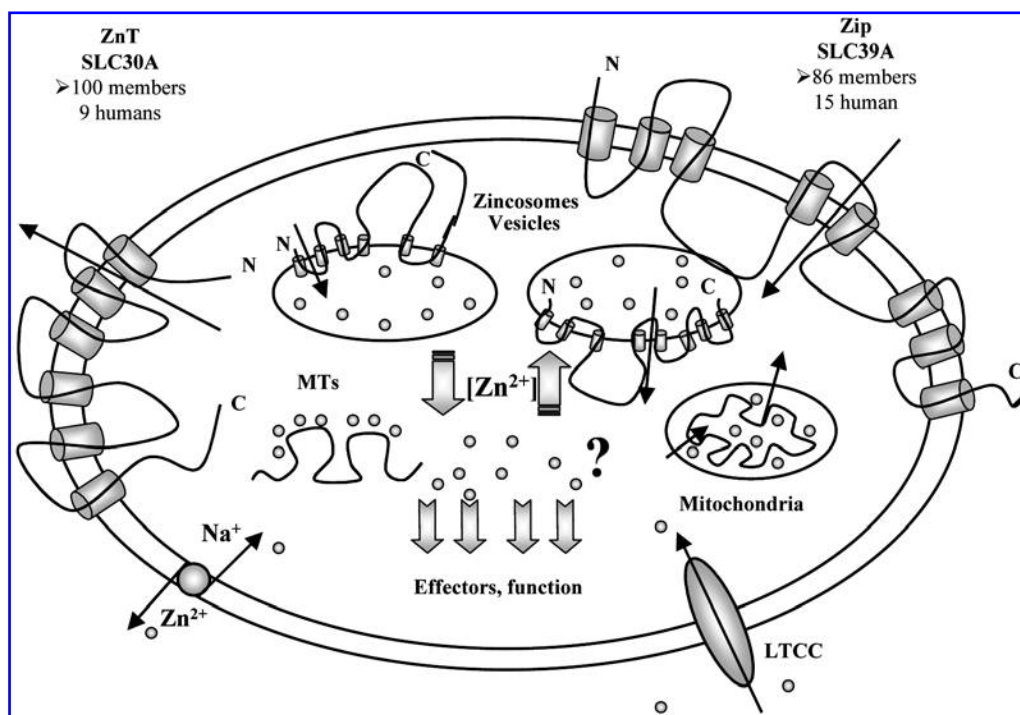
This paper presents an overview of the proteins regulating zinc homeostasis, as well as the molecular aspects of metal/redox regulation of protein function, with the accent on transcription factors and proteins of cytosolic signaling. The last part describes the hypothetical model of so-called protein "redox zinc switch," the redox sensing mechanism within the regulatory domain of protein kinase C (Fig. 1). Implications for cardiophysiology are discussed.

## ZINC TRANSPORT AND STORAGE

### Zinc transport

Tight control of cellular zinc homeostasis suggests the existence of zinc transporting systems as the first requirement, the way of elimination of excessive zinc to protect cell against zinc toxicity, and the routes for zinc entry to maintain zinc supplies for metabolic and regulatory purposes. New insights into mammalian zinc metabolism have been acquired through the identification and characterization of zinc transporters. The understanding of zinc transport at the molecular level began with the first functional evidence of zinc transport activity by ZnT-1 (90, 91). Rapid progress has been made since then, leading to the discovery of the proteins encoded by two solute-linked carrier (SLC) gene families: ZnT (SLC30) and Zip (SLC39). There are 10 ZnT and 15 Zip transporters in human cells (77). They appear to have opposite effects on  $\text{Zn}^{2+}$  homeostasis: ZnT transporters facilitate zinc efflux from cytoplasm either into various intracellular compartments (81), or across plasma membranes. Zip transporters promote extracellular zinc uptake and vesicular zinc release (Fig. 2). A common feature of ZnT transporters is a number of highly conserved histidine residues, which seem to be important for metal ion recognition and transport (77). Both transporter families exhibit tissue-specific expression and differential regulation by zinc deficiency and excess, and by signaling cascades (Fig. 2).

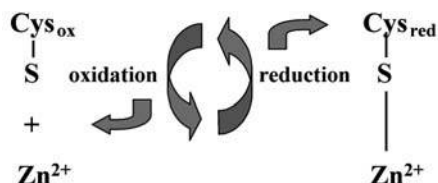
The ZnTs are a growing family of proteins involved in sequestration of intracellular zinc. ZnT-1, the first mammalian transporter discovered, has the simplest gene structure (90). With two exons, this gene predicts a 507 amino acid protein with six transmembrane domains with both N- and C-termini on the cytoplasmic side of the membrane. Like other ZnT proteins, ZnT1 has a long histidine-rich loop, which could represent a metal-binding domain. It is possible that ZnT proteins function as dimers or multimers. ZnT-1 is the most



**FIG. 1. Molecular partners of zinc homeostasis.**  $\text{Zn}^{2+}$  efflux is mediated by ZnT-1 transporter, the member of SLC30 gene family. Other ZnT proteins facilitate zinc sequestration by cytosolic vesicles: zincosomes. Sodium/zinc exchange is another mechanism for intracellular zinc extrusion. On the other hand, Zip proteins, SLC39 family members promote extracellular zinc uptake and zinc release by zincosomes. The major route of zinc entry into most cells is L-type calcium channel (LTCC). Mitochondria and zincosomes are storage compartments for excessive zinc and potential regulators of zinc-based signaling. Metallothioneins are protein-based storage sites and zinc donors to various proteins. Liberated or labile zinc regulate thousands of known and unknown proteins and as a result influence physiological responses. The transporter proteins are oversized to emphasize the structural features.

ubiquitously expressed ZnT protein. The well-documented cellular role of ZnT-1 is protection against zinc toxicity (77).

Expression of ZnT-1 is regulated in a tissue-specific manner by the level of available zinc. Zinc deficiency leads to a significant decrease in mRNA content, while zinc supplementation induces marked increase in the mRNA level (76). The molecular mechanism for ZnT-1 expression is not delineated but it appears to be identical to that of metallothionein gene (discussed further in this review), specifically the involvement of metal response element (MRE) in the ZnT-1 promoter and activation of transcription through metal responsive transcription factor (MTF) (74).



**FIG. 2. Redox chemistry of the zinc-cysteine interaction.** Oxidation and reduction of protein cysteines are linked to the release and binding of the zinc ion, respectively. Thiols can be oxidized reversibly to disulfides and cysteinesulfenic acid. Oxidation of cysteines to cysteinesulfinic and cysteinesulfonic acids is irreversible. Zinc is in turn a potential modulator of cysteine reactivity. This interdependent interaction forms a chemical basis for a protein “redox zinc switch.”

