

Toshiyuki Fukada · Taiho Kambe *Editors*

# Zinc Signals in Cellular Functions and Disorders

 Springer

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*Editors*

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# Foreword

Our understanding of the roles of the essential metal zinc in health and disease processes is advancing rapidly, as is evident from the remarkable studies presented in this book on zinc signaling mechanisms. Certainly many excellent scientists have contributed to the foundations of this field, and I trust that they will not be offended if I cannot mention them all in this limited space. However, I find the pioneering studies of several clinicians and molecular biologists particularly noteworthy of mention. The clinicians Ananda Prasad and Harold Sandstead traveled to Iran in the late 1950s and 1960s and found young adults who had failed to thrive and mature and then deduced that this was due to dietary zinc deficiency (Prasad 1984). By the early 1970s, Edward Moynahan identified acrodermatitis enteropathica as a genetic disease of zinc deficiency in humans (Moynahan 1974). These findings led the American National Academy of Sciences in the 1970s to realize that humans could, in fact, become zinc deficient and that zinc deficiency could cause disease.

The molecular biologist Richard Palmiter first described the mammalian metallothionein genes and demonstrated their dramatic transcriptional induction by zinc and then created mouse models which over-express or lack metallothioneins (MT-I and II) (Palmiter 1987; Masters et al. 1994). Subsequently Walter Schaffner identified and cloned the transcription factor MTF-1, which regulates metallothionein gene transcription in response to zinc (Radtke et al. 1993). These pivotal studies paved the way for thousands of subsequent studies. Although my group provided compelling data that the unique zinc-finger domain of MTF-1 functions as a zinc sensor (Laity and Andrews 2007), the structural basis for that mechanism remains to be resolved in detail. Nonetheless the concept that substantial changes in “available” zinc in higher eukaryotic cells and organisms are sensed by the cell was fundamental to our understanding of zinc biology and zinc homeostasis mechanisms. We now understand that zinc fluxes modify kinase signal transduction cascades and control the localization and stability of several zinc transporters. Using the MT over-expressing or knockout mice created by Richard Palmiter, we presented some of the first evidence that the mouse metallothioneins provide a biologically important labile pool of zinc (Dalton et al. 1996; Andrews and Geiser 1999). These proteins are now considered to function as zinc buffers. Richard Palmiter’s contribution did not end with the metallothioneins.

He subsequently cloned the first mammalian zinc efflux transporter (ZnT1; Slc30a1), described the ZnT gene family, and created mouse models that lacked ZnTs (Palmiter and Findley 1995; Palmiter and Huang 2004). His ZnT3 knockout mouse model has been and continues to be employed in hundreds of neurobiology studies (Cole et al. 1999).

Another fundamental advance in the field was the identification of the first ZIP family member IRT-1 in Mary Lou Guerinot's laboratory (Eide et al. 1996). In collaboration with David Eide they showed that *Saccharomyces* ZRT zinc transporters (Zhao and Eide 1996) and *Arabidopsis* IRT1 iron transporters belong to a structurally related family of metal ion transporters, thus the acronym **Zrt-Irt-like Proteins** (Guerinot 2000). The ZIP proteins are found in all eukaryotes, and orthologues are found in bacteria. Since the identification of this family of metal ion transporters, there have been hundreds of publications on their structure, regulation, and functions. Pioneering studies by Jane Gitschier (Wang et al. 2002) and Sebastien Kury (Kury et al. 2002) identified *Zip4* mutations in patients with acrodermatitis enteropathica about 30 years after the description of this devastating zinc deficiency disease by Moynahan (1974). Among the 14 known ZIP family members, we now have mouse knockout models of over half of these genes. My group created mouse knockout models of *Zip1* through *Zip5* which includes mouse models of acrodermatitis enteropathica (Kambe et al. 2008; Dufner-Beattie et al. 2007; Geiser et al. 2012, 2013). Our studies revealed that expression of the *Zip4* gene in intestinal enterocytes and embryonic visceral endoderm in mice is essential for viability and that the loss of function of this gene causes a rapid shift from anabolic to catabolic metabolism in the animal accompanied by a devastating loss of intestinal integrity and impaired stem cell differentiation.

As you will see when you read this book, the field of zinc biology has matured rapidly in the past decade. The current availability of zinc-sensing fluorescent probes, zinc-transporter genes, and expression vectors, antibodies (still a weak point), and genetic mouse models allows investigators to probe mechanistic aspects of zinc metabolism in great depth. Evidence for functions of zinc and specific zinc transporters in several diseases has emerged, including functions in cancer as well as in normal growth and development. Studies of structure–function relationships in zinc transport proteins are rapidly progressing, and an active field of investigation involves understanding the biophysics of zinc–protein interactions in regulatory proteins and the multiple mechanism of cellular and organismal zinc sensing. We can look forward to many exciting and novel findings in this field over the next few years.

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# Preface

More than five decades ago, Dr. Ananda S. Prasad discovered zinc (Zn) as the essential trace element for human life. Zn deficiency was the first discovery in Zn imbalance-related abnormality that causes growth retardation, immunodeficiency, hypogonadism, and neuronal and sensory dysfunctions. Human diseases including cancer, diabetes, osteoporosis, dermatitis, and auto-immune and neurodegenerative diseases have been shown to be associated with abnormal Zn status. Investigations of the biological roles of Zn, however, had been challenging because Zn compounds are normally colorless, and the natural status of Zn is stable as a divalent cation, unlike other bioactive metals such as iron and copper.

Until now, there have been at least four issues that advanced our knowledge about the significant roles of Zn in physiology and diseases. First: bioinformatics, which revealed that approximately 10 % of all proteins in humans may bind with Zn. Second: genetic approaches using animal models and human genetics, which contributed to demonstrating the physiological roles of Zn in cells, tissues, and the whole body. Third: investigation of Zn transporters and metallothioneins in vitro and in vivo, which provided a variety of information on the importance of Zn transportation within and between cells, which led us to the fourth issue: Zn indeed acts as a signaling factor like calcium, called “Zn signaling”. Because this is a quite new field, we were motivated to introduce the current status of the study of Zn signaling and to review the whole scheme of this area to date.

The present book overviews up-to-date information on the study of Zn signaling, describing not only the essence of Zn signaling including its history, the molecular analysis of the structures and functions of Zn transporters and metallothioneins, and detection techniques for Zn signals, but also the involvement of Zn signaling in physiology and disease status as in brain function, immunity, inflammation, skeletogenesis, diabetes, and cancer. Besides the introduction of new insights in the study of Zn signaling, this book aims to address the many unsolved problems in the field. For this reason, we made a great effort to furnish educational contexts that will provide great introductions for students, young scientists, and clinical personnel. These contexts can also be valuable references for the pioneers and aficionados among researchers involved with Zn. So that all these goals would mesh, we as editors invited contributions from investigators who are world leaders in this field.

We believe the publication of this book is timely for reviewing the nature of Zn signaling, in which there is growing evidence that Zn signals regulate intra- and extracellular events leading to biological homeostasis, as all the authors will discuss. Also, we are confident that readers will find the book valuable for teaching, lecturing, and other outreach activities that can help make known to the public the importance of Zn itself. Finally, we express our heartfelt thanks to the splendid contributions of all authors, which will lead us to our goal.

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# Chapter 1

## Introduction: “Zinc Signaling”–The Blossoming Field of Zinc Biology

Taiho Kambe

**Abstract** Zinc plays an indispensable role in life. It regulates a great number of protein functions including transcription factors, enzymes, adapters, receptors, and growth factors as a structural or catalytic factor. Recently, a further function of zinc has received extensive interest and attention because of its potential importance as a signaling mediator. Zinc plays a dynamic role as an extracellular and intracellular signaling factor, which enables communication between cells in an autocrine, paracrine, or endocrine fashion, conversion of extracellular stimuli to intracellular responses, and regulation of various intracellular signaling pathways. These zinc functions are recognized as “zinc signaling,” which has critical roles in physiology, and thus their imbalance can cause a variety of problems with regard to human health. This book extensively reviews the field from the basic aspects to the crucial roles of zinc signaling in biological processes, discussing the future directions and questions at both the molecular and the physiological level.

**Keywords** Zinc • Zinc homeostasis • Zinc signaling

### 1.1 Introduction

There are two types of zinc ions in the body. One is protein-binding zinc, which functions as a structural component and enzyme cofactor to stabilize and functionalize proteins. Proteome analyses estimate that approximately 10 % of proteins encoded in the human genome have potential zinc-binding motifs (Andreini et al. 2006). The other is labile zinc, which means “free” zinc ions. The amount of free zinc ions in the cytosol maintained is extremely low and is estimated to be less than nanomolar concentrations, while it is high in some kind of zinc containing vesicles such as insulin granules and synaptic vesicles. (Kambe et al. 2004; Maret 2011). Recent studies have revealed exciting information about the dynamic roles of free zinc ions in a great number of biological processes (Frederickson et al. 2005; Hirano et al. 2008; Sensi et al. 2009; Haase and Rink 2009, 2014; Fukada et al. 2011), which has highlighted the signaling functions of zinc, generally called “zinc signaling” (Fig. 1.1).

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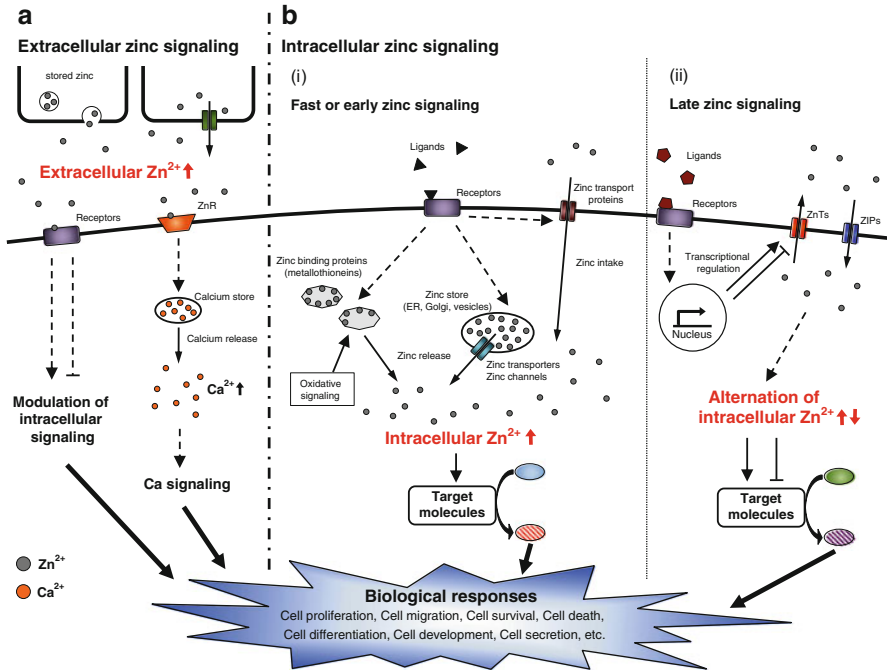
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**Fig. 1.1** Schematic diagrams of zinc signaling. Zinc signaling is caused by alternation in zinc concentrations in both the extracellular and intracellular milieu and can be divided into several types. **a** “Extracellular zinc signaling” takes place in extracellular milieu such as the synaptic cleft. In extracellular zinc signaling, zinc, which is released from cells via exocytosis of vesicular zinc or zinc efflux across the plasma membrane by zinc transport proteins, acts as a ligand of receptors expressed on the cellular membrane of target cells. One example is the ZnR (zinc receptor) signaling that activates calcium (Ca) signaling in different types of cells, and another example is  $\alpha$ -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid (AMPA) or *N*-methyl-D-aspartate (NMDA) receptor signaling, which can modulate intracellular signaling in postsynaptic cells. **b** “Intracellular zinc signaling” is the result of extracellular stimuli via their receptors, which generally can be divided into two groups depending on the timescale in which it operates. *i* “Fast or early zinc signaling” occurs within seconds or a minute after the extracellular stimulus. In fast or early zinc signaling, intracellular free zinc is influxed from the extracellular space or released from intracellular zinc stores, such as the endoplasmic reticulum (ER), Golgi, and some vesicles, by zinc transport proteins, including ZIPs (Zrt, Irt-like proteins), AMPAR, and L-type calcium channels. Furthermore, zinc is released from cytosolic zinc-binding proteins such as metallothionein (MT), which can be triggered by oxidative stimuli. The increased intracellular free zinc functions as an intracellular second messenger as does Ca. *ii* “Late zinc signaling” occurs in the timescale of hours. In late zinc signaling, extracellular stimuli induce transcriptional regulation of zinc transport proteins including ZIPs and ZnTs (Zn transporters). This regulation can contribute to the alteration in intracellular zinc concentrations and zinc distribution across the cellular membrane, leading to regulation of downstream signaling pathways. All types of zinc signaling modulate a wide variety of biological responses such as cell proliferation, cell migration, cell survival, cell death, cell differentiation, cell development, cell secretion

Zinc signaling occurs via alterations in zinc concentrations in both extracellular and intracellular sites. It contributes to multifarious physiological and pathological processes, and the mechanisms underlying zinc signaling events have begun to be elucidated at the molecular level. Thus, it is very timely to review the extensive functions of zinc signaling. This book has 15 chapters that give a comprehensive understanding of the current knowledge of zinc signaling in physiology and pathogenesis. As an introduction to the book, zinc signaling is briefly overviewed from several different perspectives.

## 1.2 “Extracellular” Versus “Intracellular”

Zinc signaling can fall into two classes from the perspective of the location where it occurs: one is extracellular zinc signaling, and the other is intracellular zinc signaling (Fig. 1.1). The former has been extensively investigated in synaptic transmission in the central nervous system (CNS) (see Chaps. 4, 8, and 9), where zinc released in synaptic clefts from presynaptic neurons can modulate neurotransmitter functions via a number of receptor channels and transporters on postsynaptic neurons through its zinc-binding sites (Frederickson et al. 2005; Sensi et al. 2009). Besides synaptic transmission, zinc released with insulin from pancreatic  $\beta$  cells reduces insulin secretion from the  $\beta$  cells and suppresses insulin clearance in the liver (see Chap. 13). Thus, extracellular zinc signaling mediates communication between cells in an autocrine, paracrine, or endocrine fashion. For sensing extracellularly released zinc, zinc receptor (ZnR), which is identical to G protein-coupled receptor 39 (GPR39), is important (see Chap. 6).

Intracellular zinc signaling, which plays a role in a great number of cell types, has been extensively investigated in immune cells (see Chaps. 10 and 11). In the cytosol, zinc functions as a second messenger of extracellular signals similarly to Ca. The “zinc wave,” which has been identified as zinc release from the perinuclear area including the endoplasmic reticulum (ER) in antigen-stimulated mast cells (Yamasaki et al. 2007), is well known (see Chap. 5). Release of zinc from proteins with zinc-thiol/disulfide coordination such as metallothionein (MT) is thought to contribute to intracellular zinc signaling (see Chaps. 2 and 4). In intracellular zinc signaling, a number of molecular targets have been identified, including protein tyrosine phosphatases (PTPs), phosphodiesterases (PDEs), caspases, and kinases (Huber and Hardy 2012; Wilson et al. 2012). In oocytes, zinc is taken up during the final stage of maturation, and then released into the extracellular milieu on fertilization, which is named the “zinc spark.” Zinc spark decreases intracellular zinc content, thereby contributing to regulation of cell signaling (see Chap. 15).



### 1.3 “Membrane Transport Protein-Mediated” Versus “Cytosolic Protein-Mediated”

Alteration of zinc concentrations initiates zinc signaling; therefore, zinc transport proteins have critical roles in this process (see Chap. 3). ZIP (Zrt, Irt-like protein) and ZnT (Zn transporter) transporters are the major two zinc transport proteins and thus have crucial roles in zinc signaling (see Chaps. 12 and 14). Both transporters are localized to the plasma membrane and membranes of the intracellular compartments, which indicates that zinc is mobilized between the extracellular space or the lumen of intracellular compartments and the cytosol across cellular membranes. In addition to ZIPs and ZnTs, it has been shown that other membrane transport proteins are involved in triggering zinc signaling (see Chaps. 3 and 5).

An alternative mechanism of zinc signaling is by zinc release from proteins with oxidation-sensitive zinc-binding sites in the cytosol, which is triggered via oxidative signaling (see Chap. 2). However, zinc released by oxidative stress can be involved in deleterious signaling pathway (see Chap. 4). Most likely, cooperative regulation of zinc signaling by zinc transport proteins and cytosolic proteins such as MT is required for crucial roles in physiology.

### 1.4 “Fast” and “Early” Versus “Late”

Extracellular stimuli can increase or decrease the cytosolic concentration of labile zinc within minutes or several hours (Fig. 1.1). Thus, intracellular zinc signaling can also be classified into several classes according to the timescale in which it acts (see Chap. 10). Zinc signaling occurring within minutes is termed “fast” or “early” zinc signaling. Fast or early zinc signaling does not need transcription of proteins (reviewed by Hirano et al. 2008; Haase and Rink 2009, 2014; Fukada et al. 2011). Fast zinc signaling occurs within seconds to a minute, and early zinc signaling, for example, a “zinc wave,” occurs within minutes after triggering; in both cases, zinc ions serve as a type of second messenger (see Chaps. 5 and 10). The other type of zinc signaling, which requires transcription of zinc transport proteins including ZIP and ZnT transporters, occurs on a timescale of hours. This type of zinc signaling is termed “late” zinc signaling. In late zinc signaling, local zinc homeostasis is changed in zinc concentrations and distribution by changes of expression levels of zinc transport proteins in response to various stimuli such as cytokines and lipopolysaccharide (Kambe 2013). Thus, late zinc signaling is important as homeostatic control mechanisms.

## 1.5 Conclusions

The increasing body of evidence clearly reveals that zinc signaling is essential for life, but it is also clear that recent findings represent the very tip of the iceberg. Zinc signaling is essential for human physiology, and its dysfunction likely causes health deterioration and diseases including cancer, inflammatory diseases, diabetes, and neurodegenerative diseases, as shown in this book. There are still many questions and ongoing discussions in the field of zinc signaling. However, novel techniques, such as genetically encoded fluorescent sensors (see Chap. 7), will contribute to clarifying those questions and discussions, similarly to the case of small fluorescent probes, which have greatly contributed to detecting and monitoring both extracellular and intracellular zinc signaling (Nolan and Lippard 2009).

This book is the first one to extensively review zinc signaling. Readers will enjoy each chapter with interest and find that zinc signaling definitely goes mainstream!

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## Chapter 2

# Molecular Aspects of Zinc Signals

Wolfgang Maret

**Abstract** Zinc ions ( $\text{Zn}^{2+}$ ) have chemical properties that make them ideally suited to carry biological information in intracellular and intercellular communication. Such zinc signaling has much in common with calcium signaling in terms of fast binding in coordination environments of proteins, but there are also important differences between the two metal ions. Biological control with zinc occurs at much lower metal ion concentrations. Zinc ions bind with higher affinity and hence dissociation rates are slower, resulting in longer-lasting biological effects. Selectivity of coordination environments is different as zinc employs oxygen, nitrogen, and sulfur donors from ligands whereas calcium binds almost exclusively to oxygen donors. Zinc and calcium ions are redox inert but sulfur donors in zinc/thiolate coordination environments confer redox activity, thereby linking zinc metabolism and redox metabolism. In humans, 24 zinc transporters and more than 12 metallothioneins exert precise control over cellular zinc homeostasis, cellular redistribution, and transients of zinc ions that are used for biological regulation. Zinc ions are stored in subcellular compartments and released by different stimuli. Rises in cytosolic  $\text{Zn}^{2+}$  concentrations target proteins and affect a variety of cellular processes, such as phosphorylation signaling and gene expression. Zinc signaling complements and interacts with calcium signaling and redox signaling and is an integral part of the cellular signal transduction network. It has fundamental importance for health and disease.

**Keywords** Zinc • Zinc buffering • Zinc homeostasis • Zinc muffling • Zinc signaling

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## 2.1 Historic Perspective: The Emerging Role of Zinc Ions in Cellular Control

Through its catalytic and structural functions in about 3,000 human proteins, zinc is associated with about 10 % of all proteins and affects most aspects of cellular biology (Andreini et al. 2006; Rink 2011). The concept that zinc has regulatory functions in multicellular organisms enhances its importance even further. The concept is recent but rooted in rather early reports. One relates to the transcription factor MTF-1 (metal regulatory transcription factor-1), which senses increased cellular zinc concentrations and mediates zinc-dependent gene expression (Günther et al. 2012). The other is the discovery of autoradiographically detectable zinc in certain parts of the brain (hippocampus), which was found to be *zinc ions* ( $Zn^{2+}$ ) stored in a yet to be defined chemical form in synaptic vesicles of specific zinc-rich neurons and secreted into the synaptic cleft when these neurons are stimulated. Acting like a classical neurotransmitter in these specialized neurons, the zinc ions affect presynaptic and postsynaptic physiology (Frederickson et al. 2005; Sensi et al. 2009; Takeda et al. 2013). These discoveries expanded into fields other than neurobiology when zinc ions were detected autoradiographically in other organs and tissues (Danscher and Stoltenberg 2005). It is now known that cells sequester zinc ions in cellular vesicles (“zincosomes”) and other organelles and that this is a way for the cell to store zinc and to make it available for specific processes. This aspect is different from iron metabolism, where ferrous ions are oxidized to ferric ions and stored in the protein ferritin. In addition to the specialized neurons, a variety of cells secrete zinc ions by vesicular exocytosis (Box 2.1). This process differs from merely exporting zinc, which is an activity of zinc transporters in every cell. The presence of subcellular pools of zinc ions was verified and thus became a much more general issue. Investigations then began to address the functional significance of the zinc ions that are not bound to proteins.

### Box 2.1 Cells Secreting Zinc Ions

- Pancreatic  $\beta$  cells and acinar cells
- Prostate epithelial cells (tubuloacinar cells)
- Mammary gland epithelial cells
- Epididymal epithelial cells
- Paneth cells (crypts of Lieberkühn)
- Somatotrophic cells (pituitary gland)
- Osteoblasts
- Platelets
- Mast cells
- Granulocytes, neutrophils
- Fertilized oocytes

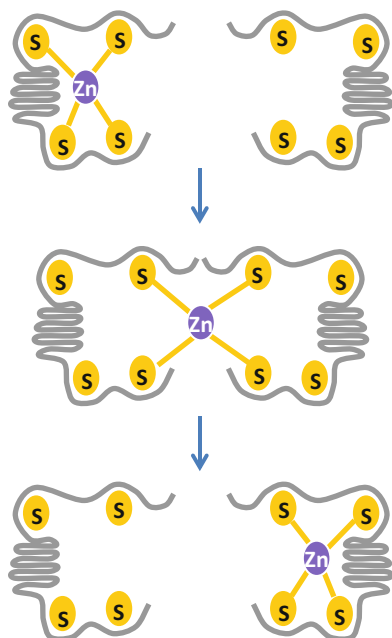
Numerous experiments demonstrated that changing zinc in cells by either adding zinc ions extracellularly or by removing them with chelating agents affects multiple signaling pathways (Beyersmann and Haase 2001). These observations gain new significance as they mimic the events that occur when transients of zinc ions are induced intracellularly. There has been an initial focus on immune cells (Hirano et al. 2008; Haase and Rink 2014), but the field is rapidly moving into investigations of other cell types (Fukada et al. 2011; Taylor et al. 2012a). In particular, with the advent of fluorescent chelating agents (“probes”) for detecting cellular zinc ions and their fluctuations it became known that zinc ions are intracrine, paracrine, and perhaps even endocrine signals. With this abbreviated account of the origins of the field, three principles are now recognized for the ways cellular zinc ions are made available for signaling functions:

1. Vesicular exocytosis
2. Opening of gated channels on vesicular/organellar stores and the plasma membrane
3. Modification of zinc/thiolate coordination environments in proteins

The first two principles involve zinc in vesicles whereas the third involves zinc in proteins.

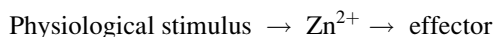
In this chapter, I discuss the molecular framework that makes signaling with zinc ions possible. To understand zinc signaling, it is critical to address and define the meaning of the terms “zinc ions” and “zinc signals.” These terms are used with ambiguity in the literature. Biologists tend to refer to “zinc,” but what they mean is chemically the zinc ion. Zinc(II) ( $\text{Zn}^{2+}$ ) is the only valence state of zinc in biology. Implied in signaling are free zinc ions that are not bound to proteins. Zinc in proteins is also in the form of zinc ions but tightly bound and hence not free. This distinction is the only basis for the term “free,” and the term does not refer to an absence of coordinating ligands. There is presently no method to examine the chemical speciation of zinc at the low concentration of free zinc ions in the cytosol or in organelles, and therefore it is not a foregone conclusion that the main species is the hydrated ion  $\text{Zn}(\text{H}_2\text{O})_6^{2+}$ . Spectroscopic analysis of zinc in cellular vesicles, where the free zinc ion concentrations are considerably higher, demonstrated interactions with ligands other than water (Wellenreuther et al. 2009). In vesicular exocytosis, zinc ions with their ligands move to an environment with a different pH value. Whether ligand exchange occurs after exocytosis is not known. Free zinc ions may have different ligands and concentrations in the cell (“i”, intracellular), outside the cell (“e”, extracellular) and in organelles (“o”, organellar), and therefore the concentrations of zinc ions in the different pools are referred to as  $[\text{Zn}^{2+}]_{\text{i,e,o}}$ . An alternative to low molecular weight complexes of zinc ions being diffusible signals would be that zinc signaling occurs via protein-mediated zinc transfer without the ion ever being free (Fig. 2.1). Such interprotein associative zinc transfer has been observed in vitro (Maret et al. 1997). However, aside from metallothioneins, metallochaperones for such zinc delivery to another protein are not known. Given the large number of structurally diverse zinc proteins, associative zinc transfer is unlikely to be the general case for zinc redistribution as it would require too many

**Fig. 2.1** Zinc/thiolate coordination environments as conduits for zinc transfer. Zinc ions can be transferred between two proteins by swapping ligands (associative mechanism). Zinc ions are never free in this reaction. Sulfur donors are particularly well suited for such reactions



chaperones for recognition of all the different zinc proteins, in contrast to copper, the most competitive ion in the Irving–Williams series (see following), which is controlled by chaperones. The fact that free zinc ion concentrations and fluctuations can be measured and that they have functions at rather low concentrations makes them not negligible and supports the role of dissociative mechanisms in zinc signaling. Such mechanisms of redistribution do not exclude the participation of other, low molecular weight ligands as such ligands have been shown to accelerate the rate of zinc removal from proteins (Jacob et al. 1998; Chong and Auld 2007).

Under which conditions zinc ions become “zinc signals” also needs further consideration as the term zinc signaling is being used quite broadly. I suggest that one uses the analogy with the classic signaling metal ion  $\text{Ca}^{2+}$  to define zinc signaling (Table 2.1) and then focuses on the differences between the two ions, namely, characteristics of zinc such as its binding to sulfur and its higher affinity for proteins and other ligands. As for calcium signaling, the term zinc signaling should be used for fast processes, induced transients of zinc ions, and subsequent binding to an effector.



This sequence does not exclude MTF-1 from participating in zinc signaling, but it is the rapid activation of MTF-1 as the direct result of a zinc signal rather than the slower consequence of this activation resulting in changes in mRNA and protein abundance.

**Table 2.1** Comparison of calcium and zinc signals

Ca <sup>2+</sup>		Zn <sup>2+</sup>
<i>Dissimilar:</i>	<i>Similar:</i> Subcellular stores involved in release Buffers and mufflers Plasma membrane receptor	<i>Dissimilar:</i>
Outward gradient		Inward gradient
O coordination environments		O, N, and S coordination environments
e.g., calmodulin (O chemistry)		e.g., metallothionein (S chemistry)
		Chemical mechanism of release
Short duration of effects		Long duration of effects
Transients >100 nM		Transients >100 pM
Mostly activation of processes		Mostly inhibition of processes

One finds terms such as labile zinc, mobile zinc, or rapidly exchanging zinc in the literature. These terms imply different characteristics of zinc or lack a chemical definition altogether. In fact, they may prevent understanding the molecular basis of zinc ion signals. I believe it is best practice to use one operational definition such as free zinc to refer to zinc ions that are not bound to proteins, albeit with the notion that the coordination environment of the zinc ions is not defined. How strongly proteins bind zinc and how zinc is buffered determine the concentrations of these free zinc ions.

## 2.2 Control of Zinc Ions

### 2.2.1 Zinc Buffering

The concepts of free zinc and zinc signaling are intricately linked to metal buffering. Metal buffering is treated as is pH buffering. In the same way that one defines a pH value (hydrogen potential,  $\text{pH} = -\log [\text{H}^+]$ ), one defines a pZn value (zinc potential,  $\text{pZn} = -\log [\text{Zn}^{2+}]$ ). pH is determined by the  $\text{p}K_a$  of the buffering acid–base pair (1), and pZn is determined by the  $\text{p}K_d$  of the buffering ligand(s) (2):

$$(1) \text{pH} = \text{p}K_a + \log ([\text{A}]/[\text{AH}])$$

$$(2) \text{pZn} = \text{p}K_d + \log ([\text{L}]/[\text{ZnL}])$$

For the most part, the zinc buffering ligands in biology are the coordinating side chains of proteins (Asp, Glu, His, Cys). The dissociation constants ( $\text{p}K_d$ ) for *cytosolic* zinc proteins are picomolar,  $\text{pZn} = <9$  and  $>12$  (Maret 2004a; Krężel and Maret 2008), although some may be lower, as discussed later. Thus, on the

basis of equilibrium constants, the concentrations of free zinc ions should also be picomolar. One could argue that biomolecules other than proteins contribute to zinc buffering. Many biomolecules bind zinc (free amino acids, carboxylic acids, peptides such as glutathione, ATP, etc.). However, these biomolecules do not bind zinc as tightly as proteins and hence it is unlikely that they contribute significantly to zinc buffering, at least not in binary or 1:1 complexes. To examine this point, the analogy to pH buffering is again helpful. A buffer with a different  $pK_a$  value contributes to a buffer at a given  $pK_a$  only if higher concentrations compensate for the differences in  $pK_a$  values. As we are concerned with logarithmic scales, one  $pK_a$  unit would need to be compensated by one order of magnitude in concentrations. Thus, ligands with different  $pK_d$  values would contribute to zinc buffering only at much higher concentrations. For zinc-binding biomolecules with lower  $pK_d$  values, such as those just mentioned, high concentrations would be required to contribute to physiological zinc buffering. An equally important consideration is how strongly zinc is buffered: this is *not* an issue of the  $pZn$  value but an issue of the *buffering capacity at the particular  $pZn$  where zinc is buffered*.

### 2.2.2 Zinc-Buffering Capacity

There is considerable uncertainty in the literature regarding cellular zinc-buffering capacity because it is often assumed to be high as a result of the many ligands that *potentially* bind zinc. It is not the buffering capacity that keeps the free zinc ion concentrations low but the affinity of the ligands. The buffering capacity determines how resistant the  $pZn$  is to change.

It is often remarked that “zinc is tightly/strongly buffered” when investigators mean that there is very little free zinc. The low free zinc ion concentrations are a consequence of the high-affinity binding sites in proteins, not the buffering capacity. Tight and weak buffering refers primarily to the buffering capacity, *which is not high as it allows  $pZn$  fluctuations to occur*. We determined the cellular buffering capacity at the physiological  $pZn$  to be only about 10 % of the total zinc ion concentrations of a few hundred micromolar (Krężel and Maret 2006). This finding has important consequences as it means that some coordination sites with high affinity for zinc are not occupied at physiological  $pZn$  and can bind zinc when free zinc ion concentrations increase. These sites determine physiological zinc buffering. Overall, the zinc-buffering capacity of all the ligands is high, but it is not relevant. Zinc is (and must be) buffered at a particular physiological  $pZn$ , and only the buffering capacity of the ligands that control this  $pZn$  is important. If the buffering capacity were high at physiological  $pZn$ , zinc signaling could not occur as any zinc signal would be quenched immediately. Changes in  $pZn$  are necessary for zinc signaling to occur. Thus, the cytosolic zinc-buffering capacity and the physiological  $pZn$  are major determinants for the role of zinc ions in signaling.



### ***2.2.3 The Role of Zinc Transporters: Muffling***

Transporters bring zinc ions into the cell and into cellular compartments or export them from the cell and from these compartments. Transport processes also contribute to biological metal ion buffering and have been referred to as muffling in the calcium field (Thomas et al. 1991). Muffling zinc ions increases the cellular zinc-buffering capacity because it removes an excess of cytosolic zinc ions (Colvin et al. 2010). Thus, what we see as buffering in a cell is a combination of (thermodynamic) buffering by ligands and (kinetic) muffling by transporters. The contribution of transporters in muffling depends on their transport characteristics and the capacity of intracellular stores. Very little quantitative information is available to define these parameters that determine the timescale, frequency, and amplitudes of zinc signals.

Computational approaches in combination with experimental data have been used to model muffling and zinc transients in neurons (Colvin et al. 2008). It became evident that a steady-state buffer model is not sufficient to explain how cells handle extracellular zinc loads, which can mimic cellular transients of zinc ions. A cellular protein that binds zinc and delivers it to a store was required. One molecule that satisfies the required characteristics is metallothionein (MT). A dual role in buffering and muffling zinc, that is, transporting zinc for the delivery to a store, resolves the issue that the concentrations of MTs are generally not high enough to account for the overall cellular zinc-buffering capacity.

This discussion explains why changing the cellular zinc muffling and buffering capacities and hence the  $pZn$  but not the total zinc concentration allows zinc redistribution.

### ***2.2.4 Quantitative Measurements***

A quantitative approach is needed to define signaling with zinc ions. Total cellular zinc concentrations are rather high, that is, a few hundred micromolar. However, the free zinc ion concentrations ( $pZn$ ) are picomolar, about six orders of magnitude lower. Free zinc ion concentrations have been estimated and reported in two classic articles. One considers that zinc inhibits muscle phosphoglucotomutase, a magnesium enzyme, with high affinity for zinc in vitro (Peck and Ray 1971). For the enzyme not to be zinc inhibited in muscle, the free zinc ion concentration must be less than 32 pM (Ray 1969). It is noteworthy that this consideration merely sets a limit on the enzyme being fully active but it leaves the possibility that free zinc ion concentrations are indeed higher than 32 pM in muscle tissue and modulate the activity of this enzyme. In the other article, free zinc ion concentrations of 24 pM in erythrocytes have been determined (Simons 1991). One expects  $pZn$  values in this range on the basis of the affinity of zinc proteins for zinc. With the advent of new molecular probes for zinc ions, that is, chelating agents that become highly fluorescent when binding zinc, picomolar values of free zinc were confirmed in different cell lines,

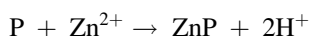
although the reported values vary between tens and hundreds of picomolar (Krężel and Maret 2006; Bozym et al. 2006; Vinkenborg et al. 2009; Qin et al. 2011). Zinc sensors based on the zinc enzyme carbonic anhydrase measure 5–10 pM, but other protein sensors as well as low molecular weight probes measure hundreds of pM (see table 1 in Maret 2013a). Any probe or sensor that is brought into the cell to measure free zinc contributes to zinc buffering and *lowers free zinc ion concentrations*. We have measured this effect as a function of different probe concentrations and applied an extrapolation to a zero probe concentration to correct for the additional buffering of the probe, and indeed found higher free zinc ion concentrations in the absence of the probe (Krężel and Maret 2006). Some investigators refer to the zinc ions that the probes measure as labile zinc. When extrapolation is applied, the zinc measured cannot be labile because there is no probe to remove zinc from other ligands. The term labile zinc should not indicate that zinc bound weakly to proteins coexists with tightly bound zinc in the same cellular compartment. The free zinc ion concentration determined in the absence of a probe is simply the result of existing equilibria. Tightly bound zinc can be kinetically labile, however. For example, MT binds zinc tightly but the sulfur ligands allow fast exchange with other zinc/thiolate coordination environments (Maret et al. 1997). Measured cellular pZn values indicate that predictions based on zinc-binding affinities of proteins are valid and that there is no buffering increment from other biomolecules that would lower the free zinc ion concentration further.

Although consensus is building regarding cellular (cytosolic) pZn values and zinc-buffering capacity, pZn values in different subcellular compartments are just beginning to be defined. Estimates are 0.9 pM for the endoplasmic reticulum (ER), 0.2 pM for the Golgi (Qin et al. 2011), 0.2 pM for the mitochondrial matrix (McCranor et al. 2012), and 0.14 pM for mitochondria (Park et al. 2012). However, there is a fundamental issue with these concentrations as well as those given for small structures such as erythrocytes. Taking the proton as an example, calculations demonstrate that there are limits to volumes and concentrations where there is essentially no longer a single free ion (Bal et al. 2012a). In other words, given the same concentrations for a larger volume such as the cell and for a much smaller volume such as an organelle leads to a seemingly unrealistically small number of ions in the latter.

Few data exist on extracellular free zinc ion concentrations. Experimental estimates are about 200 pM for horse blood plasma (Magneson et al. 1987), suggesting there is virtually no gradient between extracellular and intracellular free zinc. With higher total intracellular (>100  $\mu$ M) than extracellular (<10  $\mu$ M) zinc concentrations, one wonders about the source of energy to transport zinc into the cell against this gradient. However, recent examination of human blood plasma revealed free zinc concentrations of about 500 nM (Maarten Merckx, personal communication). This finding has important implications as it allows zinc binding to serum albumin, which has an apparent zinc-binding constant of about 100 nM (Ohyoshi et al. 1999; Bal et al. 2012b). Such zinc ion concentrations are also in the range for free zinc to be considered as the substrate of zinc transporters. For example, zebrafish ZIP1 has a  $K_m$  value for zinc of less than 500 nM (Qiu et al. 2005).

The necessity of buffering zinc in cells with resulting picomolar free zinc ion concentrations becomes evident when considering the properties and the control of

other essential metal ions. A fundamental principle in inorganic chemistry, the Irving–Williams series (Irving and Williams 1948), describes relative binding affinities of divalent transition metal ions and the free metal ion concentrations resulting from binding equilibria. For the cell to keep the biochemistry of metal ions separated from each other, every metal ion needs to be controlled in a specific range of pM. Without such control, the more competitive ions such as zinc and copper would bind to sites that need to be occupied by the less competitive ions. There is no free ranging of metal ions over concentrations needed for the control of other metal ions. According to the Irving–Williams series, the affinity of the biologically relevant divalent metals ions to the same ligands is  $\text{Mn} < \text{Fe} < \text{Co} < \text{Ni} < \text{Cu} > \text{Zn}$ ; that is, zinc is the most strongly bound divalent ion after copper. Thus, for the binding equilibrium



with picomolar affinities of the proteins (P), picomolar free zinc ion concentrations result. There is a scarcity of data about how greatly the affinities of zinc proteins for zinc differ. If there were sites with more loosely bound zinc, there would be considerable dissociation of zinc, loss of function, and interference with the functions of other metal ions. There is no evidence for a hierarchy in such a way that some proteins yield their zinc under zinc deficiency to preserve the functions of other, potentially more essential zinc proteins. Some proteins bind zinc more strongly, with femtomolar affinities for zinc (Sikorska et al. 2012). The reason for this could be that at very low protein concentrations, such as for low abundance zinc proteins, zinc would dissociate if the binding were not strong enough, thereby compromising the function of the protein.

First principles also relate free zinc ion concentrations to biological events. It has been estimated that it would take about 14 h for a zinc enzyme to obtain its zinc at a concentrations of 1 pM free zinc and with a comparatively fast on-rate (Heinz et al. 2005). Clearly, if free zinc concentrations were so low—as they appear to be in some cellular compartments (see earlier)—they could not serve as a source of zinc for enzymes unless low molecular substances enhance the transfer rates (see foregoing) (Heinz et al. 2005). Measured free zinc ion concentrations in the range of a few hundred picomolar, however, are sufficient for association rates on a biologically relevant timescale, in the range of seconds. Of course, this argument also applies to zinc signaling: Zinc ion concentrations need to be at least a few hundred picomolar to affect proteins sufficiently rapidly.

Zinc sites of most zinc proteins seem to be fully occupied with zinc. It would be a significant waste of energy to synthesize a large protein and then not have the zinc available for function. How the synthesis of a zinc protein and the supply of zinc are coordinated and how, when, and where zinc proteins acquire their zinc is not known. There is no experimental evidence that mononuclear sites in zinc proteins are regulated by zinc ion fluxes. The evidence is less clear for enzymes with a second, co-catalytic zinc. These enzymes could be regulated through zinc ion fluctuations. Zinc regulation must occur above the free zinc ion concentrations

that keep zinc proteins saturated. Regulation also requires mechanisms that restore the steady-state free zinc ion concentrations after transients have occurred.

Several investigators attempted to quantify *global* fluctuations of intracellular free zinc ion concentrations. The fluctuations are a few hundred picomolar above the steady-state concentrations of free zinc ions and may reach about one nanomolar (Table 2 in Maret 2013a). For example, when cells are deprived of extracellular zinc, they have a way of mobilizing zinc ions intracellularly (Li and Maret 2009). Also, synchronized rat pheochromocytoma (PC12) cells increase their free zinc ion concentrations at two stages during the cell cycle (Li and Maret 2009). Generally, fluctuations have been measured in different states of a cell and rarely in real time. Hence, the time period over which changes develop and persist is largely unknown.

However, *local* free zinc ion concentrations are expected to be significantly higher. They could establish microdomains akin to those in calcium signaling. Induced local zinc ion transients seem to be fast acting not to act pleiotropically or change gene expression. Although the transients are likely short lived, the effects are expected to be long lasting. Again, first principles support this prediction. With high affinity for zinc and fast on-rates, the corresponding off-rates must be slow. For example, the half-life for zinc dissociation from carbonic anhydrase with a  $pK_d$  of 11.4 (pH 7.0) is about 250 days (Ippolito et al. 1995). Of course, carbonic anhydrase is not thought to be regulated by zinc. Because proteins that are targets of fluctuating zinc ions have affinities that are not significantly lower than those of genuine zinc proteins (see following), the off-rates, and hence the duration of zinc signals, are still of the order of many hours or even days. Thus, zinc signaling is expected to elicit long-lasting effects, which is in contrast to calcium signaling. Overall, this interpretation is consistent with zinc ions being inhibitory for cellular functions (Williams 1984) and being involved in long-term adjustments of the state of a cell, such as growth, differentiation, and survival.

Genuine zinc ion signals are to be distinguished from global changes to a different steady-state concentration of free zinc ions ( $pZn$ ). For example, growth-arrested, proliferating, differentiating, and apoptotic intestinal epithelial cancer cells (HT-29) all have different  $pZn$  values (Krężel and Maret 2006), which seem to be the consequence of adjustments in buffering rather than changes in total zinc concentrations. If changes of total zinc were responsible for such adjustments, unreasonable large fluctuations in the range of hundreds of micromolar zinc would be required. Global adjustments of buffering can be brought about by changes of redox potentials that may affect specific redox pairs coupled to zinc binding and release. About 30 % of the zinc-buffering capacity at physiological pH depends on sulfur (thiol) donors and therefore is redox sensitive (Krężel et al. 2007). Changing the expression of zinc homeostatic proteins such as ZnT1 and MT, which are controlled by MTF-1, also changes zinc buffering. The dynamics of the MT pool is an example of how zinc buffering and  $pZn$  are interrelated. In different states of HT-29 cells, concentrations of total zinc, free zinc, metallothionein, buffering capacity, and the redox state are correlated (Krężel and Maret 2006). Changed buffering increases or decreases free zinc ion concentrations, and this is a cause for long-term adjustments. Indeed transcriptomics, and

more recently proteomics, investigations have shown extensive changes in protein expression profiles in response to zinc added to growth media or zinc removed by chelating agents.