Although it was discovered several years ago, it is unclear how ZnT-1 modulates zinc fluxes; it has been recently suggested that the protein may be involved in the regulation of zinc influx rather than efflux. Peculiarly, the major route of zinc entry into most cells is L-type calcium channel (LTCC) (4). When LTCC was co-expressed with the ZnT-1, the rate of  $\text{Zn}^{2+}$  influx reduced threefold (97).

Although transition metals are generally viewed as  $\text{Ca}^{2+}$  channel blockers, single channel recordings suggest that zinc can enter the myocytes through dihydropyridine-sensitive calcium channel. Therefore, activation of LTCC permeability for  $\text{Zn}^{2+}$  is the primary machinery of voltage-mediated gene expression (4). Despite the general important physiological consequences of  $\text{Zn}^{2+}$  influx, the mechanism of LTCC permeation for  $\text{Zn}^{2+}$  remains elusive. In mouse cortical neurons, an inward current detectable at micromolar doses of zinc was sensitive to a blockade by  $\text{Cd}^{3+}$  and nimodipine. Channel amplitude and voltage sensitivity depended upon doses of  $\text{Zn}^{2+}$ . Zinc ions could permeate calcium channels in the presence of  $\text{Ca}^{2+}$ . Currents recorded with  $\text{Zn}^{2+}$  were unaffected by up to equimolar calcium concentrations.  $\text{Zn}^{2+}$  current mediated by voltage-gated calcium channels was enhanced by extracellular acidity, while Ca current was inhibited by lowering pH (62).

The co-expression experiments suggest a regulatory role for ZnT-1 in permeation of the LTCC for zinc ions. ZnT-1 does not affect LTCC expression level, indicating that this regulation is based on functional interaction between the two

proteins or between ZnT-1 and LTCC regulator. It should be noted that ZnT-1 is also a regulator of Ca responses. Ca entry via LTCC was diminished with ZnT-1 overexpression. In line with this negative control, capacitive Ca entry is inhibited by ZnT-1. This inhibition is likely to occur through interaction of ZnT-1 with the redox-sensitive extracellular site of store-operated Ca channel (42). Similarly, zinc itself has a negative impact on capacitive Ca entry by affecting extracellular thiols, as shown in mouse astrocytes (71). In addition, one more route of cross communication of  $\text{Ca}^{2+}$  and  $\text{Zn}^{2+}$  homeostasis is negative regulation by zinc ions of ryanodine binding to sarcoplasmic reticulum that leads to inhibition of  $\text{Ca}^{2+}$  release in both skeletal muscle and cardiomyocytes (5).

ZnT-1 is the only mammalian zinc transporter acting as a cellular zinc exporter. All other ZnTs participate in sequestration of zinc ions into endosomes, secretory granules, synaptic vesicles, Golgi apparatus, or trans-Golgi network (77). They are unlikely to share the same channel-regulating activity. The detailed mechanism of ZnT-mediated zinc sequestration remains to be established. Recently discovered ZnT-5 is of particular interest. This vesicular transporter was reported almost simultaneously by two groups (17, 58). Unlike many other transporters, it has 12 [15, according to Kambe *et al.* (58)] transmembrane spanning domains. The protein expression is also regulated by high zinc and possibly mediated by MTF1. ZnT-5 has unusual although uncharacterized functions within the cardiovascular system. Intriguingly, male ZnT-5 null mice develop fatal arrhythmias and die of heart block and sinus bradycardia at 15 weeks of age (50). It should be noted that independent of ZnT proteins, recently discovered sodium/zinc exchange mediates extrusion of  $\text{Zn}^{2+}$  from mammalian cells. The exchange was reversible upon reversal of sodium gradient, and energy independent, consistent with a mechanism involving a secondary active transporter (85).

Zip proteins (24) have been divided into four subfamilies: I, II gufA, and the LIV-1 subfamily of ZIP transporters (LZT). Most Zip proteins have eight transmembrane domains with extracellular or intravesicular amino- and carboxy-termini. Interestingly, the LZT subfamily members have a long extracellular N terminus with 2 to 34 histidines and the novel metalloprotease motif (HEXPHE), which could suggest alternative functions (104). As ZnTs, Zip transporters are energy independent. Their expression is stimulated by elevated  $\text{Zn}^{2+}$  and may be linked to oxidative metabolism (28). LIV-1 expression is stimulated by insulin, IGF-1, TGF $\alpha$ , and EGF (25). Oxidative treatment of C6 glioma cells resulted in 50% of total zinc exported through the plasma membrane (44). Our study shows that stress imposed by ischemia and reperfusion (I/R) leads to zinc depletion of cardiac tissue. Thus, understanding the mechanism of export is crucial in cardiac cells. Although, the research on Zip family proteins shows rapid progress, no convincing data exist on their function in heart, providing a fertile field for future investigations.

### Sequestration of zinc by mitochondria

Sequestration of zinc ions into intracellular vesicles by ZnTs is not only the way of cell protection from  $\text{Zn}^{2+}$  overload. It also represents the machinery of  $\text{Zn}^{2+}$  storage. In most cell types, zinc-containing vesicles, so-called "zincosomes,"

are observed under normal conditions (28). In our experiments using neonatal cardiomyocytes, the morphological appearance of *N*-(6-methoxy-8-quinolyl)-p-toluensulfonamide (TSQ) staining changed from homogeneous cytoplasmic distribution of fluorescence in control toward a patchy distribution in phorbol-myristate-acetate (PMA)- or hydrogen peroxide-treated cells, reminiscent of the vesicle-associated zinc accumulation seen in other cells. In adult rat cardiomyocytes, an increase in TSQ fluorescence was first noticeable only at the cell periphery, then spread all over the cell forming typical vesicular structures (Korichneva *et al.*, unpublished observations).