### 2.3 Molecular Mechanisms of Proteins Involved in Cellular Zinc Homeostasis

In contrast to proteins that use zinc as a permanent cofactor, the proteins involved in regulating zinc (zinc transporters, metallothioneins, and MTF-1) and in being regulated by zinc have mechanisms for moving zinc and binding it reversibly in sites with coordination dynamics (Maret and Li 2009; Maret 2011a, 2012). MTF-1 has six zinc fingers ( $C_2H_2$  coordination of zinc: C = Cys, H = His) for DNA recognition, but it is neither entirely clear how they are involved together with a metal-responsive activation domain in zinc sensing nor whether free zinc ions are sensed in the cytosol before MTF-1 translocates to the nucleus (Laity and Andrews 2007; Günther et al. 2012). Three-dimensional (3D) structures of MTF-1 or any of the 24 mammalian zinc transporters [10 members of the ZnT family (SLC30A) and 14 members of the Zip family (SLC39A)] have not been reported and therefore there is virtually no insight into the transport and sensing mechanisms. However, detailed information about the sequences, biological regulation, and genetics of these transporters is available (Fukada and Kambe 2011). The number of zinc transporters is remarkable as homeostatic mechanisms for other metals ions such as iron and copper rely on only a few transporters. None of the mammalian zinc transporters uses ATP as a source of energy. The *Escherichia coli* YjiP protein, which belongs to the ZnT family, functions as a  $Zn^{2+}/H^+$  antiporter and has served as the only model for human ZnTs (Lu and Fu 2007). It has three different zinc-binding sites, all of which use oxygen (Asp/Glu) and nitrogen (His) donors; one is located between the transmembrane helices and one at the interface between the transmembrane domain and the cytoplasmic domain. The third site is binuclear and located between the dimer interface of the cytoplasmic domains. It is thought to be a sensor site of cytoplasmic zinc ion concentrations. Once zinc is bound at these sites, a conformational change of the protein occurs and triggers zinc transport. At present, it is not known whether transporters contribute directly to maintaining physiological pZn. If they do, they would need to have  $K_m$  values in the picomolar range, many orders of magnitude lower than their experimentally observed values. Alternatively, the substrates could be proteins that deliver zinc to the transporters by an associative mechanism. Which zinc complexes are the substrates for these transporters and which ligands receive zinc on the opposite side of the membrane is not known.

About a dozen human MT genes are expressed and participate in the control of cellular zinc homeostasis (Li and Maret 2008). Their zinc coordination involves exclusively zinc/sulfur (thiolate) interactions. They have been thought to store zinc, and there is an extensive literature about their possible functions as cellular antioxidants. At least two chemical properties of MTs and the molecular biology

of MT gene expression support a dynamic role in zinc metabolism. One is that MTs have different binding constants for the seven zinc ions. The zinc affinities of human MT-2 are in the range where zinc regulation takes place, allowing MTs to transport, accept, and donate zinc ions dependent on cellular conditions (Maret 2011b). Although four zinc ions are bound with affinities similar to those of other zinc proteins, two zinc ions bind less tightly and one zinc ion only with nanomolar affinity, making MT a protein that is not saturated with zinc at physiological pZn (Krežel and Maret 2007). These properties would allow MT to buffer zinc exactly in the range where such buffering is required. The second property is that MTs are redox-active zinc proteins. Zinc itself is redox inert and remains  $Zn^{2+}$ , and hence zinc proteins were generally not considered to be redox proteins. However, the oxidation of the sulfur donors of the cysteine ligands of zinc causes zinc dissociation whereas the reduction of cystines (disulfides) to cysteines (thiols) generates zinc-binding capacity (Maret and Vallee 1998). This property establishes a cellular redox cycle that links redox changes and the availability of zinc from MT and other proteins with zinc/thiolate sites (Chen and Maret 2001; Maret 2009). Because of the redox activity of the sulfurs, MTs are indeed “antioxidants”; however, any discussion of an antioxidant function needs to consider that MT is oxidized when it reacts with oxidants and releases zinc ions that are potent effectors at very low concentrations, and that the released zinc itself can have pro-antioxidant and pro-oxidant functions depending on its concentrations (Maret 2008a).

## 2.4 Stimulation of Zinc(II) Ion Fluctuations

This section focuses only on the three basic mechanisms of zinc release. The signaling pathways and proteins triggering or controlling zinc release are treated in considerable depth in other chapters of this book.

### 2.4.1 Vesicular Exocytosis and Paracrine Signals

Zinc transporters ZnT3, ZnT8, and ZnT2 load cellular vesicles with zinc in the brain, pancreatic  $\beta$  cells, and mammary epithelial cells, respectively, for exocytosis of zinc ions. Neither the concentration of zinc in the vesicles (millimolar?) nor the local concentration of released zinc (submicromolar?) is exactly known. Exocytotic vesicles have slightly acidic pH favoring free zinc ions, but once the zinc is exocytosed it is in an environment of higher pH, which favors zinc binding to proteins. Zinc ions secreted from neurons diffuse over a distance of 100  $\mu\text{m}$ , and the signal is eliminated within tens of seconds (Ueno et al. 2002). This investigation demonstrates the significance of the spatiotemporal characteristics of extracellular zinc signals and makes it an issue over which space and time measured zinc ion concentrations are averaged. Owing to their high affinity for proteins, free zinc ions

are “sticky” and, depending on the environment, only fleetingly existent, a phenomenon that has been referred to as a zinc “veneer” forming on the surface of cells (Nydegger et al. 2012). Zinc ions secreted from specific neurons are paracrine signals affecting postsynaptic events. Zinc secreted together with insulin from pancreatic  $\beta$  cells is discussed as an effector of pancreatic  $\alpha$  cells and, in addition, has been suggested to be an endocrine signal affecting blood insulin clearance by the liver (Tamaki et al. 2013). Potentially, there are many more functions for the zinc ions secreted from different cells (Box 2.1).

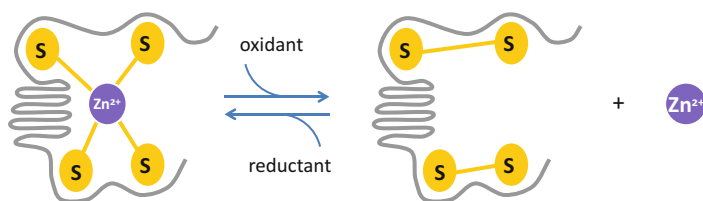
The release of zinc ions from fertilized mouse oocytes into the extracellular space follows calcium ion oscillations and has been referred to as “zinc sparks.” Whether this process involves vesicular exocytosis is not known. The role of zinc release is thought to be that the embryo needs to resume progression through the cell cycle upon fertilization; this happens after the oocyte has taken up significant amounts of zinc at the latest stage of maturation and became growth arrested after the first meiotic division (Kim et al. 2011).

#### ***2.4.2 Release from Intracellular Stores, Influx from the Plasma Membrane, and Intracrine Signals***

Stimulation of the macrophage immunoglobulin E Fc $\epsilon$ RI receptor and ERK/IP<sub>3</sub> signaling triggers first Ca<sup>2+</sup> and then Zn<sup>2+</sup> release from a vesicular store that ZnT2 loads with zinc (Yamasaki et al. 2007). The release has been referred to as a “zinc wave.” Intracellular zinc waves occur in minutes, whereas extracellular zinc sparks occur in seconds, demonstrating different dynamics of zinc signals. In neurons, the zinc store is also IP<sub>3</sub> sensitive (Stork and Li 2010). Growth factor stimulation of breast cancer cells leads to casein kinase 2-dependent phosphorylation of ZIP7, which opens an endoplasmic reticulum store for zinc release (Taylor et al. 2012b). Similarly, lysosomal zinc release in interleukin 2-stimulated T cells is a required signal for proliferation (Kaltenberg et al. 2010). Several ZIP transporters of the LIV-1 family also seem to trigger zinc signals from their location at the plasma membrane. For instance, N-terminal proteolytic cleavage of ZIP6 leads to translocation to the plasma membrane and zinc influx (Hogstrand et al. 2013). Given the high inward gradient of total zinc, it is unclear how the extracellular zinc is provided and what transport mechanism is involved.

#### ***2.4.3 Redox Mechanisms***

An alternative way to releasing zinc by opening a subcellular store is oxidative signaling in the cytosol. The basis for this zinc release mechanism is the bonding of zinc to sulfur donors in thiolate coordination environments and sulfur



**Fig. 2.2** Zinc/thiolate redox switches. Zinc/thiolate (Cys) coordination environments can react with oxidants resulting in the oxidation of sulfur (to disulfides for example, as shown here) and the release of zinc ions. Reduction of the disulfide regenerates zinc-binding capacity. In this way, redox signaling or changes of specific redox pairs can modulate free zinc ion concentrations and the function of proteins that lose their zinc and others which are targets of the released zinc. These reactions are not restricted to zinc in tetrathiolate sites

ligand-centered redox activity (Maret 2004a, 2006) (Fig. 2.2). The chemistry is specific for sulfur and does not occur in calcium coordination environments. It involves different oxidation states of sulfur, not only thiol–disulfide equilibria, in reactions with a host of physiologically significant reactive oxygen, nitrogen, and sulfur species, reactive carbonyls, and reducible selenium compounds (Chen and Maret 2001; Hao and Maret 2006).

Zinc/thiolate sites, such as those in MTs, are molecular switches operating under many pathophysiological conditions where reactive species release zinc ions that become cytotoxic, for example, for neurons (Aizenman et al. 2000). These switches are also indicated under physiological conditions where a redox signal is transduced into a zinc signal. Particular emphasis has been given to nitric oxide (NO) signaling. Metallothionein has been shown to be the source of intracellularly released zinc ions in endothelial cells, in bradykinin-induced NO signaling, and in cytokine-induced iNOS-dependent NO signaling that causes an intranuclear rise in zinc ions (Pearce et al. 2000; Spahl et al. 2003). A variety of G protein-coupled receptors generate a redox signal that then releases zinc for signaling (Sanchez-Blazques et al. 2012). Thus, in oxidative signaling associated zinc signals must be considered. Zinc protects specific redox-sensitive thiols and initiates specific responses by inhibiting enzymes or activating gene expression as part of an antioxidant response.

## 2.5 Targets of Free Zinc Ion Transients

Knowledge of pZn values and matching affinities of proteins targeted by transient or permanent rises in free zinc ion concentrations becomes critical when distinguishing physiological from pathophysiological changes. Only above their steady-state levels can zinc ions bind to additional proteins and modulate their biological activities. Zinc inhibits some enzymes with nanomolar affinities



(Maret et al. 1999). These proteins are generally not recognized as zinc enzymes because they are isolated with chelating and reducing agents to preserve their enzymatic activity. When investigating zinc inhibition, two methodological issues need to be addressed. First, zinc-buffered solutions should be employed to control free zinc ions at such low concentrations, and second, because the inhibition is assayed by enzymatic activity, only apparent  $K_i$  values will be obtained if the inhibition is competitive with respect to substrate. A full kinetic analysis is then required to determine  $K_i$  values. In the case of receptor protein tyrosine phosphatase beta, the inhibition is so strong (21 pM) that it suggests tonic inhibition of the enzyme (Wilson et al. 2012). With free zinc ion concentrations of 24 pM in human erythrocytes (Simons 1991), zinc inhibition of human erythrocyte  $\text{Ca}^{2+}$ -ATPase with a  $K_i$  of 80 pM (pH 7.4) also indicates at least partial inhibition under physiological conditions (Hogstrand et al. 1999). The affinities of proteins that are targets of free zinc ions are therefore only slightly lower than those of zinc enzymes, suggesting an important principle: whereas zinc enzymes need to be activated by binding zinc, the zinc-inhibited enzymes need to be activated by removing zinc (Maret 2013b). The number of enzymes that zinc inhibits is not known and will depend on the exact magnitude of zinc ion fluctuations and whether global changes or local transients are involved. Enzymes may be inhibited tonically or their activity modulated, and inhibition with zinc may occur under physiological or pathophysiological conditions. Zinc inhibits many thiol-dependent enzymes (protein tyrosine phosphatases, caspases, and cathepsins) and other enzymes that have diads or triads of catalytic His, Glu(Asp), and Cys residues as binding sites for metal ions (Maret 2013b). How zinc-inhibited cytosolic enzymes are reactivated is not known. In vitro investigations suggest that the activation involves zinc removal by thionein, the apoprotein of MT. A common observation is that zinc enhances tyrosine phosphorylation signaling. In most instances, the effect can be explained with phosphatase inhibition rather than kinase activation. Colocalization of protein tyrosine phosphatases, receptors, and zinc transporters/channels provides a way for zinc microdomains and gradients to modulate signaling complexes. Although enzyme inhibition is emerging as one principle of zinc signaling, there may be others, such as enzyme activation or modulating protein-protein interactions (Maret 2004b). In as much as it is discussed that ER-released calcium affects mitochondria, ER-released zinc could also have a significant effect on mitochondrial respiration (Ye et al. 2001).

Secreted zinc ions affect intercellular zinc signaling. Zinc ions released from zinc-rich neurons into the synapse inhibit the NMDA (*N*-methyl-D-aspartate) receptor postsynaptically. The inhibition constant is less than 10 nM (pH 7.3) (Paoletti et al. 1997). Zinc affects many other receptor proteins but affinities for zinc are often not known.

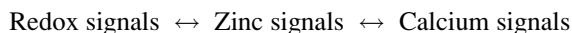
Another regulatory function, but not a zinc signal, relates to the zinc inhibition of enzymes secreted from cells. Micromolar zinc ion concentrations inhibit the zinc enzyme bovine carboxypeptidase A at a second zinc-binding site ( $K_i = 0.5 \mu\text{M}$ ) and serine proteases such as kallikreins with inhibition constants ranging from 10 nM to about 10  $\mu\text{M}$  (Maret 2008b). These interactions are thought to be physiologically

significant, although these zinc affinities are orders of magnitude lower than those discussed for inhibition of cytosolic enzymes. The reason for this is that seminal and prostatic fluids, where these kallikreins are found, contain about 10 mM zinc. Presumably, the enzymes are stored with an inhibitory zinc ion bound, which then dissociates and activates the enzymes once they are secreted and diluted.

## 2.6 Concluding Remarks

It is remarkable that dozens of proteins control cellular zinc homeostasis. These proteins redistribute zinc subcellularly and control zinc ion transients. The role of zinc as a messenger in not one but at least three different mechanisms of release with multiple functional outcomes in intracrine, paracrine, and possibly endocrine signaling leaves no doubt as to the major importance of zinc for cell biology. Its signaling functions are in addition to its functions in enzymes and in protein–DNA/RNA and protein–protein interactions in thousands of proteins. Regulation with zinc ions extends the functions of the other two redox-inert metal ions, magnesium and calcium, into a range of concentrations that are typical for hormones. Together these metals ions cover many orders of concentrations for regulation. In the series  $Mg^{2+}$ ,  $Ca^{2+}$ , and  $Zn^{2+}$ , specificity and the ratio of protein-bound metal to free metal increases commensurate with increasing affinities for proteins (Maret 2001). The metal ions have different coordination chemistries and chemical properties and hence target different proteins and are involved in different processes. Given that association (on) rates are fast and not restricted, the significant different affinities dictate very different dissociation (off) rates. The effect of zinc signals is expected to be orders of magnitude longer than that of calcium signals unless there are specific mechanisms to increase the off rates. This factor makes zinc ions ideally suited for long-term changes such as holding the cell in specific states.

Sulfur donors of cysteine confer redox activity on some zinc coordination environments, thereby linking zinc redistribution and redox signaling. There is crosstalk between calcium and zinc signaling at several levels. Thus, zinc signaling is integrated into other cellular signaling networks:



Calcium influx into cells is necessary for exocytosis of  $Zn^{2+}$ -containing vesicles. Extracellular signals that elicit calcium signals for inducing NO are also linked to generating zinc transients. Extracellular zinc ions bind to a zinc receptor (ZnR), which is a G protein-coupled receptor identified as GPR39, triggering the release of  $Ca^{2+}$  from the ER (Hershinkel et al. 2001; Holst et al. 2007; Yasuda et al. 2007). ZnT1 interacts with the L-type calcium channel (LTCC)  $\beta$ -subunit and reduces the cell-surface expression of the  $\alpha$ -subunit (Levy et al. 2009). This action is through the Ras-ERK signaling pathways and also affects activity and surface expression of

T-type calcium channels (Mor et al. 2012). The  $\alpha 1D$ -subunit of the ER resident L-type calcium channel has a role in controlling the cellular zinc wave (Yamasaki et al. 2012).

Experimentally, there continue to be tremendous challenges. Investigating free zinc ions at their very low concentrations is demanding in terms of analytical procedures and purity of reagents, which often have orders of magnitude higher zinc concentrations than the cellular free zinc ion concentrations. Zinc is buffered in the cell but not in most biological experiments in which buffers are primarily employed to control pH. Although electrophysiology is a mainstay in the field of calcium research, the electrophysiology of zinc has not been explored. Direct and quantitative zinc measurements are necessary to refine the models of zinc homeostasis and zinc signaling.

The concept that a transition metal ion is a signaling ion has major implications for health and disease. It changes the view of the micronutrient zinc as merely being a cofactor of proteins to one including global functions in cellular control and suggests that perturbation of zinc homeostasis has much wider consequences for cell proliferation, differentiation, and cell death as nutritional zinc deficiency. The many factors affecting the proteins that buffer and muffle zinc also perturb zinc status and may elicit cellular zinc deficiency or zinc overload (accumulation), if the cell can no longer handle zinc properly. How these processes affect zinc stores as a source of signaling zinc ions and how other metal ions, either essential ones out of homeostatic control or nonessential ones such as cadmium, interact with the control and signaling of zinc needs to be addressed.

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# Chapter 3

## Zinc Transport Proteins and Zinc Signaling

Taiho Kambe, Tokuji Tsuji, and Kazuhisa Fukue

**Abstract** There is an increasing body of evidence indicating that zinc transport proteins play crucial roles in a variety of biological events. The Zrt, Irt-like protein/solute carrier family 39 (ZIP/SLC39A) and Zn transporter (ZnT)/SLC30A family are proteins that are primarily involved in zinc transport across the cellular membrane. In general, the ZIP family facilitates zinc influx into the cytosol from the extracellular space and release from intracellular compartments, and the ZnT family facilitates zinc mobilization in the opposite direction. A number of articles have shown that zinc movement by both transporter families contributes to zinc signaling in cellular events such as signal transduction, immunological response, cell differentiation, cell development, and cancer progression. In addition, recent reports have revealed that some types of calcium channels and other membrane proteins are employed in zinc permeation in the cell. In this chapter, we review the current understanding of the molecular functions, and the regulation of expression and activity of these zinc transport proteins, from the perspective of zinc signaling with a focus on recent advances.

**Keywords** Calcium channel • Zinc • Zinc signaling • Zinc transporter • ZIP (Zrt Irt-like protein) • ZnT (zinc transporter)

### 3.1 Introduction: Zinc Transport Proteins

Zinc is a charged divalent cation in physiological conditions. Thus, it cannot cross the cytoplasmic membrane and membranes of the intracellular compartments by passive diffusion. Zinc transport therefore requires a set of membrane proteins that are indispensable for zinc to fulfill crucial roles in multifarious biological events. During the past two decades there have been significant advances in our understanding of zinc transport proteins. In metazoa, the Zrt, Irt-like protein/solute carrier family 39 (ZIP/SLC39A) and the Zn transporter (ZnT)/SLC30A family are primary zinc transport proteins (Gaither and Eide 2001; Kambe et al. 2004; Eide 2006; Cousins et al. 2006). Moreover, some types of calcium (Ca) channels

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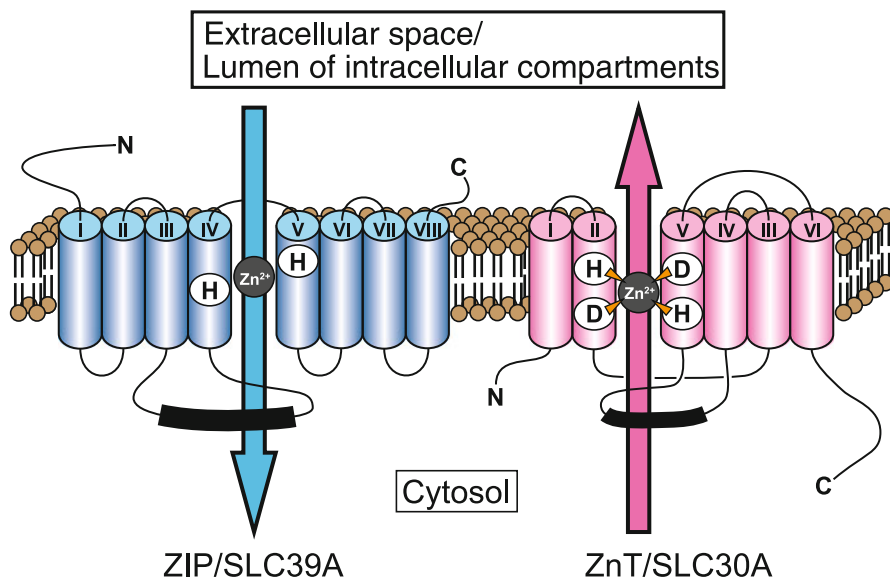
and other membrane proteins contribute to cellular zinc movement (Frederickson et al. 2005; Sensi et al. 2011; Bouron and Oberwinkler 2013). In contrast to copper and iron, the divalent zinc cation does not require a redox reaction during the membrane transport process (Kambe et al. 2008b; Kambe 2013). Thus, the expression levels of active zinc transporters and zinc permeable channel proteins at the cellular sites where they normally operate directly define the net cellular zinc transport.

Zinc transport proteins are involved in many cellular responses through modulating enzyme activation/inactivation, transcriptional activation/repression, membrane trafficking, and protein stability (Maret and Li 2009; Fukada and Kambe 2011; Maret 2013). Increasing evidence has shown that these functions are mediated by altering zinc ion concentration and distribution, that is, zinc transport proteins directly contribute to zinc signaling (Hirano et al. 2008; Haase and Rink 2009; Hogstrand et al. 2009; Fukada et al. 2011). Here, functions of the zinc transport proteins, such as ZIPs and ZnTs, and other membrane proteins including Ca channels involved in zinc transport, are reviewed from the point of view of zinc signaling.

### 3.2 Two Solute Carrier Proteins: ZIPs and ZnTs

ZIP and ZnT transporters belong to the solute carrier proteins and thus function as secondary active transporters (Gaither and Eide 2001; Kambe et al. 2004; Eide 2006; Cousins et al. 2006; Lichten and Cousins 2009; Fukada and Kambe 2011). Under physiological conditions, ZIP transporters import zinc into the cytosol from the extracellular space or intracellular compartments, and ZnT transporters mobilize zinc in the opposite direction (recently, it has been argued that ZIPs are channels, but in this chapter ZIP proteins are described as transporters) (Fig. 3.1). ZIP and ZnT members were identified by genetic, functional screenings and amino acid sequence similarities, resulting in more than 20 members (Kambe et al. 2006). They are expressed in a cell- and tissue-specific or zinc-regulatory manner, are developmentally regulated. Several ZIP transporters and most of the ZnT transporters are localized to intracellular compartments such as the secretory and endosomal-lysosomal compartments (Hennigar and Kelleher 2012; Kambe 2011), where they execute their specific functions (Fig. 3.2). Thus, in addition to zinc mobilization into and out of the cytosol across the cytoplasmic membrane, zinc mobilization into and out of these compartments by ZIP and ZnT transporters is also involved in zinc signaling. Before outlining the molecular functions of the ZIP and ZnT transporters in zinc signaling, their fundamental information is briefly reviewed.

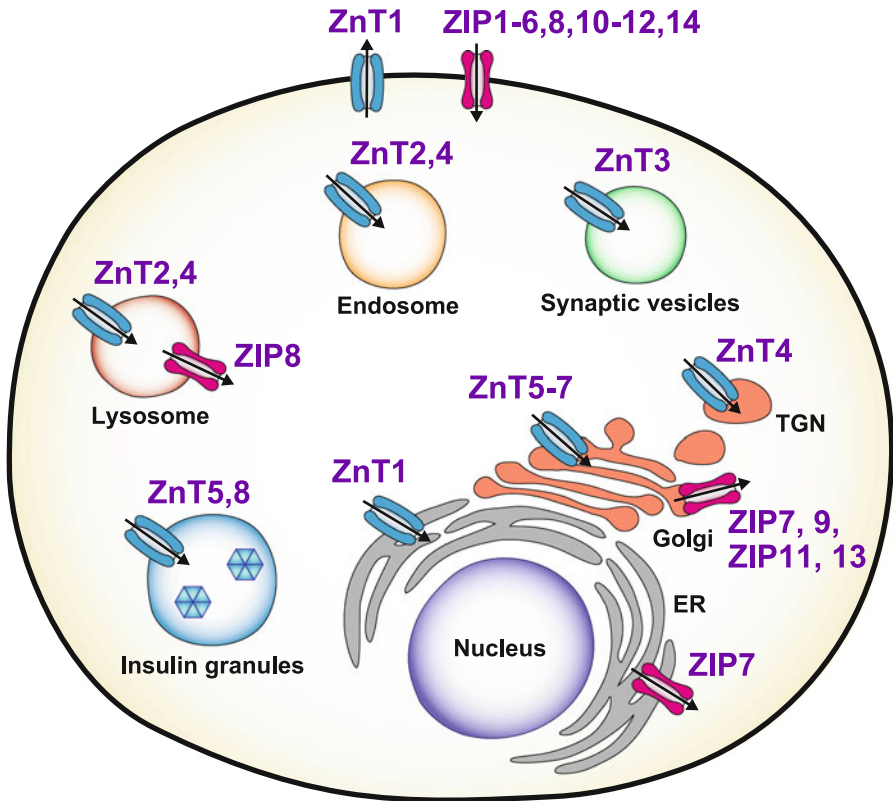




**Fig. 3.1** Predicted structures and zinc transport directions of ZIP and ZnT transporters: predicted topologies of ZIP (*left*) and ZnT (*right*) transporters. The His-rich cluster of ZIP and the His-rich loop of ZnT are indicated by *bold lines*. The highly conserved histidine (H) residues in transmembrane domain (TMD) IV and V of ZIP transporters are thought to be involved in zinc transport activity. The highly conserved aspartic acid (D) and H residues in TMD II and V of ZnT transporters are thought to form zinc-binding sites in TMDs based on the homology to YiiP. ZIP transporters mobilize zinc from the extracellular space or the lumen of intracellular compartments to the cytosol, and ZnT transporters mobilize zinc in the opposite direction

### 3.2.1 ZIP Transporters

Fourteen ZIP transporters operate in mammals (Jeong and Eide 2013). They can be divided into four subfamilies, I, II, LIV-1, and *gufA*, based on their phylogenetic relationships (Gaither and Eide 2001; Taylor and Nicholson 2003; Kambe et al. 2004). The name “ZIP” (ZRT, IRT-like protein) (Eng et al. 1998), which was named after the first identified members, the *Saccharomyces cerevisiae* Zrt1 and Zrt2 zinc transporters (Zhao and Eide 1996a, b) and the *Arabidopsis thaliana* IRT1 iron transporter (Eide et al. 1996), suggests that ZIP transporters can mobilize several divalent metals. Actually, some of the ZIP transporters have been shown to be involved in iron and manganese transport (Jenkitkasemwong et al. 2012; Fujishiro et al. 2012). In this context, a particularly interesting aspect is the recent evidence of their contribution to iron metabolism as a transporter of non-transferrin-bound iron (NTBI) in the liver (Liuzzi et al. 2006; Pinilla-Tenas et al. 2011; Beker Aydemir et al. 2012).



**Fig. 3.2** Subcellular localization and direction of zinc transport of ZIP and ZnT transporters shown according to available information. *Red-purple* and *blue* indicate ZIP and ZnT transporters, respectively. A number of ZIP and ZnT transporters are expressed in a cell type-specific manner: ZnT3 is expressed in synaptic vesicles in a subset of glutamatergic neurons, and ZnT8 is expressed in insulin granules of pancreatic  $\beta$  cells. Most ZIPs and ZnTs are thought to form homodimers, except for ZnT5 and ZnT6, which form heterodimers (see text). *TGN* *trans*-Golgi network, *ER* endoplasmic reticulum

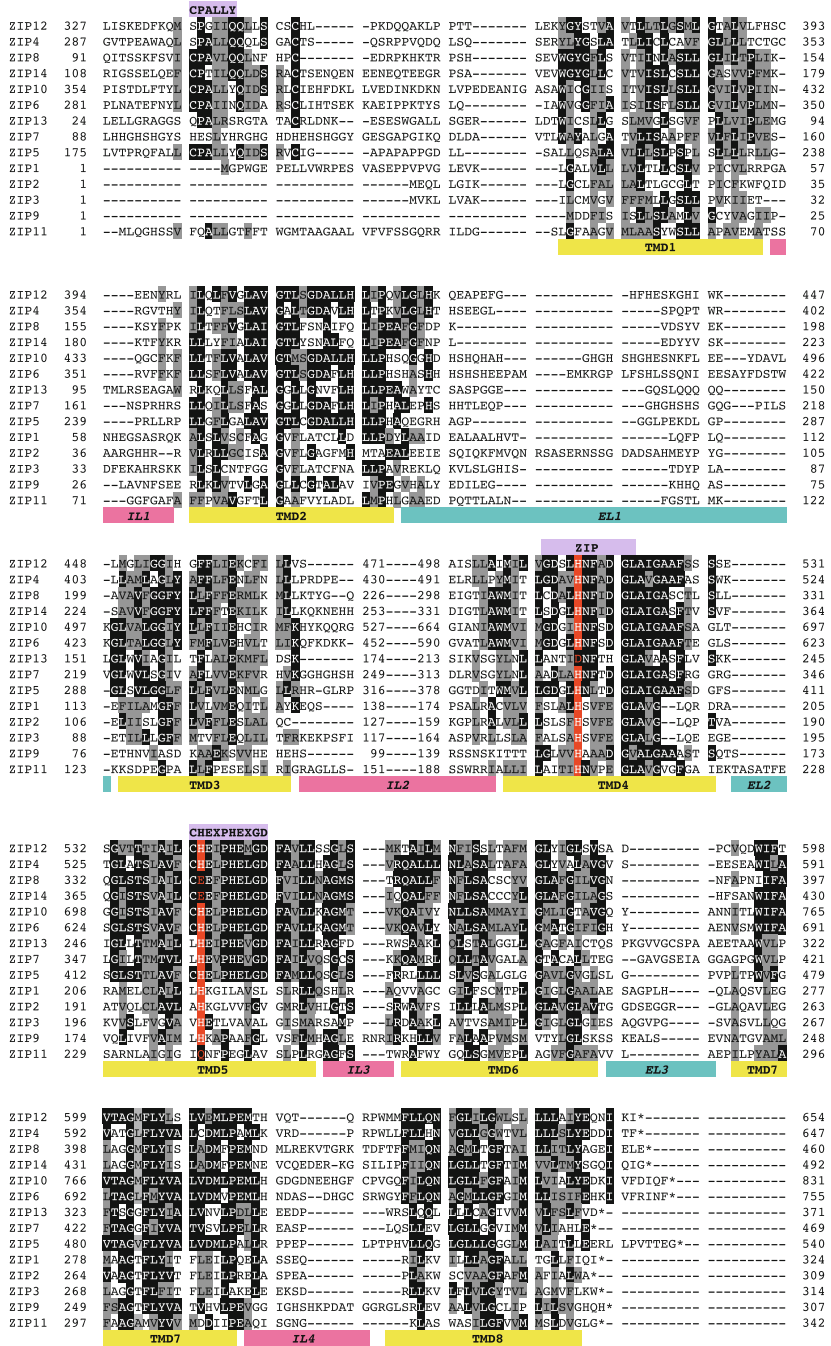
All ZIP members are predicted to have eight transmembrane domains (TMDs) with a similar membrane topology in which the amino- and carboxyl-terminal ends are located outside the cytoplasmic membrane or in the lumen of intracellular compartments (Taylor and Nicholson 2003; Kambe et al. 2004; Fukada and Kambe 2011). ZIP transporters are thought to form functional dimers, although there is not a lot of evidence to support this idea (Bin et al. 2011). Most ZIP transporters have a cytosolic His-rich cluster between TMDs III and IV, which may play a role in cytosolic zinc binding (Fig. 3.1). The most conserved portion among the members is found in TMDs IV and V, both of which are partially amphipathic and contain conserved His residues (Eng et al. 1998; Fukada and Kambe 2011)

(Fig. 3.3). It has been suggested that these domains may comprise an aqueous pore through which zinc ions pass and the conserved His residues may constitute an intramembranous zinc-binding site, but only little information about the transport mechanism of ZIP transporters has been elucidated. Using a purified bacterial ZIP homologue in reconstituted proteoliposomes has revealed a nonsaturable and electrogenic zinc transport (Lin et al. 2010). In contrast, several ZIP transporters have been shown to facilitate zinc transport in the presence of bicarbonate ions, when overexpressed in the cells (Gaither and Eide 2000; He et al. 2006). Further investigation is required to characterize the molecular mechanism of zinc transport by ZIP transporters.

### 3.2.2 ZnT Transporters

Ten ZnT transporters have been molecularly characterized in mammals thus far (Huang and Tepasamorndech 2013). However, ZnT9 (referred to as GAC63) was found to function as a nuclear coactivator, and thus generally nine ZnT transporters are thought to be operative in mammals (Kambe 2012; Fukada and Kambe 2011). They belong to the cation diffusion facilitator (CDF) family, which is a zinc efflux protein family conserved in diverse organisms from bacteria to mammals. Despite the term “diffusion facilitator,” CDF transporters do not serve as diffusion facilitators, but function as secondary active transporters. In fact, CDF transporters, including ZnTs, have been shown to function as a  $\text{Zn}^{2+}/\text{H}^{+}$  antiporter (Ohana et al. 2009; MacDiarmid et al. 2002; Kawachi et al. 2008). The  $\text{Zn}^{2+}/\text{H}^{+}$  antiport mode is reasonable for ZnTs, because most ZnTs are localized to acidic compartments such as endosomes/lysosomes (e.g., ZnT2, -3, -4, and -8). The CDF transporters are classified into three groups—Zn-CDF, Zn/Fe-CDF, and Mn-CDF—based on their phylogenetic relationships, and ZnT transporters all belong to the Zn-CDF group (Montanini et al. 2007; Kambe 2012) (Fig. 3.4). A more recent phylogenetic analysis has divided them into four groups (Gustin et al. 2011): (1) ZnT1 and ZnT10; (2) ZnT2, ZnT3, ZnT4, and ZnT8; (3) ZnT5 and ZnT7; and (4) ZnT6 (Kambe et al. 2006; Kambe 2012).

An X-ray structure of ZnT transporters has not been elucidated. However, the crystal structure of YiiP, an *Escherichia coli* homologue, provides a framework that allows exploration of the molecular basis of the ZnT transporters structure. YiiP forms a homodimer with six TMDs, and both the N- and C-termini are located in the cytosol (Lu and Fu 2007; Lu et al. 2009). Four TMDs, I, II, IV, and V, form a compact four-helix bundle with an inner core forming a channel, and the remaining TMDs III and VI cross over in an antiparallel configuration outside the bundle (Lu and Fu 2007; Lu et al. 2009). One His and three Asp residues within TMDs II and V form a zinc-binding site in the TMDs. Zinc binding to the C-terminal cytosolic domain triggers hinge movements, pivoting around four salt bridges situated at the juncture of the cytosolic domains and the TMDs. These salt bridges interlock the TMDs at the dimer interface, thereby modulating coordination



**Fig. 3.3** Sequence alignment of ZIP transporters. The order of alignment is according to the similarities among subfamilies, which was performed with amino acid sequences of ZIP transporter proteins using ClustalW2 ([www.ebi.ac.uk/Tools/msa/clustalw2/](http://www.ebi.ac.uk/Tools/msa/clustalw2/)) with some modifications.

geometry of the zinc-binding site in the TMDs for zinc transport. Based on the information of YiiP, ZnT transporters have been predicted to have a similar topology with six TMDs and intracellular N- and C-termini (Kambe et al. 2004; Kambe 2012; Fukada and Kambe 2011) (Fig. 3.1). The highly conserved His and Asp residues (two of each) within TMDs II and V are critical for zinc transport activity (Ohana et al. 2009; Fukunaka et al. 2011; Itsumura et al. 2013). In ZnT6, two of the four residues are changed to hydrophobic residues (Kambe 2012); therefore, ZnT6 does not have zinc transport activity and is instead thought to be not functional until it forms heterodimers with ZnT5 (Fukunaka et al. 2009). Moreover, in ZnT10, the His residue in TMD II is substituted by Asn, which may explain why ZnT10 can be used in manganese metabolism (Tuschl et al. 2012; Quadri et al. 2012; Kambe 2012). The distinctive cytosolic His-rich loop between TMDs IV and V has been suggested to be employed in zinc binding (Suzuki et al. 2005b) and modulate zinc recognition, acting as a selectivity filter or sensor of the cytosolic zinc level (Kawachi et al. 2008, 2012).

### 3.2.3 Physiology and Pathogenesis of ZIPs and ZnTs

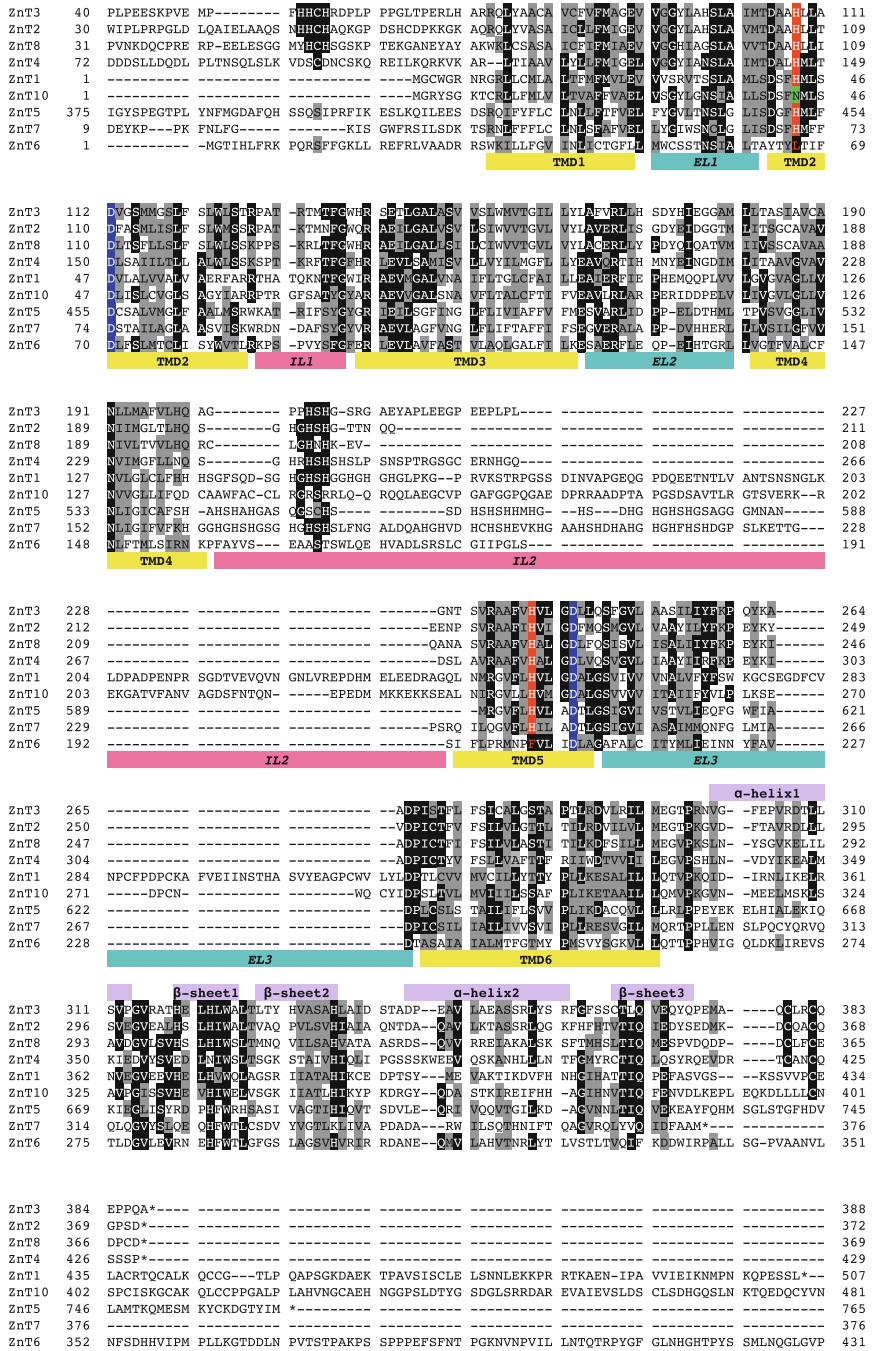
A number of ZIP and ZnT transporters have been shown to be involved in human genetic diseases. Moreover, knockout (KO) mice have been generated for almost half of these transporters. Here, phenotypes of these diseases, and mutant and KO mice and other model organisms are briefly reviewed to unveil the fundamental importance of ZIPs and ZnTs in zinc biology. The details of the mice phenotypes have been described in other reviews (Kambe et al. 2008b; Fukada and Kambe 2011).

#### 3.2.3.1 Phenotypes of Inherited Human Diseases, and Mutant and KO Mice and other Model Organisms of ZIP Transporters

There are two ZIP genes with mutations that are related to genetic diseases. *ZIP4* has been identified as the gene responsible for the rare autosomal genetic disease, acrodermatitis enteropathica (AE) (Kury et al. 2002; Wang et al. 2002). AE is



**Fig. 3.3** (continued) The putative transmembrane domains (TMD), intracellular loops (IL), and external loops (EL) are shown below the alignment in *yellow*, *pink*, and *turquoise*, respectively. “Extracellular” corresponds to the extracellular space and the lumen of the intracellular compartments. Residues highlighted in *black* and *gray* are highly conserved and semi-conserved, respectively. Residues highlighted in *red* indicate the positions of residues important for zinc transport. Conserved sequences in ZIP transporters [CPALLY, ZIP, and CHEXPHEXGD motif (Taylor and Nicholson 2003)] are indicated in *lavender*. The amino acid sequences at the N-terminal end of the LIV-1 subfamily members (the first seven proteins) are not displayed in the alignment, and the loop region corresponding to IL2 between TMDIII and TMDIV is omitted from the figure because of high sequence variations. “-” denotes a gap in the alignment



**Fig. 3.4** Sequence alignment of ZnT transporters. The order of alignment is according to similarities among subfamilies as in Fig. 3.3. The putative transmembrane domains (*TMD*), intracellular loops (*IL*), external loops (*EL*), and C-terminal cytosolic  $\alpha$ -helices and  $\beta$ -sheets

caused by defective intestinal zinc absorption, characterized by eczematous dermatitis, alopecia, and diarrhea (Maverakis et al. 2007; Schmitt et al. 2009). Mutations of the *ZIP13* gene have been shown to result in the spondylocheiro dysplastic form of Ehlers–Danlos syndrome (SCD-EDS) (Giunta et al. 2008; Fukada et al. 2008). SCD-EDS is characterized by abnormalities in hard and connective tissue development (see Chap. 12).