In addition to zincosomes, the mitochondria are now a well-established compartment taking up elevated cytosolic zinc. For the last decade, mitochondria have been known as key stations in apoptotic signaling. Myocardial cell apoptosis contributes to cardiac dysfunction, including ischemia/reperfusion injury. It has been demonstrated that components of ischemia activate the mitochondrial death pathway in cardiac myocytes. This pathway involves depolarization of the mitochondrial membrane and opening of the permeability transition pore (PTP), a channel through which molecules  $\leq 1.5$  kDa pass. Release of apoptosis-inducing factor, Smac, procaspase, and cytochrome C following membrane rupture initiates the execution process, and seals the fate of the cells. Mitochondria are firmly integrated into the cellular control circuits. The afferent signals affecting mitochondrial function are not fully understood. Among others, they appear to include ROS as redox triggers of mitochondria and activators of a number of upstream signaling molecules that are recruited to mitochondria. The subsequent generation of ROS by mitochondria may constitute a feed-forward loop to monitor the redox microenvironment and to initiate appropriate responses. While cytosolic redox triggers lead to zinc release, the equilibrium in zinc compartmentalization shifts in such a way that zinc ions are quickly taken up by mitochondria as a consequence of redox stimulation. A detailed study by Sensi and colleagues (99) clearly demonstrates opposite roles of physiological and excessive zinc on mitochondrial function. Submicromolar levels, comparable to those that might occur during strong mobilization from intracellular compartments, induce membrane depolarization, increase currents across the mitochondrial inner membrane as detected by direct patch clamp recording of mitoplasts, increase oxygen consumption, and decrease ROS generation. However, high doses of zinc decrease oxygen consumption and increased ROS generation. Therefore, excessive mitochondrial  $\text{Zn}^{2+}$  sequestration would lead to a marked dysfunction of these organelles, characterized by prolonged ROS generation (96–99). While most of the studies of zinc function in mitochondria were performed on brain cells or tissue, or even mitochondria isolated from brain, we observed the relocation of zinc pool in mitochondria of cardiac cells upon stimulation (Korichneva *et al.*, unpublished observations).

The mechanisms of zinc-induced mitochondrial dysfunction are not delineated. Several molecular targets have been identified.  $\text{Zn}^{2+}$  inhibited alpha-ketoglutarate-stimulated mitochondrial respiration and alpha-ketoglutarate dehydrogenase complex isolated from the pig heart (10).  $\text{Zn}^{2+}$  similarly to  $\text{Ca}^{2+}$ , both at 10  $\mu\text{M}$ , triggered mitochondrial permeability transition, induced cytochrome C release and ROS production by



isolated liver mitochondria (9). Zinc in cardiac mitochondria reversibly inhibited the bc1 complex. Existence of a mitochondrial target for  $\text{Zn}^{2+}$  upstream of the bc1 complex has been also suggested. Zinc is shown to be an efficient inhibitor of mitochondrial cytochrome C oxidase activity rapidly interacting with the enzyme at a site exposed to the aqueous phase corresponding to the mitochondrial matrix (73). On the whole, tissue specificity would define the level of toxic doses for zinc ions.

Zinc, taken up by mitochondria, can in turn be released in a Ca-dependent manner. At physiological pH, much of the zinc released from mitochondria is rapidly buffered by the cytosolic proteins, thus preventing large increases in  $\text{Zn}^{2+}$ .

### *Zinc storage proteins metallothioneins*

The metallothioneins (MT) deserve a special place in the area of zinc homeostasis due to their unique role as protein-based storage sites for zinc. MTs localize in the intermembrane space of mitochondria, the cytosol, and the nuclear. Thirteen forms of human MTs originate from different genes. MTs are rather small, cysteine-rich heavy metal binding proteins that have the most complex  $\text{Zn}^{2+}$ -Cys coordination of all zinc containing proteins known (27, 87, 102). One third of all amino acid residues of MTs are strictly conserved cysteines. They bind seven zinc ions in zinc-thiolate clusters. Despite the fact that zinc binding to MT has the highest affinity compared to other proteins ( $-\log K_d$  equals  $\sim 13$ ), zinc in MT is readily exchangeable (56). Experimental data suggests that the likely way the MTs exchange zinc is by direct interaction with other zinc ligands (59). These properties designate to MTs two major antistress functions: in addition to playing a central role in heavy metal detoxification, these proteins are capable of protecting the cells from oxidative stress. The latter may be exerted due to chaperone-like activities of MTs that are capable of donating zinc to target metalloproteins, which in turn could have lost zinc under stress conditions. Studies by Kang *et al.* (60), using a cardiac-specific MT-overexpressing transgenic mouse model, have demonstrated that MT inhibits myocardial injuries triggered by oxidative stress. Myocardial oxidative stress has long been known to play a major role in several pathophysiological responses, including ischemia/reperfusion injury, cardiotoxicity induced by environmental chemicals and therapeutic drugs, and heart failure resulting from multifactorial manifestations. Under acute or chronic oxidative stress, ischemia/reperfusion, doxorubicine treatment, or dietary copper restrictions, MT-overexpressing mouse hearts revealed marked resistance to damage based on biochemical and functional analysis. Clearly, ischemia/reperfusion-induced myocardial injury was inhibited by MT via suppressing apoptosis (60). MTs inhibited mitochondrial cytochrome C release and caspase 3 activation. The protective role of MT in myocardial I/R may be accomplished via zinc release in oxidized environment, followed by the transfer to zinc binding proteins necessary to support cell function in the conditions of oxidative stress. Accordingly, reactivity of sulfur ligand is the key to the mechanism of action of MTs (79). MT does not release all of its seven zinc ions except under the conditions of severe oxidative stress when modifications of thiols in MT zinc clusters occur. It contains at

least one that is prone to be released than the others, and it originates from the three-zinc cluster (57). It has now been demonstrated by direct thiol modifications that disulfides are present in MT from MT-overexpressing transgenic mouse hearts and they are increased under the conditions of oxidative stress (31).

The understanding of MT function was significantly advanced by the discovery of the apoprotein, thionein (T). It was found that T is present in the tissues in the amounts comparable to those of MT, underscoring the dynamics of zinc distribution in the MT/T pair (112). Binding of zinc to T is highly cooperative, and the MT/T ratio (but not MT on its own) correlates with the available cellular zinc (53). Different tissues have different MT/T ratios, suggesting that changes in this ratio affect availability of zinc in the cells. Zinc transfer can occur in either direction, from MT to proteins or from proteins to T. The direction of zinc transfer reactions would depend on the redox status of the cells. It has been shown that T rapidly activates a group of enzymes in which zinc is bound at an inhibitory site (78).

Translocation of MT was observed between cytosol and nucleus, cytosol and mitochondria, as well as through plasma membrane. Thus, MT participates in compartmentalization of available zinc within the cell. Import of MT into mitochondria inhibits respiration. The electron transfer chain is identified as a primary site of inhibition. MT inhibition involves zinc delivery to mitochondria (112). The transported apoform of MT, thionein, activates zinc-inhibited respiration with a 1:1 stoichiometry. It should be noted, however, that inhibition of respiration by MT was demonstrated in the liver but was not confirmed in the heart.

A critical physiological function of MTs that has been suggested is to control  $\text{Zn}^{2+}$  availability to proteins requiring  $\text{Zn}^{2+}$  for activity. The biochemical proof for the transfer was demonstrated recently in heart extracts from MT-null mice incubated with  $^{65}\text{Zn}$ MT. Myocardial proteins receiving  $^{65}\text{Zn}$  were separated electrophoretically. The analysis of a unique band revealed mitochondrial aconitase among the proteins accepting MT bound zinc. The mitochondrial but not cytosolic aconitase was immunoprecipitated with MT, confirming direct interaction (30).

Mammalian metallothionein genes are transcriptionally regulated by heavy metals through metal response elements (MREs). The MRE-binding transcription factor-1 (MTF-1) is a protein containing six C(2)H(2)-type zinc fingers. An intact zinc finger domain is required for metal-induced recruitment of MTF-1 to the MT-I promoter (55). Mutational analysis showed that the six zinc fingers are not functionally equivalent, sharing distinct roles such as direct DNA recognition and regulatory function (65). The transcription of four known MT genes is rapidly upregulated in response to high zinc or oxidative stress. DNA-binding activity of MTF-1 *in vivo* and *in vitro* was reversibly activated by zinc interaction with the zinc finger domain controlled by redox conditions. Accordingly, MTF-1 serves one of the sensors of free zinc alterations in the cell.

As mentioned earlier, ZnT-1 transporter transcription is initiated by MRE-binding to MTF-1. However, regulations of expression of ZnT-1 and MT by zinc appear to be independent processes. Transgenic mice with a null mutation in the

MT gene, and transgenic mice overexpressing the protein, exhibit normal ZnT-1 expression.

Another type of intracellular redox stress, nitrosative stress and its relation to zinc homeostasis is receiving increasing attention. Both chemical compounds that generate NO, and an endogenous source, inducible nitric oxide synthase-derived NO, trigger nuclear MT translocation and intracellular  $Zn^{2+}$  release (62). NO stress increases mRNA expression of both MT-1 and MT-2, presumably via  $Zn^{2+}$  release, in murine aortic endothelial cells. The transient nature of this phenomenon witnesses the signaling function of zinc ions, suggesting that when stress has declined, modified zinc fingers are restored to be prepared for response to the next message.

## ZINC-MEDIATED REGULATION OF CELLULAR FUNCTIONS

### *Protein regulation*

There are thousands of zinc-containing proteins in the human proteome. This review highlights a few examples of zinc involvement in regulating the function of these proteins. In support of crosstalk of zinc and redox signals, antioxidant enzymes are the first example of zinc regulation. Copper–zinc superoxide dismutase (CuZnSOD) is an antioxidative defense enzyme that attenuates myocardial ischemia/reperfusion injury. The structural interplay of conserved disulfide bond and metal-site occupancy in human SOD1 is of increasing interest, as these posttranslational modifications are known to dramatically alter the catalytic chemistry, subcellular localization, and susceptibility of the protein to aggregation. Either the addition of  $Zn^{2+}$ , or the formation of the disulfide, leads to a shift in equilibrium that favors the dimeric species, the mature form (3).

SAG/ROC/Rbx/Hrt, a zinc-containing RING (really interesting new gene) finger proteins with characteristic C3HC4 or C3H2C3 motifs appear to act as E3 ubiquitin ligases and play important role in many vital processes in myocardium. In humans, both SAG and ROC1 are ubiquitously expressed at a very high level in heart and skeletal muscle. SAG is protective against apoptosis (103). Another group of proteins containing a zinc-binding fold, BIR (baculoviral IAP repeat)-containing proteins are inhibitors of cell death and act by binding to active caspases (101).

The DNA repair enzyme, polyADP-ribose polymerase (PARP) is a zinc-dependent enzyme that is activated by binding to DNA breaks. Poly(ADP-ribosyl)ation of nuclear proteins by PARP converts DNA damage into intracellular signals that activate either DNA repair by the base-excision pathway or cell death. As a result, PARP zinc finger modules found at the N-terminus were initially described as nick sensors. The specific hypothesis that zinc toxicity might be partly mediated by PARP has been tested. PARP was activated in cultured mouse cortical astrocytes after a toxic acute  $Zn^{2+}$  exposure (350  $\mu M$   $Zn^{2+}$  for 15 min). The neurotoxicity induced by acute, but not chronic,  $Zn^{2+}$  exposure was reduced in mixed neuronal–glial cultures prepared from mutant mice lacking the PARP gene. Additionally, an acute influx of labile  $Zn^{2+}$  induced apoptosis via activation of caspase in human leukemia HL-60 cells (66).

The area of zinc regulation of proteins, classical players of apoptotic pathway, is thus far underexploited in cardiac tissue. The sole evidence of blocking caspase-3 activation by zinc chloride in cardiac allografts suggested that there may be synergistic effect of zinc ions and cyclosporine A in decrease of apoptosis (70).

There is more evidence associated with zinc regulation of cardiac matrix metalloproteinases (MMPs). MMPs are zinc-dependent endopeptidases that are traditionally known for their role in extracellular matrix degradation remodeling in physiological and pathological processes, including ischemia, myocardial infarction, and cardiomyopathy. Catalytic sites are preserved in the zymogene form by ZnHis<sub>3</sub>Cys coordination. Upon increased oxidative or nitrosative stress, a catalytically active enzyme is released via a “cysteine zinc switch” mechanism in which cysteines can be oxidized with formation of a disulfide S-oxide and zinc ion of the active site is dissociated from a cysteine residue, allowing the enzyme to function (43, 83). In the cardiovascular system, a prevalent MMP, MMP-2, can degrade such extracellular matrix proteins as collagens, fibronectin, elastic, and laminin. Loss of collagen leads to progressive contractile dysfunction (13, 88). Recent studies reveal a growing number of nonmatrix substrates: endothelin-1 yielding a novel vasoconstrictor (32), or the vasodilator calcitonin gene-related peptide (33). Studies by Schultz and colleagues uncover a novel biological role for MMPs by showing the presence of MMP-2 within myofilaments and in the nucleus, where the peptidase was able to cleave troponin I and PARP, respectively (38, 109). These biochemical events would contribute significantly to impairment of myocardial recovery in postischemic reperfusion or at other conditions of oxidative stress. Indeed, it has been shown on isolated perfused rat hearts that peroxynitrite-induced myocardial injury is mediated by MMP-2 (108). The proteolytic cleavage of myosin light chain and troponin I by MMP-2 was clearly one of the reasons for myocardial ischemia injury (96).

### *Effects of zinc on gene expression*

Many cardiac abnormalities that are induced by zinc deficiency are associated with alterations in the expression of genes that encode myocyte structural proteins and the proteins involved in signal transduction, redox responses, and growth and energy utilization. The discovery of so-called zinc fingers in the early 1980s gave a start to a series of innovations related to functional implications of zinc–sulfur ligand interactions. Since 3% of the whole human genome encode proteins with zinc fingers, the significance of physiological consequences of zinc and cysteine mutual regulation is difficult to underestimate (51). Zinc in zinc fingers can be coordinated either by two cysteines and two histidines (ZnCys<sub>2</sub>His<sub>2</sub>), three cysteines and one histidine (ZnCys<sub>3</sub>His), or cysteines only (ZnCys<sub>4</sub>). The chemistry of this interaction (*e.g.*, tight zinc binding to sulfur ligand along with redox active coordination for zinc ion in zinc fingers) allows these domains to confer multiple activities to the proteins, such as control of conformation and function, translocation, and sensing zinc concentration. Evidence exist that a disruption of thiols in zinc–sulfur clusters leads to reversible inhibition of zinc finger structures and DNA binding, providing molecular mecha-

nisms to regulate gene transcription via modulation of zinc-thiol interaction (72). A few examples will illustrate how zinc and redox signals converge on zinc fingers of transcription factors.