KO mice and other model organisms clearly show the pathophysiological importance of ZIP functions. *Zip1*-, *Zip2*-, and *Zip3*-KO mice do not show an obvious phenotype of zinc deficiency but are more likely to develop abnormal embryos when dietary zinc is limited (Dufner-Beattie et al. 2005, 2006; Peters et al. 2007). Similar phenotypes are also observed in *Zip1*, *Zip2*, and *Zip3* triple-KO mice (Kambe et al. 2008a). A recent study has revealed that *Zip3*-KO shows zinc retention in the secreted milk pool, indicating its functions in zinc reuptake from the alveolar lumen in lactating mammary glands (Kelleher et al. 2009). Moreover, *Zip1* and *Zip3* double-KO mice attenuate seizure-induced CA1 neurodegeneration (Qian et al. 2011), suggesting their involvement in zinc entry-induced neural degeneration. Complete *Zip4*-KO mice are embryonically nonviable, showing its indispensability during development (Dufner-Beattie et al. 2007). Furthermore, intestine-specific conditional *Zip4*-KO shows pivotal roles of *Zip4* in intestinal integrity (Geiser et al. 2012). Recently, complete *Zip5*-KO mice and tissue-specific *Zip5*-KO mice have been generated (Geiser et al. 2013), clearly showing that *Zip5* participates in the control of zinc excretion. The *in vivo* functions of *Zip6* and *Zip7* have not been yet found in mouse KO studies, but their importance has been confirmed in model organisms. In *Drosophila*, a *Zip6* mutant (FOI) shows abnormal cell migration (Pielage et al. 2004) and defects in gonad formation (Mathews et al. 2006). In zebrafish, using an antisense *Zip6* morpholino (MO), ZIP6 (zLiv1) has been shown to be essential for gastrulation by controlling epithelial-mesenchymal transition (Yamashita et al. 2004). In a *Zip7* *Drosophila* mutant (Catsup) showing semidominant lethality (Stathakis et al. 1999), catecholamine-related functions, and membrane protein trafficking including Notch and epidermal growth factor receptor are impaired (Stathakis et al. 1999; Groth et al. 2013). Morpholino-antisense gene knockdown of *Zip7* in zebrafish has demonstrated its requirement for eye, brain, and skeleton formation during early embryonic development (Yan et al. 2012). The hypomorphic *Zip8* mice show a fetal and postnatal lethal phenotype because of hypoplasia of multiple organs such as spleen, liver, kidney, and lung



**Fig. 3.4** (continued) based on the crystal structure of YiiP are indicated in *yellow*, *pink*, *turquoise*, and *lavender*, respectively. Residues highlighted in *red* and *yellow* indicate H and D, respectively, essential for zinc binding in TMDs. Residues highlighted in *black* and *gray* are highly conserved and semi-conserved, respectively. The asparagine residue in TMD II of ZnT10, which has been speculated to be involved in recognition of manganese, is indicated in *green*. The amino acid sequences at the C-terminal end of ZnT6 (30 aa) and ZnT10 (4 aa) are not displayed in the alignment. The TMDs indicated in ZnT5, which is predicted to have fifteen TMDs, correspond to TMDs X and XV. “–” denotes a gap in the alignment

(Galvez-Peralta et al. 2012). The neonates also show defects in hematopoiesis. Thus, *Zip8* plays indispensable roles in both multiple organ organogenesis and hematopoiesis from early embryogenesis (Galvez-Peralta et al. 2012). Recent analysis using *Zip12* antisense MO knockdown in *Xenopus* indicated its important role in nervous system development, including neurulation and neuronal differentiation. (Chowanadisai et al. 2013). *Zip13*-KO mice show phenotypes similar to those of SCD-EDS patients, such as delayed growth and skeletal and connective tissue abnormalities (Fukada et al. 2008). *Zip14*-KO mice have recently been generated, exhibiting growth retardation and impaired gluconeogenesis (Hojo et al. 2011) (see Chap. 12). *Zip14*-KO mice also show greater body fat, hypoglycemia, and higher insulin levels, as well as increased liver glucose (Beker Aydemir et al. 2012), and decreased hepatocyte proliferation during liver regeneration (Aydemir et al. 2012).

### 3.2.3.2 Phenotypes of Inherited Human Diseases, and Mutant and KO Mice and other Model Organisms of ZnT Transporters

*ZnT2* has been identified as the gene responsible for transient neonatal zinc deficiency, which is caused by low-zinc breast milk (Chowanadisai et al. 2006; Lasry et al. 2012; Itsumura et al. 2013). The nonsynonymous single nucleotide polymorphism (SNP), rs13266634, of the *ZnT8* gene increases the risk for type 2 diabetes mellitus (Sladek et al. 2007). The rs13266634 SNP has also been shown to be a determinant of humoral autoreactivity to ZnT8, which is found in approximately 60–80 % of type 1 diabetes mellitus patients at the onset of the disease (Wenzlau et al. 2008; Kawasaki et al. 2008). Homozygous mutations of the *ZnT10* gene are involved in parkinsonism, which is characterized by hepatic cirrhosis, polycythemia, dystonia, and hypermanganesemia. Thus, ZnT10 is probably involved in manganese transport.

In addition to *Zip*-KO mice, a number of *Znt*-KO mice have been generated. *Znt1*-KO mice are embryonically nonviable from an early stage (Andrews et al. 2004), revealing its indispensability during early development. In *Drosophila*, gut-specific silencing of *Znt1* has increased lethality under zinc-deficient conditions (Wang et al. 2009). *Znt3*-KO mice show lack of zinc in synaptic vesicles (Cole et al. 1999). Older *Znt3*-KO mice exhibit deficits in learning (Adlard et al. 2010), contextual discrimination and spatial working memory (Sindreu et al. 2011), and fear memory (Martel et al. 2010). A spontaneous *Znt4* mutant mouse, named lethal milk, is characterized by reduced milk zinc levels; thereby, pups nursed by affected dams die before weaning (Huang and Gitschier 1997). *Znt5*-KO mice show poor growth, osteopenia, and male-specific sudden cardiac death because of the bradyarrhythmia (Inoue et al. 2002). *Znt5*-KO mice also show defects in high-affinity immunoglobulin E receptor (FcεRI)-induced cytokine production in mast cells, because of impaired nuclear factor kappa-light-chain enhancer of activated B cell (NF-κB) activation through protein kinase C (PKC) translocation to the plasma membrane (Nishida et al. 2009) (see Chap. 5). *Znt7*-KO mice display poor growth,



decreased adiposity, and reduced absorption of dietary zinc, although no typical symptoms of zinc deficiency are found (Huang et al. 2007). Male *Znt7*-KO mice fed with a high-fat diet have severe glucose intolerance and show insulin resistance (Huang et al. 2012). *Znt8*-KO mice have been generated in a number of research groups (Pound et al. 2009; Lemaire et al. 2009; Nicolson et al. 2009; Wijesekara et al. 2010; Hardy et al. 2012; Tamaki et al. 2013) (see Chap. 13). The importance of ZnT8 for the formation of zinc-insulin crystals has been consistent, but phenotypes related to glucose tolerance, insulin processing/secretion, and body weight have been variable among these mice. The molecular mechanism that causes these differences in *Znt8*-KO mice may give a clue about how the rs13266634 SNP in the *ZnT8* gene affects the pathogenesis of type 2 diabetes mellitus.

### 3.2.4 ZIP and ZnT Transporters and Zinc Signaling

Zinc mobilized by ZIP and ZnT transporters is engaged in zinc signaling. The best characterized zinc transporter related to zinc signaling is ZIP7 (Taylor et al. 2012) (Table 3.1). ZIP7 participates in the activation of signaling pathways including Akt and extracellular signal-regulated kinase (ERK) 1/2 by releasing zinc from the endoplasmic reticulum (ER) when phosphorylated by CK2 protein kinase in response to extracellular signals such as epidermal growth factor (EGF) (Taylor et al. 2012) (see Chap. 14). The zinc release from the perinuclear area including the ER is called a “zinc wave,” which was first found in mast cells stimulated by FcεRI (Yamasaki et al. 2007) (see Chap. 5). A similar release of zinc from intracellular organelles and vesicles has been found with a number of ZIP transporters; ZIP13 releases zinc from the Golgi, which is important in the nuclear translocation of Smad proteins, thereby operating in the bone morphogenetic protein (BMP)/transforming growth factor-β (TGF-β) signaling pathway (Fukada et al. 2008) (see Chap. 12). ZIP13 has also been shown to be involved in zinc release from intracellular vesicle stores to maintain ER homeostasis by controlling ER stress (Jeong et al. 2012). ZIP9 functions in zinc release from the Golgi and is required for the regulation of Akt and ERK activation in the B cell-receptor signaling pathway (Matsuura et al. 2009; Taniguchi et al. 2013). ZIP8, when located to lysosomes, mediates lysosomal zinc release and is shown to control TCR-mediated T-cell activation, probably through inhibiting calcineurin, and thus sustaining cAMP response element-binding protein (CREB) activity (Aydemir et al. 2009).

Needless to say, zinc mobilized from the extracellular space into the cytosol by ZIP transporters is important for zinc signaling. ZIP8 plays a critical role in zinc signaling, when localized to the plasma membrane, by regulating host defense through inhibition of NF-κB via zinc-mediated down-modulation of IκB kinase (IKK) activity (Liu et al. 2013) (see Chap. 11). The closest homologue, ZIP14, facilitates G protein-coupled receptor-mediated cAMP-CREB signaling by suppressing the basal phosphodiesterase (PDE) activity in the growth plate, pituitary gland, and liver through mediating the zinc influx (Hojo et al. 2011)

**Table 3.1** Subcellular localization of ZIP transporters and their zinc signaling functions

Protein	Primary subcellular localization	Zinc signaling functions	References
ZIP1	Plasma membrane	–	
ZIP2	Plasma membrane	–	
ZIP3	Plasma membrane	–	
ZIP4	Plasma membrane	CREB signaling in pancreatic cancer	Zhang et al. (2010)
ZIP5	Plasma membrane	–	
ZIP6	Plasma membrane	Activation of Snail	Yamashita et al. (2004), Hogstrand et al. (2013)
		Phosphorylation of ERK1/2, inactivation of GSK-3 $\beta$	Zhao et al. (2007), Hogstrand et al. (2013)
ZIP7	ER, Golgi apparatus	CK2-mediated “zinc wave” for Akt and ERK1/2 activation	Taylor et al. (2012), Hogstrand et al. (2009)
ZIP8	Plasma membrane, lysosomes	T-cell activation by sustaining CREB activity, inhibition of NF- $\kappa$ B signaling	Aydemir et al. (2009)
			Liu et al. (2013)
ZIP9	Golgi apparatus	B-cell receptor signaling	Taniguchi et al. (2013)
ZIP10	Plasma membrane	–	
ZIP11	Plasma membrane	–	
ZIP12	Plasma membrane	CREB activation	Chowanadisai et al. (2013)
ZIP13	Golgi apparatus, vesicles	BMP/TGF- $\beta$ signaling	Fukada et al. (2008)
ZIP14	Plasma membrane	GPCR-mediated cAMP-CREB signaling	Hojyo et al. (2011)
		Inhibition of IRS-1/2 phosphorylation	Beker Aydemir et al. (2012)

(see Chap. 12). Moreover, zinc (and iron) mediated by ZIP14 is involved in inhibition of insulin receptor substrate (IRS) 1/2 phosphorylation through interleukin (IL) 6-mediated STAT3 signaling and cAMP-induced suppressors of cytokine signaling (SOCSs) (Beker Aydemir et al. 2012). Zinc mobilized by ectopically expressed ZIP4 is important for CREB activity (Zhang et al. 2010), which increases miR-373 expression, leading to promotion of pancreatic cancer growth (Zhang et al. 2013). ZIP6 negatively regulates Toll-like receptor (TLR) signaling, and thus a decrease in the intracellular zinc level caused by downregulation of ZIP6 is an important maturation signal in dendritic cells (Kitamura et al. 2006). ZIP6 also

**Table 3.2** Subcellular localization of ZnT transporters and their zinc signaling functions

Protein	Primary subcellular localization	Zinc signaling functions	References
ZnT1	Plasma membrane	Activation of Ras/Raf/MEK/ERK pathway	Bruinsma et al. (2002), Jirakulaporn and Muslin (2004)
	ER	Downregulation of signaling via MTF-1, c-Jun, and Elk	Lazarczyk et al. (2008)
ZnT2	Endosomes/lysosomes	–	
ZnT3	Synaptic vesicles	Modulation of synaptic transmission, ERK signaling in presynaptic neurons	Sindreu et al. (2011)
ZnT4	Endosomes/lysosomes, TGN	–	
ZnT5	Early secretory pathway	NF- $\kappa$ B signaling via PKC in mast cells	Nishida et al. (2009)
		Regulation of PKC/NF- $\kappa$ B and PI3K/Akt pathways	Zhang et al. (2012)
ZnT6	Early secretory pathway	–	
ZnT7	Early secretory pathway	Regulation of PKC/NF- $\kappa$ B, PI3K/Akt, and MAPK/ERK pathways	Zhang et al. (2012), Liang et al. (2013)
ZnT8	Insulin granules	Insulin clearance from bloodstream	Tamaki et al. (2013)
ZnT10	Golgi apparatus, recycling endosomes	ERK signaling	Patrushev et al. (2012)

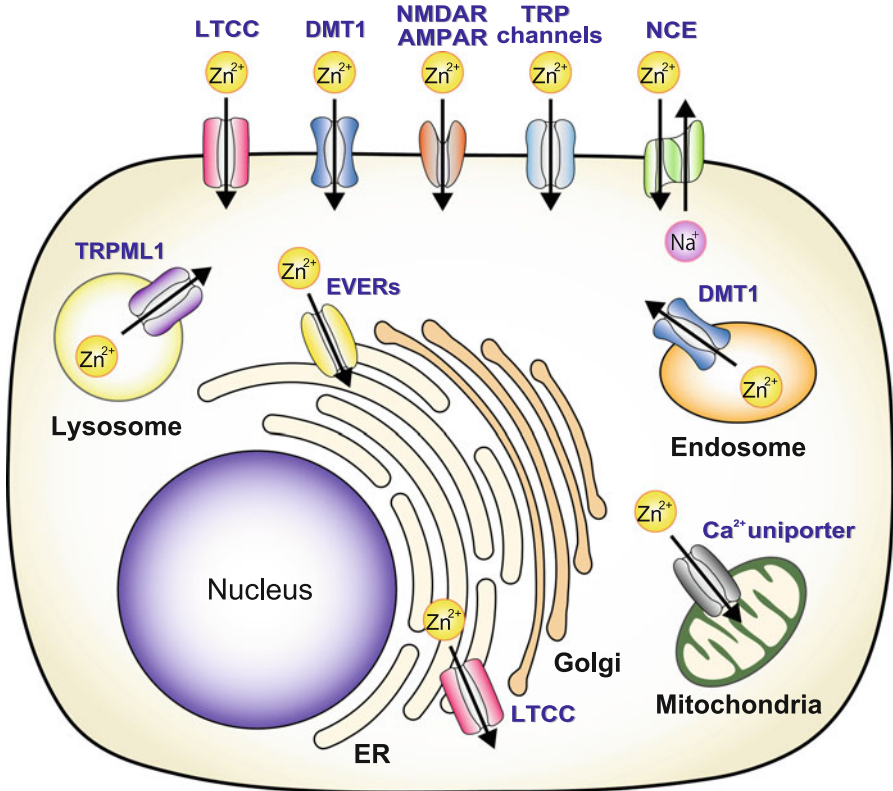
has a role in T cell-receptor (TCR)-mediated T-cell activation by controlling Src homology region 2 domain-containing phosphatase-1 (SHP-1) recruitment to the TCR activation complex (Yu et al. 2011). Moreover, ZIP6 is involved in expression and phosphorylation of ERK1/2 (Zhao et al. 2007) and can inactivate glycogen synthase kinase 3 $\beta$  (GSK-3 $\beta$ ) directly or indirectly via Akt by increasing the zinc influx, which results in activation of the zinc-finger transcription factor Snail in tumor cells (Hogstrand et al. 2013). In zebrafish, ZIP6 regulates the nuclear translocation of Snail, which is indispensable for the epithelial-mesenchymal transition (EMT) during early development (Yamashita et al. 2004). ZIP12, which is highly expressed in brain, has been shown to play crucial roles in neuronal differentiation, and neurite extension via CREB activation, by mobilizing zinc into neurons (Chowanadisai et al. 2013).

Important biological functions of zinc signaling associated with ZnTs are also abundant (Table 3.2), although the molecular mechanism is less clear in some cases. ZnT1 promotes Raf-1 activation by binding to the amino-terminal regulatory portion of Raf-1, which may be regulated by removing zinc from the Raf-1 cysteine-rich domain, because zinc inhibits the binding between Raf-1 and ZnT1

(Jirakulaporn and Muslin 2004). In nematodes, the ZnT1 orthologue, CDF1, plays a crucial role in fine-tuning Ras-mediated signaling (Bruinsma et al. 2002); thereby, the signaling functions of ZnT1 in the Ras/Raf/MEK/ERK pathway are highly conserved among metazoa. The Ras-ERK activation by ZnT1 also contributes to the enhancement of T-type Ca channel activity by increasing its surface expression (Mor et al. 2012), and in the brain it is important for protection of cells from simulated ischemia–reperfusion (Beharier et al. 2012). Moreover, ZnT1 has been shown to downregulate transcription factors stimulated by metal regulatory transcription factor 1 (MTF1), c-Jun, and Elk, when localized to the ER, by forming a hetero-complex with EVER1 and EVER2 in keratinocytes (Lazarczyk et al. 2008). In dendritic cells, ZnT1 controls TLR signaling by decreasing the intracellular zinc level (Kitamura et al. 2006). ZnT3 is important in ERK1/2 MAPK signaling via inhibition of the zinc-sensitive MAPK tyrosine phosphatase activity in presynaptic neurons, although the contribution of ZnT3 is indirect, because the effects occur after zinc, which ZnT3 transports into presynaptic vesicles, is synaptically released and then taken up again in presynaptic neurons (Sindreu et al. 2011). ZnT5 is employed in zinc signaling by NF- $\kappa$ B activation through PKC translocation to the plasma membrane (Nishida et al. 2009) (see Chap. 5). ZnT5 and ZnT7 contributes to maintain secretory pathway homeostasis and regulate zinc-requiring enzyme activities (Ishihara et al. 2006; Suzuki et al. 2005a; Fukunaka et al. 2011). ZnT5 and ZnT7 have also been suggested to be involved in PKC/NF- $\kappa$ B and phosphatidylinositol 3-kinase (PI3K)/Akt signaling (Zhang et al. 2012). ZnT7 has been shown to protect cells from oxidative stress-induced apoptosis via activating the PI3K/Akt-mediated survival pathway and the MAPK/ERK pathway (Liang et al. 2013). Zinc is accumulated by ZnT8 in insulin granules for insulin crystallization in pancreatic  $\beta$  cells (Chimienti et al. 2005). Zinc released from  $\beta$  cells in response to increased glucose levels decreases insulin secretion from  $\beta$  cells and reduces insulin clearance from the bloodstream by the liver, which indicates that ZnT8 is involved in zinc signaling in both an autocrine and endocrine fashion (Tamaki et al. 2013). ZnT10 functions in the regulation of ERK signaling by controlling cellular zinc levels (Patrushev et al. 2012). All the information clearly shows that ZIP- and ZnT-mediated zinc is indispensable in zinc signaling.

### 3.3 Zinc Permeable Channels and Membrane Proteins

Membrane transport proteins other than ZIP and ZnT transporters have also been shown to contribute to cellular zinc mobilization across the cellular membrane (Frederickson et al. 2005; Sensi et al. 2011; Bouron and Oberwinkler 2013) (Fig. 3.5). However, comprehensive understanding is limited, and many cases need to be investigated more closely to elucidate their importance in zinc physiology and pathogenesis. In this section, membrane transport channels that have been shown to be involved in zinc transport are summarized.



**Fig. 3.5** Subcellular localization and direction of zinc mobilization of Ca channels and other membrane proteins involved in zinc transport shown according to available information. The L-type calcium channel (*LTCC*) localized to the ER is lacking the  $\beta$ -subunit. The contribution of divalent metal transporter 1 (*DMT1*) to zinc transport is thought to be minor. *NCE* Na<sup>+</sup>-Ca<sup>2+</sup> exchanger

### 3.3.1 Ca Channels

Ca ions are the most common second messengers in eukaryotic cells. Thus, all cells finely tune the Ca signal using broad groups of channels and pump proteins (Rizzuto and Pozzan 2003). The Ca permeable channels are generally divided into a number of groups: (1) voltage-gated Ca channels, (2) receptor-operated Ca channels, (3) second messenger-operated channels, and (4) transient receptor potential (TRP) channels. These groups are subdivided into a great diversity of protein families based on molecular, biophysical, pharmacological, and functional properties. Ca channels such as Ca release-activated Ca channels, InsP3 receptor, and ryanodine receptor channels increase the Ca levels in the cytosol, thus eliciting Ca signaling, whereas sarcoplasmic/endoplasmic reticulum Ca ATPases (SERCAs)

and plasma membrane Ca ATPases (PMCAs) remove Ca from the cytosol, thus terminating Ca signaling (Feske et al. 2012). The tuning of Ca influx versus Ca efflux/mobilization depends on the stimulus and the cell type.

Among the Ca channels, proteins belonging to voltage-gated Ca channels (VGCCs), glutamate-gated receptors, and TRP channels are thought to be involved in zinc transport (Bouron and Oberwinkler 2013) and to contribute to the cellular zinc metabolism in specific cellular events.

VGCCs are known as selective Ca channels, but many evidences have indicated that they can permeate zinc. Most VGCCs are large protein complexes composed of a pore-forming  $\alpha$ -subunit and one or more auxiliary  $\beta$ -subunits that regulate channel properties (Burraei and Yang 2013). The L-type Ca channel (LTCC), a member of VGCC, is involved in some forms of pathological death of neurons as a zinc entry route from the extracellular space (Sensi et al. 1997; Kim et al. 2000), but probably contributes to a physiological zinc entry route in pancreatic  $\beta$  cells under stimulatory conditions during the depolarization of the plasma membrane (Gyulkhandanyan et al. 2006). In mast cells, the pore-forming  $\alpha 1D$  subunit of LTCC has been shown to be located to the ER, probably because of very low expression of the  $\beta$ -subunit, and thus is operative for zinc release from the ER after stimulation through Fc $\epsilon$ RI (Yamasaki et al. 2012): this is an important mechanism of the “zinc wave” in mast cells (Yamasaki et al. 2007) (see Chap. 5).

Glutamate-gated receptors are known to bind extracellular zinc, and thus their activities are modulated by synaptic zinc (see Chaps. 8 and 9). Some glutamate receptors also function as zinc permeable channels in postsynaptic neurons, mainly in pathological aspects such as ischemic injury. Ca permeable  $\alpha$ -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid (AMPA)/kainite-type glutamate receptors and N-Methyl-D-aspartate (NMDA)-type glutamate receptors provide zinc entry routes in postsynaptic neurons and astrocytes during neuronal excitation (Frederickson et al. 2005; Sensi et al. 2009). Zinc inhibits NMDA receptors, which seems somewhat paradoxical considering its zinc permeation property. An interesting finding has been reported about the zinc-permeable activity of AMPA receptor channels. Prion protein facilitates zinc uptake mediated by AMPA receptors containing GluA1, but lacking GluA2 subunits, in neuronal cells (Watt et al. 2012). In this case, the N-terminal polybasic region of the prion protein is important for interaction with the AMPA receptor, and the octapeptide repeat of the prion protein (Walter et al. 2007), which is known to bind with zinc, is required for facilitating zinc uptake by AMPA receptors (Watt et al. 2012). Moreover, zinc permeation by nicotinic acetylcholine receptors has been shown at higher concentrations of zinc (Ragozzino et al. 2000), but the pathophysiological meaning is unclear.

The mammalian TRP channels superfamily comprises 28 members, which are divided into seven subfamilies: TRPA, TRPC, TRPM, TRPN, TRPV, TRPP, and TRPML (Venkatchalam and Montell 2007). A number of TRP channel proteins have been shown to operate in zinc transport. TRPA1, which is a cation channel primarily expressed in sensory nerves, is activated by the psychoactive component in marijuana, environmental irritants, pungent compounds (Venkatchalam and Montell 2007), and zinc (Banke and Wickenden 2009). TRPA1 can operate as a

zinc influx route for extracellular zinc, and the cytosolic aspartate residue at position 915 of TRPA1 is indispensable for its zinc mobilization (Hu et al. 2009). The D915A TRPA1 mutant cannot permeate zinc or be activated by extracellular zinc; however it can be activated by intracellular zinc (Hu et al. 2009), indicating its physiological relevance in zinc mobilization. TRPC6, but not TRPC3, facilitates intracellular zinc accumulation when overexpressed (Gibon et al. 2011). TRPM7 is well known as a magnesium (Mg) conducting channel in addition to Ca (Schmitz et al. 2003; Ryazanova et al. 2010). TRPM7 appears to permeate zinc in the presence of Ca and Mg (Monteilh-Zoller et al. 2003) and has been shown to contribute to zinc-induced neurotoxicity (Inoue et al. 2010). TRPM7 is known to form heterodimers with TRPM6, which can also permeate zinc (Li et al. 2006). TRPM1, another member of the TRPM subfamily, is not permeable to zinc (Lambert et al. 2011), which excludes the possibility that all the members of this subfamily are involved in zinc transport. TRPV5 and TRPV6 have been shown to contribute to a zinc influx route when overexpressed in cells, but their physiological relevance in mammals remains unknown (Qiu and Hogstrand. 2004; Kovacs et al. 2013).

TRPML1 functions as a nonselective cation channel including Ca and other metals such as iron (Dong et al. 2008). Loss of TRPML1 causes the lysosomal storage disorder, mucopolipidosis IV (MLIV), resulting in large hyperacidic lysosomes, membranous vacuoles, mitochondrial fragmentation, and autophagic dysfunction (Dong et al. 2008). The lysosomes of TRPML1-knockdown cells accumulate chelatable zinc ions, suggesting TRPML1 is involved in zinc release from lysosomes (Eichelsdoerfer et al. 2010). A recent study has reported that TRPML1 works in concert with ZnT4 to regulate zinc translocation between the cytosol and lysosomes (Kukic et al. 2013) and is thereby important for proper cell function.

### 3.3.2 *Other Membrane Proteins*

A number of reports show the involvement of membrane proteins in zinc transport; representative examples are described here. Transmembrane channel-like (TMC) proteins constitute eight members in mammals, which are thought to operate as ion channels (Hahn et al. 2009). The ER membrane proteins, EVER1 and EVER2, described earlier, are identical to TMC6 and TMC8, which contribute to the regulation of intracellular zinc distribution by forming complexes with ZnT1 (Lazarczyk et al. 2009). EVER proteins are also probably involved in the activation-dependent regulation of zinc concentration in T cells (Lazarczyk et al. 2012).

Divalent metal transporter 1 (DMT1) is well known as an essential iron transporter (Gunshin et al. 1997). Because DMT1 can transport various divalent cations, DMT1 generally is thought to be involved in zinc transport. However, some reports have shown that DMT1 can transport zinc poorly (Mackenzie et al. 2007; Illing et al. 2012). A putative member of the Na<sup>+</sup>-Ca<sup>2+</sup> exchanger superfamily can mobilize zinc in or out of the cytosol, depending on the Na<sup>+</sup> gradient

**Table 3.3** Subcellular localization of Ca channels and their zinc signaling functions

Protein	Primary subcellular localization	Zinc signaling functions	References
L-type Ca channel	ER	“Zinc wave”-mediated by FcεRI in mast cells	Yamasaki et al. (2012)
AMPA receptors	Plasma membrane	Inhibition of zinc-sensitive tyrosine phosphatases	Watt et al. (2012)

(Sensi et al. 2009). Mobilization of zinc into mitochondria is thought to be conducted through a cation-permeable channel or the mitochondrial Ca uniporter, which can prevent cytosolic zinc accumulation in neurons undergoing excitotoxicity (Sensi et al. 2009).

Although they are not transport proteins, membrane proteins may contribute to the regulation of zinc transport activity. An intriguing example is presenilin. Presenilin 1 and 2 are serpentine integral membrane proteins with nine TMDs known for their role as the catalytic subunit of  $\gamma$ -secretase, which is involved in proteolysis of type I integral membrane proteins, including amyloid precursor protein and Notch receptor (Tomita and Iwatsubo 2013). Zinc uptake from the extracellular space is decreased in cells lacking presenilins, and thus presenilins may be involved in the regulation of the zinc uptake process (Greenough et al. 2011).

### 3.3.3 Zinc Signaling via Ca Channels

There is little information indicating that Ca channels and other membrane proteins directly contribute to zinc signaling (Table 3.3). However, an important evidence has been reported for the “zinc wave” process, in which the pore-forming  $\alpha 1D$ -subunit of LTCC plays a role in zinc release from the ER, as described earlier (Yamasaki et al. 2012) (see Chap. 5). Recently, it has been reported that under control of prion protein, zinc mediated by Ca-permeable AMPA receptors regulates the activity of zinc-sensitive tyrosine phosphatases (Watt et al. 2012). The enhanced zinc uptake by prion protein is lost in familial-associated mutants of prion protein (Watt et al. 2012), which suggests that zinc mobilization regulated by prion protein via AMPA receptors may affect learning and memory and promote neuronal survival. This kind of zinc signaling may have some roles in many cases of zinc permeation through Ca channels and other membrane proteins. Moreover, zinc influx into the cytosol of the postsynaptic cells, probably via NMDA, AMPA, or VGCCs, regulates Src activity, which contributes to the activation of receptor tyrosine kinase TrkB and synaptic potentiation (Huang et al. 2008). Zinc influx via these receptors and channels also contributes to activation in multiple intracellular pathways leading to necrotic, apoptotic, and autophagic neuronal death (Sensi et al. 2009).



### 3.4 Concluding Remarks and Perspectives

A growing body of evidence indicates that zinc transport proteins play pivotal roles in zinc signaling. However, the molecular basis explaining how zinc signaling conducted by zinc transport proteins controls each specific event is far from being complete and thus should be intensively investigated. The impaired zinc signaling caused by loss or reduced functions of zinc transport proteins can be partially rescued by zinc supplements in some cases, but not in other cases (Fukada et al. 2008; Hojyo et al. 2011; Taylor et al. 2012; Taniguchi et al. 2013; Liu et al. 2013), which suggests that zinc signaling conducted by zinc transport proteins is controlled by sophisticated regulation mechanisms. One mechanism may be that the concentration and distribution of zinc ions mobilized by zinc transport proteins is strictly controlled spatially and temporally, and the other may be that zinc transport process is modulated by other specific proteins for strict regulation (Taylor et al. 2012). The latter may include the case in which a putative zinc chaperone protein supports zinc signaling by specifying zinc handling to zinc transport proteins or target proteins (Fukada and Kambe 2011; Fujimoto et al. 2013). Considering the involvement of zinc signaling in multifarious pathophysiological processes, the answers to these questions would provide novel insight and may lead to therapeutic progress.

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# Chapter 4

## Oxidative Stress and Neuronal Zinc Signaling

Hirokazu Hara and Elias Aizenman

**Abstract** Zinc ( $\text{Zn}^{2+}$ ) is an abundant transition metal that is found in the central nervous system (CNS) at relatively high concentrations. A small fraction of this metal is located within synaptic vesicles in a subpopulation of excitatory neurons along with glutamate, as “chelatable”  $\text{Zn}^{2+}$ , and can be synaptically released in an activity-dependent fashion. Vesicular  $\text{Zn}^{2+}$  can thus act as a neurotransmitter or neuromodulator under physiological conditions. However, under certain pathological conditions excessive synaptically released  $\text{Zn}^{2+}$  can translocate into postsynaptic neurons, inducing cell death. There is mounting additional evidence that reactive oxygen species (ROS) and reactive nitrogen species (RNS) are critically involved in the pathophysiology of many neuronal diseases, including ischemic stroke. The majority of neuronal  $\text{Zn}^{2+}$  exists not within synaptic vesicles, but tightly bound to  $\text{Zn}^{2+}$ -binding proteins including metallothionein (MT), as well as transcription factors with zinc-finger domains. Under pathological conditions, oxidative and nitrosative stress causes oxidation and S-nitrosylation of cysteine thiols in  $\text{Zn}^{2+}$ -containing proteins, liberating the bound metal. Oxidative stress-induced elevation of intracellular  $\text{Zn}^{2+}$  can activate various deleterious cell-signaling pathways, sometimes with disastrous consequences. As such,  $\text{Zn}^{2+}$ -containing proteins such as MT serve as redox-sensitive molecular switches for zinc signals, playing a critical role in the regulation of neuronal function and viability.

**Keywords** Cerebral ischemia • Metallothionein • Neurotoxicity • Oxidative stress • Potassium channel • Zinc

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## 4.1 Introduction

Reactive oxygen species (ROS) are by-products of the cellular metabolism of oxygen in aerobic cells. These molecules are powerful oxidants and can lead to oxidative damage of cellular components, resulting in cytotoxicity. To limit oxidative damage, cells have several antioxidant defense systems, including antioxidant metabolites, as well as enzymes having ROS-scavenging activity. Injurious oxidative stress is thus caused by an imbalance between the production of ROS and the ability of antioxidant defense systems to protect cells. Mounting evidence suggests that ROS are closely associated with pathophysiological processes present in many neurological disorders including ischemic stroke, amyotrophic lateral sclerosis, Alzheimer's disease, and Parkinson's disease (Grunblatt et al. 2000; Moro et al. 2005; Butterfield et al. 2006; Boillee and Cleveland 2008; Clark and Simon 2009). Because neuronal cells are nondividing and thus especially vulnerable to the deleterious consequences of oxidative stress, excessive ROS generated under pathological conditions can lead to extensive and permanent neuronal damage. As such, ROS are generally regarded as harmful molecular moieties in the nervous system. Recent reports, however, have demonstrated that ROS can serve as signaling molecules, altering the redox state of specific target molecules that affect cellular function (Stamler et al. 2001; Spickett et al. 2006). These redox-signaling events include stress responses, which can sometimes trigger cellular protective mechanisms (Shih et al. 2003; Itoh et al. 2004; Hara et al. 2006).

Zinc ( $\text{Zn}^{2+}$ ) is an abundant transition metal in bioorganic molecules and is essential for life (Geiser et al. 2012).  $\text{Zn}^{2+}$  is required for the function of many enzymes and the structural stability of a large number of proteins, including transcription factors containing so-called zinc-finger domains (Shi and Berg 1996). In all, approximately 3,000 proteins, roughly 10 % of the translational output of the human genome, contain  $\text{Zn}^{2+}$  as either a regulatory or a structural component (Maret and Li 2009). In the central nervous system (CNS), approximately 10 % of the  $\text{Zn}^{2+}$  content is located within synaptic vesicles of a subpopulation of excitatory neurons, along with glutamate. This population of  $\text{Zn}^{2+}$  is labile or "chelatable" [i.e., easily visualized with traditional autometallographic methods such as Timm's staining (Haug et al. 1971)] and is synaptically co-released with glutamate in an activity-dependent manner (Assaf and Chung 1984; Howell et al. 1984). Therefore, this metal is now generally considered a neuromodulator, perhaps even a neurotransmitter (Paoletti et al. 1997; Besser et al. 2009; Perez-Rosello et al. 2013).

Under certain pathological conditions such as cerebral ischemia and severe epilepsy, excess vesicular  $\text{Zn}^{2+}$  released into the synaptic cleft has been shown to enter postsynaptic neurons through a variety of ion channels including calcium ( $\text{Ca}^{2+}$ ) permeable glutamate receptors (Weiss et al. 1993; Sensi et al. 1999) and voltage-gated  $\text{Ca}^{2+}$  channels (Sensi et al. 1997; Canzoniero et al. 1999), leading to the activation of neuronal cell death-inducing cellular pathways. Most of the  $\text{Zn}^{2+}$  in the CNS, however, exists in a tightly bound form to metal-binding proteins, including metallothionein (MT). As such, cytoplasmic levels of free or unbound

$\text{Zn}^{2+}$  are virtually nonexistent, perhaps reaching the low picomolar or even femtomolar range (Canzoniero et al. 1997; Outten and O'Halloran 2001; Thompson et al. 2002). MT and other  $\text{Zn}^{2+}$ -binding proteins, however, are very susceptible to oxidative changes within cells. In fact, MT itself has a very negative redox potential [below  $-366$  mV (Maret and Vallee 1998)], and even mild oxidative stress can promptly lead to the liberation of  $\text{Zn}^{2+}$  from this protein. This rise of intracellular  $\text{Zn}^{2+}$  may serve as a messenger signal to regulate a wide array of cell functions (Aizenman et al. 2000b; Bossy-Wetzel et al. 2004; Yamashita et al. 2004; Yamasaki et al. 2007). In this chapter, we focus on the molecular mechanism of oxidative stress-induced zinc signaling and role of this metal in neuronal cell death.

## 4.2 Basis of Oxidative Stress

Oxygen is an essential component for prokaryotic and eukaryotic aerobic metabolism. ROS are generated as by-products of oxygen consumption under normal physiological conditions. Generally, the primary intracellular source of the generation of ROS is the mitochondria. Approximately 95 % of the oxygen is metabolized by cytochrome *c* oxidase in the mitochondria, which transfers four electrons to oxygen, with two molecules of water produced as the product. However, about 1–2 % of oxygen is not completely consumed, leading to the formation of ROS (Boveris and Chance 1973).

### 4.2.1 Reactive Oxygen and Nitrogen Species

A free radical is defined as any molecular species capable of independent existence containing one or more unpaired electrons, an unpaired electron being one that is alone in an orbital. ROS, oxygen-derived reactive species, generally include oxygen radicals [e.g., superoxide ion ( $\text{O}_2^-$ ), hydroxyl radical ( $\text{OH}^*$ )], as well as certain nonradical species [e.g., hydrogen peroxide ( $\text{H}_2\text{O}_2$ ), singlet oxygen ( $^1\text{O}_2$ )].

Superoxide ion ( $\text{O}_2^-$ ), which is produced by the one-electron reduction of oxygen, is generated by electron leakage from the mitochondrial electron-transport chain, cytochrome P450, and redox-cycling enzymes such as xanthine oxidase and NADPH oxidase. In some cases, superoxide is intentionally produced in activated phagocytic cells to attack and kill invading bacteria. Hydrogen peroxide ( $\text{H}_2\text{O}_2$ ), a reduced form by two electrons, is produced by the dismutation of superoxide ion. Although superoxide has extremely limited permeability through lipid membranes, hydrogen peroxide has the capability to cross the membrane freely and diffuse considerable distances (Takahashi and Asada 1983; Antunes and Cadenas 2000). Hydroxyl radical ( $\text{OH}^*$ ) is generated from hydrogen peroxide through the Fenton reaction, catalyzed by  $\text{Fe}^{2+}$ . This molecule, the most reactive radical species in this

group, can attack and damage a very large number of molecules found in cells. As such, the half-life of this species is very short.

Reactive nitrogen species (RNS), including nitric oxide (NO), are nitrogen-containing oxidants and are sometimes considered to be a subset of ROS. NO is a free radical gaseous molecule that has a wide array of biological functions. NO is synthesized from L-arginine by NO synthases (NOSs). There are three isoforms of NOS: neuronal NOS (nNOS), endothelial NOS (eNOS), and inducible NOS (iNOS). NO can very rapidly react with superoxide to form peroxynitrite ( $\text{ONOO}^-$ ), a potentially highly damaging free radical that has also been shown to generate hydroxyl radicals (Beckman et al. 1990).

### ***4.2.2 Antioxidant Defense Systems***

Unregulated levels of ROS cause damage to cellular components, including nucleic acids, proteins, and lipids, leading to cell injury. To counteract these deleterious effects of ROS, cells have various antioxidant defense systems involving antioxidant enzymes such as superoxide dismutase (SOD), glutathione peroxidase (GPx), and catalase. SODs are specific antioxidant enzymes that catalyze the dismutation of superoxide to hydrogen peroxide and oxygen. There are three isoforms of SODs: copper/zinc SOD (Cu/Zn-SOD, cytosolic isoform), manganese SOD (Mn-SOD, mitochondrial isoform), and extracellular-SOD (EC-SOD, extracellular isoform). GPx, at the expense of glutathione (GSH), and catalase convert hydrogen peroxide to water. Besides these antioxidant enzymes, there are nonenzymic antioxidant compounds such as  $\alpha$ -tocopherol (vitamin E),  $\beta$ -carotene, ascorbate (vitamin C), and GSH. However, in spite of these various antioxidant defense systems, oxidative stress can and does arise as a consequence of an imbalance between ROS or RNS production and antioxidant defense systems.

### ***4.2.3 Redox Modification of Proteins***

There is significant evidence that certain kinds of oxidants reversibly influence protein activity, and, as such, the concept of protein oxidation as a functional posttranslational modification is a topic generating some attention (Stamler et al. 2001; Forman et al. 2004; Spickett et al. 2006; Winterbourn and Hampton 2008). For example,  $\text{Ca}^{2+}$ /calmodulin-dependent protein kinase II (CaMK II), which is usually activated by elevation of intracellular  $\text{Ca}^{2+}$ , has been shown to be also activated via a  $\text{Ca}^{2+}$ -independent mechanism. As such, the activity of CaMK II can be regulated via oxidation of methionine residues, located in the autoinhibitory motif of the enzyme, with the oxidation normally reversed by methionine sulfoxide reductase A (Erickson et al. 2008; He et al. 2011). Methionine residues possess reactive sulfur-containing side chains that are susceptible to

oxidation (Hoshi and Heinemann 2001). Oxidants are also known to react with protein cysteine thiols, and indeed, oxidation and reduction of thiol-containing proteins are thought to be a primary mechanism by which ROS/RNS modulate signaling pathways. Therefore, endogenously generated reactive species can, in theory, be considered second messengers under certain circumstances. Cysteine thiols are initially oxidized to cysteine sulfenic acid ( $-SOH$ ) by ROS such as hydrogen peroxide. In general, sulfenic acids can either quickly form disulfide bonds or can be further oxidized to sulfinic ( $-SO_2H$ ) or sulfonic ( $-SO_3H$ ) acids. Oxidation to sulfenic acid and formation of disulfide bonds are reversible modifications, whereas further oxidation to sulfinic and sulfonic acids is generally considered an irreversible modification of cysteine residues (Spickett et al. 2006).

Previously, we and others showed that *N*-methyl-D-aspartate (NMDA) receptor activation is regulated via oxidation of cysteine residues (Aizenman et al. 1989, 1990; Tang and Aizenman 1993; Sullivan et al. 1994; Brimacombe et al. 1999). Oxygen free radicals generated by xanthine and xanthine oxidase, or the oxidizing agents, 5,5'-dithiobis(2-nitrobenzoic acid), decrease NMDA-evoked cation currents in cortical neurons in culture. In contrast, the sulfhydryl reducing agent dithiothreitol enhances NMDA-evoked currents. Sullivan et al. (1994) demonstrated that two cysteine residues (Cys774 and Cys798) on the NMDA receptor subunit (NR) 1 contribute to redox modification of the NMDA receptor. Although there are now many examples of ion channels being modified by reversible oxidation processes, a recent report described that the oxidation of the potassium channel Kv2.1 promotes oligomerization of the channels, contributing to apoptosis in neuronal cells (Cotella et al. 2012; Wu et al. 2013). The formation of disulfide bridges between cytoplasmic residues Cys73 and Cys710 caused by oxidants is involved in the oligomerization. This voltage-dependent channel is highlighted at this juncture, because, as we shall see later on, it is a critical component of zinc signaling processes mediating neuronal cell death.

NO is a free radical gaseous molecule that has been known to have pleiotrophic effects on biological systems. NO is generated from L-arginine by NO synthase and serves as a signaling molecule. The three NOS isoforms, which are neuronal NOS (nNOS), endothelial NOS (eNOS), and inducible NOS, are differentially expressed in various tissues. Both nNOS, predominantly expressed central and peripheral neurons, and eNOS, expressed in endothelial tissues of blood vessels, are  $Ca^{2+}$  dependent. In contrast, activation of iNOS, primarily expressed in immune and glial cells, is  $Ca^{2+}$  independent. NO and its derivatives can rapidly react with cysteine thiols to generate *S*-nitrosothiols. These NO-mediated thiol modifications can lead to significant changes in protein structure and function, and it has been established that transcription factor, membrane channels, and metabolic enzymes can be readily modified by these reactions (Denninger and Marletta 1999; Stamler et al. 2001; Spickett et al. 2006). Thus, *S*-nitrosylation represents an important signaling mechanism as many proteins have been identified as targets for this form of modification (Jaffrey et al. 2001). For example, the activity of SHP-1 and SHP-2 protein tyrosine phosphatases (PTPs) has been shown to be suppressed by NO (Forman et al. 2004). The redox-sensitive cysteine in a conserved motif in the active

site of these PTPs undergoes *S*-nitrosylation, leading to inhibition of their phosphatase enzymatic function. NO has also been reported to inhibit the DNA-binding activity of transcription factors containing zinc fingers (Matthews et al. 1996; Tabuchi et al. 1996; Nikitovic et al. 1998; Hara and Adachi 2002). This structure is one class of  $Zn^{2+}$ -binding motifs consisting of cysteine and histidine residues (Shi and Berg 1995). A large group of proteins have also been reported to have other different  $Zn^{2+}$ -binding motifs, including RING, LIM, and PHD-finger domains (Matthews and Sunde 2002; Krishna et al. 2003), and are thus potential targets for oxidant-mediated regulation of their function. The common feature of these structures (e.g., Cys<sub>4</sub> and Cys<sub>2</sub>His<sub>2</sub>) is that  $Zn^{2+}$  coordination is in most cases tetrahedral in geometry, providing the structural stabilization of protein. Although  $Zn^{2+}$  is a redox inert metal, zinc/cysteine coordination in the zinc-finger structures is thought to act as a redox-sensitive molecular switch (Krezel et al. 2007; Kroncke and Klotz 2009).