The transcription factor p53 controls the proliferation and survival of cells exposed to DNA damage. Targeted deletion of p53 prevents cardiac rupture after myocardial infarction in mice (80). The specific DNA-binding domain of p53 (residues 102–292) has a complex tertiary structure that is stabilized by zinc. It has been shown that the exposure of cultured cells to the membrane-permeable zinc chelator N,N,N', N'-tetrakis(2-pyridylmethyl)ethylenediamine (TPEN) induces wild-type p53 to accumulate in an immunologically “mutant” form (PAb240+, PAb1620-) with decreased DNA-binding activity. Removal of TPEN from culture medium allowed p53 to refold into the immunologically wild-type form, followed by a transient increase in DNA binding, expression of the cyclin-dependent kinase inhibitor p21WAF1, and cell-cycle delay in the G1 phase. Thus, modulation of intracellular zinc induced conformational changes in p53 that activated wild-type function, suggesting that metalloregulation may play a role in controlling p53. This redox and metal sensitivity may be one of the biochemical mechanisms by which p53 acts as a “sensor” of multiple forms of stress. The involvement of thioredoxin, redox factor 1, and metallothionein in control of p53 protein conformation and activity has been discussed (46).

Retinoic acid-mediated gene expression is essential for cardiovascular morphogenesis. DNA-binding domain of nuclear retinoic acid receptor contains two zinc fingers with zinc tetrahedrally coordinated by four cysteines. Under oxidative stress conditions, DNA binding of zinc finger is abolished and zinc is released. The effect is reversible: the combination of reduced glutathione and  $Zn^{2+}$  restores activity. The Early Growth Response protein (Egr-1) is a classical C(2)H(2)-zinc-containing transcriptional regulator involved in the control of cell proliferation and apoptosis. Its DNA binding activity is redox regulated *in vitro* via oxidation/reduction of Cys residues (92).

The cardiac-restricted zinc finger transcriptional factor GATA-4 has been implicated as a critical regulator of inducible cardiac gene expression and as a potent mediator of the hypertrophic program. By interacting with NFATc in endothelin-1 treated cardiomyocytes, GATA-4 mediates protection against oxidant-induced apoptosis (23). GATA-4 induces transcription of survival factors, including anti-apoptotic molecule bcl-2 in cardiac tissue. Zinc deficiency induced cardiac abnormalities associated with alterations in the expression of genes regulated by GATA-4. Thus, two genes critical for heart development,  $\alpha$ -myosin heavy chain and cardiac troponin I, were downregulated in Zn-deficient rat fetuses. (23). It has also been suggested that GATA-4 DNA binding is upregulated by a mechanical stretch in the isolated rat atria via p38 and extracellular signal-regulated protein kinase (105).

### *Zinc control of cytosolic signaling*

Zinc deficiency may indirectly lead to the activation of transcription factors that do not possess zinc finger domains in their structure. Thus, oxidant-sensitive transcription factors NF- $\kappa$ B and AP-1 are generally activated in zinc deficiency,

which occurs possibly as a result of oxidative stress followed by activation of p38 and JNK (86).

The work of Keen and colleagues contributed significantly to our understanding of the effects of zinc deficiency on both transcription factors and signaling kinases (15). In general, zinc deficiency is characterized by attenuation of growth factor signaling pathways and an amplification of p53 pathways. This outcome is achieved by hypophosphorylation of anti-apoptotic kinases, AKT and ERK, under the conditions of zinc deficiency, and activation of p38 and JNK. It is not clear, however, to what extent the production of ROS is involved in these effects and whether zinc may have direct regulatory function on the enzymes. It could be also important to understand time-dependency of zinc regulation of signaling kinases. The complexity of zinc effects on MAP kinases contributes to controversy between the *in vitro* and *in vivo* studies. As such, opposite to zinc deficiency, zinc chelation inhibits activation of p38. Tissue specificity and doses studied are other crucial factors playing a part in the controversy. How zinc affects MAPK function in cardiac tissue is still an open question.

As another group of regulators of protein phosphorylation, protein phosphatases are also subject to zinc control. Zinc is an effector of insulin/IGF signaling. Tight inhibition of PTPs is likely responsible for insulinomimetic properties of zinc ions. The study by Haase and Maret established that zinc inhibits protein tyrosine phosphatases (PTPs) as a cause for these effects (45). *In vitro* inhibition of PTPs occurs at nanomolar zinc concentrations. Incubation of cultured cells with zinc and zinc ionophore pyrithione augments tyrosine protein phosphorylation, while chelation of intracellular zinc with TPEN suppresses insulin- and IGF-1-stimulated tyrosine phosphorylation.

The principle of signal transduction and definition of a second messenger first evolved from the discovery of hormone-regulated adenylate cyclase, an enzyme that converts the signal from G-protein coupled receptor to synthesis of cAMP. Since then, multiple consequences of cAMP-dependent signaling have been investigated in detail, including regulation by hormones,  $\alpha$  and  $\beta\gamma$  subunits of G-proteins, feedback phosphorylation by associated kinases, control by ionic environment, and plasma membrane lipids. Recent interest to zinc signals provoked analysis of its effects on membrane associated and soluble adenylate cyclase. It has been shown that zinc inhibits hormone and forskolin stimulation of cAMP synthesis in N18TG2 cells. Crystallographic data of the truncated soluble AC suggest a possible mechanism by which zinc could inhibit AC activity. It turned out that micromolar concentrations of  $Zn^{2+}$  bound to a site different from  $Mg^{2+}$  binding sites involved in catalysis. Using extrinsic and intrinsic fluorescent measurements, the authors showed a conformational response of the enzyme to zinc binding (63). Zinc deficiency and altered myocardial adenylate activity commonly occur in diabetes with hormonal-stimulated enzymatic activity, which is significantly lower in diabetic rats on a low zinc diet (82).

Zinc has also been shown to influence cAMP signaling by affecting cyclic nucleotide phosphodiesterases (PDE). After first observations of an inhibition of cAMP and cGMP hydrolysis by zinc in bovine heart, there have been several reports of both activating and inhibitory effects of zinc on different PDE subfamilies. For example, cGMP specific PDE V

is activated by zinc at submicromolar levels and inhibited at higher doses of zinc (37).