Finally, nitrotyrosination is the reaction of tyrosine residues in proteins with peroxynitrite to form 3-nitrotyrosine, which has been used as a biomarker of nitrosative stress under pathological conditions. The formation of 3-nitrotyrosine has been widely reported to be present in a wide range of neurodegenerative disorders including Alzheimer's disease and Parkinson's disease (Beckman et al. 1993; Smith et al. 1997; Beal 2002).

### 4.3 Oxidative Stress in Cerebral Ischemia

#### 4.3.1 ROS Generation in Cerebral Ischemia

Stroke is an acute cerebrovascular event. About 85 % of all strokes are the result of ischemia caused by occlusion of a major cerebral artery by a thrombus or embolism. Interruption of blood flow results in a major decrease in the supply of oxygen and nutrients to the affected region, leading to brain damage. Focal cerebral ischemia has been studied extensively using an animal model of middle cerebral artery occlusion (MCAO), causing a reduction of cerebral blood flow in both the striatum and the cortex. Reperfusion following transient MCAO is a good model of focal cerebral ischemia/reperfusion (I/R) injury. ROS have been implicated in the pathophysiology associated with the restoration of blood flow following a cerebrovascular accident (Chan 2001; Warner et al. 2004; Kahles and Brandes 2012). As such, overexpression of Cu/Zn-SOD and antioxidants protect against ischemic brain injury following ischemia and reperfusion (Chan et al. 1998; Amemiya et al. 2005). In addition, in barbiturate-anesthetized rats, transient MCAO followed by reperfusion has been reported to robustly produce ROS compared to permanent MCAO (Peters et al. 1998). These findings suggest the possibility that ROS play a major role in brain injury caused by cerebral ischemia, especially following I/R.

Mitochondria have been thought of as a principal source of ROS generation in ischemic stroke. Indeed, infusion of the complex I inhibitor rotenone into the hippocampus is shown to inhibit ROS generation during reperfusion after *in vivo* ischemia (Piantadosi and Zhang 1996). Furthermore, studies using mitochondrial Mn-SOD transgenic and knockout mice revealed that  $O_2^-$  derived from mitochondria contributes to neuronal cell death after cerebral ischemia (Keller et al. 1998; Murakami et al. 1998; Kim et al. 2002). Overexpression of Mn-SOD protects against neuronal cell death in MCAO models. In contrast, knockout of Mn-SOD increases infarct volume. In addition to mitochondria, pro-oxidant enzymes such as xanthine oxidase and NADPH oxidase are likely involved in ROS generation caused by cerebral I/R (Kahles and Brandes 2012). It has been observed that expression levels of the NADPH oxidase isoforms NOX2 and NOX4 increases in brain microvessels and endothelial cells after ischemic stroke. Deletion of the NOX2 gene, which is normally predominantly expressed in neutrophils, has also been reported to reduce infarct volume after MCAO (Walder et al. 1997). Moreover, as described next, overload of  $Zn^{2+}$  into neurons is thought to contribute to neuronal cell death following cerebral ischemia. Related to the aforementioned discussion, Noh and Koh (2000) showed that exposure of cortical neurons to a high concentration of  $Zn^{2+}$  induces and activates NADPH oxidase.

### 4.3.2 NO Generation in Cerebral Ischemia

As already described, there are three isoforms, nNOS, eNOS, and iNOS. All three isoforms of NOS have shown to be involved in neuronal cell death following cerebral ischemia. During and following injury, excitotoxic concentrations of glutamate released from excitatory synaptic terminals lead to the activation of NMDA and  $Ca^{2+}$ -permeable AMPA receptors, promoting influx of  $Ca^{2+}$ . The rise of intracellular  $Ca^{2+}$  induces activation of nNOS, resulting in NO production. In nNOS knockout mice, infarct volumes are decreased after MCAO and neurological deficits are much less pronounced when compared to wild-type mice (Huang and Lo 1998). Moreover, nNOS inhibitors protect against global ischemia in gerbils and provides some reduction in infarct volume following transient MCAO in rats (O'Neill et al. 2000). Importantly, PDZ domains, which mediate protein–protein interaction, have been shown to be critically relevant in NMDA-mediated neuronal cell death process (Aarts and Tymianski 2004; Cui et al. 2007). PSD-95 and nNOS bind to NMDA receptors via the C-terminal PDZ domain of NMDA receptor subunit GluN2 (Kornau et al. 1995; Christopherson et al. 1999). PSD-95 plays a critical role in NO-induced toxicity via direct interaction with NMDA receptors, whereby  $Ca^{2+}$  influx via the receptor channel can activate nNOS, but only when the synthase is tethered to the receptor (Sattler et al. 1999). In fact, a peptide mimicking the NR2B PDZ domain (TAT-NR2B9c) has been shown to inhibit pro-death NMDA receptor signaling, leading to protection against MNDNA-induced excitotoxicity (Soriano et al. 2008). Importantly, a small-scale clinical trial with



TAT-NR2B9c suggests the possibility that the peptide may be useful in attenuating brain tissue damage in humans, although clearly these findings are only preliminary (Hill et al. 2012). It must be mentioned, however, that eNOS knockout mice develop significantly larger vertebral infarcts after MCAO (Huang et al. 1996). Therefore, NO derived from eNOS may have contrasting, beneficial effects on neuronal injury caused by cerebral ischemia (Samdani et al. 1997).

Inducible iNOS differs fundamentally from nNOS and eNOS as it is not activated by  $\text{Ca}^{2+}$ . Under normal conditions the expression levels of iNOS are very low. The activity of iNOS is normally regulated in response to pathogen recognition and cytokine release. Because the activation of iNOS occurs later than that of nNOS and eNOS, iNOS is thought to contribute to delayed neuronal cell death in stroke and other forms of injury. Indeed, infarct volume in iNOS knockout mice was similar to that of wild-type mice 24 h after permanent ischemia. However, a reduction of infarct volume was observed in iNOS knockout mice at later times (Iadecola et al. 1997). These findings do suggest, however, that selective iNOS inhibition may be an important component for useful therapeutic intervention following a stroke.

## 4.4 Zinc Neurotoxicity

### 4.4.1 *Entry of Extracellular $\text{Zn}^{2+}$ into Neurons*

In the CNS, “chelatable”  $\text{Zn}^{2+}$  is present in the synaptic vesicles of excitatory neurons along with glutamate. “Zincergic” neurons are widely distributed in the cortex, hippocampus, and amygdala and have been suggested to play a role in learning and memory cellular processes (Frederickson et al. 2000; Takeda 2001).  $\text{Zn}^{2+}$ -containing neurons are also located in the olfactory bulb and the auditory brainstem (Frederickson et al. 1988; Perez-Clausell et al. 1989).  $\text{Zn}^{2+}$  is released in an activity-dependent manner into the synaptic cleft and serves as a neuromodulator or perhaps even as a neurotransmitter. This metal allosterically inhibits NMDA and  $\gamma$ -aminobutyric acid receptors (Peters et al. 1987; Christine and Choi 1990; Li et al. 1994; Ruiz et al. 2004), while potentiating glycine receptor function (Lynch et al. 1998; Hirzel et al. 2006). Synaptically released  $\text{Zn}^{2+}$  has also been reported to activate a postsynaptic,  $\text{Zn}^{2+}$ -sensing metabotropic receptor, GPR39 (Besser et al. 2009). Through this receptor, synaptic  $\text{Zn}^{2+}$  promotes postsynaptic insertion of the potassium-chloride co-transporter 2 (KCC2), thereby enhancing synaptic inhibition (Chorin et al. 2011; Saadi et al. 2012). More recently, synaptically released  $\text{Zn}^{2+}$  was reported to stimulate postsynaptic synthesis of the endocannabinoid 2-arachidonoylglycerol (2-AG) via activation of GPR39 (Perez-Rosello et al. 2013). 2-AG suppresses neurotransmitter release through activation of cannabinoid receptor 1 (CB1R) in presynaptic terminals. Finally, synaptic  $\text{Zn}^{2+}$

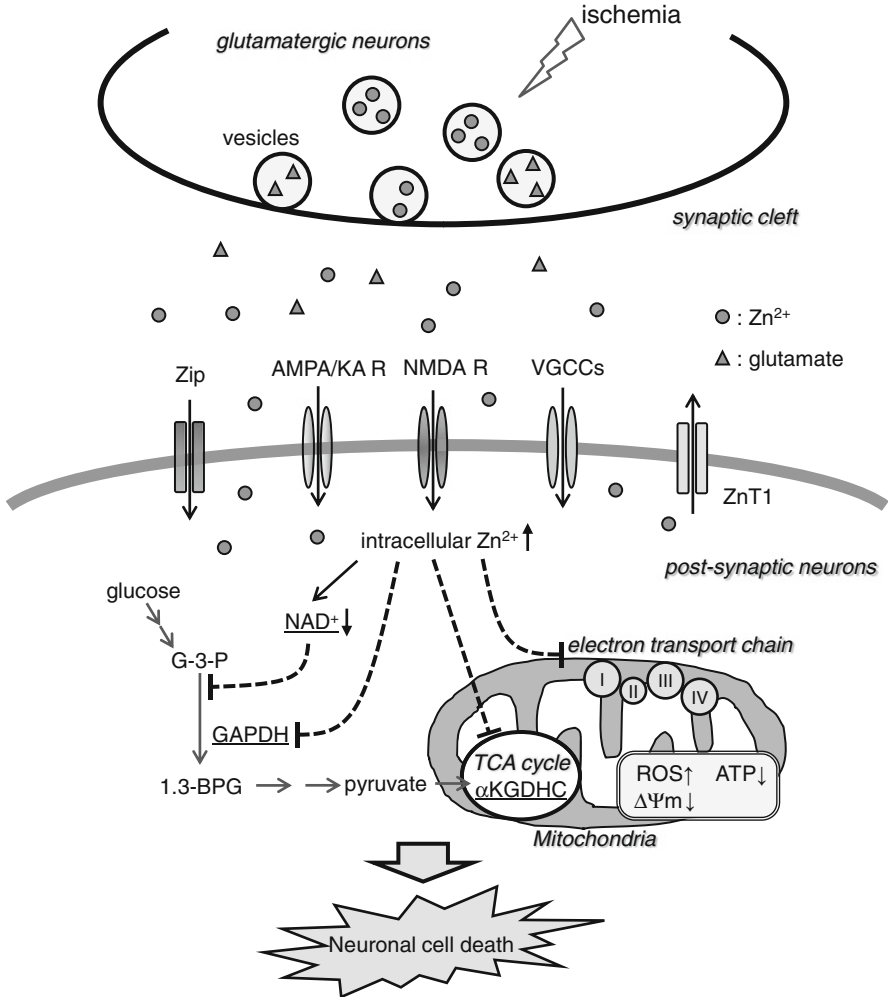
may influence the activity of other proteins following its activity-dependent release, including T-type  $\text{Ca}^{2+}$  channels (Grauert et al. 2014).

In contrast to the physiological roles for  $\text{Zn}^{2+}$ , under pathological conditions, such as transient global ischemia and epileptic seizures, excess  $\text{Zn}^{2+}$  can be released from vesicles along with glutamate into the extracellular space. As elevations of extracellular  $\text{Zn}^{2+}$  have been shown to cause neuronal cell injury (Fig. 4.1), the extracellular  $\text{Zn}^{2+}$  chelator Ca-EDTA can block neurotoxicity following transient global cerebral ischemia (Tonder et al. 1990; Koh et al. 1996).  $\text{Zn}^{2+}$  released into the synaptic cleft has been shown to enter into postsynaptic neurons through a variety of channels and transporters, including voltage-gated  $\text{Ca}^{2+}$  channels (VGCCs), NMDA receptors,  $\text{Ca}^{2+}$ -permeable AMPA receptors, as well as TRP channels (Weiss et al. 1993; Sensi et al. 1997, 1999; Marin et al. 2000; Inoue et al. 2010). Of interest, a recent in vivo study revealed that hippocampus CA1 damage following kainic acid injection was attenuated in Zip-1 and -3 null mice (Qian et al. 2011). Therefore, Zip family transporters might also be involved in  $\text{Zn}^{2+}$  translocation and neurotoxicity following ischemia.

Spreading depression (SD) is an intense depolarization wave that spreads throughout brain tissue (Leo 1944). SD-like events occurring after ischemia and trauma are shown to be involved in spreading brain injury (Leao 1947). Although  $\text{Ca}^{2+}$  influx through  $\text{Ca}^{2+}$  channels has been tightly linked to SD-related damage, more recent studies have suggested that  $\text{Zn}^{2+}$  entry through L-type  $\text{Ca}^{2+}$  channels or NMDA receptors may substantially contribute to SD-related injurious processes (Dietz et al. 2009). Moreover, Carter et al. (2011) have recently reported that  $\text{Zn}^{2+}$  release and accumulation during SD caused by oxygen-glucose deprivation is abolished in brain slices prepared from ZnT3 knockout mice. These findings suggest the possibility that SD-induced  $\text{Zn}^{2+}$  release contributes to neuronal injury following cerebral ischemia.

#### ***4.4.2 $\text{Zn}^{2+}$ -Induced Energy Failure and Mitochondrial Dysfunction***

There is widespread evidence that exposure of cortical neurons to  $\text{Zn}^{2+}$  causes energy failure and mitochondrial dysfunction, leading to neuronal cell death (Fig. 4.1) (Dineley et al. 2003). Elevation of intracellular  $\text{Zn}^{2+}$  levels has been shown to reduce cellular nicotinamide adenine dinucleotide ( $\text{NAD}^+$ ) levels, leading to inhibition of glyceraldehyde-3-phosphate dehydrogenase (GAPDH), which is an important enzyme in the regulation of glycolysis (Sheline et al. 2000; Cai et al. 2006). In addition,  $\text{Zn}^{2+}$  also directly inhibits GAPDH (Krotkiewska and Banas 1992) and partially inhibits phosphofructokinase (Ikeda et al. 1980). These events provoke inhibition of glycolysis, resulting in decrease in ATP levels and energy failure. Restoration of  $\text{NAD}^+$  can attenuate neuronal cell death induced by



**Fig. 4.1** Synaptic Zn<sup>2+</sup>-dependent neuronal cell death. During injurious conditions, such as cerebral ischemia, excess Zn<sup>2+</sup> can be released from glutamatergic neurons to the synaptic cleft along with glutamate. Released Zn<sup>2+</sup> has been shown to translocate into postsynaptic neurons through a variety of channels, including voltage-gated Ca<sup>2+</sup> channels (VGCCs), the *N*-methyl-D-aspartate (NMDA) receptor, and AMPA/kinate (KA) receptors, as well as zinc transporters. Elevation of intracellular Zn<sup>2+</sup> inhibits glycolysis, the tricarboxylic acid (TCA) cycle, and the mitochondrial electron-transport chain, leading to energy failure and, ultimately, neuronal cell death. *G3P* glyceraldehyde-3-phosphate, *1,3-BPG* 1,3-bisphosphoglycerate, *α-KGDHC* α-ketoglutarate dehydrogenase complex

Zn<sup>2+</sup> (Cai et al. 2006). Zn<sup>2+</sup> also inhibits α-ketoglutarate dehydrogenase complex (α-KGDHC) of the TCA cycle (Brown et al. 2000). In sum, these studies strongly suggest that zinc neurotoxicity is caused, at least in part, by suppressing cellular energy production.

In addition to the aforementioned studies,  $Zn^{2+}$  influx through  $Ca^{2+}$ -AMPA channels was shown to induce neuronal cell death via mitochondria-mediated generation of ROS (Sensi et al. 1999). As such, the vitamin E-derivative antioxidant trolox was shown to ameliorate  $Zn^{2+}$ -induced neurotoxicity (Kim et al. 1999). These observations indicate the possibility that ROS generation caused by  $Zn^{2+}$  exposure also contributes to  $Zn^{2+}$  toxicity. Mitochondria are thought to be the primary source of  $Zn^{2+}$ -generated ROS and play a critical role in  $Zn^{2+}$ -induced neuronal cell death, primarily by producing an increase in intramitochondrial  $Zn^{2+}$  levels and mitochondrial dysfunction (Sensi et al. 2000).  $Zn^{2+}$  has also been shown to inhibit the mitochondrial electron-transport chain (Skulachev et al. 1967). For example, the cytochrome  $bc_1$  complex, also known as complex III of the respiratory chain, can be reversibly inhibited by  $Zn^{2+}$  by interfering with proton transfer reactions at the  $Q_p$  center of the complex (Link and von Jagow 1995). Importantly, mitochondrial dysfunction caused by inhibition of the electron-transfer chain often leads to ROS production (Sensi et al. 1999; Dineley et al. 2005).

In addition to inhibition of respiration, some reports show that  $Zn^{2+}$  taken up by mitochondria induces reduction of the mitochondrial membrane potential and opening of the mitochondrial permeability transition pore (mPTP) in isolated nonneuronal and neuronal mitochondria (Brierley and Knight 1967; Wudarczyk et al. 1999; Jiang et al. 2001). The mPTP allows the passage of any molecule of  $<1,500$  Da across the mitochondrial membrane. Opening of the mPTP causes mitochondrial swelling and release of cytochrome  $c$  (Cyt- $c$ ), as well as apoptosis-inducing factor (Kroemer and Reed 2000). Additionally, entry of  $Zn^{2+}$  into the mitochondria through the  $Ca^{2+}$  uniporter causes mPTP-dependent mitochondrial swelling, as well as release of Cyt- $c$  and apoptosis-inducing factor (Jiang et al. 2001). Of interest, Bonanni et al. (2006) demonstrated that  $Zn^{2+}$ -dependent activation of large, multi-conductance channels were present in mitochondria isolated from ischemic rat brain. A contrasting study (Dineley et al. 2005; Devinney et al. 2009), however, reported that  $Zn^{2+}$  was unable to induce mPTP opening in rat liver mitochondria. Thus, although it is clear that  $Zn^{2+}$  can alter mitochondrial function in a number of ways, the specific actions of this metal on the organelle under injurious conditions require further study.

#### **4.4.3 Intracellular $Zn^{2+}$ Liberation and Neuronal Cell Death**

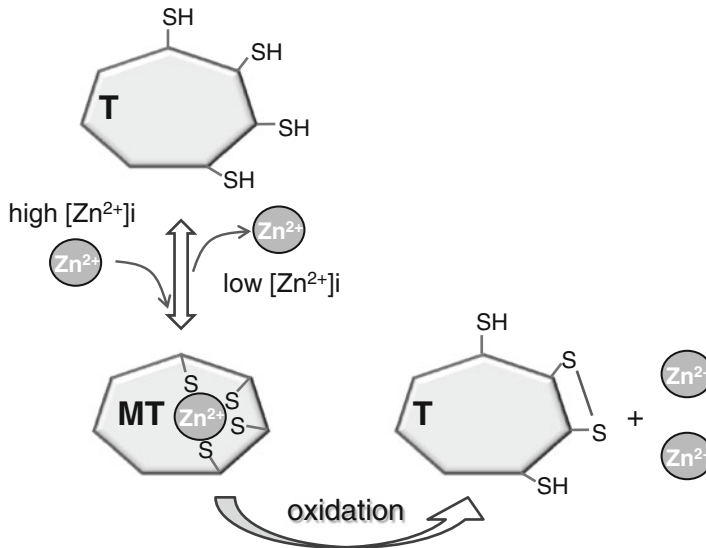
As already described, extracellular  $Zn^{2+}$  has been shown to be elevated in focal and global cerebral ischemia. Influx of  $Zn^{2+}$  from the extracellular space into neurons through multiple pathways induces accumulation of neuronal  $Zn^{2+}$ , leading to  $Zn^{2+}$  toxicity.  $Zn^{2+}$  is accumulated in synaptic vesicles via the action of the vesicular  $Zn^{2+}$ -specific transporter (ZnT3) (Wenzel et al. 1997). In fact, vesicular  $Zn^{2+}$  is conspicuously absent in mice with a genetic ablation of *ZnT3* (Wenzel et al. 1997). In a critically important study, Lee et al. (2000) demonstrated that  $Zn^{2+}$  continued to remain elevated in the hippocampus of *ZnT3*<sup>-/-</sup> mice treated with kainate

intraperitoneally, leading to  $Zn^{2+}$ -dependent cell death. This key observation suggested that synaptic vesicular  $Zn^{2+}$  may not be either necessary or sufficient for the cytoplasmic accumulation of the metal in dying neurons, and, importantly, that synaptic source of  $Zn^{2+}$  may not be unique for this injurious process. Because  $Zn^{2+}$  accumulation and  $Zn^{2+}$  neurotoxicity occur even in the absence of vesicular  $Zn^{2+}$ , it was hypothesized that  $Zn^{2+}$  released from intracellular stores could play a critical role in neural injury (Aizenman et al. 2000b).

#### 4.4.4 Metallothioneins

As mentioned earlier, the majority (80–90 %) of  $Zn^{2+}$  in the brain is tightly bound to a large number of proteins. There has been evidence that ROS and RNS react with  $Zn^{2+}$ /thiol clusters to induce the release of  $Zn^{2+}$  from various proteins, most notably MT, but also including proteins such as protein kinase C, as well as zinc-finger transcription factors (Kroncke et al. 1994; Maret 1994; Knapp and Klann 2000). MTs are a family of small cysteine-rich metal-binding proteins with a major role in regulation of intracellular  $Zn^{2+}$  homeostasis and heavy metal detoxification. In the adult mammalian CNS, there are three principal MT isoforms: MT-I, MT-II, and MT-III. MT-I and MT-II are widely expressed in most tissues and MT-III is predominantly expressed in the CNS. MT-III was first isolated and identified as a growth inhibitory factor (GIF) in a series of Alzheimer's disease-directed studies (Uchida et al. 1991; Tsuji et al. 1992). An additional MT isoform has been described, MT-IV; its expression is restricted to stratified squamous epithelia including upper stomach and skin (Quaife et al. 1994). MTs are formed by peptide chains of 61–68 amino acids, structurally resembling a dumbbell-shaped molecule, with metal-binding domains ( $\alpha$  and  $\beta$ ) at either end (Romero-Isart and Vasak 2002). MTs contain 20 cysteine residues, which can coordinate up to seven zinc ions. In the  $\alpha$ -domain, four  $Zn^{2+}$  ions are bound to 11 cysteines, whereas in  $\beta$ -domain, three  $Zn^{2+}$  ions are bound to 9 cysteines. In this way, each  $Zn^{2+}$  ion is bound tetrahedrally to four cysteines. In general, the zinc cluster in the C-terminal  $\alpha$ -domain tends to be more stable than that in the  $\beta$ -domain.

Biochemical analysis of the association of  $Zn^{2+}$  ion with the apoprotein, thionein, has revealed that there are  $Zn^{2+}$ -interacting sites with different binding affinity (Krezel and Maret 2007b). The sites are classified into strong, moderate, and weak groups, depending on the binding affinity to  $Zn^{2+}$  ions (stability constant  $\log K_d$  11.8, ~10, and 7.7, respectively). As four  $Zn^{2+}$  ions can be tightly bound to the strong  $Zn^{2+}$ -interacting sites, thionein functions as a potent metal chelator (Fig. 4.2). In contrast,  $Zn^{2+}$  ions bound to MT with weak and moderate strength can be transferred to thionein and, importantly, to other  $Zn^{2+}$ -binding proteins. As such, MT can also serve as a  $Zn^{2+}$  donor. Differential fluorescent labeling of cysteine clusters of MT revealed that tissues contain almost as much thionein as metal-bound MT. The different binding properties of MT provide a role for buffering  $Zn^{2+}$  ions at a wide range of intracellular  $Zn^{2+}$  concentrations. Because



**Fig. 4.2** Metallothionein (*MT*) regulates intracellular zinc dynamics. The *MT*/thionein (*T*) system controls intracellular  $Zn^{2+}$  concentrations in a wide range of physiological conditions. However, because cysteine residues in *MT* are highly redox sensitive, *MT* is readily oxidized by extracellular or intracellular oxidants, resulting in the unregulated liberation of previously coordinated  $Zn^{2+}$ . In turn, the liberated  $Zn^{2+}$  can initiate various deleterious cell signaling pathways

this protein has a high cysteine content (20/mol) and cysteine thiols in thionein are highly reactive, this molecule likely contributes to the total cellular thiol redox buffering capacity (Fig. 4.2). Indeed, some studies have shown that *MT* has functions to scavenge ROS and can serve as an important cellular antioxidant (Lazo et al. 1998; Reinecke et al. 2006; Krezel and Maret 2007a; Chiaverini and De Ley 2010).

#### 4.4.5 $Zn^{2+}$ -Mediated Gene Expression

$Zn^{2+}$  has been shown to trigger *MT* expression by inducing the binding of metal regulatory element-binding transcription factor 1 (MTF-1) to specific DNA motifs termed metal responsive elements (MRE), located in the 5'-flanking regulatory region of  $Zn^{2+}$ -inducible genes, including *MT*-I, *MT*-II, and several zinc transporters (*ZnTs*), such as *ZnT1* (Andrews 2000; Langmade et al. 2000). MTF-1 is a zinc-finger protein in the Cys<sub>2</sub>His<sub>2</sub> family of transcription factors and has six zinc-finger domains. Binding to the MRE and transcriptional activation is reversibly regulated by interaction of  $Zn^{2+}$  with the zinc-finger domains in MTF-1 (Andrews 2000). Although under normal conditions MTF-1 is preferentially sequestered in the cytoplasm, various stimuli (e.g., heavy metals and oxidative stress-induced  $Zn^{2+}$

release) promote translocation of MTF-1 to the nucleus to induce gene transcription. Cadmium ( $\text{Cd}^{2+}$ ), known as a strong MT inducer, can activate MTF-1, but does so by displacing  $\text{Zn}^{2+}$  from MT. Using a cell-free MTF-1-dependent transcription system, Zhang et al. (2003) demonstrated that  $\text{Zn}^{2+}$ -saturated MT is indispensable for  $\text{Cd}^{2+}$ -induced MTF-1/MRE activation. These results suggest that zinc is the only metal that can directly mediate MTF-1 activation and nuclear translocation. Because  $\text{Cd}^{2+}$  binds to MT with a much higher affinity than  $\text{Zn}^{2+}$ , upon entry of  $\text{Cd}^{2+}$  into cells,  $\text{Cd}^{2+}$  displaces bound  $\text{Zn}^{2+}$  from  $\text{Zn}^{2+}$ -saturated MT or other  $\text{Zn}^{2+}$ -containing proteins. Similarly, hydrogen peroxide, a known inducer of MTF-1 activation, does so by oxidation of thiol of cysteine residues in MT (Zhang et al. 2003), leading to promotion of  $\text{Zn}^{2+}$  release from MT (described next). As such, liberation of  $\text{Zn}^{2+}$  by  $\text{Cd}^{2+}$  and hydrogen peroxide is necessary for MTF-1-mediated transactivation of *MT* gene by these stressors. Because MTF-1 serves as a selective intracellular  $\text{Zn}^{2+}$  sensor, a method using a MRE-driven luciferase construct was developed (Chen et al. 1998; Giedroc et al. 2001) and has been utilized to monitor alterations in intracellular  $\text{Zn}^{2+}$  levels (Daniels et al. 2002; Bi et al. 2004). We have showed that this system can be applied effectively to detect liberated  $\text{Zn}^{2+}$  caused by oxidative stress in primary cortical neurons (Hara and Aizenman 2004; Aras et al. 2009).

#### 4.4.6 Redox-Dependent $\text{Zn}^{2+}$ Release

Oxidative and nitrosative stress can modify cysteine residues in the  $\text{Zn}^{2+}$ /thiolate complex of  $\text{Zn}^{2+}$ -containing proteins (Stamler et al. 2001; Forman et al. 2004; Spickett et al. 2006; Winterbourn and Hampton 2008). As such,  $\text{Zn}^{2+}$ /thiolate clusters provide a redox-active coordination environment for the redox-inert  $\text{Zn}^{2+}$  ion (Maret 1994, 2000; St Croix et al. 2002; Krezel and Maret 2007a). Because the redox potential of the clusters is very negative (Maret and Vallee 1998), MT is oxidized easily even under mild oxidative stress and releases  $\text{Zn}^{2+}$  ions. Therefore, oxidants release  $\text{Zn}^{2+}$ , whereas reductants restore the full potential of the sulfur ligands to bind  $\text{Zn}^{2+}$  (Fig. 4.2).  $\text{Zn}^{2+}$  release from  $\text{Zn}^{2+}$ /thiolate clusters of MT can be induced by several ROS species. MT-III is significantly more reactive to NO than MT-I and MT-II and readily forms *S*-nitrosothiols, while released  $\text{Zn}^{2+}$  levels from MT-III induced by other ROS/RNS (e.g., hydrogen peroxide) are similar to those generated by MT-I/II (Chen et al. 2002). It was reported that basic and acidic amino acids in the vicinity of target cysteine residue facilitate its *S*-nitrosylation by acid–base catalysis. Because MT-III contains such sequences in its  $\alpha$ - and  $\beta$ -domains, MT-III tends to be preferentially *S*-nitrosylated. Lee et al. (2003) observed that when sodium nitroprusside (SNP), a NO donor, was injected into the lateral ventricle of wild-type mice,  $\text{Zn}^{2+}$  accumulation and neuronal cell death occurred in the C1A region of the hippocampus. Moreover,  $\text{Zn}^{2+}$  chelation was shown to block SNP-induced  $\text{Zn}^{2+}$  accumulation and neuronal cell death (Lee et al. 2003). Because it has also been observed that neuronal cell death is

significantly decreased in MT-III<sup>-/-</sup> mice, the metal-binding protein may represent a significant source of the Zn<sup>2+</sup>-mediating damage under these conditions (Lee et al. 2003).

Thiol oxidants and NO have been shown to induce the release of Zn<sup>2+</sup> from MTs in a variety of experimental paradigms. Pierce et al. (2000) constructed a fusion protein consisting of MT sandwiched between two mutant green fluorescent proteins (CFP and YFP), termed FRET-MT [based on the Ca<sup>2+</sup>-sensitive cameleon probe (Miyawaki et al. 1999)], and showed that MT is an important component of intracellular redox signaling using this FRET-MT system. Our group also assayed for intracellular Zn<sup>2+</sup> release induced by the thiol-oxidizing agent, 2,2'-dithiodipyridine (DTDP), and peroxynitrite using the same FRET-MT detection system in cultured cortical neurons (Zhang et al. 2004). When neurons were exposed to these agents, change of emission intensity ratio in FRET-MT transfected neurons was observed, reflecting Zn<sup>2+</sup> liberation from the MT-containing chimeric indicator.

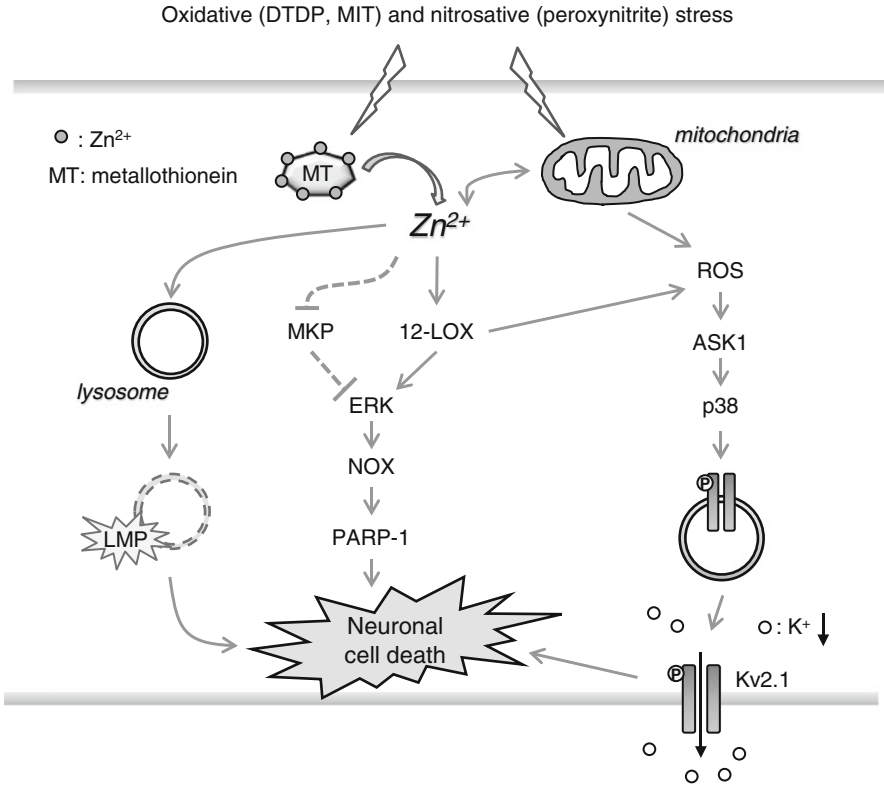
## 4.5 Signaling Pathway in Liberated Zn<sup>2+</sup>-Induced Neuronal Apoptosis

Oxidants induce the liberation of intracellular Zn<sup>2+</sup> in neurons and other systems. The liberated Zn<sup>2+</sup>, in turn, was observed to lead to the activation of signaling pathways leading to neuronal apoptosis (Aizenman et al. 2000b; McLaughlin et al. 2001).

### 4.5.1 Zinc Signaling in Neuronal Death

Our group demonstrated that DTDP-liberated Zn<sup>2+</sup> induced neuronal apoptosis via apoptosis signal-regulating kinase 1 (ASK1)-mediated p38 activation, enhancement of potassium currents, enabling caspase activation (Aras and Aizenman 2005; Knoch et al. 2008) (Fig. 4.3). Treatment with the K<sup>+</sup> channel blocker tetraethylammonium (TEA) or high extracellular K<sup>+</sup> can attenuate DTDP-induced neuronal apoptosis. We observed a robust, delayed increase in TEA-sensitive potassium channel currents following a brief exposure to DTDP. Because DTDP-induced enhancement of potassium currents is blocked by p38 inhibitors, p38 is an upstream regulator of this process. In contrast, a spin-trap agent can prevent DTDP-induced neuronal cell death and p38 activation, suggesting an additional ROS-mediated step in the signaling cascade, likely the result of 12-lipoxygenase activation (McLaughlin et al. 2001; Zhang et al. 2004). Free Zn<sup>2+</sup> can also be taken up by mitochondria, resulting in changes in mitochondrial membrane potential and additional ROS generation (Sensi et al. 1999, 2000; Dineley et al. 2003, 2005).





**Fig. 4.3** Oxidative stress-induced  $Zn^{2+}$  signaling in neuronal cell death. Oxidative and nitrosative stress induce  $Zn^{2+}$  release from MT or mitochondria. Liberated  $Zn^{2+}$  provokes mitochondrial dysfunction as well as activation of ASK1 and p38 MAPK. The latter phosphorylates Kv2.1, leading to an apoptotic  $K^+$  current surge. Interestingly, different stimuli have been shown to trigger activation of other signaling pathways by  $Zn^{2+}$ . For example, the biocide MIT, which is known to induce oxidative stress, activates a 12-LOX-mediated ERK-, but not a p38-dependent signaling pathway, leading to reactive oxygen species (ROS) production, DNA damage, and overactivation of PARP-1. In addition, elevation of intracellular  $Zn^{2+}$  caused by oxidative stress can promote neuronal cell death via lysosomal membrane permeability (LMP). MKP MAPK phosphatase

Therefore, ROS are required for DTDP-induced p38 activation. ASK1 is a ubiquitously expressed MAP kinase kinase kinase and has been shown to play a critical role in apoptosis in response to various stimuli. Under normal conditions, ASK1 is bound to thioredoxin (Trx) and its kinase activity is inactivated. Under stress conditions, however, ROS oxidize sulfhydryl groups of Trx and oxidized Trx is dissociated from ASK1, leading to activation of ASK1 and its downstream kinases, primarily p38 and c-jun-N-terminal kinase (JNK) (Ichijo et al. 1997; Saitoh et al. 1998). We found that dominant-negative ASK1 or overexpression of Trx prevented DTDP-induced surge of potassium currents (Aras and Aizenman 2005), directly implicating this upstream kinase system in  $Zn^{2+}$ -triggered enhancement of apoptotic-enabling potassium currents.

### 4.5.2 *Involvement of Kv2.1 in DTDP-Induced Neurotoxicity*

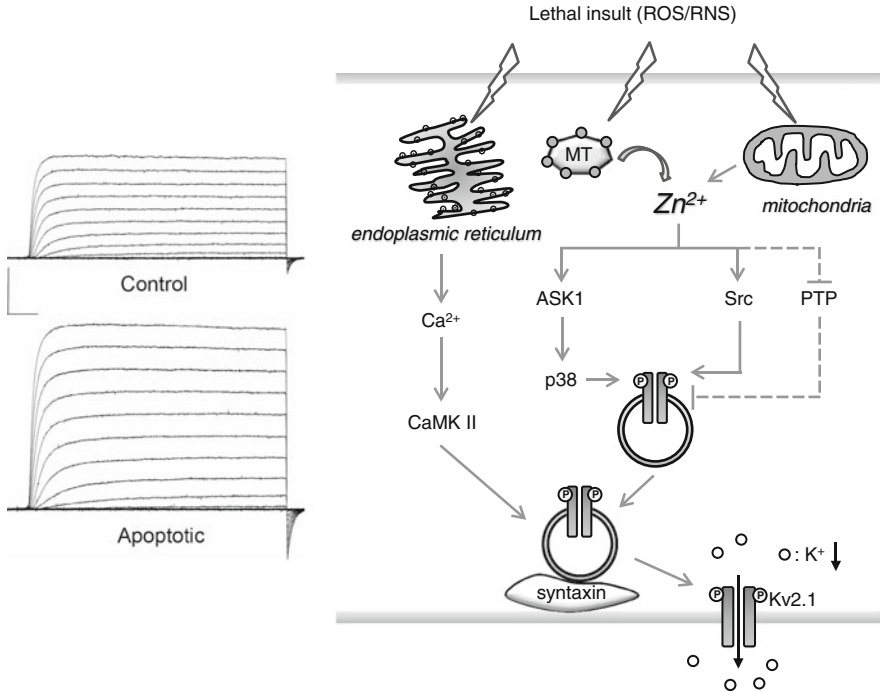
Cellular  $K^+$  efflux has been shown to be an essential step in the apoptotic cascade in various types of cells (Yu et al. 1997; Bortner and Cidlowski 1999; Aizenman et al. 2000b; McLaughlin et al. 2001). In neurons, the loss of potassium is mediated by a dramatic enhancement in potassium currents. When cultured cortical neurons are exposed to serum deprivation, staurosporine (Yu et al. 1997), or  $\beta$ -amyloid peptides (Yu et al. 1998), a prominent surge of voltage-gated  $K^+$  current is observed. Appropriately, apoptosis caused by these various stimuli can be prevented by TEA, a  $K^+$  channel blocker.

Kv2.1 is the principal component of delayed rectifying  $K^+$  currents in several neuronal populations (Murakoshi and Trimmer 1999; Malin and Nerbonne 2002; Guan et al. 2013). We observed that dominant-negative constructs of Kv2.1 can effectively decrease basal delayed rectifier currents in cortical neurons and, more importantly, completely abrogate the apoptotic surge of potassium currents and increasing neuronal viability (Pal et al. 2003). These observations strongly indicate that Kv2.1-encoded channels are responsible for the apoptotic surge of  $K^+$  currents we have observed following DTDP exposure and other forms of cell injury (Aizenman et al. 2000b; McLaughlin et al. 2001; Knoch et al. 2008), entirely consistent with the protective actions of TEA or elevated extracellular  $K^+$  concentration.

In a separate set of studies, we reported that the enhancement of  $K^+$  currents during apoptosis was caused by the translocation of new Kv2.1 channels to the plasma membrane (Pal et al. 2006). This delivery of Kv2.1 was sensitive to botulinum neurotoxins, suggesting that *N*-ethylmaleimide-sensitive factor attachment protein receptor (SNARE) proteins support this trafficking of Kv2.1. We have more recently shown that  $Ca^{2+}$ -dependent activation of  $Ca^{2+}$ /calmodulin-dependent protein kinase II (CaMK II) is required for DTDP-induced Kv2.1 activation (McCord and Aizenman 2013) (Fig. 4.4). DTDP also promotes intracellular  $Ca^{2+}$  release and activation of CaMK II, which regulates exocytosis via a specific interaction with the SNARE protein syntaxin. Subsequently, CaMK II promotes interaction of Kv2.1-encoded  $K^+$  channel Kv2.1 with syntaxin, leading to enhancement of  $K^+$  currents. Of note, syntaxin has a well-described and specific association with the proximal C-terminus of Kv2.1 (Leung et al. 2003; Singer-Lahat et al. 2007). These novel findings have uncovered a crucial cooperative convergence of  $Zn^{2+}$ - and  $Ca^{2+}$ -mediated signals to regulate oxidative-induced neuronal cell death.

### 4.5.3 *Phosphorylation of Kv2.1*

Phosphorylation and dephosphorylation of a number of cytoplasmic residues, Kv2.1, strongly affects channel gating, influencing cellular excitability (Murakoshi et al. 1997; Misonou et al. 2004; Mohapatra et al. 2007). In addition to this type of



**Fig. 4.4** Regulation of Kv2.1 channel by zinc signaling. *Left panel:* Oxidative stress-induced  $Zn^{2+}$  liberation triggers a surge of  $K^+$  currents. CHO cells transfected with Kv2.1 were exposed to either vehicle (*Control*) or 25  $\mu$ M DTDP (*Apoptotic*) for 5 min and recorded 3 h later. Calibration is 5 nA and 20 ms. *Right panel:* Liberated  $Zn^{2+}$  activates several signaling pathways and promotes membrane insertion of new Kv2.1 channels. The channel is phosphorylated by p38 MAPK and Src kinase, whereas  $Zn^{2+}$  prevents dephosphorylation via inhibition of protein phosphatase. The dual phosphorylated channels are inserted in the cell membrane via a syntaxin-dependent process, leading to enhanced  $K^+$  currents and cytoplasmic  $K^+$  efflux, enabling apoptosis. Translocation of the channel is also regulated by  $Ca^{2+}$ -dependent activation of CaMKII, which interacts with the syntaxin/Kv2.1 complex

regulation of Kv2.1 function, phosphorylation events are also at the heart of Kv2.1-mediated apoptotic currents. The MAPK p38 directly phosphorylates C-terminal serine residue 800 (S800) in Kv2.1, a process essential for the expression of the apoptotic  $K^+$  current surge (Redman et al. 2007). Moreover, Kv2.1 N-terminal tyrosine 124 (Y124) must also be phosphorylated for the apoptotic process to ensue. Phosphorylation at Y124 is ensured not only by Src kinase activity, but by  $Zn^{2+}$ -dependent inhibition of tyrosine phosphatase  $\epsilon$  (Cyto-PTP $\epsilon$ ) (Redman et al. 2009) (Fig. 4.4). This kinase/phosphatase was previously shown to be specific for the Y124 residue, a process that was tightly coupled to the regulation of Kv2.1-mediated current amplitude (Tiran et al. 2003, 2006). Previous reports have shown that  $Zn^{2+}$  can directly act on the highly conserved active site of protein tyrosine phosphatases at nanomolar concentrations (Maret et al. 1999; Haase and Maret 2003).

Together, these findings suggest that two amino acid residues on Kv2.1, Y124 and S800, are critical determinants of neuronal viability by regulating the expression of apoptotic  $K^+$  currents (Fig. 4.4).

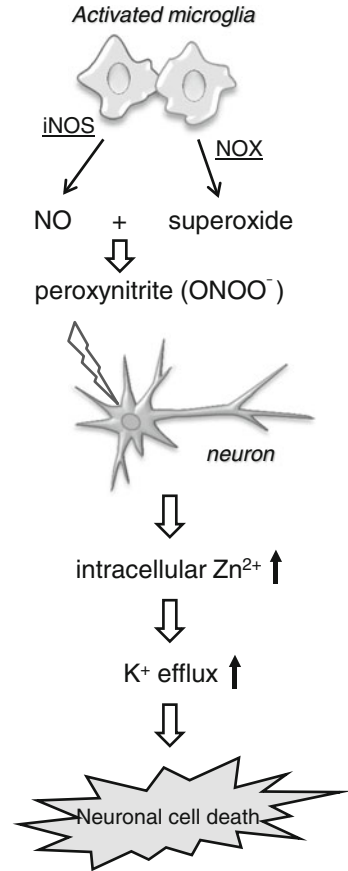
#### **4.5.4 Phosphatase Inhibition**

Phosphorylation signaling is tightly regulated through the coordinated action of protein kinases and phosphatases. Several phosphatases such as protein tyrosine phosphatases 1B (PTP-1B) are redox sensitive and inhibited by direct thiol oxidation. PTPs have conserved C(X)<sub>5</sub>R motif at their active sites, in which the cysteine thiol possesses a low  $pK_a$  (~5) and is highly susceptible to reduction and oxidation (Tanner et al. 2011). Not surprisingly,  $Zn^{2+}$  can readily interact with these thiols to inhibit phosphatase activity (Maret 2013). In addition to Cyto-PTP,  $Zn^{2+}$  has been reported to inhibit other types of protein phosphatases, including PTP-1B and MAPK phosphatase (Haase and Maret 2003; Ho et al. 2008). For example, intracellular  $Zn^{2+}$  elevation inhibits PTP-1B and augments tyrosine phosphorylation of insulin/insulin-like growth factor receptors (Haase and Maret 2003). Moreover, Ho et al. (2008) observed that glutamate-induced oxidative stress inhibits ERK2-directed phosphatases, resulting in sustained ERK1/2 activation, the process being mediated by oxidant-induced  $Zn^{2+}$  liberation. Interestingly, as  $Zn^{2+}$  failed to affect JNK3 phosphatase activity, endogenous  $Zn^{2+}$  might be more selective for ERK2-directed phosphatase inhibition under these conditions.

#### **4.5.5 Microglia-Mediated Neuronal Cell Death**

There is growing evidence that inflammation is involved in the pathogenesis of neurodegeneration in many CNS disorders (Perry et al. 2010). Microglia, resident immune cells in the CNS, serve beneficial functions in neuronal maintenance and innate immunity. However, microglia can be activated in response to neuronal injury and release injurious signals such as NO, superoxide, and proinflammatory cytokines, leading to enhanced neuronal injury (Weinstein et al. 2010). The induction of iNOS is mediated via activation of Toll-like receptor 4 (TLR4) in microglia, and, indeed, several reports have demonstrated that TLR4 participates in the exacerbation of ischemic brain injury (Caso et al. 2007; Hua et al. 2007; Yang et al. 2010). Lipopolysaccharide (LPS) activates TLR4 and initiates several signaling pathways within microglia, including activation of nuclear factor- $\kappa$ B (NF- $\kappa$ B) and MAPKs (JNK, p38, and ERK). Damaged or dying cells after cerebral ischemia release damage-associated molecular pattern molecules (DAMPs), such as high mobility group box 1, as well as heat shock proteins, which are known to be endogenous TLR4 ligands that promote neuroinflammation (Kim et al. 2006; Marsh et al. 2009; Zhang et al. 2011). Recently, peroxiredoxin family proteins

**Fig. 4.5** Activated microglia-mediated  $Zn^{2+}$ -dependent neuronal cell death. Activated microglia induce iNOS expression, which in turn produces NO. NO rapidly reacts with NADPH oxidase-produced superoxide to form  $ONOO^-$ . This reactive nitrogen species (RNS) induces liberation of intraneuronal  $Zn^{2+}$  and activation of  $Kv2.1$ -enabled apoptosis



were shown to be released extracellularly from necrotic brain cells and induce expression of inflammatory cytokines through activation of Toll-like receptor 2 (TLR2) and TLR4, promoting neural cell death (Shichita et al. 2012).

As described earlier, NO produced by iNOS rapidly reacts with superoxide to form  $ONOO^-$ , a highly reactive and cytotoxic oxidant (Beckman et al. 1990; Espey et al. 2002). Because  $ONOO^-$  can rapidly permeate plasma membranes and target a large number of molecules, it has been closely associated with injurious processes in neurons. We observed that activated microglial-derived  $ONOO^-$  promoted the liberation of  $Zn^{2+}$  from intracellular stores in cultured neurons, resulting in a pronounced  $Zn^{2+}$ -dependent  $K^+$  current surge (Knoch et al. 2008) (Fig. 4.5). The  $K^+$  current surge was abolished by apocynin, an NADPH inhibitor, and 5,10,15,20-tetrakis(4-sulfonatophenyl)porphyrinato iron(III) chloride, a  $ONOO^-$  decomposition catalyst. Importantly, activated microglia-dependent neurotoxicity was prevented by neuronal overexpression of MT-III, which provided not only additional antioxidant levels within cells, but likely also additional binding sites for the liberated  $Zn^{2+}$ .

Of interest,  $Zn^{2+}$  itself has been shown to directly activate microglia. Kauppinen et al. (2008) observed that  $Zn^{2+}$  exposure to cultured mouse microglia caused morphological changes and triggered NO and cytokine productions via NADPH oxidase, poly(ADP-ribose) polymerase 1 (PARP-1), or NF- $\kappa$ B activation. In addition, microglial activation observed following cerebral ischemia-reperfusion was shown to be suppressed by injection of the  $Zn^{2+}$  chelator Ca-EDTA (Kauppinen et al. 2008). Thus, a positive feedback model emerges in which ischemic injury leads to microglial activation causing DAMPs and subsequent ROS/RNS production, which in turn leads to the intraneuronal liberation of  $Zn^{2+}$ . In addition to activating cell death signaling pathways in neurons, the accumulation of free  $Zn^{2+}$  may overwhelm homeostatic buffering mechanisms that lead to the release of  $Zn^{2+}$  from neurons, further activating microglia. A late, possibly secondary involvement of  $Zn^{2+}$ -mediated injury processes in the ischemic brain has been reported by various investigators (Calderone et al. 2004; Carter et al. 2010).

## 4.6 Additional Zinc Signaling Injury Pathway

### 4.6.1 12-Lipoxygenase (12-LOX)

Lipoxygenases (LOXs) are dioxygenases that incorporate molecular oxygen into specific positions of polyunsaturated fatty acids and, as such, are generally classified as 5-, 12-, or 15-LOXs (Shimizu and Wolfe 1990). 12-LOX, which is predominantly expressed in the brain, has been implicated in neuronal oxidative injury in various models. For example, glutamate-induced glutathione depletion causes 12-LOX activation and ROS generation, ultimately inducing neuronal cell death (Li et al. 1997). Furthermore, 12-LOX is also involved in peroxynitrite-induced,  $Zn^{2+}$ -dependent neurotoxicity in cortical neurons (Zhang et al. 2004) (Fig. 4.3). As TPEN, a  $Zn^{2+}$  chelator, was observed to block the membrane translocation and the activity of 12-LOX,  $Zn^{2+}$  liberation occurs upstream of 12-LOX activation, via a yet to be defined signaling pathway. As explained in an earlier section, ROS produced by 12-LOX are likely responsible for ASK1 activation via thioredoxin oxidation (Aras and Aizenman 2011), a critical step in p38 phosphorylation of Kv2.1. Other studies also reported that oxidative and nitrosative stressors could trigger intracellular  $Zn^{2+}$  liberation in astrocytes (Malaiyandi et al. 2004) and oligodendrocytes (Zhang et al. 2006), contributing to deleterious signaling pathways in those cells via 12-LOX activation. Of note, however, although p38 MAPK plays an important role in peroxynitrite-induced/12-LOX-dependent cell death, this MAPK appears not to be involved in oligodendrocyte toxicity. Rather, 12-LOX activation appears to occur downstream from the phosphorylation of another MAPK, ERK, which itself is activated by the liberated  $Zn^{2+}$  (Fig. 4.3). This is a unique pathway not commonly observed in neurons, although a connection between

12-LOX activity and ERK has been reported to occur in other types of neuronal toxicity, as described below.

Methylisothiazolinone (MIT), a commonly used industrial and household biocide that also triggers intracellular  $Zn^{2+}$  liberation, can lead to neuronal cell death (Du et al. 2002). Curiously, the mechanism of cell death triggered by this compound is remarkably different from that activated by either DTDP or  $ONOO^-$ . Indeed, the elevation of intracellular  $Zn^{2+}$  induced by MIT activates ERK, but not p38, but in this case MAPK activation occurs downstream from 12-LOX (Du et al. 2002). MIT was also observed to induce a decrease in intracellular GSH levels. Although in this case intracellular GSH depletion is also directly correlated with 12-LOX activation, TPEN was observed to inhibit MIT-induced GSH depletion. At this point we are not sure how to reconcile both sets of studies, but clearly there are different signaling mechanisms at play in oligodendrocytes versus neurons. We must mention that MIT-induced toxicity is dependent on subsequent NADPH oxidase activation, ROS generation, and DNA damage, leading to overactivation of PARP-1,  $NAD^+$  depletion, and nonapoptotic cell death (Fig. 4.3). All these signaling pathway components are  $Zn^{2+}$ - and ERK dependent. Thus,  $Zn^{2+}$  can activate both caspase-dependent and caspase-independent cell death pathways in neurons following its liberation from intracellular binding sites.

#### 4.6.2 Preconditioning

Preconditioning is a very interesting cellular phenomenon whereby exposure to sublethal injury triggers an adaptive response that results in tolerance to a subsequent, normally lethal stimulus. Ischemic preconditioning (IPC) in the brain can be triggered, for example, by brief (10-min) ischemic events, such as transient MCAO (Dirnagl et al. 2003; Stetler et al. 2009). Preconditioning stimuli such as this one can substantially protect brain tissue, even from subsequent permanent MCAO, at least within a certain time window (Barone et al. 1998). Although all the mechanisms underlying neuronal tolerance have yet to be completely understood, it is generally believed that preconditioning induces modest activation of molecules that are normally associated with cell damage (e.g., ROS). These signaling molecules trigger adaptive rather than deleterious responses in neurons (Ravati et al. 2000; Thompson et al. 2012). Of note, our group (McLaughlin et al. 2003), as well as others (Garnier et al. 2003; Tanaka et al. 2004; Lee et al. 2008), observed that ischemic preconditioning induces sublethal activation of caspase 3 both in vivo and in vitro.

Sublethal increases in intracellular  $Zn^{2+}$  are also important contributors to the adaptive response of neurons during preconditioning. Treatment of cultured cortical neurons with transient chemical ischemia (KCN in glucose-free conditions) can render neurons tolerant to excitotoxic injury within 24 h (Aizenman et al. 2000a; McLaughlin et al. 2003). Preconditioning leads to the liberation of intracellular  $Zn^{2+}$ , and  $Zn^{2+}$  itself, in the presence of an ionophore, can serve alone as a

preconditioning stimulus (Aras et al. 2009). Koh and coworkers further noted that  $Zn^{2+}$  was necessary for sublethal caspase activation in preconditioned neurons (Lee et al. 2008). These findings suggest that intracellular  $Zn^{2+}$  elevation during preconditioning process is an essential step in the expression of neuronal tolerance. Indeed, pretreatment with exogenous, nontoxic levels of  $Zn^{2+}$  has been reported to protect against neuronal cell death in both in vivo and in vitro cerebral ischemia models (Matsushita et al. 1996; Lee et al. 2008). Because oxidative stress caused by cerebral ischemia/reperfusion can affect zinc homeostasis in the brain, preconditioning-derived  $Zn^{2+}$  may upregulate the expression of MT or zinc transporters that could contribute to  $Zn^{2+}$  buffering during the normal lethal stimulus. Consistent with this observation, we observed that NMDA-triggered intraneuronal  $Zn^{2+}$  elevations were significantly dampened in preconditioned neurons (Aras et al. 2009).

### 4.6.3 Autophagy

In addition to the aforementioned mechanisms, labile  $Zn^{2+}$  liberated by oxidative stress has recently been shown to cause lysosomal changes, leading to neuronal cell death (Hwang et al. 2008; Lee and Koh 2010; Lee et al. 2010). The lysosome is a cytosolic vesicle containing numerous acidic hydrolases that are involved in degradation of cellular components. It has been reported that ischemic brain injury and epileptic stimuli cause lysosomal membrane disintegration in neuronal cells (Hwang et al. 2008; Windelborn and Lipton 2008). Hwang et al. (2008) showed that hydrogen peroxide induces the translocation of labile  $Zn^{2+}$  into lysosomes and  $Zn^{2+}$ -laden lysosomes undergo membrane disintegration, resulting in lysosomal membrane permeability (LMP) (Fig. 4.3). LMP, in turn releases the lysosomal enzyme cathepsin D, resulting in cathepsin D-dependent cell death (Boya and Kroemer 2008). Because TPEN can attenuate oxidative stress-induced LMP and subsequent cell death,  $Zn^{2+}$  is thought to play a critical, upstream role in this process. In astrocytes, exposure to hydrogen peroxide produces an increase in autophagic vacuoles positive for microtubule-associated protein 1 light chain 3 lipidated form (LC3-II), an autophagosomal marker, leading to autophagosome formation (Lee et al. 2009). Under oxidative stress conditions, accumulation of  $Zn^{2+}$  in the autophagic vacuoles is observed. As these events are also blocked by TPEN, intracellular  $Zn^{2+}$  accumulation induced by oxidative stress is likely upstream from autophagy itself. Interestingly, Lee et al. (2010) showed that MT-III has an important role in regulation of lysosomal function in astrocytes.



## 4.7 Concluding Remarks

Oxidative stress substantially contributes to neuronal injury after ischemic stroke. However, clinical trials have revealed that antioxidants have limited therapeutic benefit for ischemic stroke. Although intravenous administration of thrombolytic drugs such as recombinant tissue plasminogen activator (t-PA) has been shown to have therapeutic efficacy in this disease, there is a very narrow therapeutic window for the use of this drug, as well as an increased risk for intracranial bleeding. Therefore, it is imperative to develop alternative therapeutic strategies for stroke and related conditions. More than a decade of experimental evidence has demonstrated that intracellular  $Zn^{2+}$  is associated with ischemic neuronal cell death. Oxidative stress induces elevation of intracellular  $Zn^{2+}$  levels, which, in turn, activates multiple signaling pathways that can lead to the demise of neurons. Therefore, conversion of oxidative stress into a zinc signal is likely a key component of the molecular mechanisms contributing to ischemic neuronal damage. As such, a better understanding of the signaling pathways triggered by oxidative stress-induced zinc signals may provide novel therapeutic targets for cerebral ischemia in the coming years.

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# Chapter 5

## Zinc Signaling by “Zinc Wave”

Keigo Nishida and Satoru Yamasaki

**Abstract** Zinc (Zn) is an essential heavy metal for all organisms. Zn homeostasis is maintained in mammalian cells through the activity of Zn transporters and Zn-permeable channels and through metallothionein expression levels. Zn is important in nucleic acid metabolism, cell replication, and tissue growth and repair. Zn deficiency is associated with a wide range of pathological conditions, such as impaired immunity, growth retardation, disorders in brain development, and delayed wound healing. Zn binds and affects the activity of several signaling molecules and of transcription factors that have a Zn-binding motif. However, whether Zn itself, as does calcium, acts as an intracellular signaling molecule has been a point of speculation. Recently, we and other groups have demonstrated that Zn does indeed act as an intracellular signaling molecule, converting extracellular stimuli to intracellular signals and controlling various cell functions. This chapter summarizes our current understanding of Zn signaling, especially with regard to the *Zn wave* and the role of Zn signaling in immune cells, and discusses how these processes contribute to allergic responses.

**Keywords** Immune response • Mast cell • Second messenger • Signal transduction • Zinc • Zinc transporter • Zinc wave

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## 5.1 Introduction

Zinc (Zn), an essential trace element, is an important structural component in a great number of proteins, including intracellular signaling enzymes and transcription factors (Prasad 1995; Vallee and Auld 1993). The wide-ranging effects of Zn in the immune and nervous systems have been demonstrated both *in vivo* and *in vitro*, and these effects mainly depend on Zn concentration (Frederickson et al. 2005; Rink and Gabriel 2000). Many researchers have reported that Zn depletion decreases immune function. Natural killer cell-mediated cytotoxic activity, antibody-mediated responses, and host defenses against pathogens and tumors are all reduced in Zn-deficient mice (Fernandes et al. 1979; Fraker et al. 1982; Keen and Gershwin 1990).

Zn plays an essential constitutive role in the conformation and activity of many enzymes, transcription factors, signaling molecules, and other components involved in cellular processes. However, high concentrations of Zn can be cytotoxic, and can induce apoptosis in T and B cells (Ibs and Rink 2003; Telford and Fraker 1995). Zn concentration and distribution within and between cells are controlled by Zn transporters, such as those in the Slc39/ZIP and Slc30/ZnT families, which increase and decrease intracellular Zn levels, respectively (Fukada and Kambe 2011; Kambe et al. 2004; Lichten and Cousins 2009), and Zn is buffered by Zn-binding molecules (Palmiter 2004; Vallee 1995).

We recently showed that Fc epsilon receptor I (FcεRI) stimulation induces an increase in intracellular free Zn, and we named this phenomenon the “Zn wave” (Yamasaki et al. 2007). The Zn wave occurs within several minutes after FcεRI stimulation and originates from the endoplasmic reticulum (ER). Thus, extracellular stimuli can affect intracellular Zn levels through Zn transporters and Zn-permeable channels, and Zn acts as an intracellular signaling molecule (Taylor et al. 2012; Yamasaki et al. 2012). We have proposed that intracellular Zn signaling can be classified into at least two categories: late Zn signaling, which depends on transcriptional changes in Zn-transporter expression, and early Zn signaling, which involves the Zn wave, in which Zn is directly released from the cell organelle by an extracellular stimulus such as FcεRI (Fukada et al. 2011; Hirano et al. 2008; Murakami and Hirano 2008; Nishida et al. 2011).

Many studies have shown that Zn is important in the immune system and that imbalances in Zn homeostasis lead to various disorders, but several questions remain as to how Zn homeostasis and signaling are regulated in mast and other immune cells, and whether Zn transporters are involved in immune cell function. In this chapter, we briefly describe aspects of the Zn-wave phenomenon and discuss the role of Zn signaling in allergic responses.

## 5.2 Cellular Zn Homeostasis by Zn Transporters and Metallothioneins

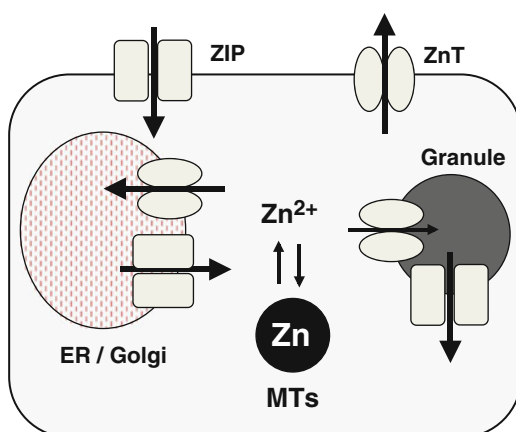
Computational analysis suggests that approximately 10 % of the genes in the human genome may contain Zn-binding motifs (Andreini et al. 2006), reflecting the physiological relevance of Zn and Zn-binding proteins for life in general. In fact, Zn has wide-ranging effects on cellular functions (Vallee and Falchuk 1993), and imbalances in Zn homeostasis can impair growth and cause hair loss, thickening and hyperkeratinization of the epidermis, and testicular atrophy in humans and animal models (Prasad 1991). The concentration and distribution of both intracellular and extracellular Zn are controlled via buffering by Zn-binding molecules, such as metallothioneins, and by Zn transporters, including Slc39/ZIP and Slc30/ZnT family members, which increase or decrease the intracellular Zn levels, respectively (Fig. 5.1).

Metallothioneins (MTs), small cysteine-rich proteins that bind Zn and other metal ions, are thought to be responsible for regulating intracellular Zn concentrations and detoxifying nonessential heavy metals. When intracellular free Zn reaches a threshold concentration, activation of the Zn sensor MTF-1 induces the expression of MTs, which sequester Zn ions (Andrews 2001). Thus, MTs serve as a biochemical device that controls free Zn concentrations by sequestering or releasing Zn in response to oxidative signaling and other biochemical events.

## 5.3 Zn Signaling

Cytosolic and cellular concentrations of free Zn change dynamically in many cells in response to various stimuli. Three major sources for cytosolic free Zn have been identified: uptake from the extracellular environment, reversible storage in vesicles,

**Fig. 5.1** Subcellular localization of Zn transporters and metallothioneins. An illustration of the subcellular localization and potential functions of ZIP- and ZnT family members, based on currently available information. *Arrows* indicate the predicted direction of Zn mobilization. *MTs* metallothionein1/2, *ER* endoplasmic reticulum



and oxidative release from storage proteins. Thus, Zn is increasingly recognized as a potential signaling molecule (Frederickson and Bush 2001; Haase and Rink 2009; Hirano et al. 2008; Sensi et al. 2009).

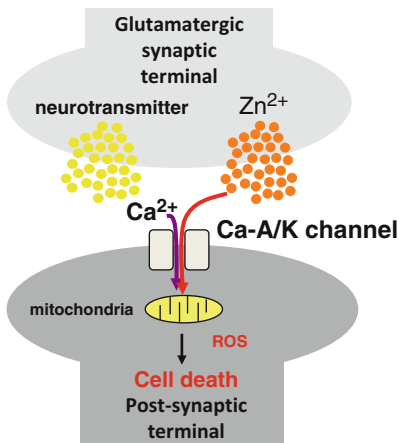
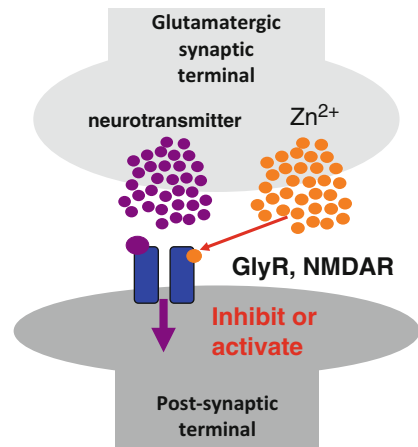
### 5.3.1 *Zn Acts as a Neurotransmitter*

Zn is highly concentrated in synaptic vesicles and is released with glutamate in an activity-dependent manner (Assaf and Chung 1984). Recently, Zn imaging techniques that allow the real-time analysis of Zn concentration and distribution using fluorescent sensor molecules have been widely applied (Kikuchi 2010). Microfluorescence imaging of Zn secretions in rodents showed that exocytotic presynaptic stimulation prompts the release of Zn from hippocampal mossy fiber terminal vesicles into the surrounding milieu (Li et al. 2001; Qian and Noebels 2005; Ueno et al. 2002), where it is taken up into the cytoplasm of neighboring cells through gated Zn channels. A rapid influx of Zn through calcium ion-permeable AMPA/kainate (Ca-A/K) channels triggers the generation of reactive oxygen species (ROS) and is potentially neurotoxic (Weiss and Sensi 2000).

In the foregoing scenario, Zn activity is similar to that of neurotransmitters, which are stored in membrane-enclosed synaptic vesicles, are released by exocytosis, and activate postsynaptic cells through transmitter-gated ion channels (Colvin et al. 2003; Hershfinkel et al. 2001; Xie and Smart 1994). Because Zn modulates both the current response (mediated by excitatory and inhibitory neurotransmitter receptors) and the efficacy of transporter-driven neurotransmitter re-uptake (Smart et al. 2004), synaptically released Zn has been proposed to function as an important regulator of synaptic transmission and plasticity (Lu et al. 2000; Vogt et al. 2000).

ZnT3/Slc30a3, which is highly expressed on synaptic vesicle membranes, is essential for Zn uptake into the vesicles. Although *ZnT3*-KO mice show a loss of stainable Zn in synapses (Cole et al. 1999), they are behaviorally normal except for an enhanced susceptibility to kainite-induced seizures (Lopantsev et al. 2003). In the Tg2576 transgenic mouse model for Alzheimer's disease (AD), Zn release during synaptic transmission induces cerebral  $\beta$ -amyloid (A $\beta$ ) deposits. When these mice are crossed with the *ZnT3*-KO mice, which lack synaptic Zn, the cerebral A $\beta$  deposition is nearly abolished in the Tg2576/*ZnT3*<sup>-/-</sup> progeny (Lee et al. 2002). A recent study by Tamaki et al. provides evidence that Zn is co-secreted with insulin in a ZnT8-dependent manner, and that the secreted Zn not only affects neighboring endocrine cells, but also plays an important role in hepatic insulin clearance by inhibiting clathrin-dependent insulin endocytosis (Tamaki et al. 2013). This finding suggests that Zn release is involved in various pathologies, such as AD and diabetes.

Recent studies have shown that Zn is an endogenous agonist for GPR39, an orphan receptor that is structurally and functionally related to G protein-coupled receptors. The concept of GPR39 as a Zn-sensing receptor in the brain is consistent with the role of Zn as a neurotransmitter (Besser et al. 2009; Yasuda et al. 2007).

**a Zn induces neuronal cells directly****b Zn interacts with and modifies receptors**

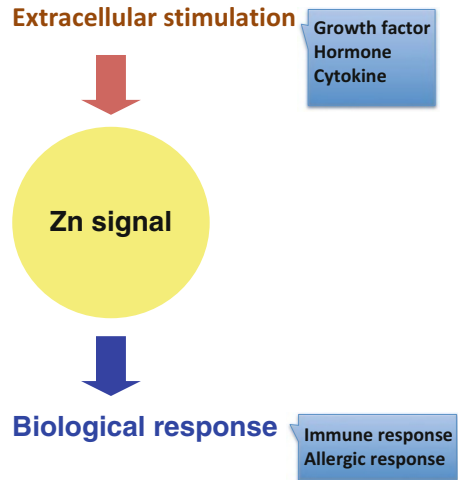
**Fig. 5.2** Zn acts as a neurotransmitter. Zn behaves as a neurotransmitter in neuronal cell communication. **a** Zn is released from vesicles into the surrounding milieu upon exocytotic presynaptic stimulation, and is then taken up into the cytoplasm of neighboring cells through gated Zn channels. The rapid influx of Zn through calcium (Ca) ion-permeable AMPA/kainate (Ca-A/K) channels triggers the generation of reactive oxygen species (ROS) and is potentially neurotoxic. **b** Zn released from glutamatergic synaptic vesicles can bind to the Zn-binding sites of GlyR and NMDAR on postsynaptic neurons to modulate neurotransmission

Intercellular Zn communication mediated through the Zn-sensing receptor GPR39 is also involved in regulating epithelial cell repair (Sharir et al. 2010) and endocrine pancreatic function (Holst et al. 2009). Also supporting the role of Zn as a neurotransmitter, Hosie et al. identified two Zn-binding sites and characterized a third in the GABA receptor using site-directed mutagenesis (Hosie et al. 2003). Hirzel et al. produced knock-in mice carrying a constructed Zn-binding site (a D80A mutation) in the glycine receptor alpha-1-subunit gene (*Glr1*) and demonstrated that Zn modulates neurotransmission (Hirzel et al. 2006). Zn is also known to inhibit *N*-methyl-D-aspartate receptor (NMDAR) activity through a dual mechanism: a voltage-dependent channel block, and a voltage-independent reduction in the probability of the channel opening (Christine and Choi 1990; Legendre and Westbrook 1990; Mayer and Vyklicky 1989). Thus, Zn appears to act as a neurotransmitter in addition to its other roles in the neural system (Fig. 5.2).

### 5.3.2 Zn Acts as a Second Messenger

cAMP was the first intracellular second messenger to be discovered (Berthet et al. 1957), and calcium was the second. At present, only a limited number of intracellular signaling effectors are known, including cAMP, calcium, NO, lipid

**Fig. 5.3** Zn as an intracellular second messenger candidate. Second messengers are molecules that receive signals from stimuli such as hormones, growth factors, and cytokines at the cell surface and relay these signals to target molecules in the cytosol or nucleus. This action, in turn, induces intracellular events that can regulate various biological responses. Zn functions are consistent with those of second messenger molecules



mediators, and G proteins (Gomperts et al. 2002). Interestingly, Zn has also been recognized to have an essential role as a second messenger. Zn itself affects a variety of signaling molecules, including PKC, Ca/calmodulin-dependent protein kinase II (CaMKII), Erk1/2, cAMP-dependent protein kinase (PKA), protein tyrosine phosphatase, and caspase-3 (Brautigan et al. 1981; Haase and Maret 2005; Hubbard et al. 1991; Lengyel et al. 2000; Murakami et al. 1987; Park and Koh 1999; Perry et al. 1997). In addition, Zn activates ion channels such as the transient receptor potential ankyrin 1 (TRPA1) (Andersson et al. 2009; Hu et al. 2009), ATP-sensitive  $K^+$  (Prost et al. 2004), and large-conductance Ca-activated  $K^+$  (Hou et al. 2010) channels. Together, these findings suggest that Zn may function as an intracellular signaling molecule or second messenger if extracellular stimuli, such as cytokines or growth factors, cause the intracellular Zn status to change, whether dependently or independently of transcriptional changes in MTs or Zn transporters (Fig. 5.3).

It is important to determine whether Zn transporters are involved in Zn signaling. We reported that the ZIP6/SLC39A6 is required for the epithelial-mesenchymal transition (EMT) in the zebrafish gastrula organizer, as it is essential for nuclear retention of the E-cadherin-repressor Snail (Yamashita et al. 2004). Because ZIP6/SLC39A6 expression in the zebrafish organizer is dependent on STAT3 activation, any extracellular stimulus that regulates STAT3 activation could change the intracellular Zn level by inducing changes in ZIP6/SLC39A6 or other Zn transporters. TLR4 decreases the intracellular free Zn level by inducing changes in Zn transporter expression in dendritic (Kitamura et al. 2006) and pulmonary endothelial cells (Thambiayya et al. 2011). These observations support the role of Zn as an intracellular second messenger, that is, as a molecule whose intracellular status is altered in response to an extracellular stimulus and that is capable of transducing the extracellular stimulus into an intracellular signaling event.



The role of Zn as a second messenger is further supported by our findings that ZIP13/Slc39a13 is required for the BMP/TGF- $\beta$ -induced nuclear localization of Smad proteins (Fukada et al. 2008), that ZIP14/Slc39a14 is involved in GPCR-mediated signal transduction through cAMP basal-level regulation (Hojo et al. 2011), and that Fc $\epsilon$ RI-stimulation-induced PKC activation is dependent on ZnT5/Slc30a5 in mast cells (Nishida et al. 2009). Thus, extracellular stimuli can, by changing the expression of Zn transporters, affect intracellular signaling pathways by changing the intracellular Zn status.

Besides Zn signaling mediated by Zn transporter expression, Zn signaling is also exemplified by the Zn wave phenomenon, which is a transcription-independent increase in intracellular Zn that occurs in mast cells relatively rapidly (several minutes) after extracellular stimulation (Yamasaki et al. 2007). Zn waves, which originate from the ER, depend on calcium influx and Erk1/2 activation in mast cells. Because the Zn wave does not involve extracellular Zn, and is induced within several minutes of Fc $\epsilon$ RI stimulation, Zn here acts as an intracellular signaling molecule. Using the Zn probe FluoZin-3, Haase et al. revealed that the intracellular Zn level is elevated in peripheral blood mononuclear cells (PBMCs) after polymethyl acrylate (PMA) stimulation (Haase et al. 2006), and in human leukocytes, especially monocytes, after physiological stimulation (Haase et al. 2008). In addition, ZIP7/SIC39A7 is reported to regulate intracellular Zn at the ER membrane (Taylor et al. 2008). It is also possible that transporters and channels other than ZIP or ZnT family members generate Zn waves in individual cell types with various types of stimulation. In any case, the precise molecular mechanisms generating the Zn wave have not been clarified.

### 5.3.3 Zn-Signaling Gatekeepers

Recently, three independent groups reported rapid increases in free Zn, as seen in the Zn wave, in mast cells and lymphocytes upon stimulation with antigens such as Fc $\epsilon$ RI, B-cell receptors (BCRs), and T-cell receptors (TCRs) (Taniguchi et al. 2013; Yamasaki et al. 2012; Yu et al. 2011). Interestingly, these studies reported that the dynamic changes in cytosolic free Zn were regulated by Zn-permeable channels and Zn transporters.

In this section, we briefly describe gatekeepers of Zn signaling, their regulation, and their molecular targets.

#### 5.3.3.1 LTCC-Mediated Zn Signaling in Mast Cells

L-type calcium channels (LTCCs) conduct Zn and can act as Zn-permeable channels on the plasma membrane of neurons and pancreatic  $\beta$  cells (Atar et al. 1995; Gyulkhanyan et al. 2006; Sensi et al. 1997). However, whether LTCCs can function in releasing Zn from intracellular organs has not been clarified. It was

recently revealed that LTCCs have the potential to act as a gatekeeper for the Zn wave that occurs when Fc $\epsilon$ RI induces intracellular Zn signaling in mast cells (Yamasaki et al. 2012).

It is well established that LTCCs function as voltage-gated calcium channels on the plasma membrane. LTCC complexes include  $\alpha_1$ -,  $\beta$ -, and  $\alpha_2/\delta$ -subunits. The  $\alpha_1$ -subunit functions as the voltage sensor, selective filter, and ion-conducting pore (Catterall 2000). The  $\alpha_1$ -subunit on the cell surface is thought to require an association with the  $\beta$ -subunit, which masks one or more ER retention signals (Bichet et al. 2000; Cornet et al. 2002).

In bone marrow-derived mast cells (BMMCs), the dominantly expressed  $\alpha_1$ -subunit ( $\alpha_{1D}$ ) is *cacna1d*, the  $\alpha_1$ -subunit for the LTCC. The expression of LTCC  $\beta$ -subunits, which are required for the localization of  $\alpha_1$ -subunits to the plasma membrane, is very low in mast cells. Furthermore, mast cells express high levels of ZnT-1/Slc30a1, which interacts with  $\beta$ -subunits on the plasma membrane, reducing their availability to bind  $\alpha_1$  and inhibiting  $\alpha_1$ -subunit trafficking to the plasma membrane (Levy et al. 2009). Therefore,  $\alpha_{1D}$  in mast cells localizes to the intracellular area; it co-localizes partially with the ER marker calnexin but not with F-actin, which accumulates beneath the plasma membrane. These observations indicate that  $\alpha_{1D}$  localizes preferentially to intracellular organelle membranes, such as the ER membrane, rather than to the plasma membrane. This intracellular localization of  $\alpha_{1D}$  in BMMCs suggests that it plays a different role in BMMCs than in other cells, in which it is located on the plasma membrane and acts as a calcium channel.

Consistent with this idea, treating mast cells with verapamil, an LTCC inhibitor, reduces their Zn waves compared to control cells, without disturbing cell survival, Fc $\epsilon$ RI expression, or the Fc $\epsilon$ RI-mediated calcium elevation. Diltiazem, another type of LTCC antagonist, also inhibits Zn waves without disturbing the calcium elevation. Not only does verapamil have no effect on the Fc $\epsilon$ RI-mediated calcium elevation in BMMCs, but calcium-mediated signaling, such as the normal nuclear translocation of NFAT2 in response to calcium elevation, is also unaffected (Yamasaki et al. 2012).

On the other hand, treatment with the LTCC agonist (*s*)-(-)-BayK8644 without antigen stimulation elevates the intracellular Zn level but not the calcium level in mast cells (Yamasaki et al. 2012). These findings indicate that LTCC function in mast cells differs from its function as a calcium channel in other cell types, such as neurons and pancreatic  $\beta$  cells. LTCC may have little effect on the intracellular calcium regulation in mast cells because the main mode of calcium influx in these cells, as in lymphocytes, is store-operated calcium (SOC) entry (Vig and Kinet 2009). LTCC agonists induce an increase in intracellular Zn even in the absence of calcium, and this increase is inhibited by verapamil. Fc $\epsilon$ RI induces similar Zn increases in BMMCs in the presence or absence of an LTCC agonist, indicating that the mechanisms responsible for the Fc $\epsilon$ RI-induced Zn wave and the LTCC agonist-induced Zn elevation are probably similar.

Although the Fc $\epsilon$ RI-induced Zn wave is significantly reduced in  $\alpha_{1D}$ -knockdown BMMCs, the Fc $\epsilon$ RI-induced calcium elevation is intact in these cells, as is the case

with verapamil-treated cells. Moreover, the ectopic expression of wild-type  $\alpha_{1D}$  rescues the inhibitory effect of  $\alpha_{1D}$  siRNA knockdown on the Zn wave. These results suggest that the LTCC  $\alpha_{1D}$  subunit is a gatekeeper for the Zn wave.

This finding raises the question of how LTCC regulates the release of Zn from the ER into the cytoplasm. The  $\alpha_1$ -subunit of LTCC contains a voltage-sensor domain, and channel activity is elevated after membrane depolarization. The plasma-membrane potential in BMMCs is hyperpolarized after Fc $\epsilon$ RI stimulation (Shumilina et al. 2008; Vennekens et al. 2007). However, inhibiting the Fc $\epsilon$ RI-mediated plasma-membrane hyperpolarization by high KCl treatment does not impair the induction of the Zn wave. Treatment with bongkreikic acid, which inhibits ADP/ATP transport, inhibits Fc $\epsilon$ RI-mediated intracellular membrane depolarization but does not inhibit the induction of the Zn wave. These observations suggest that regulation of the membrane potential might not affect the Zn wave generation.

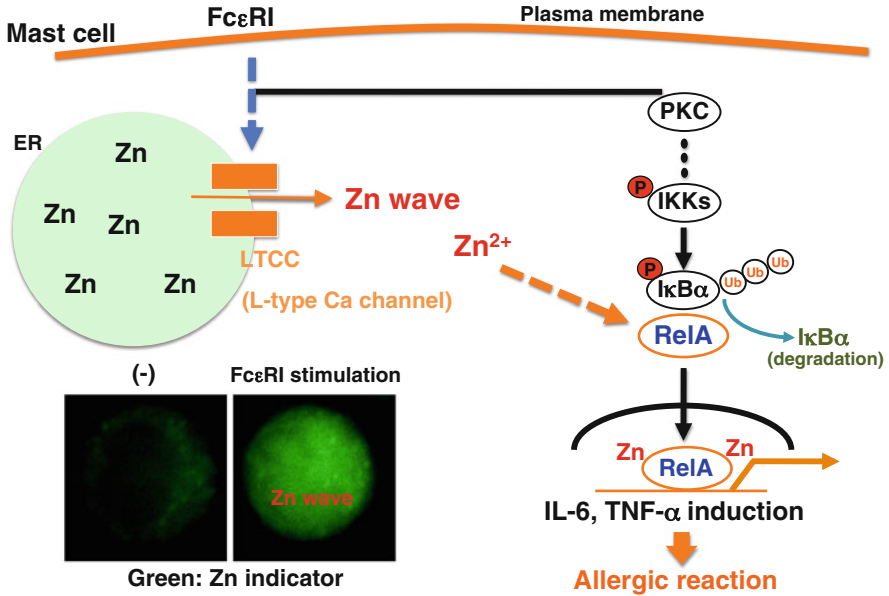
Phosphorylation of the pore-forming  $\alpha_1$ -subunit has an additional effect on channel activity; in fact, cAMP-mediated channel activity is reduced by site-directed mutagenesis of the PKA consensus sites of  $\alpha_{1D}$  (Ramadan et al. 2009). However, a PKA inhibitor did not inhibit the Zn wave. Therefore, PKA might not assist in regulating the Zn wave, at least not in mast cells. This event may be controlled by as yet unidentified regulatory proteins and mechanisms on the ER membrane.

These results show that the LTCC pore-forming  $\alpha_{1D}$ -subunit, when expressed on the ER membrane, functions as a gatekeeper for the Zn wave in mast cells, and that this LTCC-mediated Zn wave may function as an intracellular Zn signal that can positively modify signal transduction to produce inflammatory cytokines (Fig. 5.4).

### 5.3.3.2 ZIP9-Mediated Zn Signaling in B Cells

Taniguchi et al., using the DT40 chicken B-cell line as a model, found that the Zn transporter ZIP9/SLC39A9 induces an increase in intracellular Zn. In contrast to the Zn wave, which originates from the ER, the source of intracellular free Zn in these chicken ZIP9-knockout DT40 (cZip9KO) cells is thought to be the Golgi bodies. Consistent with this scenario, ZIP9 is thought to function in releasing Zn from the Golgi bodies to the cytosol (Taniguchi et al. 2013).

The BCR-signaling pathway is critical for many cellular events, including cell growth, cell proliferation, and apoptosis (Dal Porto et al. 2004; Harwood and Batista 2008, 2010). BCR activation transduces the signal to several cascades, including the PI-3K/Akt, PLC $\gamma$ 2/PKC, and Ras/Raf/ERK cascades (Brazil and Hemmings 2001; Hashimoto et al. 1998; Kurosaki 2011). These cascades are important for the differentiation of antibody-producing cells and memory B cells. ZIP9-mediated Zn signaling affects BCR-mediated Akt and ERK phosphorylations. In fact, BCR-induced Akt and ERK phosphorylations are significantly decreased, along with the enzymatic activity of protein tyrosine phosphatase (PTPase), in cZip9KO cells. Consistent with this observation, overexpressing hZIP9 decreases



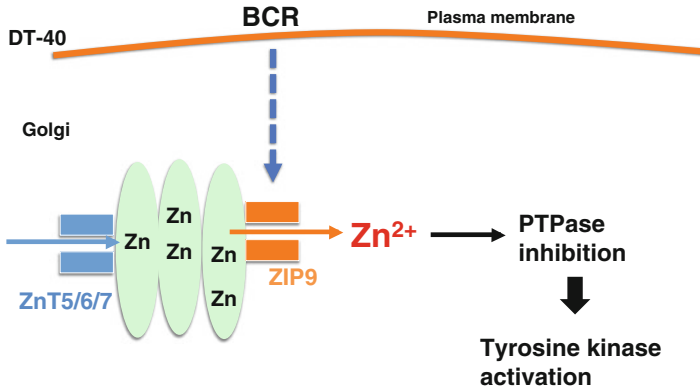
**Fig. 5.4** The Zn wave in FcεRI-mediated mast cell activation. In a phenomenon we named the *Zinc wave*, FcεRI stimulation induces the rapid elevation of intracellular Zn in mast cells by releasing Zn from the ER at the perinuclear region. The LTCC $\alpha_{1D}$  subunit expressed on the ER membrane acts as the Zn-wave gatekeeper in mast cells. LTCC-mediated Zn waves positively regulate the NF- $\kappa$ B DNA-binding activity and are involved in regulating cytokine production

the PTPase activity in Zn-treated cZip9KO cells (Taniguchi et al. 2013). At present, it is not known how ZIP9-mediated Zn signaling is regulated by BCR stimulation. ZIP7 is reported to be activated by its phosphorylation by protein kinase CK2 in a human breast cancer cell line (Taylor et al. 2012). This finding raises the possibility that CK2 can phosphorylate ZIP9 and regulate ZIP9-mediated Zn signaling.