As a separate issue, it is worth noting the so-called “zinc sensing receptor” role in the modulation of classical signaling pathways. Extracellular zinc may not only mediate physiological responses by entering the cells but also by stimulating a zinc-sensing receptor (ZnR) on the surface of some cell types. This receptor, though not yet cloned, appears to be coupled to phospholipase C via pertussis toxin sensitive G-protein and linked to intracellular Ca release and MAP kinase pathway activation (48). Desensitization of ZnR by high doses of zinc is followed by approximately 90% inhibition of  $\text{Zn}^{2+}$ -dependent ERK1/2 phosphorylation. Physiological importance of ZnR activation was supported by robust activation of Na/H exchanger in colon epithelial cells, which was blocked by MAPK pathway inhibitor U0126 (6). These observations are in line with several others that show that treatment of cells with  $\text{ZnCl}_2$  increases phosphorylation of ERKs (47). The apparent affinity of the putative receptor is estimated to be close to 80  $\mu\text{M}$ . A critical related question would be whether zinc-sensing receptor is functional *in vivo* given the extracellular zinc level of 10–20  $\mu\text{M}$ . In certain pathological conditions, such as brain ischemia, zinc is massively released from synaptic vesicles into the extracellular space. Consequently, elevated zinc can activate the receptors of postsynaptic membranes. If the zinc-sensing receptor exists on cardiomyocytes, its activation during myocardial ischemia/reperfusion would have significant physiological impact. In fact, since we have suggested that zinc is extruded from the cells under oxidative stress in myocardium (68), zinc ions could play a role of autocrine regulator providing feedback loop controlling cardiac responses.

## “REDOX ZINC SWITCH” HYPOTHESIS

### *Redox chemistry of zinc interactions*

Despite skepticism that the strongly reducing intracellular environment would permit significant oxidation of cysteine residues within zinc finger proteins, there is compelling evidence that oxidation occurs both *in vivo* and *in vitro*. The reports demonstrating reversible oxidation of zinc-coordinated cysteines with loss of zinc binding function *in vitro* were shown to reflect accurately the changes in intact cells, and these in turn have been linked to physiological changes. A critical biological partnership of zinc and sulfur ligand is reviewed by Maret (78).

Chemical flexibility of transition metal allows zinc to impose conformational changes on the proteins it binds (75). Being redox inert, zinc plays a part in electron transfer complex shifting protein electron density. In proteins, zinc can bind mainly to cysteine, histidine, aspartate, and glutamate residues. Cysteines possess the unique structural features that allow them to combine metal binding properties with catalytic activity and extensive redox chemistry. Within the zinc coordination center, zinc ions potentially can modulate reactivity of cysteine thiol groups towards oxidation. Interdependency of these three aspects permits the redox regulation of proteins, metal control of redox activity, and redox control of metal-based catalysis. The most important and extraordinary

property of zinc–sulfur ligand interaction is release of zinc under oxidative environment, converging the redox signaling and zinc metabolism (Fig. 1). Cysteine-rich zinc binding protein domains are therefore able to act as “redox zinc switches” to sense the concentrations of both zinc and oxidants. Therefore, unlike thiol oxidation/reduction, “redox zinc switches” are controlled by zinc availability. Remarkably, until recently it was assumed that the redox inert zinc protects thiolates from oxidation. However, the recent studies suggest that a strong binding of zinc enhances the redox sensitivity of thiolates (79).

The unsurpassed study of the mechanism of the “redox zinc switch” operation was performed in a relatively simple cell model of the *Escherichia coli* chaperone bacterial chaperon Hsp-33. Hsp33 contains a C-terminal zinc finger domain that modulates activity by a redox-regulated, reversible hinge (8, 54). In an oxidizing microenvironment, thiols were converted to disulfide, zinc became uncoupled, and the unfolding of the protein led to the active enzyme. The reduced form in the presence of zinc was inactive. The solution structure of a recombinant 61-residue protein containing zinc-binding domain of Hsp33 suggests that loss of the bound zinc ions disrupts the well-folded structure, allowing the ligand cysteine residues to be oxidized (8). This finding implies that the redox response of zinc–cysteine clusters is biphasic and emphasizes a separate role for zinc in redox control mechanism. Our laboratory demonstrated that similar redox zinc switch operates the activation of protein kinase C (PKC), and perhaps other serine/threonine kinases containing homologous zinc finger domains (69).

It should be noted that in some instances the thiols of different polypeptides are oxidized under stressed conditions. For example, in nitric oxide synthase, the zinc site links two protomers, oxidation releases zinc and uncouples the enzyme. Ischemic conditions create more complexity on the redox switches. As such, the equilibrium of free versus chelated zinc is sensitive to environmental factors, in particular to acidosis. Acidification appears to rapidly destabilize zinc–thiol binding, shifting equilibrium towards free  $\text{Zn}^{2+}$ . Taken together, chemistry of zinc–sulfur ligand interactions suggests that zinc homeostasis may play a very significant role in ischemic damage of tissues, including myocardium.

### *Zinc hypothesis of PKC activation: operation of the mammalian “redox zinc switch”*

Perhaps a better understanding of the regulation of signaling kinases by zinc and redox changes is accomplished in the studies of PKC isoforms. PKC has always been the focus of increased interest due to the key role of this enzyme in signal transduction (111). Different isoforms translocate to different compartments to close proximity to substrates and perform multiple cellular functions. Like other Ser/Thr kinases, PKC is sensitive to variations of zinc concentration. More than 10 years ago, Forbes and Zalewski demonstrated that micromolar concentrations of zinc chloride induced specific association of PKC with the plasma membrane or cytoskeleton (34–36). The attachment of protein kinase C to the cytoskeleton was accompanied by an enhanced expression of binding sites for 3H-phorbol ester, a regulatory ligand of protein kinase C. The heavy-metal chelating agent 1,10-phenanthroline com-



pletely reversed the increased [3H]PDBu binding in cells pretreated with  $^{65}\text{Zn}$  and ionophore, which was associated with a decline of about 20% in cell-associated  $^{65}\text{Zn}$ , suggesting that a relatively small pool of intracellular  $\text{Zn}^{2+}$  acts on PKC. The authors suggested that this could be a membrane-associated pool. The active factor in the cytoskeleton was labile to protease, suggesting that protein kinase C binds to a cytoskeletal protein. PKC bound to a  $\text{Zn}^{2+}$  affinity column and was eluted by a metal chelator, confirming that  $\text{Zn}^{2+}$  interacts directly with PKC. The authors further proposed that putative binding sites for zinc were present in the regulatory domain of protein kinase C; however, no distinct role for zinc was obvious at that time.