This study concluded that ZIP9 on the Golgi body membrane regulates cytosolic Zn, enhancing the Akt and ERK phosphorylations in B cells (Fig. 5.5). Thus, Zn signaling in B cells may occur via a mechanism similar to that of the Zn wave in mast cells.

### 5.3.3.3 ZIP6-Mediated Zn Signaling in T Cells

Yu et al. found Zn signaling in T cells; TCR stimulation triggers an increase in cytoplasmic Zn concentration within 1 min (Yu et al. 2011). This increase is dependent on extracellular Zn concentration, suggesting that TCR stimulation induces an influx of extracellular Zn into the T cell. Moreover, this influx of Zn is inhibited by silencing the Zn transporter ZIP6, which is expressed on the cytoplasmic membrane.

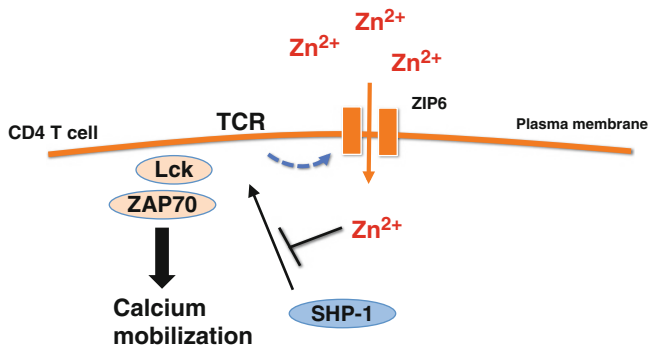


**Fig. 5.5** Proposed action sites of intracellular Zn release by ZIP9 in the activation of B-cell receptor signaling in DT40 cells. An illustration of the proposed mechanism by which Zn induces the inhibition of protein tyrosine phosphatase (PTPase) by ZIP9 in DT40 cells, leading to the activation of B-cell receptor (*BCR*) signaling. Intracellular Zn is incorporated into Golgi bodies by ZnT5/6/7, and ZIP9 induces its release from the Golgi back into the cytosol. This Zn inhibits PTPase activity and induces tyrosine kinase activation probably indirectly by regulating upstream components of the signal transduction

Early TCR signaling events include the tyrosine phosphorylation of several signaling molecules. The Src protein kinase Lck is primarily responsible for the early phosphorylation of tyrosines within the ITAM motifs of CD3 $\zeta$  and ZAP70 (Palacios and Weiss 2004). Extracellular Zn influences ZAP70 phosphorylation and inhibits negative regulatory feedback loops, accounting at least in part for the increase in ZAP70 phosphorylation. SHP-1, which dephosphorylates tyrosines within the ITAM motifs of ZAP70 and other signaling molecules after being recruited to Lck (Altan-Bonnet and Germain 2005), is a prime candidate target for the ZIP6-mediated Zn signaling. In fact, an increase in Zn influx reduces SHP-1 recruitment to the TCR activation complex, augments ZAP70 phosphorylation, and sustains calcium influx. Thus, Yu et al. proposed that the influx of Zn after TCR stimulation leads to a local increase in cytoplasmic Zn that modifies early TCR signaling events (Fig. 5.6).

## 5.4 Zn and Zn Signaling in Allergies

Many studies have reported that Zn depletion decreases immune function, indicating that Zn acts as a positive regulator in immune responses. However, the precise roles of Zn and the molecular mechanism(s) of its function in allergic responses have not been clarified. Here, we describe the effect of Zn and Zn homeostasis on biological events, especially those of mast cell-mediated allergy responses, and outline our current understanding of the physiological role of the Zn wave.



**Fig. 5.6** Zn functions as an ionic signaling molecule after T-cell activation. Cytoplasmic Zn concentrations increase within 1 min after T-cell receptor (*TCR*) triggering as a result of Zn influx via the transporter *ZIP6*. This increase, which is most pronounced in the immediate subsynaptic area, enhances TCR signaling, at least partly by inhibiting the recruitment of *SHP-1*

#### 5.4.1 The role of Zn in Mast Cell-Mediated Allergic Responses

Allergy-related cells, such as mast cells, eosinophils, and basophils, are involved in allergic reactions such as anaphylaxis, asthma, and atopic dermatitis (Galli et al. 2008; Kawakami et al. 2009; Metz et al. 2007). Mast cell activation leads to the secretion of two classes of mediators. The first consists of preformed mediators that are stored in granules and can be quickly secreted in activated cells. The second class of mediators, the cytokines and chemokines, must be newly synthesized and are secreted more slowly. These released molecules play pivotal roles in the inflammatory reactions observed in patients with allergies.

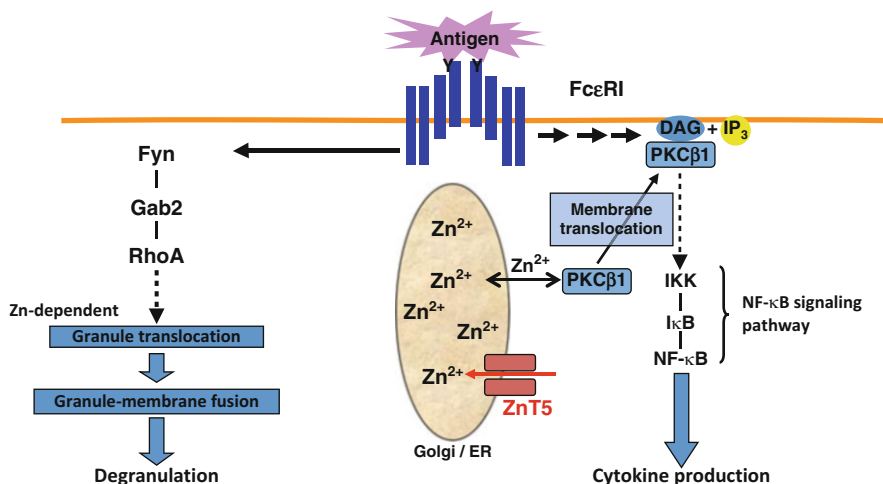
Intracellular Zn levels and distribution can be analyzed using the Zn probe Zinquin, which allows the imaging of distinct pools of Zn in allergy-related cells. Granules in mast cells, for instance, fluoresce intensely with Zinquin (Ho et al. 2004). Airway epithelial cells are also rich in Zn (Truong-Tran et al. 2000). Furthermore, Zn deficiency is reported to increase allergic eosinophilic inflammation, whereas dietary Zn supplementation attenuates its intensity (Richter et al. 2003a). Interestingly, Zn deficiency is a risk factor for asthma development (Riccioni and D’Orazio 2005; Zalewski et al. 2005). These reports suggest that Zn is involved in the development of allergic disease. In addition, high levels of *ZIP2* are observed in the leukocytes of asthmatic infants (Xu et al. 2009). However, the precise role of Zn and Zn transporters in allergy-related cells is poorly understood.

We showed that Zn is required for both degranulation and cytokine production in mast cells. The Zn chelator TPEN [*N,N,N,N*-tetrakis (2-pyridylmethyl) ethylenediamine] inhibits histamine release, cytokine production, and lipid mediator secretion. The inhibitory effects of TPEN are rescued by Zn supplement, and chelators of other metals do not affect mast cell function (Kabu et al. 2006). These observations indicate that Zn is crucial for degranulation and cytokine production in mast cells. Similarly, it has been reported that Zn depletion by TPEN or by the

clinically used heavy metal chelator DMPS (Torres-Alanis et al. 1995) inhibits the mRNA expression of eotaxin and other chemokines in human lung cell lines (Richter et al. 2003b). All together, these reports suggest that Zn chelators and their derivatives are a promising source of anti-allergy drugs that may act differently from histamine antagonists and other currently available allergy treatments.

It is not clear exactly how Zn chelators inhibit mast cell function. We reported that the degranulation of mast cells can be divided into two processes. First, FcεRI stimulation triggers microtubule polymerization and granule translocation to the plasma membrane in a calcium-independent manner. Fyn/Gab2/RhoA signaling, but not Lyn/SLP-76 signaling, is critical in this calcium-independent microtubule-dependent pathway (Nishida et al. 2005). Second, the granules fuse with the plasma membrane in a well-characterized calcium-dependent manner. To clarify the mechanisms behind the effect of Zn chelators, we first examined whether TPEN interfered with either of these two processes. Although TPEN had little effect on calcium mobilization or the early FcεRI-induced tyrosine phosphorylation of various signaling molecules, it suppressed the FcεRI-induced granule translocation. Given that granule translocation depends on cytoskeletal proteins such as tubulin and actin (Goode et al. 2000), and that microtubules are critical for granule translocation and vesicle transport (Nishida et al. 2005; Smith et al. 2003), we speculated that TPEN might affect microtubule assembly. However, such an effect by TPEN on FcεRI-induced microtubule formation has not been found, suggesting the existence of Zn-regulated molecule(s) that are directly linked to microtubules and granules. Kinesin receptors, or linker-cargo proteins, have been identified as key molecules for microtubule-dependent vesicle trafficking (Schnapp 2003); thus, the TPEN target might have a kinesin-interacting region through which it links kinesin to vesicles. In addition, TPEN suppresses FcεRI-mediated cytokine production and the transcription of interleukin (IL)-6 and tumor necrosis factor (TNF)-α mRNAs. PKC is activated upon FcεRI stimulation and is involved in cytokine production through NF-κB activation (Klemm et al. 2006; Nechushtan et al. 2000), and TPEN inhibits the FcεRI-mediated plasma membrane translocation of PKC (Kabu et al. 2006). These results suggest PKC as one of the TPEN targets in regulating cytokine production. This hypothesis is supported by findings from other groups showing that the Zn-binding domain of PKC is required for PKC translocation to the plasma membrane after stimulation (Oancea et al. 1998).

We demonstrated that ZnT5 is crucial in mast cell activation and mast cell-mediated allergic reactions. *Znt5* is expressed at high levels in mast cells, and its transcription is enhanced by FcεRI stimulation, suggesting that *Znt5* is involved in mast cell-mediated allergic reactions. *ZnT5-KO* mice have defects in mast cell-mediated, delayed-type allergic reactions such as contact hypersensitivity, but not in immediate-type reactions such as anaphylaxis (Nishida et al. 2009). Consistent with this in vivo analysis, ZnT5 is required for FcεRI-mediated cytokine production, but not for degranulation, in mast cells. In *ZnT5-KO* mast cells, the FcεRI-induced IL-6 and TNF-α mRNAs are reduced. Finally, we showed that ZnT5 is required for the FcεRI-induced translocation of PKC to the plasma membrane and for the nuclear translocation of NF-κB. Thus, ZnT5 is selectively required for mast cell-mediated, delayed-type allergic responses, and is a novel player in PKC/NF-κB



**Fig. 5.7** Zn and Zn transporters are involved in FcεRI-mediated mast cell activation. Zn is required in multiple steps of FcεRI-induced mast cell activation, including degranulation and cytokine production. Zn levels depend on FcεRI-induced granule translocation, regulated by the Fyn/Gab2/RhoA-mediated signaling pathway. Zn and ZnT5 are also required for PKC translocation to the plasma membrane and NF-κB's subsequent nuclear translocation, leading to the production of cytokines such as interleukin (IL)-6 and tumor necrosis factor (TNF)-α

signaling. How ZnT5 regulates PKC translocation to the plasma membrane is still unknown. PKC contains a Zn-binding motif, and Zn is essential for maintaining the structure of PKC (Corbalan-Garcia and Gomez-Fernandez 2006). Mutational analysis showed that the Zn-binding domain of PKC is essential for the plasma membrane translocation of PKC. Furthermore, in experiments utilizing *ZnT5-KO* DT40 cells, Suzuki and colleagues showed that ZnT5 expressed on the ER–Golgi membrane is required for the enzymatic activity of the Zn-dependent alkaline phosphatases (ALPs), which are processed from apoALPs to holoALPs in the ER–Golgi (Suzuki et al. 2005a, b). Together, these findings indicate that ZnT5 may be involved in supplying Zn to the Zn finger-like domain in PKC and ALP.

All these findings suggest that Zn and Zn transporters are involved in mast cell-mediated allergic responses by regulating degranulation and cytokine production, and that Zn transporters modulate the PKC/NF-κB signaling pathway, which regulates the gene expression levels of cytokine and chemokines (Fig. 5.7).

#### 5.4.2 Role of the Zn Wave in Mast Cell-Mediated Allergic Responses

As already mentioned, we found that the pore-forming  $\alpha_{1D}$ -subunit of LTCC on the ER membrane is involved in generating the Zn wave in mast cells. Using siRNA or an LTCC antagonist, we found that the Zn wave can regulate cytokine gene



induction. LTCC antagonist-treated mast cells cannot increase the intracellular concentration of free Zn, either through a Zn wave or through the mRNA induction and protein synthesis of IL-6 and TNF- $\alpha$ . Furthermore, both Fc $\epsilon$ RI-induced Zn waves and cytokine gene induction are inhibited in mast cells treated with siRNA against the LTCC  $\alpha_{1D}$ -subunit. These results suggest that the Zn wave is required for the Fc $\epsilon$ RI-induced cytokine production in mast cells.

It is not certain how the Zn wave acts to induce cytokine genes. We found that the LTCC-mediated intracellular Zn signal upregulates NF- $\kappa$ B DNA-binding activity and transactivation of inflammatory cytokines. This NF- $\kappa$ B-mediated transactivation can be divided into three steps: NF- $\kappa$ B first dissociates from I $\kappa$ B after I $\kappa$ B phosphorylation and degradation, then translocates from the cytosol to the nucleus, and finally binds to its target sequences. We found that the frequency of NF- $\kappa$ B p65 nuclear translocation is reduced in LTCC antagonist-treated cells, even though upstream regulators are unaffected. Treatment with the exportin inhibitor LMB enhances the amount of NF- $\kappa$ B in nuclei in both LTCC antagonist-treated and LMB-treated cells, suggesting that the Zn wave is not involved in NF- $\kappa$ B nuclear translocation. However, our evidence indicates that the Zn wave is required for NF- $\kappa$ B DNA-binding activity. In further support of this scenario, LTCC antagonist treatment reduces NF- $\kappa$ B DNA-binding activity, whereas supplementing cell lysates with Zn enhances it. These findings suggest that Zn wave-induced increases in intracellular Zn positively regulate NF- $\kappa$ B DNA-binding activity (Fig. 5.4).

Finally, we evaluated the role of the Zn wave in allergic reactions *in vivo* using an LTCC antagonist. Mast cells are effector cells for allergic responses *in vivo*, and mast cell-derived cytokines, which are induced by the Fc $\epsilon$ RI-mediated activation of the PKC/Bcl10/Malt1/NF- $\kappa$ B signaling pathway, are involved in delayed-type allergic responses such as contact hypersensitivity (CHS) (Klemm et al. 2006; Nishida et al. 2009). Mast cell-derived TNF is required for a maximum CHS response; it induces leukocyte infiltration at the inflammation site (Biedermann et al. 2000), enhances the elongation of cutaneous nerves (Kakurai et al. 2006), and enhances the dendritic cell migration to draining lymph nodes (Suto et al. 2006). In this study, we revealed that treating mice with the LTCC antagonist verapamil inhibits CHS, which is a delayed-type immune response, without affecting passive cutaneous anaphylaxis (PCA), which is an immediate-type response. Consistent with these results, we showed that verapamil treatment inhibits the Fc $\epsilon$ RI-mediated activation of NF- $\kappa$ B DNA-binding activity and cytokine gene induction, but not calcium elevation or degranulation in BMMC. Thus, the inhibitory effect of verapamil on CHS might depend at least partly on the reduction of mast cell-derived cytokine production and be independent of histamine and other mediators.

In future studies, knocking out the LTCC $\alpha_{1D}$ -subunit in mice will further clarify Zn wave *in vivo* roles in allergic and other immune responses.

## 5.5 Perspective

We have discussed new insights into the relevance of Zn, its channels, and its transporters in immune cell responses, particularly focusing on the role of Zn as a signaling molecule. Our studies and those of other researchers indicate that Zn signals affect a variety of immune-signaling pathways to produce biological outputs. Thus, we propose that Zn functions as a signaling molecule (Fukada et al. 2011; Hirano et al. 2008; Murakami and Hirano 2008; Nishida et al. 2011). Many questions about the role of Zn in signaling remain to be answered. We do not yet know the other targets, the biological significance in vivo, or the regulatory mechanisms of Zn signaling, particularly in the Zn wave. As with calcium, it is likely that Zn is an important intracellular signaling molecule in various systems including immune system. We hope that recognition of the importance of Zn signaling and Zn biology will open new avenues for future research.

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# Chapter 6

## The Zinc-Sensing Receptor, ZnR/GPR39: Signaling and Significance

Michal Hershfinkel

**Abstract** The structural role of  $Zn^{2+}$  in stabilizing numerous enzymes and zinc fingers of transcription factors has been well established for several decades. Therefore, the major effects of this metal ion on growth, development, and cognitive function were not surprising. The importance of cellular homeostasis of  $Zn^{2+}$  is underlined by the identification of more than 20 proteins involved in transport of  $Zn^{2+}$  into the cytoplasm and various organelles. In the past decade, evidence for a signaling role of  $Zn^{2+}$  is emerging, suggesting this ion acts as a first and second messenger. Thus, transient changes in extracellular and intracellular  $Zn^{2+}$  were monitored and  $Zn^{2+}$ -dependent regulation of multiple signaling pathways was shown. We have identified the function of ZnR, a Gq protein-coupled receptor that triggers the release of  $Ca^{2+}$  via the IP3 pathway. This ZnR-dependent signaling regulates cellular pathways involved in survival and proliferation, such as the MAP and PI3 kinase pathways, as well as modulation of ion transport systems such as the  $Na^+/H^+$  exchanger or the  $K^+/Cl^-$  co-transporter. The GPR39 was then shown to mediate extracellular  $Zn^{2+}$ -dependent ZnR signaling. Here we discuss the major role of ZnR/GPR39 as the link between extracellular  $Zn^{2+}$  and intracellular signaling pathways regulating the physiological function of epithelial and neuronal cells. A major future challenge will be to identify the role of ZnR/GPR39 in diseases linked to  $Zn^{2+}$  dyshomeostasis.

**Keywords** GPCR • Zinc signaling • Zn-sensing receptor • ZnR/GPR39

### 6.1 Introduction

$Zn^{2+}$  is an essential micronutrient that is required for proper development and function of the digestive, immune, nervous, secretory, and integumentary systems (Prasad 1995, 2008; Sandstead et al. 2000; Kambe et al. 2008; Kelleher et al. 2011; Roohani et al. 2013). The role of  $Zn^{2+}$  as a cofactor or structural element in numerous proteins, enzymes, and transcription factors has been established for

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several decades (Vallee and Falchuk 1993; Maret 2001b). More recent work has shown that changes in extracellular  $Zn^{2+}$  as well as intracellular  $Zn^{2+}$  affect cellular signaling (Hershinkel 2006; Fukada et al. 2011; Maret 2001a). Changes in extracellular  $Zn^{2+}$  may result by its release from vesicles containing high concentrations of this ion that are present in the pancreas, brain, mammary gland, salivary glands, and digestive system (Frederickson et al. 1987, 1992; Frederickson and Danscher 1990; Ishii et al. 1999; Danscher and Stoltenberg 2003; McCormick et al. 2010).  $Zn^{2+}$  is packed into these vesicles by specific  $Zn^{2+}$  transporters from the ZnT family that transport this ion from the cytoplasm (Liuzzi and Cousins 2004; Eide 2006; Sekler et al. 2007). Changes in extracellular  $Zn^{2+}$  may also occur following the release of this ion from injured cells. For example, following injury of keratinocytic cells, endogenous  $Zn^{2+}$  is released and may act as a paracrine agonist to a  $Zn^{2+}$ -sensing receptor ZnR, leading to activation of intracellular signaling pathways associated with wound healing (Sharir et al. 2010). These transient changes are quickly reversed either by re-uptake of  $Zn^{2+}$  via an extensive transporter system consisting of Zip and ZnT proteins or by the buffering of free  $Zn^{2+}$  by proteins such as metallothioneins (Vasak 2005; Krezel and Maret 2006; Sekler et al. 2007; Fukada et al. 2011). The dramatic changes in the extracellular concentration of  $Zn^{2+}$  may be recruited for cellular signaling; thus, a mechanism for sensing the changes is required. Regulation of key cellular functions based on these changes may be implicated by the fact that  $Zn^{2+}$  has a major role in the physiological functions of virtually all organ systems. Indeed, at the cellular level  $Zn^{2+}$  triggers proliferation of cells, particularly epithelial cells. Its deficiency is associated with cell death and growth retardation, as well as impaired wound healing, and it is considered an important factor in various forms of diarrhea (Prasad 1995, 2008; MacDonald 2000; Walker and Black 2010; Sandstead 2012). Among the most studied roles of  $Zn^{2+}$  is its role as an essential micronutrient for cognitive functions: its deficiency results in neurological disorders and in neuronal death (Sandstead et al. 2000; Takeda 2001; Takeda et al. 2003; Sensi et al. 2011). Indeed,  $Zn^{2+}$  dyshomeostasis is implicated in neuronal loss during Alzheimer's disease, ischemia, and stroke, as well as epilepsy (Choi and Koh 1998; Weiss et al. 2000; Bush 2003; Stoltenberg et al. 2007; Sensi et al. 2011).

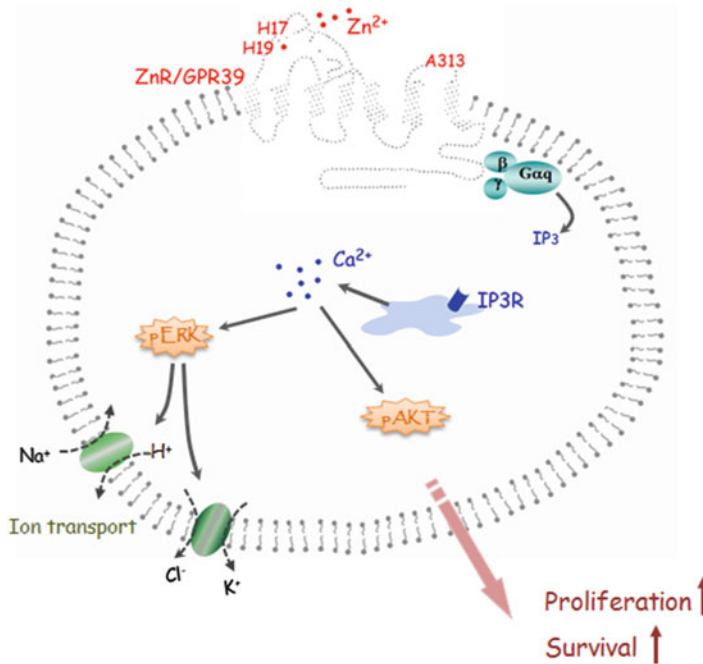
Numerous studies have shown that extracellular  $Zn^{2+}$  indirectly activates cell signaling via allosteric modulation. For example,  $Zn^{2+}$  interacts with all major neuronal membrane transporters: the dopamine transporter, NMDA, glycine and the GABA ionotropic receptors (Paoletti et al. 1997; Lynch et al. 1998; Han and Wu 1999; Hosie et al. 2003; Herin and Aizenman 2004). Regulation of the purinergic receptors and store-operated channel (SOC), which are found on most cell types and tissues, links between  $Zn^{2+}$  and the important second messenger,  $Ca^{2+}$  (Wildman et al. 1999; Acuna-Castillo et al. 2000; Gore et al. 2004). A role for intracellular and extracellular  $Zn^{2+}$  was suggested as a trigger of intracellular pathways that induce cell proliferation and survival. For example, extracellular  $Zn^{2+}$  upregulated the PI3 kinase pathway, leading to activation of AKT in fibroblasts (Kim et al. 2000). Another major pathway linked to cell proliferation is the mitogen-activated kinase (MAPK) pathway that was also activated by extracellular  $Zn^{2+}$ , which in turn,

induced expression of p21(CiP/WAF1) and cyclin D1 (Oh et al. 2002). It was suggested that intracellular  $Zn^{2+}$  induces transactivation of epidermal growth factor receptor (EGFR) by Src in airway epithelial cells (Wu et al. 2002, 2003, 2005). Although binding sites were found on intracellular kinases and membrane receptors, a direct and distinct mechanism linking extracellular  $Zn^{2+}$  to cellular signaling was unknown for many years. We hypothesized that such a mechanism exists and subsequently described the interaction of extracellular  $Zn^{2+}$  with a specific target, an extracellular  $Zn^{2+}$ -sensing receptor that we have functionally termed ZnR (Hershinkel et al. 2001, 2007). We then showed that ZnR is the major mediator of  $Zn^{2+}$ -dependent intracellular signaling, as is discussed in the current review.

## 6.2 The ZnR/GPR39 Is Mediating $Zn^{2+}$ -Dependent Signaling

### 6.2.1 Functional Identification of a Putative $Zn^{2+}$ -Sensing Receptor, the ZnR

Because of the crosstalk between the ions and the central role of  $Ca^{2+}$  in regulating many of the signaling pathways known to be activated by  $Zn^{2+}$ , we asked if  $Zn^{2+}$ -dependent signaling triggers changes in intracellular  $Ca^{2+}$ . Indeed, application of extracellular  $Zn^{2+}$  triggered a rise in intracellular  $Ca^{2+}$  released from thapsigargin-sensitive stores via the IP<sub>3</sub> pathway (Hershinkel et al. 2001; Maret 2001a, b) (Fig. 6.1). Focusing on physiologically relevant tissues, we and others have shown  $Zn^{2+}$ -dependent  $Ca^{2+}$  release in colonocytes, keratinocytes, pancreatic cells, prostate cancer cells, and salivary gland cells, all epithelial cells with high proliferation rates (Azriel-Tamir et al. 2004; Sharir and Hershinkel 2005; Dubi et al. 2008; Holst et al. 2009).  $Zn^{2+}$ -dependent activation of this pathway was also shown in neurons (Besser et al. 2009). Inhibitors of  $G\alpha_q$  (Takasaki et al. 2004; Taniguchi et al. 2004), inositol 1,4,5-trisphosphate (IP<sub>3</sub>) receptor, and phospholipase C (PLC) attenuated this  $Zn^{2+}$ -dependent  $Ca^{2+}$  rise, indicating that the  $Ca^{2+}$  release is mediated by activation of a  $G\alpha_q$ -coupled receptor (Hershinkel et al. 2001; Azriel-Tamir et al. 2004). The  $Zn^{2+}$ -dependent  $Ca^{2+}$  rise was not attenuated by an inhibitor of tyrosine kinase, suggesting that the response is not mediated by this family of receptors. The specificity of the receptor to  $Zn^{2+}$  was also shown, as the  $Ca^{2+}$  response was not triggered by other heavy metal ions tested, such as  $Mn^{2+}$ ,  $Cu^{2+}$ , and  $Fe^{2+}$  (Hershinkel et al. 2001). This finding was in agreement with another study, which also showed that cation-sensing receptors are not activated by  $Zn^{2+}$  (Riccardi 1999). The other well-described cation receptor is the  $Ca^{2+}$ -sensing receptor (CaSR) (Brown 2000; Brennan et al. 2013); despite the link between these ions, the  $Zn^{2+}$ -dependent  $Ca^{2+}$  increase was distinct from the activity of the CaSR as overexpression of CaSR did not produce an increase in  $Ca^{2+}$  following application of extracellular  $Zn^{2+}$  (Hershinkel et al. 2001). Thus, our



**Fig. 6.1** A scheme for ZnR/GPR39 signaling. ZnR/GPR39, found on the cellular membrane, binds  $Zn^{2+}$  via the indicated residues. Asp313 serves as pH sensor on ZnR/GPR39. Shown are the cellular pathways activated by ZnR/GPR39 and the physiological roles of the receptor

experiments revealed a Gq-coupled,  $Zn^{2+}$ -sensing receptor, ZnR, linking changes in extracellular  $Zn^{2+}$  and downstream signal transduction pathways. Following the  $Ca^{2+}$  rise triggered by  $Zn^{2+}$ , enhanced activation of the mitogen-activated protein (MAP) kinase pathway and the PI3 kinase pathways was observed. These pathways are closely linked to enhanced cell survival and proliferation (Chappell et al. 2011), and thus the ZnR may be the mediator of the well-established role of  $Zn^{2+}$  (MacDonald 2000). In neurons, ZnR activation was also shown to activate the calcium calmodulin (CAM) kinase II pathway, an essential pathway related to cognitive function (Rongo 2002). Finally, ZnR was shown to have a paracrine role triggering signaling in neighboring cells via inducing release of ATP from salivary gland ductal cells, HSY (Sharir and Hershinkel 2005). Using a coculture of ZnR-expressing HSY cells and vascular smooth muscle cells (VSMCs), which do not express a functional ZnR, it was shown that application of  $Zn^{2+}$  induced a  $Ca^{2+}$  rise in both HSY cells and VSMC. The  $Ca^{2+}$  rise in the VSMC was inhibited by the ATP scavenger apyrase. Such a paracrine effect of ZnR extends the effect of the receptor by enhancing the  $Ca^{2+}$  signals also in neighboring cells that do not express a ZnR. For example, this phenomenon may enhance wound-healing effects of  $Zn^{2+}$  by promoting the proliferation and migration of both fibroblasts and keratinocytes (Huang et al. 1999), although fibroblasts do not have a functional ZnR (Hershinkel et al. 2001).

A hallmark of Gq protein-coupled receptor (GPCR) activity is a desensitization process that occurs after a brief exposure to their ligands in which the receptor undergoes internalization and degradation (McDonald and Lefkowitz 2001; Kohout and Lefkowitz 2003). There are striking differences in the degree of functional desensitization among GPCRs, mainly reflecting the ratio between the recycling versus degradation of the receptor. The degree of desensitization thus regulates the cellular signaling triggered by these receptors (Mohan et al. 2012). The fact that  $Zn^{2+}$  is not scavenged as are most ligands of GPCRs suggested that protection of cells from excessive  $Ca^{2+}$  signaling must occur via desensitization of the ZnR. Indeed, brief exposure of the epithelial and neuronal cells to subtoxic concentrations of  $Zn^{2+}$  led to profound and prolonged desensitization of the ZnR (Azriel-Tamir et al. 2004; Dubi et al. 2008; Besser et al. 2009). Remarkably,  $Zn^{2+}$  in the presence of citrate, an extracellular chelator of  $Zn^{2+}$ , also induced desensitization of the ZnR signaling (Dubi et al. 2008). This desensitization effectively inhibited  $Zn^{2+}$ -dependent signaling, suggesting that the ZnR is the major regulator of cellular  $Zn^{2+}$  signaling.

### 6.2.2 *GPR39 Is the Molecular Moiety of ZnR*

Although the functional and physiological relevance of the ZnR was established, the molecular moiety that mediates its function was unknown. The activity of the G protein-coupled receptor 39 (GPR39) was suggested to be modulated by zinc, but the physiological relevance of this ion was not addressed (Holst et al. 2004; Elling et al. 2006). GPR39 was an orphan receptor related to the ghrelin/neurotensin receptor subfamily (McKee et al. 1997). GPR39 is expressed in all vertebrates; it is expressed in a range of tissues including adipose tissue, thyroid, and heart, but it is mostly expressed in the pancreas, GI tract, liver, and kidney (Jackson et al. 2006; Egerod et al. 2007). The receptor is composed of 435 amino acids, encoded via two exons (Popovics and Stewart 2011). A splice variant has been identified that is encoded by the first exon only and is assumed to be nonfunctional (Egerod et al. 2007). Although obestatin was originally suggested to activate GPR39 and have an opposing effect to ghrelin regulating food intake (Zhang et al. 2005), subsequent studies could not verify this activity (Lauwers et al. 2006; Holst et al. 2007). It was then established that  $Zn^{2+}$  activates GPR39 signaling, and this ion was also singled out as the trigger of GPR39 signaling within serum (Holst et al. 2007; Yasuda et al. 2007). GPR39 signaling is mediated through  $G\alpha_q$ , which stimulates IP<sub>3</sub> and downstream release of  $Ca^{2+}$ , but it was also shown to activate the cAMP response element that mediated transcription via MAPK activation. A major role for ZnR/GPR39 in enhancing epithelial cell proliferation and survival was indeed shown, as is discussed next. Interestingly, GPR39 activity was suggested to be neuroprotective in a hippocampal cell line (Dittmer et al. 2008), but the role of  $Zn^{2+}$  in this system was not described. GPR39 was suggested to have high constitutive activity as measured by the levels of IP<sub>3</sub> (Dittmer et al. 2008), which may be

insufficient to trigger downstream  $\text{Ca}^{2+}$  signaling or MAP and PI3 kinase phosphorylation, as activation of these pathways was not observed in cells endogenously expressing the receptor as well as in overexpressing HEK-293 cells (Cohen et al. 2012a, b). Another explanation, to the constitutive activity as well as the response to obestatin, may be that the activation of signaling likely resulted from residual  $\text{Zn}^{2+}$  often found in physiological solutions (Kay 2004; Maret 2012; Wilson et al. 2012).

Although cellular studies addressed the signaling triggered by the ZnR/GPR39, in vivo studies regarding the physiological role of GPR39 were done using GPR39 knockout (KO) mice (Moechars et al. 2006). These mice were characterized by accelerated gastric emptying and with a higher volume of gastric fluid secretion, which were not related to higher acid secretion; however, in this work a link to  $\text{Zn}^{2+}$  or its deficiency was not shown (Moechars et al. 2006). The relevance of this receptor to systems where  $\text{Zn}^{2+}$  deficiency plays a major role led us to hypothesize that GPR39 is the functionally described ZnR. We therefore established an siRNA silencing paradigm in which we silenced the expression of GPR39 and determined the signaling pathway activated by  $\text{Zn}^{2+}$  (Besser et al. 2009). In several experiments we have shown that ZnR activity is mediated by GPR39 in keratinocytes, colonocytes, salivary gland ductal cells, and prostate cancer cells as well as in neurons (Besser et al. 2009; Sharir et al. 2010; Cohen et al. 2012a, b; Asraf et al. 2014). In agreement, we monitored loss of ZnR-dependent signaling in native colon tissue and hippocampal CA3 neurons (Chorin et al. 2011; Cohen et al. 2012a, b). Thus, we conclude that ZnR and GPR39 are one and the same receptor, termed ZnR/GPR39.

### 6.2.3 Regulation of ZnR/GPR39

The  $\text{Zn}^{2+}$ -binding site on GPR39 consists of three residues: His 17, His19, and Asp313 (Storjohann et al. 2008). The Asp residue was suggested to act as a tethered inverse agonist that is diverted upon binding of  $\text{Zn}^{2+}$  to trigger signaling. The physiologically relevant  $\text{PK}_a$  of the residues acting as the  $\text{Zn}^{2+}$ -binding site raised the hypothesis that ZnR/GPR39 may be regulated by changes in pH (Cohen et al. 2012a, b). Epithelial cells that express ZnR/GPR39 may face changes in extracellular pH within the digestive system lumen or in the epidermis during physiological activity, and also in the brain, most likely during pathological conditions (Perdikis et al. 1998; Sharma et al. 2005; Holzer 2009, 2011; Sandoval et al. 2011). Indeed, the colonocytic ZnR/GPR39-dependent  $\text{Ca}^{2+}$  responses are maximal at pH 7.4 but are completely abolished at pH 6.5. ZnR/GPR39-dependent activation of MAP or PI3 kinases was abolished at an acidic extracellular pH of 6.5 (Cohen et al. 2012a, b). Surprisingly, the histidine residues forming the  $\text{Zn}^{2+}$ -binding site, His17 or His19, or other extracellular-facing histidines, did not affect the pH dependence of ZnR/GPR39. In contrast, replacing Asp313 to alanine

resulted in loss of the pH dependence of the ZnR/GPR39 response, as similar  $\text{Ca}^{2+}$  responses were triggered by  $\text{Zn}^{2+}$  at pH 7.4 or 6.5. Importantly, although substitution of Asp313 to Ala abolished the pH dependence, substitution to His or Glu residues restored pH sensitivity of the receptor. Thus, Asp313 is an essential residue of the pH sensor of ZnR/GPR39 that is tuned to sense physiologically relevant changes in extracellular pH regulating its activity (Cohen et al. 2012a, b).

The important role of heterodimerization of GPCRs that diversifies the physiological response of these receptors to their ligands (Gomes et al. 2004; Albizu et al. 2006) raised the question whether ZnR/GPR39 also interacts with other GPCRs. Notably, only two ion-sensing receptors were described thus far, the  $\text{Ca}^{2+}$  sensing receptor, CaSR (Brown 2000; Chattopadhyay et al. 1997) and the ZnR/GPR39. Both the ZnR/GPR39 and the CaSR exhibit similarity in the signaling pathway, which they activate via a Gq-dependent pathway. However the CaSR is related to GPCR family-C receptors and the ZnR/GPR39 is a family-A member. Importantly,  $\text{Zn}^{2+}$ -dependent activity does not require  $\text{Ca}^{2+}$  per se and is not directly mediated by the CaSR, as was shown using a dominant negative as well as siRNA. Moreover, the CaSR is not activated by  $\text{Zn}^{2+}$  although other divalent ions may activate this receptor. Nevertheless, extracellular  $\text{Ca}^{2+}$  alters the apparent cooperativity and affinity of ZnR/GPR39 to  $\text{Zn}^{2+}$  (Sharir and Hershfinkel 2005). Similar to the effect of  $\text{Ca}^{2+}$ , spermine, a CaSR ligand, synergistically increased the cellular response when applied with  $\text{Zn}^{2+}$ , although it did not activate the ZnR/GPR39 itself. In contrast, silencing of the CaSR downregulated the response to  $\text{Zn}^{2+}$ , suggesting that direct interaction between the receptors regulates the signaling triggered by ZnR/GPR39. Direct interaction between the CaSR and ZnR/GPR39 was indeed monitored using coimmunoprecipitation (Asraf et al. 2014). Changes in CaSR surface expression occur following exposure to its ligand (Grant et al. 2011). Thus, changes in CaSR localization induced by spermine or  $\text{Ca}^{2+}$  may have affected surface expression of ZnR/GPR39, thereby enhancing the  $\text{Zn}^{2+}$ -dependent response.

## 6.3 Physiological Aspects of ZnR/GPR39 Signaling

### 6.3.1 *The Digestive System*

Zinc is essential for digestive system function, and its deficiency is manifested in severe diarrhea and pathogenesis of ulcerative colon disease (Luk et al. 2002; Maret and Sandstead 2006; Walker and Black 2010). The World Health Organization (WHO) suggests zinc supplementation for effective treatment of diarrhea, and  $\text{Zn}^{2+}$  has been also suggested to reduce the severity and prolong the relapse of episodes of inflammatory ulcerative disease, such as Crohn's disease and colitis (Krasovec and Frenk 1996; Sturniolo et al. 2001; Luk et al. 2002; El-Tawil 2003; Walker and Black 2010; Alam et al. 2011). The general role of  $\text{Zn}^{2+}$  in preserving the digestive

epithelium in human diseases is underscored by the following: (1)  $Zn^{2+}$  supplementation dramatically reduces diarrhea-related symptoms and mortality (Scrimgeour and Lukaski 2008; Walker and Black 2010), and (2)  $Zn^{2+}$  reduces the permeability of the gut and enhances remission in ulcerative diseases (Sturniolo et al. 2001).  $Zn^{2+}$  plays a major role in enhancing proliferation and survival of colon epithelial (colonocytes) cell cultures (Hershinkel 2006; Cohen et al. 2012a, b) as well as differentiation of colonocytes and barrier formation (Glover et al. 2003, 2004; Finamore et al. 2008; Geiser et al. 2012). Zinc deficiency, dietary or genetically induced by loss of the transporter that is responsible for absorption of  $Zn^{2+}$ , impairs barrier function and increases permeability and cell death, and its supplementation can reverse these processes (Hoque and Binder 2006; Finamore et al. 2008; Geiser et al. 2013).

In colonocytes, ZnR/GPR39 mediates  $Zn^{2+}$ -dependent activation of the MAP kinase and the PI3 kinase pathways that are essential for cell proliferation and survival (Azriel-Tamir et al. 2004). Silencing of ZnR/GPR39 in vivo, GPR39 KO, or in vitro using siRNA, as well as functional downregulation of its activity via desensitization by  $Zn^{2+}$ , is followed by inhibition of the  $Zn^{2+}$ -dependent  $Ca^{2+}$  rise and phosphorylation of ERK1/2, indicating that the ZnR is a principal link between extracellular  $Zn^{2+}$  and ERK1/2. Activation of ZnR/GPR39 signaling pathway was shown to upregulate the  $Na^+/H^+$  exchanger (NHE) and enhance the recovery from acidic pH in colon cells and in native tissue (Azriel-Tamir et al. 2004; Cohen et al. 2012a, b). It should be noted that colonocytes are chronically exposed to short-chain fatty acids, which induce acid load on these cells (Busche et al. 1997; Topping and Clifton 2001; Tang et al. 2011). Thus, ZnR-dependent upregulation of NHE may be an effective trigger to enhance pH recovery in these cells.

Among the short-chain fatty acids found in the colon, butyrate, produced by bacterial fermentation in the colon, is found at high concentrations. Butyrate is essential for colonocyte nutrition but imposes an acidic stress that may lead to apoptosis of colonocytes and has been implicated in ulcerative colon diseases (Bordonaro et al. 2008; Scharlau et al. 2009; Yu et al. 2010; Zhang et al. 2010). Acidification of the colonocytes by application of extracellular  $Zn^{2+}$  before butyrate treatment significantly enhanced recovery of the colonocytes from the acid load produced by butyrate (Cohen et al. 2012a, b). Furthermore, short exposure of colonocytes to concentrations of  $Zn^{2+}$  sufficient to activate but not desensitize the ZnR/GPR39, or to induce changes in intracellular  $Zn^{2+}$ , attenuated butyrate-induced cell death (Cohen et al. 2012a, b). This effect was not mediated by regulation of intracellular pH, because the inhibition of the  $Na^+/H^+$  exchanger did not alter colon cell survival. Moreover, molecular silencing of ZnR/GPR39 or desensitization of the receptor reversed the protective effect of  $Zn^{2+}$ . Similarly, inhibition of the MAP and PI3 kinase pathways that are activated by  $Zn^{2+}$  via ZnR/GPR39 (Azriel-Tamir et al. 2004) also reversed the protective effect of  $Zn^{2+}$ . Thus, a clear role for ZnR/GPR39 is enhancing cell survival via upregulation of intracellular signaling. A candidate for mediating these effects of ZnR/GPR39 is the pro-survival glycoprotein, clusterin (also known as apolipoprotein J) (Pajak and Orzechowski 2006; Shannan et al. 2006; Djeu and Wei 2009; Mazarrelli

et al. 2009), which is upregulated by intracellular  $\text{Ca}^{2+}$  signaling such as is triggered by the ZnR/GPR39. Activation of the ZnR/GPR39 signaling pathway synergistically with butyrate treatment led to enhancement of the expression of the secreted isoform of clusterin (sCLU). Interestingly, ZnR/GPR39-dependent upregulation of sCLU expression required activation of the PI3 kinase pathway, further suggesting a survival role for the ZnR/GPR39-dependent pathway (Cohen et al. 2012a, b). The level of expression, moreover, was enhanced further by application of  $\text{Zn}^{2+}$  and butyrate, suggesting a synergistic mechanism. Using siRNA silencing of clusterin, the role of this pathway was shown to be essential for the  $\text{Zn}^{2+}$ -dependent prevention of butyrate-induced cell death (Cohen et al. 2012a, b). As butyrate was shown to induce colon cancer cell apoptosis, this may suggest a role for ZnR/GPR39 in the etiology of colon cancer that is yet to be addressed. A role for GPR39 in enhancing human esophageal squamous cell carcinoma was suggested, but this was not related to activation of the receptor by  $\text{Zn}^{2+}$  (Xie et al. 2011).

### 6.3.2 The Prostate

The highest concentration of  $\text{Zn}^{2+}$  in soft tissues is monitored in the prostate where millimolar concentrations were documented. Notably, dramatic changes in extracellular  $\text{Zn}^{2+}$ , resulting in a tenfold decrease in  $\text{Zn}^{2+}$  and its binding protein citrate (Costello et al. 1999; Huang et al. 2006), are observed during tumorigenesis in this organ. We have shown that an androgen-independent prostate cancer cell line, PC-3, mediates  $\text{Zn}^{2+}$ -dependent intracellular  $\text{Ca}^{2+}$  signals via ZnR/GPR39. The intracellular  $\text{Ca}^{2+}$  release mediated by ZnR/GPR39 subsequently triggers activation of MAP and PI3 kinases shown to enhance prostate cell proliferation and survival (Papatsoris et al. 2007; Agoulnik et al. 2011; Bartholomeusz and Gonzalez-Angulo 2012). The PI3K pathway is particularly prominent in prostate cancer, where constitutively activated PI3K has been correlated with severity of the tumor (Arcaro and Guerreiro 2007). Surprisingly, ZnR/GPR39 expression was shown to upregulate not only activation but also the total AKT expression level, which is associated with a more malignant phenotype of adrenal carcinomas (Fassnacht et al. 2005). This mechanism also upregulated the phosphorylation of this kinase, as basal phosphorylated AKT level measured in control cells treated with EDTA was higher than in the siGPR39 cells.

Intracellular  $\text{Ca}^{2+}$  changes may also regulate the calcium-binding proteins S100A that enable cell migration and invasion and are specifically linked to enhanced prostate cancer growth (Hermani et al. 2005, 2006; Grebhardt et al. 2014). Indeed, extracellular  $\text{Zn}^{2+}$  treatment, at concentrations that activate ZnR/GPR39, increased the expression of S100A4 protein in PC3 cells. Similarly, a decrease in S100A4 expression was monitored in siGPR39 cells. The S100A4 enhanced PC3 cell proliferation and invasiveness via induction of the metalloprotease MMP-9 (Joiner et al. 2012).



Thus, ZnR/GPR39 is a mediator of  $Zn^{2+}$ -dependent activation of signaling pathways that are all major pathways enhancing prostate cancer malignancy. An apparent paradox may be suggested by the fact the ZnR/GPR39 signaling is largely associated with enhanced cell growth and survival whereas a profound reduction in  $Zn^{2+}$  is seen during prostate cancer. Interestingly ZnR/GPR39 is completely desensitized by high  $Zn^{2+}$  concentrations such as found in the normal prostate (Costello and Franklin 2000; Franklin et al. 2005; Singh et al. 2006; Franklin and Costello 2007, even in the presence of citrate. Such desensitization renders ZnR/GPR39 quiescent in the nonneoplastic prostate. In contrast, reduced  $Zn^{2+}$  concentrations in the neoplastic prostate may allow expression of ZnR/GPR39, and thus  $Zn^{2+}$ -dependent signaling may be activated, leading to enhanced cell growth. Release of  $Zn^{2+}$  from cells following tissue destruction, such as seen for the skin cells, may activate ZnR/GPR39 signaling and enhance cell proliferation and survival. Thus, we suggest that ZnR/GPR39 may be a major target for reducing prostate cancer cells growth.

### 6.3.3 *Keratinocytes of the Skin*

High concentrations of  $Zn^{2+}$  accumulate in the intracellular and extracellular matrix of the skin, these are particularly high following injury (Andrews and Gallagher-Allred 1999; Nitzan et al. 2004; Lansdown et al. 2007). Severe zinc deficiency in a genetic disorder, acrodermatitis enteropathica, resulting from dysfunction of the zinc transporter Zip4, is manifested by skin lesions (Andrews 2008). A similar phenotype was recently described in a case of neonatal  $Zn^{2+}$  deficiency caused by a mutation in the ZnT-2 transporter in the mammary gland of the lactating mother (Lasry et al. 2012). Thus, dietary or genetic  $Zn^{2+}$  deficiency is manifested by severe skin lesions and impaired wound healing that can be reversed by  $Zn^{2+}$  supplementation (Jensen et al. 2008; Takahashi et al. 2008). For many years it has been accepted that topical addition of zinc, in ointments or bandages, stimulates wound healing and the re-epithelialization process (Lansdown 1996; Barceloux 1999; Schwartz et al. 2005; Lansdown et al. 2007). Although an antimicrobial effect was suggested as a role for  $Zn^{2+}$  during injury, subsequent studies identified  $Zn^{2+}$ -dependent signaling that is linked to enhanced proliferation and migration also in keratinocytes. Extracellular  $Zn^{2+}$ , at the concentrations found in the epidermis and released during injury, triggers  $Ca^{2+}$  release from thapsigargin-sensitive stores (Sharir et al. 2010). The response to  $Zn^{2+}$  is mediated through a  $G\alpha_q$ -coupled receptor, ZnR/GPR39, which activates PLC and the  $IP_3$  pathway and the downstream MAP kinase. Analysis of the  $Zn^{2+}$ -dependent  $Ca^{2+}$  response indicated that the keratinocytic-ZnR has high affinity and selectivity for  $Zn^{2+}$ . ZnR/GPR39-dependent signaling induces upregulation of the activity of the  $Na^+/H^+$  exchanger NHE1 and thereby enhances the recovery of intracellular pH from acid load. The enhanced activity of NHE1 also forms a local extracellular microenvironment with acidic pH that strengthens the epithelial permeability barrier (Hachem et al. 2005;

Stuwe et al. 2007; Stock et al. 2008). Thus, ZnR/GPR39 activation may regulate the formation of the permeability barrier and thereby enhance the antiinflammatory effects of  $Zn^{2+}$ . The physiological significance of the keratinocytic-ZnR/GPR39 activity is further demonstrated by the fact that ZnR/GPR39 is essential for keratinocyte proliferation and migration, as the activation of ZnR/GPR39 enhanced the rate of scratch closure and silencing of the receptor or its signaling pathway reversed the effects of  $Zn^{2+}$  (Sharir et al. 2010). Importantly, Zn/GPR39, inhibition of the  $Zn^{2+}$ -induced NHE1 upregulation, also resulted in attenuated migration and scratch closure. Interestingly, although in colonocytes ZnR/GPR39 regulation of NHE did not affect cell survival, albeit it enhanced the recovery from acid load, in keratinocytes NHE activation enhanced recovery from acid load and enhanced cell proliferation. Altogether, it has been shown that ZnR/GPR39 is mediating the beneficial effects of  $Zn^{2+}$  on wound healing, and thus generation of agonists that will activate, but will not desensitize, this receptor may provide novel and effective drugs to accelerate wound healing.

### 6.3.4 *The Pancreas*

$Zn^{2+}$  is packed into the insulin-containing vesicles by a specific  $Zn^{2+}$  transporter (ZnT8) and is released together with this hormone (Chimienti et al. 2004, 2006; Seve et al. 2004; Wenzlau et al. 2007; Gyulkhandanyan et al. 2008). It was first suggested that  $Zn^{2+}$  has a structural stabilizing function to the insulin hexamers; however, its concentration within the vesicles is much higher than required for this function and may suggest signaling activity mediated by this ion. Furthermore,  $Zn^{2+}$  release from pancreatic cells was monitored following glucose stimulation (Gee et al. 2002; Qian et al. 2003). Indeed, ZnR/GPR39 expression was identified in pancreatic  $\beta$  cells and within the duct epithelium (Holst et al. 2009). GPR39 expression was decreased in cells differentiated toward the exocrine phenotype but increased in the cells programmed to the endocrine phenotype (Tremblay et al. 2009); this suggests that similar to the autocrine effect of insulin itself, binding to insulin receptors on  $\beta$  cells,  $Zn^{2+}$  co-released with the hormone also has a specific target on the cells. The role of ZnR/GPR39 on the ductal cells has not been addressed, yet previous studies on salivary ductal epithelium indicated that ZnR/GPR39 activation in these cells triggers release of ATP (Sharir and Hershinkel 2005), likely inducing a paracrine response in neighboring cells. Smooth muscle cells that do not express a functional ZnR/GPR39, for example, may be a target for the ATP release following ZnR/GPR39 activation in ductal epithelial cells; this signal may regulate muscle contraction and release of secretagogues through the duct.

In the initial studies describing GPR39 KO mice, no effect on metabolic function was observed. Further studies of older animals found impaired glucose tolerance and altered glucose-induced insulin secretion from isolated islets from GPR39 KO mice (Moechars et al. 2006). Interestingly, the phenotype of the GPR39 KO mice

was revealed under conditions of “increased demand” such as age-dependent or diet-induced insulin resistance.

Although the morphology of the pancreatic islets in GPR39 KO mice was normal, the expression of key regulators of islet development was decreased. The transcription factor HNF-1 $\alpha$  was also downregulated, and in agreement with other studies, this showed a gender difference in the phenotype, leading to more severe glucose intolerance in female mice (Holst et al. 2009). Among the pathways regulated by the ZnR/GPR39, the NFAT was shown to be effectively increased in HEK293 cells transfected with GPR39. This pathway was shown to be an important regulator for the expression of genes that control  $\beta$ -cell differentiation, proliferation, and adaptive islet responses in vivo. Thus, a possible explanation for the effects of Zn<sup>2+</sup> would be via ZnR/GPR39-dependent regulation of this pathway and thereby serve as a therapeutic target for diabetes (Popovics and Stewart 2011).

### 6.3.5 *The Brain*

One of the most notable pools of free Zn<sup>2+</sup> ions is found in neurons (Frederickson and Moncrieff 1994; Frederickson 2003b). The development of fluorescent tools enabled the study of this specific pool of Zn<sup>2+</sup> (Burdette et al. 2001, 2003; Frederickson 2003a; Pan et al. 2011). Extensive research indicated that Zn<sup>2+</sup> bound to intracellular proteins can be liberated into the cytoplasm during oxidative or nitrosative neuronal injury, leading to cell death (Aizenman et al. 2000; Zhang et al. 2004; Zhang et al. 2006; Redman et al. 2009; McLaughlin et al. 2001), but the role of the second pool of synaptic free Zn<sup>2+</sup> was less understood. Synaptic Zn<sup>2+</sup> is transported into vesicles by the Zn<sup>2+</sup> transporter 3 (ZnT3) and is released into the synaptic cleft during neuronal activity in a Ca<sup>2+</sup>-dependent manner (Qian and Noebels 2005, 2006; Frederickson et al. 2006). Using ZnT3 KO mice, it was shown that the synaptic Zn<sup>2+</sup> regulates neuronal excitability and can strongly influence seizure activity (Vogt et al. 2000; Smart et al. 2004; Sensi et al. 2011). Similarly, removal of synaptic Zn<sup>2+</sup> by dietary means or chemical chelation also led to enhanced susceptibility to epileptic seizures (Cole et al. 2000; Takeda et al. 2003; Blasco-Ibáñez et al. 2004; Takeda et al. 2005). Interestingly Zn<sup>2+</sup> deficiency was also linked to some forms of human epilepsy (Goldberg and Sheehy 1982; Ganesh and Janakiraman 2008; Seven et al. 2013).

Synaptic Zn<sup>2+</sup> is tightly packed in the mossy fiber terminals of the hippocampus, facing the CA3 neurons (Frederickson and Danscher 1990; Frederickson et al. 1992). ZnR/GPR39 expression in these postsynaptic cells induces metabotropic Ca<sup>2+</sup> signaling following Zn<sup>2+</sup> release (Besser et al. 2009). Blockade of synaptic transmission by tetrodotoxin or CdCl inhibited the ZnR-mediated Ca<sup>2+</sup> rises. The Zn<sup>2+</sup>-dependent Ca<sup>2+</sup> signaling then induced phosphorylation of extracellular-regulated kinase (ERK1/2) and Ca<sup>2+</sup>/calmodulin kinase II (CAMK). Importantly, although the metabotropic response may be triggered by other released factors, application of a nonpermeable Zn<sup>2+</sup> chelator, CaEDTA, largely abolished

the response. Moreover, the response was also diminished in ZnT3 knockdown mice lacking synaptic  $Zn^{2+}$  (Besser et al. 2009).

KCC2 is the major outward transporter of chloride in neurons, necessary and sufficient for creating a chloride equilibrium potential that is negative to the resting membrane voltage (Lu et al. 1999; Lee et al. 2005), thereby rendering GABA<sub>A</sub>- and glycine-mediated synaptic potentials inhibitory (Farrant and Kaila 2007; Viitanen et al. 2010). Increases in KCC2 activity may thus enhance the inhibitory actions of GABA and glycine (Zhu et al. 2005, 2008; Huberfeld et al. 2007; Khirug et al. 2010). To address a physiological role for ZnR/GPR39 activation that may link it to the effects of  $Zn^{2+}$  in seizure, it was suggested that ZnR/GPR39 may regulate the  $K^+/Cl^-$  cotransporter, KCC2, that is strongly associated with inhibitory activity (Stein et al. 2004; Lee et al. 2005; Blaesse et al. 2006; Khirug et al. 2010). Activation of ZnR/GPR39 by synaptic  $Zn^{2+}$  enhanced KCC2 activity and surface expression, thereby inducing a hyperpolarizing shift in GABA<sub>A</sub> reversal potential (Chorin et al. 2011). Direct phosphorylation of KCC2 regulates its activity (Strange et al. 2000; Rinehart et al. 2009; Kahle et al. 2010) and may also lead to enhanced KCC2 surface expression (Lee et al. 2007, 2010; Wake et al. 2007; Watanabe et al. 2009). The upregulation of KCC2 activity by ZnR/GPR39 was mediated by phosphorylation of ERK1/2 and induced higher surface expression of the cotransporter (Chorin et al. 2011). The insertion of KCC2 into the plasma membrane was dependent on the SNARE proteins that are associated with exocytotic processes (Saadi et al. 2012). By identifying a physiological role for ZnR/GPR39 in regulating the neuronal  $Cl^-$  gradient via KCC2 activity, the relevance of this pathway to the anticonvulsive actions of  $Zn^{2+}$  was established. Indeed, the fact that synaptic  $Zn^{2+}$  can profoundly influence inhibitory drive is concordant with the enhanced susceptibility to kainate-triggered seizures present in ZnT3 KO mice (Buhl et al. 1996; Cole et al. 2000; Elsas et al. 2009). The release of vesicular  $Zn^{2+}$  during application of kainate (Frederickson et al. 1988a) could trigger the activity of ZnR/GPR39 and enhance KCC2 activity, thus limiting kainate-triggered epileptic activity by rendering the GABA<sub>A</sub> receptor inhibitory drive more effective.

Another brain region that contains a large pool of synaptic  $Zn^{2+}$  is the dorsal cochlear nucleus (DCN), which is part of the auditory brainstem (Frederickson et al. 1988a, b). Similar to the hippocampus, ZnR/GPR39-dependent  $Ca^{2+}$  signaling was also monitored in this brain region (Perez-Rosello et al. 2013). Following its activation, ZnR/GPR39 induced retrograde endocannabinoid signaling; this, in turn, affected the probability of release from glutamatergic terminals. Although a single action potential could induce synaptic  $Zn^{2+}$  release (Qian and Noebels 2005; Pan et al. 2011), the release of endocannabinoids required a train of presynaptic action potentials, and a similar train was also required to trigger ZnR/GPR39 activation in the hippocampus (Besser et al. 2009; Perez-Rosello et al. 2013). These results support a physiologically interesting role for the synaptic  $Zn^{2+}$  and the ZnR/GPR39 that acts as a sensor for increased release of excitatory neurotransmitter, activates negative feedback, and enhances the inhibitory drive.

## 6.4 Conclusions

The identification of the ZnR as a functional GPCR that mediates Zn<sup>2+</sup>-dependent signaling in epithelial and neuronal cells provided the basis for understanding of many physiological roles of this ion. The subsequent link to GPR39 now establishes the required molecular machinery to address the mechanistic aspects of ZnR and Zn<sup>2+</sup> signaling. Although Zn<sup>2+</sup> was described as an important structural element for many years, the identification of free Zn<sup>2+</sup> ions in many systems suggested that this ion has a signaling role as well. Identification of ZnR/GPR39 as a distinct target for Zn<sup>2+</sup> implicates this ion as an important ligand mediating physiological signaling. The importance of Zn<sup>2+</sup> signaling in numerous diseases and the major role of the ZnR/GPR39 in mediating the effects of this ion, as described in this review, presents this receptor as a key candidate for novel therapeutic approaches. Moreover, ZnR is a member of the Gq protein-coupled receptor family (GPCR), which is at present a major focus of the pharmaceutical industry (Custodi et al. 2012; Wootten et al. 2013). Using high-throughput systems for identification of novel and specific agonists may elucidate a whole new battery of therapeutic tools to efficiently modulate cellular signaling linked to disease.

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# Chapter 7

## Genetically Encoded Fluorescent Probes for Intracellular Zn<sup>2+</sup> Imaging

Anne M. Hessels and Maarten Merkx

**Abstract** In this chapter we provide an overview of the various genetically encoded fluorescent Zn<sup>2+</sup> sensors that have been developed over the past 5 to 10 years. We focus on sensors based on Förster resonance energy transfer (FRET), as these have so far proven to be the most useful for detecting Zn<sup>2+</sup> in biological samples. Our goal is to provide a balanced discussion of the pros and cons of the various sensors and their application in intracellular imaging. Following the description of the various sensors, several recent applications of these sensors are discussed. We end the chapter by identifying remaining challenges in this field and discussing future perspectives.

**Keywords** Fluorescence • FRET • Imaging • Microscopy • Sensor • Zinc

### 7.1 Introduction

Transition metals such as zinc pose an interesting dilemma for living organisms because they are essential cofactors for numerous enzymes and proteins, but at the same time are toxic even at low concentrations in their free form (Valiko et al. 2005). Mechanisms to control this delicate balance may vary for different metal ions and also between organisms. Copper homeostasis in eukaryotes has been shown to involve specific copper chaperone proteins that transfer Cu<sup>+</sup> to various cellular targets without releasing it into the cytosol (Rae et al. 1999). Similar chaperones have not been identified for Zn<sup>2+</sup>; instead, a general Zn<sup>2+</sup>-buffering mechanism has been proposed in which the free cytosolic Zn<sup>2+</sup> concentration in mammalian cells is kept constant at pM–nM levels (Cousins et al. 2006; Krezel and Maret 2006). The free concentration of Zn<sup>2+</sup> is also likely to differ substantially between subcellular locations, as mM concentrations of total Zn<sup>2+</sup> have been reported for pancreatic  $\beta$ -cell granules (Hutton et al. 1983) and inferred for secretory vesicles in neuronal (Linkous et al. 2008) and mast cells (Ho et al. 2004).

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To advance our understanding of zinc homeostasis and the putative role of  $Zn^{2+}$  in (intracellular) signal transduction, tools are required that allow direct (sub)cellular imaging of  $Zn^{2+}$  concentrations in single living cells in real time. Fluorescence is ideally suited for this purpose, because it combines high sensitivity with subcellular resolution (Kikuchi 2010). Such fluorescent sensors should have an appropriate affinity for  $Zn^{2+}$  under physiological conditions, show high selectivity for  $Zn^{2+}$  over other biologically abundant metals, and translate  $Zn^{2+}$  binding into a strong increase in fluorescence, or even better, a ratiometric change in fluorescent properties. Currently,  $Zn^{2+}$ -sensitive fluorescent dyes are still the most commonly imaging probes for monitoring  $Zn^{2+}$  in biological samples. The development of synthetic sensors continues to be an active area in chemical biology, and an impressive variety of  $Zn^{2+}$ -sensitive fluorescent dyes (such as Zinquin, rhodzin-3, and FluoZin-3) has been developed, some of which have also been applied to monitor  $Zn^{2+}$  fluctuations in living cells (Domaille et al. 2008; Nolan and Lippard 2009). However, synthetic probes come with some intrinsic limitations, notably a lack of full control over subcellular localization and the need to achieve high intracellular concentrations of the dye, which may perturb free levels of  $Zn^{2+}$ . In addition, it has proven challenging to create synthetic dyes that rival the affinity and specificity typically observed with metalloproteins, which is important to reliably determine the extremely low concentrations of  $Zn^{2+}$  and other transition metal ions (Krezel and Maret 2006; Bozym et al. 2006; Van Dongen et al. 2007).

Genetically encoded fluorescent sensors offer several advantages compared to small molecule-based probes. Small-molecule probes need to enter the cell via diffusion over the cell membrane. Although these probes can be trapped by hydrolysis of methylesters by intracellular esterases, controlling their concentration over prolonged time intervals remains challenging. Even more importantly, once inside the cell, little control over subcellular localization is possible, which is an important caveat given that  $Zn^{2+}$  concentrations can vary considerably between different organelles. Protein-based, genetically encoded probes are produced by the cell itself, which in principle allows control over their intracellular concentration, prevents leakage, and provides excellent control over intracellular localization. A second advantage of genetically encoded probes is that they allow one to take advantage of the excellent affinity and specificity displayed by natural metal-binding proteins, which can be further improved by both rational and directed evolution approaches. Although adding a fluorescent dye to a cell maybe slightly easier than relying on DNA transfection, the choice of useful commercially available  $Zn^{2+}$  dyes is limited, which presents an important restriction for those scientists who cannot synthesize these probes themselves. DNA-encoded probes, on the other hand, can be easily replicated by standard molecular biology techniques and distributed through depositories such as AddGene.

Most applications of genetically encoded fluorescent sensors have been limited to studies in immortalized cell lines using transient transfection, but genetically encoded fluorescent sensors can also be applied in primary cells using viral vectors or even entire organisms. Although at present the latter still requires a substantial effort, new developments in genetic engineering are expected to make the latter



possibility more readily accessible in the future. In this chapter we provide an overview of the various genetically encoded fluorescent Zn<sup>2+</sup> sensors that have been developed during the past 5 to 10 years. We focus on sensors based on Förster resonance energy transfer (FRET), as these have so far proven to be the most useful for detecting Zn<sup>2+</sup> in biological samples. Our goal is to provide a discussion of the pros and cons of the various sensors and their application in intracellular imaging. Following the description of the various sensors, several recent applications of these sensors are discussed. We end the chapter by identifying remaining challenges in this field and discussing future perspectives.

## 7.2 Genetically Encoded Zn<sup>2+</sup> Sensors

### 7.2.1 *Sensor Principles*

Several strategies have been explored to develop Zn<sup>2+</sup>-responsive fluorescent proteins. One approach is to introduce a Zn<sup>2+</sup>-binding site close to the chromophore of the fluorescent protein. This principle was first reported by Barondeau et al., who created a Zn<sup>2+</sup>-binding variant of green fluorescent protein (GFP) in which the tyrosine that is part of the original fluorophore was replaced by a metal-coordinating histidine (Barondeau et al. 2002). This sensor binds both Zn<sup>2+</sup> and Cu<sup>2+</sup> with micromolar affinity. A twofold increase in fluorescence intensity was observed upon addition of Zn<sup>2+</sup>, whereas Cu<sup>2+</sup> binding resulted in quenching of fluorescence. This sensor has not been used beyond the initial proof of concept study, however, most likely because its affinity for Zn<sup>2+</sup> is too weak for intracellular Zn<sup>2+</sup> detection and because it is not easily calibrated. Another strategy for single-domain fluorescent Zn<sup>2+</sup> sensors was reported by Mizuno et al., who fused de novo designed metal ion-responsive coiled-coil peptides with circularly permuted green fluorescent protein (cpGFP) (Mizuno et al. 2007). Metal binding to histidine residues in these peptides induces a structural change from a random coil structure to an  $\alpha$ -helical, trimeric, coiled-coil structure, which stabilizes the cpGFP domain and results in an increase in fluorescence. Although the Zn<sup>2+</sup> affinity for this probe was higher than the sensor reported by Barondeau ( $K_d = 570$  nM), binding of Cu<sup>2+</sup> and Ni<sup>2+</sup> resulted in similar increase in fluorescence.

More recently, incorporation of metal-chelating, non-natural amino acids has been explored to obtain metal-responsive fluorescent proteins. Wang and coworkers developed a circularly permuted variant of super folder GFP in which the tyrosine present in the chromophore was replaced by 8-hydroxyquinolin-alanine (HqAla), yielding a fluorescent sensor that showed a sevenfold increase in fluorescent intensity in the presence of Zn<sup>2+</sup> ( $\lambda_{ex} = 495$  nm;  $\lambda_{em} = 537$  nm) (Liu et al. 2013b). In contrast to the two other examples just discussed, Zn<sup>2+</sup> binding also results in a blue shift of both excitation and emission spectra, allowing ratiometric detection. At present the applicability of this probe is still limited, not

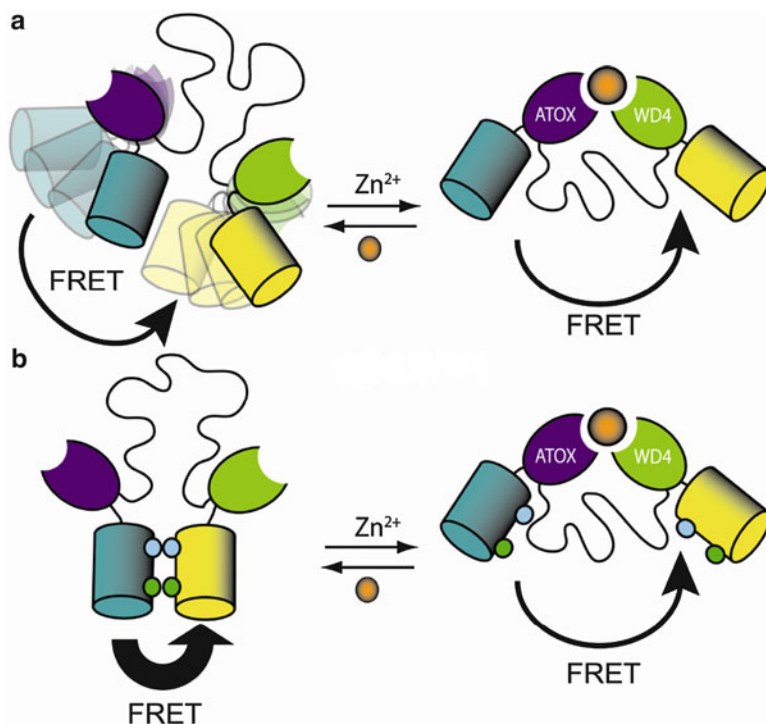
only by the requirement to use non-natural amino acids but also because of the relatively weak  $\text{Zn}^{2+}$  affinity ( $K_d = 50\text{--}100\ \mu\text{M}$ ). Besides their relatively low  $\text{Zn}^{2+}$  affinities and metal specificity, most single-domain fluorescent sensor proteins are intensity based, that is, they show an increase or decrease in fluorescence but their spectral properties do not change. This is a disadvantage for quantitative intracellular applications (Liu et al. 2013a), because fluorescence intensity is not only a function of the  $\text{Zn}^{2+}$  concentration but also depends on expression levels and can be affected by photobleaching.

The most commonly used strategy to design fluorescent sensor proteins takes advantage of the principle of Förster resonance energy transfer (FRET). FRET is a mechanism in which excitation energy is transferred from a donor to an acceptor fluorescent domain. The efficiency of this process is distance- and orientation dependent and therefore useful to detect conformational changes as a result of metal binding to a receptor domain. FRET-based  $\text{Zn}^{2+}$  sensors consist of one or more metal-binding domains flanked by a donor and acceptor fluorescent domain. The most frequently used FRET pair consists of cyan fluorescent protein (CFP) and yellow fluorescent protein (YFP), although more red-shifted FRET pairs have recently also been reported (Lindenburg et al. 2013; Miranda et al. 2012). A key advantage of FRET-based sensors is that they are ratiometric, that is, the ratio of acceptor and donor emission provides a measure of the metal-binding state that is independent of the sensor concentration. In principle, FRET sensor design is also more modular, although developing FRET sensors with a large change in emission ratio can be challenging and often requires much optimization. Other important properties that determine the performance of FRET-based sensors for intracellular  $\text{Zn}^{2+}$  imaging are their  $\text{Zn}^{2+}$  affinity and specificity, their binding kinetics, and their pH sensitivity. In the next paragraph we discuss the various FRET-based  $\text{Zn}^{2+}$  sensor systems that have been developed thus far and discuss these aspects. The first family of  $\text{Zn}^{2+}$  sensors that we discuss, the CALWY-sensors, will also be used to introduce some of the general issues that are important when considering the applications of these sensors.

## 7.2.2 *Genetically Encoded FRET-Based Sensors*

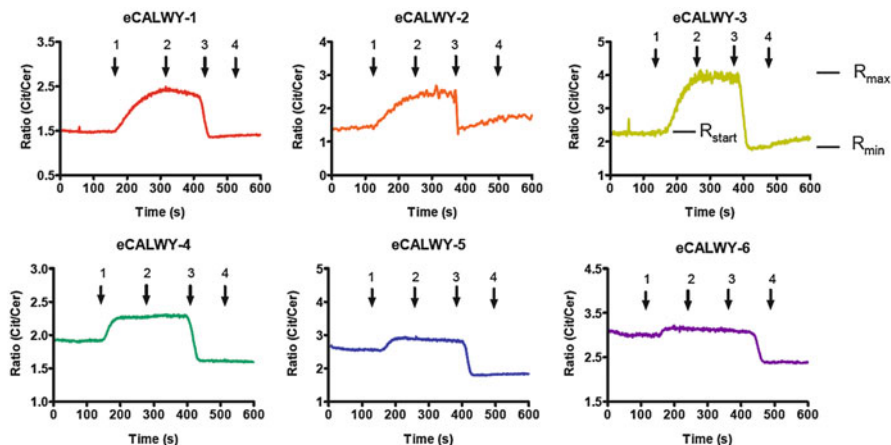
### 7.2.2.1 CALWY Sensors

Sensors from the CALWY family consist of two small metal-binding domains, Atox1 and WD4, that each contain a metal-binding CXXC motif, fused by a long and flexible linker. In the original sensor (CALWY), the metal-binding domain was flanked by cyan and yellow fluorescent domains, hence their name (CFP-Atox1-Linker-WD4-YFP) (Fig. 7.1a) (Van Dongen et al. 2006; Van Dongen et al. 2007). ATOX 1 and WD4 are native Cu(I)-binding domains that play a role in maintaining copper homeostasis, and the sensor was initially developed to create a genetically encoded  $\text{Cu}^+$  sensor based on the  $\text{Cu}^+$ -induced dimerization of these two domains.



**Fig. 7.1** Schematic representation of the CALWY (a) and eCALWY-1 (b) sensor designs, both consisting of two metal-binding domains, ATOX1 and WD4, connected via a flexible peptide linker and flanked by two fluorescent domains. **a** The CALWY sensor yielded a small Förster resonance energy transfer (FRET) change between the  $\text{Zn}^{2+}$ -free and  $\text{Zn}^{2+}$ -bound state. **b** In the eCALWY constructs two mutations, S208F and V224L, were introduced on both fluorescent domains, leading to high energy transfer in the  $\text{Zn}^{2+}$ -free state.  $\text{Zn}^{2+}$  binding disrupts the complex, resulting in a large decrease in FRET. (Adapted from Vinkenborg et al. 2009)

However, it was discovered that  $\text{Zn}^{2+}$  was able to form a very stable tetrahedral complex by binding the four cysteines present in the two copper-binding domains, yielding a  $K_d$  of approximately 0.23 pM at pH 7.1. Unfortunately, the change in emission ratio of the original CALWY sensor was small, showing a 15 % decrease in emission ratio upon  $\text{Zn}^{2+}$  binding. Because this poor dynamic would make the sensor less suitable for intracellular  $\text{Zn}^{2+}$  imaging, improved variants were developed, resulting in the so-called eCALWY series of  $\text{Zn}^{2+}$  sensors. First, ECFP and EYFP were replaced by cerulean and citrine, respectively, fluorescent domains with increased intensity (cerulean) and pH stability (citrine). Most importantly, the ratiometric response was improved sixfold by introduction of two mutations (S208F and V224L) on both cerulean and citrine that promote intramolecular complex formation between the two fluorescent domains in the absence of  $\text{Zn}^{2+}$ . Binding of  $\text{Zn}^{2+}$  to ATOX1 and WD4 disrupts the interaction between the fluorescent domains, resulting in a large decrease in FRET corresponding to a twofold



**Fig. 7.2** Responses of single INS-1(832/13) cells expressing eCALWY-1–6 to addition of 50  $\mu\text{M}$  TPEN (1), 5  $\mu\text{M}$  pyrithione (2), 5  $\mu\text{M}$  pyrithione/100  $\mu\text{M}$   $\text{Zn}^{2+}$  (3), and no additives (4). Traces show the responses of individual cells. In the response trace of eCALWY-3, the emission ratios used for  $R_{\text{max}}$ ,  $R_{\text{min}}$ , and  $R_{\text{start}}$  are displayed. (Adapted from Vinckenborg et al. 2009)

change in emission ratio. As the interaction between the fluorescent domains competed with  $\text{Zn}^{2+}$  binding, the  $K_d$  for  $\text{Zn}^{2+}$  binding was attenuated by a factor of 10, resulting in a  $K_d$  of 2 pM at pH 7.1 (Fig. 7.1b) (Vinckenborg et al. 2009).

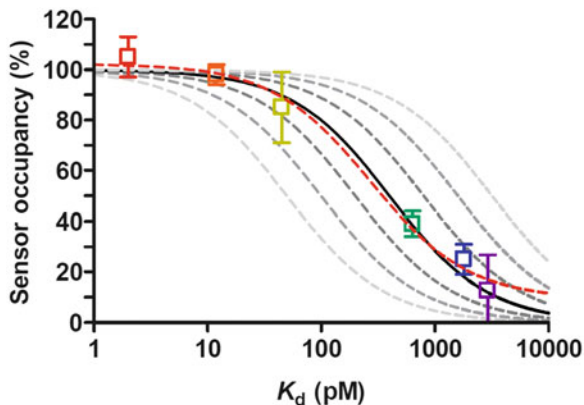
Without knowing the free cytosolic  $\text{Zn}^{2+}$  concentration in mammalian cells beforehand, eCALWY-1 was tested in HEK293 cells and INS-1(832/13) cells. Figure 7.2 shows the ratio of citrine to cerulean emission of a single cell using excitation of cerulean. Addition of the strong cell-permeable  $\text{Zn}^{2+}$  chelator TPEN results in an increase in emission ratio, consistent with dissociation of  $\text{Zn}^{2+}$  from the sensor. As expected, subsequent addition of the  $\text{Zn}^{2+}$  ionophore pyrithione and excess  $\text{Zn}^{2+}$  resulted in a decrease in emission ratio. This experiment showed that at the start of the experiment, the eCALWY-1 sensor was already fully occupied with  $\text{Zn}^{2+}$ , suggesting that the free cytosolic  $\text{Zn}^{2+}$  concentration was substantially higher than the 2 pM  $\text{Zn}^{2+}$  affinity of eCALWY-1. Therefore, a toolbox of eCALWY-based sensors was developed by systematically tuning the  $\text{Zn}^{2+}$  affinity of eCALWY-1. First, eCALWY-4 was created by introducing a single cysteine-to-serine mutation in the  $\text{Zn}^{2+}$ -binding pocket of the sensor, resulting in a 300-fold weakening of the affinity for  $\text{Zn}^{2+}$  ( $K_d = 630$  pM) This mutation also abrogated  $\text{Cu}^+$  binding to the protein, as eCALWY-4 did not show any response up to micromolar  $\text{Cu}^+$  levels. Because the free cellular copper concentration has been estimated to be about  $10^{-18}$  M (Wegner et al. 2010),  $\text{Cu}^+$  binding will not interfere with  $\text{Zn}^{2+}$  binding inside living cells. Further fine tuning of the  $\text{Zn}^{2+}$  affinity was achieved by shortening the flexible peptide linker between the metal-binding domains, yielding a series of  $\text{Zn}^{2+}$  sensors (eCALWY-1–6) with affinities ranging from low picomolar to low nanomolar and at least a twofold change in emission ratio upon  $\text{Zn}^{2+}$  binding at a physiological relevant pH (Table 7.1). Figure 7.2 shows the fluorescence

**Table 7.1** Sensor properties of different Förster resonance energy transfer (FRET)-based Zn<sup>2+</sup>

Sensor variant	Ratiometric change (in vitro)	$K_d$ (pH 7.1)	Zn <sup>2+</sup> -binding pocket
CALWY (Van Dongen et al. 2007)	15 %	0.2 pM	Cys <sub>4</sub>
eCALWY-1 (Vinkenburg et al. 2009)	240 %	2 pM	Cys <sub>4</sub>
eCALWY-2 (Vinkenburg et al. 2009)	270 %	9 pM	Cys <sub>4</sub>
eCALWY-3 (Vinkenburg et al. 2009)	215 %	45 pM	Cys <sub>4</sub>
eCALWY-4 (Vinkenburg et al. 2009)	250 %	630 pM	Cys <sub>3</sub>
eCALWY-5 (Vinkenburg et al. 2009)	300 %	1,850 pM	Cys <sub>3</sub>
eCALWY-6 (Vinkenburg et al. 2009)	200 %	2,900 pM 0.5 μM (pH 6.0)	Cys <sub>3</sub>
redCALWY-1 (Lindenburg et al. 2013)	62 %	12.3 pM	Cys <sub>4</sub>
redCALWY-4 (Lindenburg et al. 2013)	30 %	234 pM	Cys <sub>3</sub>
ZifCY1 (Dittmer et al. 2009)	220 %	1.7 μM	Cys <sub>2</sub> His <sub>2</sub>
ZifCY2 (Dittmer et al. 2009)	400 %	160 μM	His <sub>4</sub>
ZapCY1 (Qin et al. 2011)	130 %	2.5 pM	Cys <sub>4</sub>
ZapCY2 (Qin et al. 2011)	70 %	811 pM	Cys <sub>2</sub> His <sub>2</sub>
ZapOC2 (Miranda et al. 2012)	12 % (in situ)	Nd	Cys <sub>2</sub> His <sub>2</sub>
ZinCh-9 (Evers et al. 2007)	360 %	213 nM (pH 8.0)	Cys <sub>2</sub>
eZinCh-1 (Evers et al. 2007)	800 %	8.2 μM 253 nM (pH 8.0) 250 μM (pH 6.0)	Cys <sub>2</sub>
CLY9-2His (Evers et al. 2008)	65 %	47 nM (pH 8.0)	2 His <sub>6</sub> tags

responses of INS-1(832/13) cells transiently expressing each of these six eCALWY variants upon addition of the membrane permeable Zn<sup>2+</sup> chelator TPEN and subsequent treatment of Zn<sup>2+</sup> and pyrithione. A consistent trend between sensor response and sensor affinity was observed, with the high-affinity eCALWY-1 being fully saturated whereas the sensor with the lowest affinity (eCALWY-6) was nearly empty at the start of the experiment.

For each of these sensors, the Zn<sup>2+</sup> occupancy at the start of the experiment was calculated using Eq. (7.1).  $R_{\max}$  and  $R_{\min}$  are the steady-state ratios after TPEN and



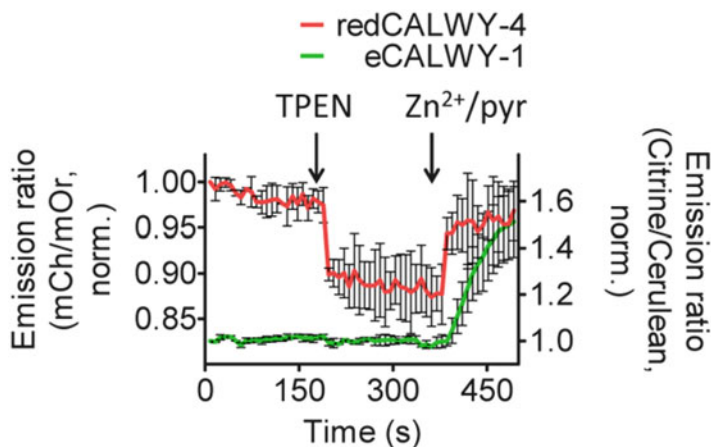
**Fig. 7.3** Sensor occupancy in INS-1(832/13) cells as a function of the sensor  $K_d$ . Data points show the occupancy of the different eCALWY variants, determined from the traces of individual cells. A nonlinear least-squares fit yielded a free  $Zn^{2+}$  concentration of  $\sim 0.4$  nM. The *dashed lines* depict the expected responses assuming free  $Zn^{2+}$  concentrations of 0.05, 0.1, 0.2, (0.4 *solid line*), 0.8, 1.6, and 3.2, respectively. (Adapted from Vinkenborg et al. 2009)

pyrithione/ $Zn^{2+}$  addition, respectively, and  $R_{\text{start}}$  is the ratio at the start of the experiment (Fig. 7.2).

$$\text{Occupancy} = \frac{R_{\text{max}} - R_{\text{start}}}{R_{\text{max}} - R_{\text{min}}} \cdot 100 \% \quad (7.1)$$

Plotting the sensor occupancies for all six variants as a function of their  $K_d$  revealed that the sensor occupancies were consistent with a free  $Zn^{2+}$  concentration of about 0.4 nM (Fig. 7.3). The same results were obtained in mouse pancreatic beta cells (INS-1(832/13)) and in HEK293 cells. Although the cytosolic free  $Zn^{2+}$  concentration may also depend on cell type and conditions, subsequent work in other cell types and using these and other sensors (see following) has confirmed that the cytosolic  $Zn^{2+}$  in mammalian cells is relatively well-buffered between 100 pM and 1 nM. The observation that a single free  $Zn^{2+}$  concentration of 400 pM was sufficient to explain the occupancies of both high- and low-affinity sensors also indicates that the sensors do not significantly perturb the free  $Zn^{2+}$  concentration. In contrast to synthetic fluorescent  $Zn^{2+}$  sensors, which are added to the cells in relatively high concentrations at the time of the imaging experiment, genetically encoded fluorescent proteins are constitutively expressed and in this way become part of the cellular  $Zn^{2+}$  buffer machinery (Qin et al. 2013).

To gain further insight into the regulation of intracellular  $Zn^{2+}$  homeostasis and the possible role of  $Zn^{2+}$  as a secondary messenger, one would like to be able to monitor  $Zn^{2+}$  in different cellular compartments in the same cell at the same time or simultaneously monitor the relationship between  $Zn^{2+}$  concentration and other important signal transduction pathways such as  $Ca^{2+}$ , cAMP, and kinase activities. Therefore, spectrally distinct variants of the eCALWY sensors have recently been



**Fig. 7.4** Response of HeLa cells expressing both eCALWY-1 (*green*) and redCALWY-4 (*red*) to the addition of  $Zn^{2+}$ /pyrithione followed by excess TPEN. Traces represent the average of multiple cells after normalization of the emission ratio at  $t = 0$ . Error bars represent SEM. (Adapted from Lindenburg 2013)

developed that can be used together with CFP-YFP-based sensors (Lindenburg et al. 2013). These red fluorescent FRET sensors (redCALWYs) were obtained by replacing cerulean and citrine by mOrange and mCherry, respectively. Functional sensors were only obtained after reengineering the surface of both fluorescent domains to promote association of mOrange and mCherry in the  $Zn^{2+}$ -free state. Red versions were created of eCALWY-1 and eCALWY4.

In vitro characterization of redCALWY-1 and redCALWY-4 yielded  $K_d$  values of  $12.3 \pm 2$  pM and  $234 \pm 5$  pM, respectively (Table 7.1), which are comparable to the affinities of their CFP-YFP counterparts, showing that the replacement of the fluorescent domains had no effect on the ligand-binding properties. In situ characterization showed that the redCALWY-1 showed a response to addition of TPEN and  $Zn^{2+}$  similar to the original eCALWY-1 (Fig. 7.2), with both high-affinity sensors being completely saturated with  $Zn^{2+}$  under normal physiological conditions. Similarly, the lower-affinity redCALWY-4 was found to be mostly empty when expressed in the cytosol of HeLa cells. To explore the feasibility of using these redCALWY variants together with CFP-YFP-based systems, the high-affinity eCALWY-1 (CFP/YFP) was coexpressed with the lower-affinity redCALWY-4 in the cytosol of HeLa cells (Fig. 7.4). As expected, addition of  $Zn^{2+}$ /pyrithione to the cells resulted in a decrease in the redCALWY-4 emission ratio without affecting the eCALWY-1 emission ratio. Subsequent addition of TPEN resulted in a quick response for redCALWY-4, followed by a slower increase in emission ratio for the high-affinity eCALWY-1 sensor. In this case, simultaneous expression of spectrally distinct  $Zn^{2+}$  sensors with different affinities in the same cellular compartment increases the range over which the  $Zn^{2+}$  concentration can be monitored. More importantly, the experiment showed the feasibility of monitoring  $Zn^{2+}$

concentrations at different subcellular localizations that otherwise cannot be easily distinguished, such as the ER and the cytosol.