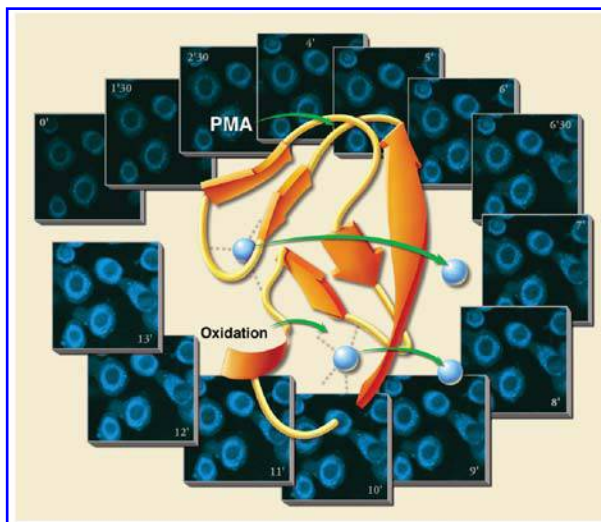
Later, zinc was shown to activate PKC in neurons and platelets (71), and was required for cellular response mediated by PKC in lymphocytes. Timely studies by Keen and colleagues of the effects of zinc depletion on function of kinases revealed that decreased zinc lowered classical PKC activity and led to proteolysis of the novel PKC family member, PKC $\delta$ , to its 40 kDa fragment, a positive regulator of apoptosis via caspase-3 activation (14). This effect of zinc deficiency could be a direct impact on the PKC molecule, or it may be executed via increased oxidative stress, possibly by influence on copper-mediated ROS production.

The ability of PKC to regulate many cardiovascular functions is supported by the facts that many cardiovascular growth factors, such as angiotensin, endothelin, vascular endothelial growth, and permeability factor target PKC (12, 18, 22, 29, 84). The physiological importance of PKC can be surmised by the existence of multiple isoforms, which are usually arranged into groups according to their structure and cofactor requirements. Conventional PKCs ( $\alpha$ ,  $\beta_{1/2}$ , and  $\gamma$ ) are  $\text{Ca}^{2+}$  dependent and activated by diacylglycerol (DAG); novel PKCs ( $\delta$ ,  $\epsilon$ ,  $\eta$ , and  $\theta$ ) are  $\text{Ca}^{2+}$  independent but activated by DAG; atypical PKCs ( $\zeta$  and  $i/\lambda$ ) are  $\text{Ca}^{2+}$  and DAG independent (12, 61). It has been shown that restricted physiological functions are limited to specific isoforms. Thus, cardiac PKC $\delta$  is activated by ischemia, and PKC $\epsilon$  is involved in ischemic preconditioning, linking PKC function to redox control (7, 12, 16). Supplementation of perfusion solution with  $\delta$ -specific RACK-derived peptide inhibitor confers protection of myocardium against ischemic injury.

Independent of the classical lipid-mediated pathway, PKC is also controlled by a redox mechanism. PKCs embrace two independent target sequences susceptible to oxidative modification (41). The two domains of PKC respond differently to redox changes. Thus, oxidation of thiols in the catalytic domains blocks enzymatic kinase function. More interestingly, oxidation within the regulatory sequence converts the protein to the catalytically competent form, while reduction reverses this process (40, 49, 64, 66). Physiologically, it would mean that the regulatory domain should be sensitive to lower doses of oxidants. Another manner in which such preferential oxidation might occur is through the facilitation of electron transfer by retinoids. It has been found that the redox activation of the kinase requires cofactors, retinol or its metabolites, since the high affinity retinoid binding site was mapped to the cysteine-rich regions in the regulatory domains of Ser/Thr kinases (49). Remarkably, metabolism of vitamin A (retinol) increases in heart after myocardial infarction (89).

In the N-terminal regulatory domain, the 50 amino acid-long, highly homologous stretches containing six conserved cysteine and two conserved histidine residues, tetrahedrally coordinated by two  $\text{Zn}^{2+}$  ions into a composite zinc finger are targets of redox control (113). When oxidized, the autoinhibitory function of the regulatory domain is compromised and, consequently, cellular PKC activity is stimulated. This topological change is believed to be complemented by phosphorylation, translocation, and  $\text{Ca}^{2+}$  and phosphatidylserine binding, to lock the catalytic domain into an active form. As a part of crosstalk, PKC $\delta$  becomes phosphorylated on Tyr at residues 512 and 523 under the conditions of oxidative stress (67).

Remarkably, both classical and redox activation of PKC trigger the same event, namely zinc release from the regulatory domain. Phorbol esters mimic the action of second messenger diacylglycerol by binding to the same motif within regulatory domain and activating catalytic activity. Neonatal rat cardiomyocytes treated with PMA and with hydrogen peroxide released substantial amounts of  $\text{Zn}^{2+}$ , which could be detected within minutes of the treatment as visualized by confocal microscopy, using TSQ as indicator (68). Of course, oxidation could trigger zinc release from multiple targets. More intriguing is a similar response to classical PKC activation. PMA-induced zinc increase along with the measurements in the cells overexpressing different PKC isoforms may suggest that PKC itself, as well as PKC-triggered signaling events, are among the sources of free intracellular  $\text{Zn}^{2+}$  (illustrated in Fig. 3). The proof was obtained experimentally by evaluating *in vitro* the glutathione-S-transferase fusion proteins, containing the human PKC $\delta$  C1A,  $\delta$ C1B,  $\zeta$ C1, or cRaf C1 peptides using a spectrofluorimetric or the commonly used colorimetric based on 4-(2-pyridylazo-resorcinol) colorimetric quantitative assays. Both 1,3-diolein and PMA triggered the release



**FIG. 3. Zinc release from protein kinase C.** Confocal images of insect cells overexpressing PKC $\alpha$  show increase of free  $\text{Zn}^{2+}$  over time with PMA treatment. Structural properties of PKC zinc finger: the additive effect of oxidants and lipid activators on the release of chelated zinc. (Adapted from Korichneva *et al.* 2002). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article at [www.liebertonline.com/ars](http://www.liebertonline.com/ars).)

of stoichiometric amounts of zinc, each mole of lipid generating one equivalent of free  $\text{Zn}^{2+}$  (69). Although the exact number of the binding constant of  $\text{Zn}^{2+}$  to PKC zinc finger is not available from our measurements, it can be estimated to exceed that of the probes, TSQ, and PAR. Upon oxidation, or PMA binding to the cyst domain, the chelation status of  $\text{Zn}^{2+}$  is changed, allowing  $\text{Zn}^{2+}$  to partition to the probes. Indeed, in a separate study the electrospray ionization mass spectrometry allowed to determine dissociation constant of zinc from the zinc finger of 0.66 nM (100).

Since the cells in culture may change certain phenotypic features, we did confirm our observations of PMA-triggered zinc release on the model of whole Langendorff perfused rat hearts by monitoring tissue sections after ischemia/reperfusion. In addition, our results suggested that heart tissue becomes zinc-depleted after ischemia/reperfusion. More importantly, the capacity to liberate labile zinc was significantly diminished (68).

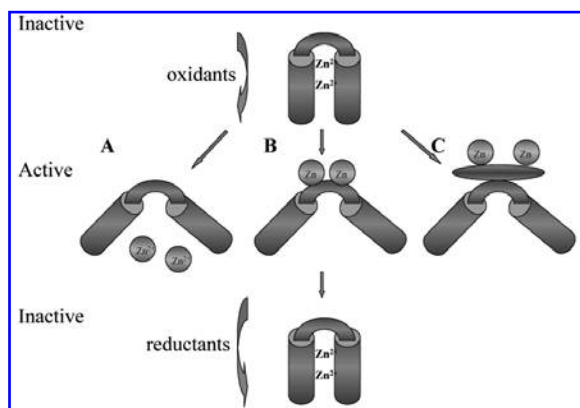
The concept that zinc movements are important for PKC to gain enzymatic capacity was validated by comparing the  $\text{Zn}^{2+}$  contents in resting and active PKC, with the expectation that the former should contain more  $\text{Zn}^{2+}$ . Indeed, zinc content correlated inversely with PKC activity (69). These results are in complete agreement with those of Knapp and Kann (64) who had previously underscored the importance of zinc release during PKC activation by the redox mechanism. Altogether, the data present the evidence defining cysteine-rich domain of the kinase as a redox sensor and a reversible redox zinc switch.

It is unclear how the loss of zinc during PKC activating agrees with the fact that PKC is activated by zinc in many experiments. To solve this controversy, based on the published accounts and our unpublished data, we suggest a possible explanation (Fig. 4). The model advocating the dynamic regulatory role for zinc ions is in agreement with zinc release upon

one activation cycle. However, liberated zinc cannot diffuse far away; rather it needs to be in close proximity for the recovery of the kinase. There are three possible scenarios in this instance: free zinc is compartmentalized within the kinase domain, it can bind with lower affinity to another site on the kinase to be available upon reduction of sulfur ligand, or it can repartition to a kinase partner that would provide the ion to the kinase, not to miss the next message. The reversible activation would be a normal physiological response to stress, while irreversible overoxidation would trigger protein degradation, and consequently apoptosis.

On the whole, zinc coordination centers of the kinases represent a redox zinc switch mechanism that is more complex than described earlier for bacterial chaperone (8). Zinc ions would function as linchpins in that switch to start the clock, initiating precisely the kind of conformational changes that have been postulated by others for the commencement of PKC catalytic activity. These changes involve the removal of the regulatory N-terminus from the catalytic domain, the exposure of hydrophobic surfaces that facilitate translocation to membranes, and the accessibility to substrate and cofactors. The importance of the mechanism of the reversible redox zinc switch is highlighted by the fact that the two signaling pathways of PKC activation converge on the zinc finger. Due to the oxidation of cysteines, or by affecting zinc affinity to histidine via the chain of hydrogen bonds and consequently redox microenvironment of cysteine cluster (in case of PMA), the two different stimuli cause principally the same effect.

It is very probable that other serine/threonine kinases sharing high homology in a composite zinc finger are operated by similar redox zinc switch. Along with different PKC isoforms, they include Raf-1, Rac1 exchange factor Vav (115), chimaerins, Rac-GTPas-activating protein (11), and others. The two pathways, although utilizing messengers of different chemical nature, trigger basically the same event—zinc release from the regulatory domain thus converging on the zinc finger of the kinase. In the equilibrium of oxidants and antioxidants, “Redox Status of Individual Molecules,” specifically the status of zinc cysteine cluster may become the most valid biomarker of a stressed tissue and its capacities to respond to stimuli. Possibly the most effective protection from ischemic damage, preconditioning sets up the redox zinc switch on the vital regulatory molecules. Better knowledge of the operation of this switch would help to find the clue to the mechanism of such protection.



**FIG. 4. Hypothetical model of PKC activation by zinc release.** Oxidation of cysteines triggers zinc release and unfolds the kinase into an active conformation. The three possible scenarios embrace free zinc compartmentalization within the kinase domain (A), zinc binding to the kinase with lower affinity to another site on the kinase (B), or participation of a partner to which zinc can repartition during one oxidation cycle (C). The proximity of zinc ions to the regulatory domain is required for conformational recovery that allows the kinase to respond to the next message. Irreversible oxidation would trigger protein degradation.

## CONCLUDING REMARKS

The complexity of the signaling system based on zinc has been partially deconvoluted over the past several years. An important part of the puzzle, one that reveals the major players in zinc homeostasis, is now solved, leaving more questions than answers, particularly relating to the tissue-specific role of these regulators. Here are a few:

- (a) Based on the experimental evidence of regulation by  $\text{ZnT}$  of LTCC, it could be of immense importance to verify the phenomenon in cardiac tissue, where LTCC is the key regulator of conductance. Effects of zinc on

calcium homeostasis are to be studied in detail. In regard to zinc transport, the cross-regulation by different ion transporting systems should be examined.

- (b) Since zinc effect on mitochondrial function is tissue specific, zinc targets in heart mitochondria must be characterized.
- (c) We still need to understand the phenotype of MT knockout mouse model. It would be required to turn off all of the isoforms to confirm the exceptional role of MT as a zinc storage protein and a zinc donor under critical conditions.
- (d) We need to develop a better understanding of zincosomes. How different they are from calcium storage compartments? What are their similarities?
- (e) The recognition of temporal and spatial fluctuation of intracellular zinc suggests its potential role in signal transduction. We need to expand the record of the proteins that are regulated by the redox zinc switch.
- (f) Finally, we definitively need to proceed with the creation of new faster, more selective, and more sensitive probes for zinc detection.

These and many more questions are within the area of exploration over the next decade. The diversity of zinc functions is fascinating, and it is promising for future biomedical and pharmacological research. The success would be determined by picking the right target and understanding the biology of the target. The new knowledge in the area of zinc homeostasis will improve our understanding of cardiac disorders and suggest new strategies for pharmacological interventions.

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## ABBREVIATIONS

CuZnSOD, copper-zinc superoxide dismutase; DAG, diacylglycerol; MRE, metal response element; MT, metallothionein; MTF, metal responsive transcription factor; PDE, cyclic nucleotide phosphodiesterases; PKC, protein kinase C; PMA, phorbol-myristate-acetate; PTP, permeability transition pore; PTPs, protein tyrosine phosphatases; SLC, solute-linked carrier; T, thionein; TPEN, *N*'-tetrakis(2-pyridylmethyl)ethylenediamine; TSQ, *N*-(6-methoxy-8-quinolyl)-p-toluensulfonamide.

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