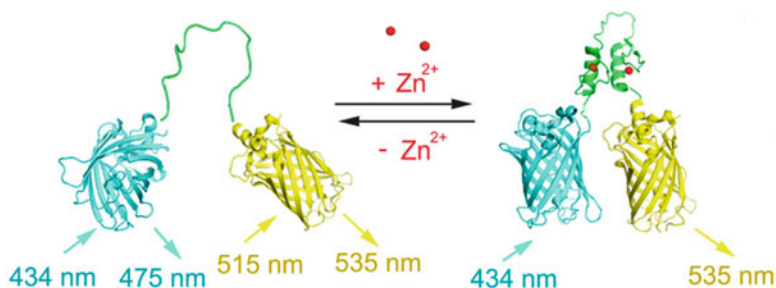
In conclusion, the accurate determination of the cytosolic free  $Zn^{2+}$  concentration using the eCALWY sensors relies on several factors:

1. *The availability of sensors with a range of  $Zn^{2+}$  affinities.* Although the free  $Zn^{2+}$  concentration can be determined based on the occupancy of a single  $Zn^{2+}$  sensor and its in vitro determined  $K_d$ , such determinations are inherently less reliable than measurements based on sensors with different affinities, particularly when the sensor's affinity is not close to the free  $Zn^{2+}$  concentration. In the case of the eCALWY sensors, determination of the free  $Zn^{2+}$  concentration using eCALWY-4 is therefore more reliable than using for example eCALWY-2.
2. *Accurate determination of  $R_{max}$  and  $R_{min}$ .* The absolute emission ratio observed for cells expressing the same sensor may vary substantially between cells for example because of varying contributions of background fluorescence. Accurate determination of  $Zn^{2+}$  concentration therefore requires the determination of the emission ratio in the absence of  $Zn^{2+}$  ( $R_{max}$  in this case) and in the presence of  $Zn^{2+}$  ( $R_{min}$ ). Accurate determination of  $R_{max}$  and  $R_{min}$  is helped in this case by the relatively fast association and dissociation kinetics of the sensor, allowing the establishments of stable plateau values within minutes following TPEN addition or even seconds after addition of  $Zn^{2+}$ /pyrithione.
3. *In situ calibration.* The calculation of the free  $Zn^{2+}$  concentration is based on the experimentally observed occupancies and the  $K_d$  of the sensor, which is most accurately determined in vitro. However, to rule out the possibility that the  $Zn^{2+}$  affinity is strongly affected by the intracellular conditions such as macromolecular crowding, ideally the sensor's affinity is also determined in situ. In situ calibration of eCALWY-4 using the pore-forming protein  $\alpha$ -toxin and a  $Zn^{2+}$  buffer solution revealed that the in situ  $K_d$  was only slightly lower than that obtained in vitro using purified sensor protein.

### 7.2.2.2 Sensors Based on Zinc Fingers: Zif- and Zap-Based FRET Sensors

Because zinc fingers (ZFs) display metal-dependent protein folding and they typically show a high affinity and specificity for  $Zn^{2+}$ , they provide an attractive class of  $Zn^{2+}$ -binding domains for FRET sensor development. Although  $Zn^{2+}$  in most ZF domains plays solely a structural role, several examples of ZnF domains have also been reported that act as  $Zn^{2+}$ -dependent transcriptional regulators. The Palmer group has developed FRET sensors based on several different zinc-finger domains, providing access to FRET sensors with a range of affinities. The first series of FRET sensors was constructed using a ZF domain derived from the mammalian transcription factor Zif268, which contains a Cys<sub>2</sub>His<sub>2</sub> binding motif (Dittmer et al. 2009). This well-characterized ZF is known to be largely unstructured in the absence of the metal ion and only folds upon  $Zn^{2+}$  binding. Two sensors were constructed by flanking the ZF domain with CFP and YFP, one containing the

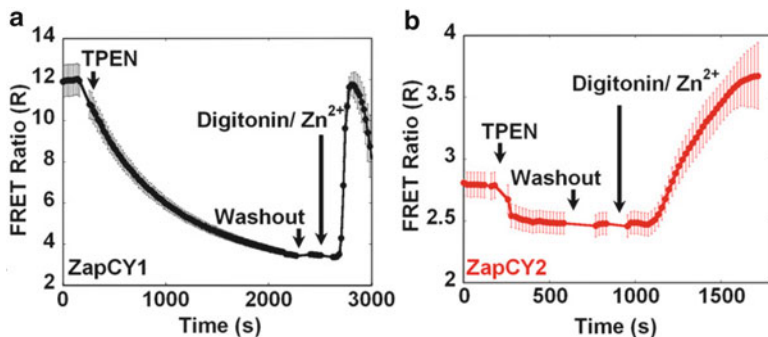




**Fig. 7.5** Schematic representation of the high-affinity  $Zn^{2+}$  sensor ZapCY1, which consists of the first and second zinc finger of *Saccharomyces cerevisiae* Zap1 flanked by two fluorescent proteins, truncated CFP and citrine. (Adapted from Qin et al. 2013)

wild-type zinc-finger domain (ZifCY1) and a variant in which the cysteines in the original Cys2His2 motif were replaced by two other histidines (ZifCY2). In vitro, a large increase in emission ratio was observed for both the ZifCY1 (2.2-fold) and the ZifCY2 (4-fold) sensors upon addition of  $Zn^{2+}$ . These in vitro  $Zn^{2+}$  titration experiments revealed  $Zn^{2+}$  affinities of 1.7 and  $\sim 160 \mu M$  for the ZifCY1 and ZifCY2 sensors, respectively. This affinity of the ZifCY1 sensor was surprisingly weak compared to the original Zif268 domain that contains a site with nanomolar affinity for  $Zn^{2+}$ . The origin of this large attenuation of  $Zn^{2+}$  affinity is not well understood but was attributed to the attachment of the fluorescent proteins. Both sensors were also tested by transiently expressing them in mammalian cell lines and monitoring their response to the addition of TPEN, followed by addition of digitonin (to permeabilize the cells) and subsequent  $Zn^{2+}$  addition. Unfortunately, the dynamic range of the ZifCY1 sensor was reduced to 25 %, possibly reflecting the effect of molecular crowding on decreasing the distance between the two fluorophores in the absence of zinc, resulting in an overall smaller ratiometric change. Despite the low  $Zn^{2+}$  affinity, the response of the ZifCY1 sensor was still used to estimate the cytosolic free  $Zn^{2+}$  concentration to be approximately 180 nM. This number merely reflected the lower limit of detection for this sensor, however, which also explained why higher sensor concentrations resulted in an apparent increase in the estimated intracellular  $Zn^{2+}$  level. This example illustrates the difficulty of measuring analyte concentrations that are outside the affinity range of a sensor, as the cytosolic  $Zn^{2+}$  concentration was subsequently shown to be 1,000 fold lower.

To overcome the low affinity and limited in situ dynamic range of the Zif268-based FRET sensors, Palmer and coworkers subsequently developed a series of FRET sensors based on zinc-finger domains from the yeast transcriptional regulator Zap1 (Qin et al. 2011). Instead of just a single ZF domain, these so-called Zap sensors consist of the first and second zinc fingers of *Saccharomyces cerevisiae* Zap1, which have low nanomolar affinity for  $Zn^{2+}$  (Fig. 7.5). FRET sensors based on these ZFs were actually first reported by Eide and coworkers (Qiao et al. 2006), who used them to learn more about the kinetics of  $Zn^{2+}$  binding and release to the



**Fig. 7.6** FRET responses of ZapCY1 (a) and ZapCY2 (b) in the cytosol of HeLa cells ( $n = 5$  cells). **a** ZapCY1 was fully saturated in the cytosol under resting conditions. **b** ZapCY2 was only partially saturated at the start of the experiment; free cytosolic  $Zn^{2+}$  concentration was estimated to be  $\sim 80$  pM. (Adapted from Qin et al. 2011)

Zap1 zinc-finger domains. In the original study the sensors were not characterized *in vitro* and not used to measure the free  $Zn^{2+}$  concentration at the single-cell level. Palmer and coworkers improved these probes by introducing a truncated version of CFP and replacement of EYFP by the more pH stable citrine. To increase the dynamic range, the linker in the construct was also replaced by one previously used in genetically encoded  $Ca^{2+}$  sensors.

Determination of the  $Zn^{2+}$  affinity of the ZapCY1 sensor *in vitro* yielded a  $K_d$  of 2.5 pM at pH 7.4 (Fig. 7.6a). The  $Zn^{2+}$  affinity could be attenuated by replacing two of the cysteines in the zinc-finger domains by histidines again, yielding the ZapCY2 sensor, with a  $K_d$  of 811 pM. When ZapCY-1 was expressed in the cytosol of HeLa cells, a large fourfold decrease in emission ratio was observed upon treatment with a zinc-chelating reagent, which was completely reversed upon treatment of the cells with digitonin and excess  $Zn^{2+}$ . This response shows that the high-affinity ZapCY1 sensor was fully saturated under normal conditions. The lower-affinity ZapCY-2 sensor was only partially saturated in the cytosol under resting conditions (Fig. 7.6b), showed a 1.4-fold dynamic range, and could be used to estimate the free  $Zn^{2+}$  concentration in the cytosol to be  $\sim 80$  pM, which is in the same range as determined using the eCALWY series.

A striking feature of the ZapCY-1 sensor is that prolonged incubations with TPEN are required to reach the  $Zn^{2+}$ -free state of the sensor. Part of this slow response may be an inherent feature of such high-affinity sensors, as the high-affinity eCALWY-1 sensor also showed a slower response than the intermediate-affinity eCALWY-4 sensor. Despite their similar affinities, the  $Zn^{2+}$ -free state of eCALWY-1 is reached within a few minutes, however, whereas this takes at least 30 min for ZapCY-1. The response of the lower-affinity ZapCY-2 to TPEN addition is much faster, making this the preferred Zap-based sensor for measuring cytosolic  $Zn^{2+}$  concentrations.

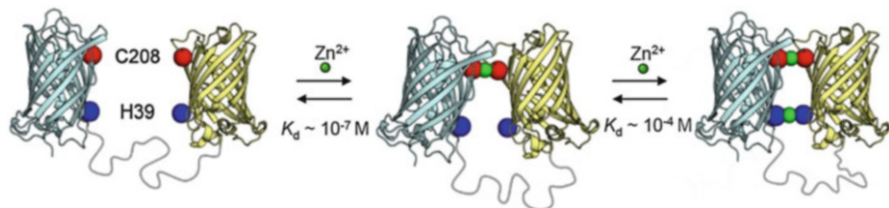
As for the eCALWY sensors, red-shifted variants have also been developed for the Zap-based FRET sensors. The CFP and YFP domains of the ZapCY1 and

ZapCY2 sensors were replaced by a variety of red-shifted donor and acceptor fluorescent domains, and sensor performance was tested for both cytosolic and nuclear-targeted sensors in HeLa cells, by doing an in situ calibration using TPEN and Zn<sup>2+</sup>. Sensors with orange and red fluorescent domains, which are spectrally well separated from the CFP-YFP-based sensors, displayed relatively small changes in emission ratio of about 10 %. The highest in vivo dynamic range (40 %) was observed for sensors that used the green fluorescent protein Clover as donor and the red fluorescent protein mRuby2 as an acceptor. Using the latter sensors allowed the simultaneous measurement of Zn<sup>2+</sup> concentration in different organelles, such as the nucleus and the cytosol, or the nucleus and the ER, Golgi, or mitochondria. The relatively modest dynamic range of the red-shifted sensor variants and the substantial spectral overlap between CFP/YFP- and Clover/mRuby2-based sensors precluded measurements in the same or overlapping intracellular compartments. The occupancies of the various sensors were sometimes found to be different, which suggests that replacing the fluorescent domains also affected Zn<sup>2+</sup> affinity. Unfortunately, in vitro determination of the Zn<sup>2+</sup> affinities of these new sensor variants was not reported.

### 7.2.2.3 eZinCh FRET Sensors and His-Tag-Based Sensors

The relatively high Zn<sup>2+</sup> affinity of both the eCALWY and zinc-finger-based FRET sensors makes these the sensors of choice for imaging free cytosolic Zn<sup>2+</sup> in mammalian cells. However, concentrations of free Zn<sup>2+</sup> can differ substantially between cellular compartments, and the extracellular free Zn<sup>2+</sup> concentration is known to be significantly higher. An example is provided by the insulin-secreting vesicles in pancreatic beta cells. The free Zn<sup>2+</sup> concentrations in these vesicles was found to be high enough to completely saturate eCALWY-6, which at pH 6 binds Zn<sup>2+</sup> with a  $K_d$  of 0.5  $\mu$ M. Reliable measurements of these higher Zn<sup>2+</sup> concentrations thus require the development of FRET sensors with sensitivities in the high nanomolar to micromolar region and sensors that cover a broader concentration range.

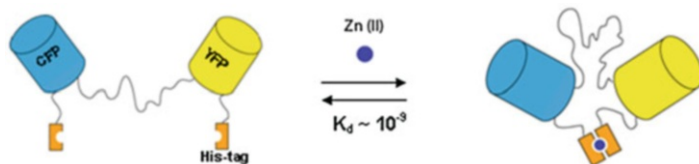
One example of these moderate-affinity sensors are the so-called ZinCh sensors (Evers et al. 2007). The ZinCh sensors do not contain separate Zn<sup>2+</sup>-binding domains but consist of a fusion protein of ECFP and EYFP connected via a long flexible peptide linker of different lengths, in which two Zn<sup>2+</sup>-coordinating amino acids (Y39H and S208C) were introduced at the dimer interface of both fluorescent domains (Fig. 7.7). A biphasic fourfold increase in emission ratio was observed upon addition of Zn<sup>2+</sup>, corresponding to an increase in energy transfer efficiency from 50 % to 85 %. The first binding event ( $K_d = 200$  nM at pH 8) involves the two Cys208 residues and results in formation of an intramolecular complex of ECFP and EYFP in a parallel orientation. After binding of Zn<sup>2+</sup> to the high-affinity site, the two His39 are pre-organized to form a second, low-affinity Zn<sup>2+</sup>-binding site ( $K_{d2} \sim 88$   $\mu$ M at pH 8.0), which results in a further increase in FRET. This sensor protein thus showed a large, fourfold increase in emission ratio over a broad range of Zn<sup>2+</sup> concentrations between 100 nM and 1 mM. Importantly, ZinCh was shown



**Fig. 7.7** Design of  $\text{Zn}^{2+}$ -chelating ECFP-EYFP chimera ZinCh-9. ECFP was fused to EYFP by a flexible  $(\text{GGSGGS})_9$  linker. A biphasic response was observed upon increasing  $\text{Zn}^{2+}$  concentrations, yielding a fourfold increase in emission ratio. (Adapted from Evers et al. 2007)

to be specific for  $\text{Zn}^{2+}$  over other divalent metal ions such as  $\text{Cd}^{2+}$ ,  $\text{Ni}^{2+}$ ,  $\text{Mg}^{2+}$ , and  $\text{Ca}^{2+}$ . More recently, the ECFP and EYFP domains were replaced by cerulean and citrine and the low-affinity site was deleted. This sensor, eZinCh-1, showed an even larger, eightfold increase in emission ratio and a similar  $\text{Zn}^{2+}$  affinity of  $K_d = 258$  nM. The  $\text{Zn}^{2+}$  affinity of eZinCh-1 was also established under physiological relevant conditions, by determination of the  $\text{Zn}^{2+}$  affinity at pH 7.1 (cytosolic) and pH 6.0 (vesicular). Changing the pH from 8.0 to 7.1 resulted in a decrease in affinity to a  $K_d$  of 8.2  $\mu\text{M}$  for  $\text{Zn}^{2+}$ , and  $K_d$  of  $\sim 250$   $\mu\text{M}$  at pH 6.0, most likely due to protonation of the cysteine residues ( $\text{p}K_a = 8.3$ ) at lower pH. An initial effort to further increase the  $\text{Zn}^{2+}$  affinity of the eZinCh platform by introduction of additional flanking cysteine residues to create a tetrahedral  $\text{Cys}_4$  site was not successful, as the  $\text{Zn}^{2+}$  affinities were in the same range as eZinCh-1. This unimproved affinity suggests that only two of the four cysteines are involved in  $\text{Zn}^{2+}$  binding because the binding pocket is too large to tightly bind the  $\text{Zn}^{2+}$ . Indeed,  $\text{Cd}^{2+}$ , which has a larger ionic radius, was found to strongly bind to some of these  $\text{Cys}_4$  variants (Vinkenborg et al. 2011). Recently, our group found other eZinCh variants that display a substantially higher  $\text{Zn}^{2+}$  affinity, with a  $K_d$  of 1 nM at pH 7.1 and 200 nM at pH 6.0 (Hessels et al., unpublished results).

All the sensors discussed here rely at least partially on cysteines for  $\text{Zn}^{2+}$  binding, which renders these sensors redox sensitive and is the main reason for their pH sensitivity. Sensors based on histidine coordination are insensitive to oxidation and are predicted to be less sensitive to pH because of the lower  $\text{p}K_a$  of histidine. Based on the serendipitous discovery that  $\text{Zn}^{2+}$  forms a relatively stable 1:2 complex with His-tags, a FRET sensor was created by incorporating His-tags at the N- and C-termini of a fusion protein of ECFP and EYFP connected via a flexible peptide linker (Fig. 7.8). Addition of  $\text{Zn}^{2+}$  to this CLY9-2His sensor yielded a 1.6-fold increase in emission ratio, corresponding to a  $K_d$  of about 47 nM. The  $\text{Zn}^{2+}$  affinity of CLY9-2His is slightly higher than the afore-described ZinCh constructs. This sensor has not been used for intracellular imaging but has recently been applied to measure the free  $\text{Zn}^{2+}$  concentration in blood serum (Arts et al., unpublished results). This sensor variant may be improved further by replacing the ECFP and EYFP by cerulean and citrine and optimization of the linkers between the His-tags and the fluorescent domains. Such improved variants could be useful for intracellular imaging in oxidizing or acidic intracellular compartments.

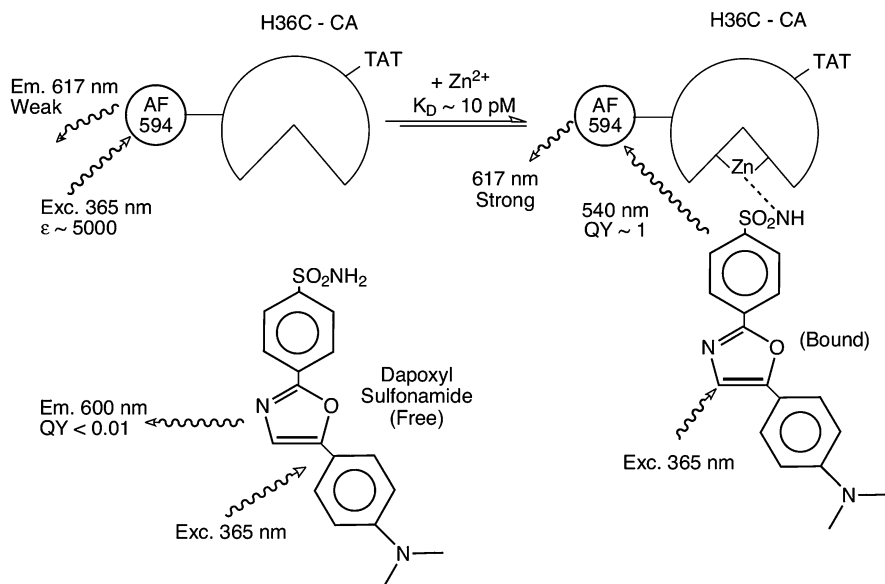


**Fig. 7.8** Design of CLY9-2His containing both an N-terminal and a C-terminal His-tag.  $Zn^{2+}$  binding results in the formation of a compact intramolecular  $Zn^{2+}$  complex with a moderate  $Zn^{2+}$  affinity. (Adapted from Evers et al. 2008)

### 7.2.2.4 FRET Sensors Based on Binding of Fluorescently Labeled Sulfonamide to Carbonic Anhydrase

Thompson and coworkers have been developing fluorescent sensors based on carbonic anhydrase (CA), an enzyme with a single  $Zn^{2+}$ -binding site with picomolar affinity at pH 7.5 (Bozym et al. 2006). Carbonic anhydrase is one of the best studied enzymes, and a wealth of mutations are available that allow tuning of its  $Zn^{2+}$  affinity and  $Zn^{2+}$ -binding kinetics. In the original design, a FRET-based sensor was obtained by covalent attachment of Alexa Fluor 594 at a cysteine introduced at position 36, which acted as an acceptor for fluorescence from dapoxyl-sulfonamide, a fluorescent sulfonamide that binds strongly to the active site  $Zn^{2+}$ . The ratio of fluorescence observed at 617 nm obtained using dapoxyl excitation at 365 nm and direct AF594 excitation at 594 nm was used as a measure of the  $Zn^{2+}$  occupancy of the CA domain. To allow intracellular uptake of the fluorescently labeled CA, the probe was fused to a TAT peptide (Fig. 7.9).

Dissociation constants were obtained by determining calibration curves both on the microscope and a steady-state fluorometer, yielding  $K_d \sim 70$  and  $\sim 137$  pM, respectively. PC-12 cells were incubated with apoTAT-H36C-AF594-CA and dapoxyl-sulfonamide to measure free zinc levels inside the cell. A free  $Zn^{2+}$  concentration of 5 pM was obtained by direct comparison of the excitation ratio observed in the cell and the calibration curves. However, because no changes in emission ratio were observed upon addition of excess  $Zn^{2+}$  or strong  $Zn^{2+}$  chelators, in situ calibration of the sensor was not possible in this case, making the measurements more susceptible to variations in background fluorescence. Moreover, the performance of this system relies on the formation of a ternary complex between sensor,  $Zn^{2+}$ , and sulfonamide and thus assumes the presence of saturating concentrations of the latter of 1  $\mu$ M. A fully genetically encoded version of the sensor protein was subsequently developed by fusing CA to dsRed2 as a FRET acceptor. This variant no longer requires protein transfection using the TAT peptide and could be targeted to the mitochondria of PC12 cells (McCranor et al. 2012). In situ calibration in isolated mitochondria revealed a  $K_d$  of 0.15 pM, which was substantially lower than the 17 pM determined for wtCA-dsRed2 in buffer and 70 pM determined for H36C-AF594-CA. Direct comparison of the excitation ratio yielded an apparent free  $Zn^{2+}$  concentration in the mitochondria of 0.15 pM.



**Fig. 7.9** Schematic representation of zinc ratiometric zinc determination with apoTAT-H36C-AlexaFluor 594 carbonic anhydrase and dapoxyl sulfonamide. In the absence of zinc, dapoxyl sulfonamide does not bind CA; therefore, no FRET occurs and very weak emission at 617 nm is observed. In the presence of zinc, dapoxyl sulfonamide binds to zinc, and FRET occurs from dapoxyl to the AlexaFluor 594. (Adapted from Bozym et al. 2006)

Both sensors just described are excitation ratiometric, which requires switching between two different lasers, and excitation of dapoxyl requires the use of 365-nm light, which may be damaging to the cells. Another sensor based on CA was therefore recently developed by the Thompson group (Zeng et al. 2013), in which the AF594 that is covalently attached to the CA acts as a donor. Chesapeake blue (CB) was coupled to the sulfonamide and can bind to the active protein in the presence of  $Zn^{2+}$ . In the absence of  $Zn^{2+}$ , the AF594 emits at 617 nm; when  $Zn^{2+}$  is bound to the protein, it promotes binding of the CB sulfonamide, resulting in emission at 650 nm. This red-shifted emission ratiometric sensor displayed a twofold change in emission ratio and bound  $Zn^{2+}$  with a  $K_d \sim 5.8 \pm 3.1$  pM. The CB sulfonamide is highly charged, however, which prevents its application in intracellular imaging.

### 7.3 Applications of Genetically Encoded Sensors

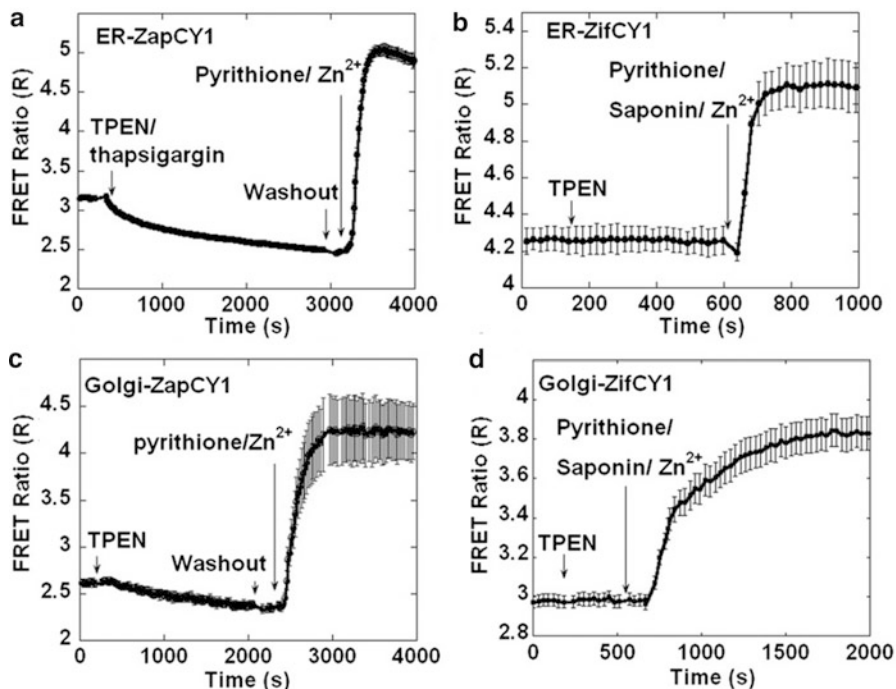
In the previous section, the various types of genetically encoded fluorescent  $Zn^{2+}$  sensors were introduced and their *in vitro* and initial *in situ* characterization was described. In this section we discuss various subsequent applications such as their targeting to various subcellular compartments and their application in different cell types and organisms.

### 7.3.1 Subcellular Targeting of Genetically Encoded Sensors

One of the key distinguishing features of genetically encoded sensors is the relative ease by which they can be targeted to specific subcellular locations. Genetically encoded FRET sensors have been instrumental in establishing the concentration of free Zn<sup>2+</sup> in a variety of cell types, revealing that cytosolic Zn<sup>2+</sup> is well buffered between 0.1 and 1 nM. Successful determination of cytosolic Zn<sup>2+</sup> concentrations critically depended on the availability of FRET sensors with the appropriate  $K_d$  and a robust calibration procedure to determine for each individual cell the emission ratio corresponding to Zn<sup>2+</sup>-free and Zn<sup>2+</sup>-bound state. In an effort to determine the free Zn<sup>2+</sup> concentration in other organelles, several of the ZF-based FRET sensors developed in the Palmer laboratory were targeted to the ER, Golgi, and the mitochondrial matrix. Both the high-affinity ZapCY1 ( $K_d \sim 2.5$  pM) and the low-affinity ZifCY1 ( $K_d \sim 1.7$   $\mu$ M) sensor were targeted to the lumen of the ER and the inner surface of the Golgi membrane (Qin et al. 2011). The targeting was confirmed by colocalization using commercially available markers to the desired organelles. HeLa cells expressing ER-ZapCY1 showed a slow and small decrease in emission ratio following addition of TPEN (Fig. 7.10a), followed by a much larger increase in emission ratio upon addition of excess Zn<sup>2+</sup>. For cells expressing the low-affinity ER-ZifCY1 (Fig. 7.10b), no decrease in FRET was observed upon TPEN addition, suggesting that the free Zn<sup>2+</sup> level in the ER was below the detection limit of this sensor. Equation 7.1 was used to calculate the free Zn<sup>2+</sup> concentration in the ER under resting conditions by using  $R_{\min}$  and  $R_{\max}$  for calibration, yielding a free Zn<sup>2+</sup> in the ER of 0.9 pM. The same experiments were performed in the Golgi (Fig. 7.10c, d), yielding a similarly low free Zn<sup>2+</sup> of 0.6 pM.

These data would suggest that the free Zn<sup>2+</sup> concentration in the ER and Golgi of mammalian cells is maintained at an even lower concentration than is present in the cytosol. One potential caveat of these measurements is the slow rate of Zn<sup>2+</sup> release from the sensor upon TPEN addition, which makes it more difficult to accurately determine  $R_{\min}$ . Very different results were recently obtained by the Rutter and Merx groups, who used ER-targeted eCALWY-4 to probe the Zn<sup>2+</sup> concentration in the ER. This probe, which has an affinity of 600 pM, was found to be mostly saturated with Zn<sup>2+</sup> in a variety of cell lines and primary cardiomyocytes (Chabosseau et al. 2014). These results would suggest that the free Zn<sup>2+</sup> concentration in the ER is at least 5 nM, which would be consistent with recent suggestions that the ER acts as a store for Zn<sup>2+</sup> (Taylor et al. 2012). Taylor and coworkers recently proposed a model whereby phosphorylation of ZIP7 plays a role in release of Zn<sup>2+</sup> from ER stores into the cytosol.

FRET sensors have also been targeted to the mitochondrial matrix. Palmer and coworkers appended an N-terminal mitochondrial targeting sequence from human cytochrome *c* oxidase subunit 8a to both Zif- and Zap-based FRET sensors, yielding



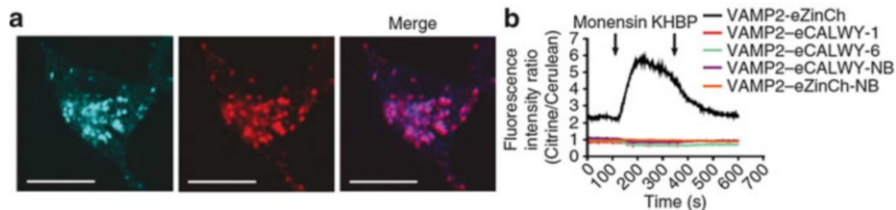
**Fig. 7.10** Representative traces for ER-ZapCY1 (a) and ER-ZifCY1 (b). **a** The FRET ratio decreased upon addition of 150  $\mu\text{M}$  TPEN/10  $\mu\text{M}$  thapsigargin and increased with addition of 5  $\mu\text{M}$  pyrithione and 10 nM  $\text{Zn}^{2+}$ . **b** No change in FRET ratio was observed upon TPEN addition, but addition of 25  $\mu\text{M}$  pyrithione/saponin/500  $\mu\text{M}$   $\text{Zn}^{2+}$  resulted in an increase in emission ratio. Representative traces for Golgi-ZapCY1 (c) and Golgi-ZifCY1 (d). **c** The FRET ratio decreased upon addition of 150  $\mu\text{M}$  TPEN and increased with addition of 5  $\mu\text{M}$  pyrithione and 10 nM  $\text{Zn}^{2+}$ . **d** No change in FRET ratio was observed upon TPEN addition, but addition of 25  $\mu\text{M}$  pyrithione/saponin/500  $\mu\text{M}$   $\text{Zn}^{2+}$  resulted in an increase in emission ratio. (Adapted from Qin et al. 2011)

mito-ZapCY1 and mito-ZifCY1. Colocalization studies using MitoTracker Red confirmed excellent targeting. Based on measurements with the low-affinity mito-ZifCY1, the mitochondrial free  $\text{Zn}^{2+}$  concentration was initially reported to be 680 nM. However, this number was found to be unreliable because of the poor dynamic range of mito-ZifCY1 as new variants with a larger dynamic range were found to be essentially unsaturated (Park et al. 2012; Dittmer et al. 2009). Targeting of the high-affinity ZapCY1 sensor to the mitochondria showed a response to TPEN and  $\text{Zn}^{2+}$ /pyrithione addition that is very similar to that of ER- and Golgi-targeted Zap-CY1; that is, addition of TPEN induces a small decrease in emission ratio over a period of an hour, whereas subsequent addition of excess  $\text{Zn}^{2+}$  results in a much larger and rapid increase in emission ratio. Based on this response and correcting for the even higher affinity of ZapCY1 at the mitochondrial pH of 8, the free mitochondrial  $\text{Zn}^{2+}$  concentration was estimated to be 0.22 pM in HeLa cells.



Somewhat higher sensor occupancies of 50 % were observed in MIN6 and primary neurons. These surprisingly low concentrations are 300 fold lower than what was recently determined using a small-molecule Zn<sup>2+</sup> fluorescent sensor (Xue et al. 2012) that contained a triphenylphosphonium (TPP) group as an effective mitochondrial targeting ligand. The  $K_d$  of this probe was determined to be about 150 pM at mitochondrial pH and a free mitochondrial Zn<sup>2+</sup> concentration of about 72 pM was measured in NIH 3T3 cells. Recent measurements of mitochondrial Zn<sup>2+</sup> using the eCALW-4 sensor targeted to the mitochondrial matrix consistently yielded free Zn<sup>2+</sup> concentrations of 200–300 pM in a number of cell lines and primary cells (Chabosseau et al. 2014). Thus, the ER and mitochondrial zinc concentrations determined using the eCALWY probes are three orders of magnitude higher than calculated using the targeted ZapCY1 probes (Park et al. 2012; Qin et al. 2011). This discrepancy is likely not the result of an error in determining the Zn<sup>2+</sup> affinities of one of the sensors, as the eCALWY sensors and ZapCY1/CY2 sensors give much more consistent results when applied in the cytosol. A striking feature of the ZapCY1 sensor is its slow dissociation kinetics, which required more than 1 h incubation in TPEN to achieve the fully Zn<sup>2+</sup>-depleted state (Qin et al. 2011) compared to 2–3 min for the equivalent eCALWY probe (Fig. 7.2). In general, rapid equilibration makes the determination of  $R_{0\%}$  and  $R_{100\%}$  less sensitive to baseline drift, and prolonged incubations with TPEN have also been reported to be cytotoxic (Hashemi et al. 2007; Donadelli et al. 2008). Nonetheless, why the eCALWY- and ZapCY-based sensors behave so differently when targeted to the ER and mitochondria remains to be explained. One way to resolve these discrepancies might be to use FRET sensors that have alternative binding mechanisms. The current sensors depend on cysteines for Zn<sup>2+</sup> coordination, which may result in formation of disulfide bonds or misfolding in the oxidizing environment of the ER lumen.

Secretory vesicles in many cell types contain highly elevated Zn<sup>2+</sup> concentrations including those involved in neurotransmission, the prostate, and the insulin-containing vesicles of pancreatic  $\beta$  cells. The only example of a genetically encoded sensor targeting a secretory vesicle has been reported by Vinkenborg et al. Both the high-affinity sensors eCALWY-1 and eCALWY-6 and the low-affinity eZinCh-1 sensor were targeted to the secretory granules of INS-1(832/13) cells by fusion to vesicle-associated membrane protein 2 (VAMP2). Zn<sup>2+</sup> is known to be important for insulin storage and secretion, and stable insulin Zn<sup>2+</sup> complexes are formed in the acidic (pH 6.0) interior of these vesicles. Mutations in Znt8, a Zn<sup>2+</sup>-specific importer protein that is exclusively localized in the secretory granules, have also been linked to the development of diabetes (Murgia et al. 2009). Colocalization studies of these vesicular-targeted constructs showed exclusive localization in insulin-containing granules (Fig. 7.11a). Emission ratios of the cells expressing either one of the sensors were monitored; for the eCALWY variants, low emission ratios were observed, indicating that the sensors were already fully saturated with Zn<sup>2+</sup> at the start of the experiment. On the other hand, the low affinity eZinCh-1 appeared to be empty at this stage. None of the sensors showed changes in emission ratio upon addition of either TPEN or Zn<sup>2+</sup>/pyrithione, suggesting that at high free



**Fig. 7.11** Subcellular targeting of  $\text{Zn}^{2+}$  probes to insulin-storing vesicles. **a** Confocal laser microscopy images of INS-1(832/13) cells transfected with plasmids encoding VAMP2-eCALWY-1 (*left*) and neuropeptide Y-mCherry (*middle*). **b** Ratiometric response of INS-1 (832/13) cells expressing different VAMP2 constructs to  $10\ \mu\text{M}$  monensin (1), followed by buffer without compounds (2). (Adapted from Vinkenborg et al. 2009)

$\text{Zn}^{2+}$  concentrations TPEN is unable to remove the  $\text{Zn}^{2+}$  from the high-affinity eCALWY variants ( $K_d = 0.5\ \mu\text{M}$  at pH 6.0 for eCALWY-6). At the same time, it is probably also difficult to raise the free  $\text{Zn}^{2+}$  concentration inside the vesicles to the millimolar (mM) concentrations that are required to saturate the low-affinity eZinCh-1 sensor ( $K_d\ 250\ \mu\text{M}$  at pH 6.0; Table 7.1). To test the hypothesis that eZinCh-1 was indeed nearly empty because of the low vesicular pH, cells were treated with the  $\text{Na}^+/\text{H}^+$  exchanger monensin, which transiently increases the pH from 6 to 7. As expected, a reversible increase in emission ratio was observed for cells expressing VAMP2-eZinCh-1 as a result of simultaneous  $\text{Zn}^{2+}$  release from the insulin- $\text{Zn}^{2+}$  and increase in affinity of eZinCh-1 (Fig. 7.11b). Although this experiment established the functionality of vesicular-targeted eZinCh-1, it also showed that accurate determination of (fluctuations in) vesicular free  $\text{Zn}^{2+}$  concentrations requires the development of less pH sensitive FRET sensors with a  $\text{Zn}^{2+}$  affinity of about  $10\ \mu\text{M}$  at pH 6.0.

### 7.3.2 Applications in Primary Cells and Plants

Genetically encoded fluorescent  $\text{Zn}^{2+}$  sensors have been mostly used in cell lines using transient transfection. To study  $\text{Zn}^{2+}$  homeostasis in primary pancreatic  $\beta$  cells, Rutter and coworkers cloned several eCALWY-variants into a pShuttle vector to allow transfection of primary cells using adenovirus (Bellomo et al. 2011). pShuttle-eCALWY constructs were digested with Pme1 and electroporated into competent BJ5183-AD-1 cells. Recombined pADEasy1 clones were screened, and positive clones were then digested with Pac1 and transfected into HEK293 cells for the generation of adenoviral particles. Primary islet cells were infected with eCALWY-4-expressing adenovirus and used to measure free cytosolic  $\text{Zn}^{2+}$ . High glucose concentrations were found to induce an increase in the cytosolic free  $\text{Zn}^{2+}$  concentration. Cytosolic free  $\text{Zn}^{2+}$  concentrations were found to be twofold higher in cells 24 h after being treated with high glucose concentrations (16.7 mM) compared to cells treated with low (3 mM) glucose concentrations,

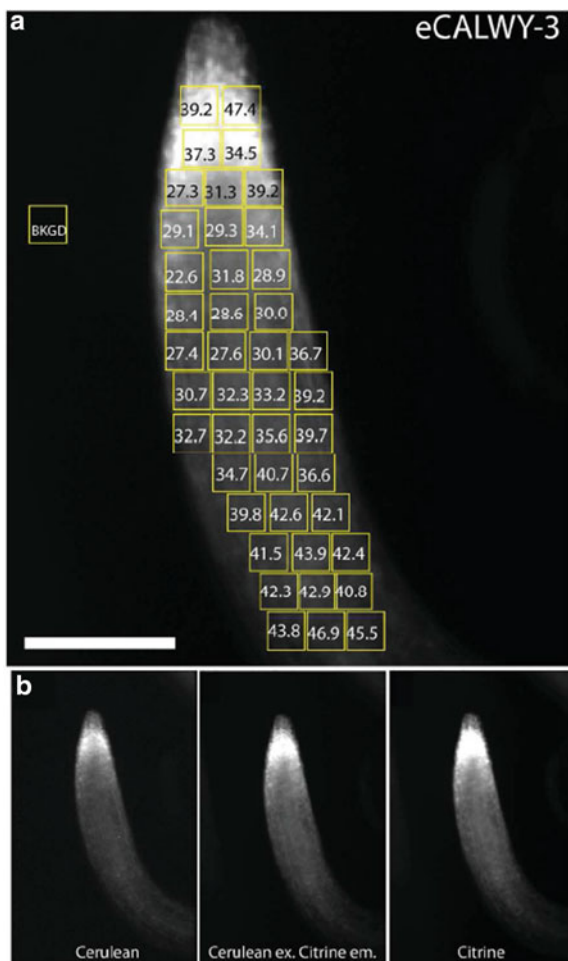
853 pM Zn<sup>2+</sup> versus 452 pM Zn<sup>2+</sup>, respectively. These findings are in contrast with the work done by Zalewski et al., who observed a decrease in cytosolic Zn<sup>2+</sup> in islet cells in response to glucose (Zalewski et al. 1994). They used a synthetic probe (Zinquin) to perform their measurements, however, which partly localizes in granules and other membrane-bound organelles where the free Zn<sup>2+</sup> concentration is higher than in the cytosol. Therefore, the observed free Zn<sup>2+</sup> concentrations and changes may be caused by degranulation of cells in response to glucose. Other primary cells in which FRET sensors have been used include primary neurons (Park et al. 2012) and cardiomyocytes (Chabosseau et al. 2014).

Several techniques have been used to investigate cellular distribution of total Zn<sup>2+</sup> in plants, but until recently genetically encoded sensors have not been used in plants (Lanquar et al. 2005). The chemical probe Zinpyr-1 was used to study the role of Zn<sup>2+</sup> in plants (Sinclair et al. 2007), but several issues were apparent, including problems with cellular penetration, control over intracellular localization, and long-term imaging possibilities. The Frommer group therefore recently constructed transgenic *Arabidopsis thaliana* lines that each constitutively express different cytosolic eCALWY variants (Lanquar et al. 2014). Low or no fluorescence was observed in the Col-O ecotype, indicating transgene-induced silencing. Therefore, the eCALWY variants were also expressed in the rgr6 line, which is deficient in transgene-induced silencing. Transgenic plant lines showing high and homogeneous fluorescence in this genetic background were selected. These eCALWY-expressing *Arabidopsis* lines looked normal and healthy and did not show a change in bulk Zn concentration. To avoid background fluorescence and easy imaging, Zn<sup>2+</sup> homeostasis was imaged in root cells using the so-called RootChip setup. To determine the cytosolic Zn<sup>2+</sup> concentration, the sensor occupancy was measured for each sensor as a function of the  $K_d$  of the sensor. For the plants grown in the presence of normal concentrations of Zn<sup>2+</sup> (5 μM), the free cytosolic Zn<sup>2+</sup> concentration was determined to be about 420 pM, the same value was found in mammalian cells using the same FRET sensors (Fig. 7.12). A concentration of about 2 nM was found for plants grown at excess Zn<sup>2+</sup>, and the estimated free cytosolic Zn<sup>2+</sup> concentration in starved root cells was about 1.5 nM, although a high standard error was observed under Zn<sup>2+</sup>-depleted conditions. Monitoring the dynamic response of cytosolic Zn<sup>2+</sup> to external supply suggested the involvement of high- and low-affinity uptake systems as well as release from internal stores.

## 7.4 Conclusion

Genetically encoded Zn<sup>2+</sup> sensors have proven themselves as a valuable alternative to the use of synthetic fluorescent dyes for monitoring intracellular Zn<sup>2+</sup> homeostasis and signaling. FRET-based fluorescent sensor proteins are attractive because they do not require cell-invasive procedures, they allow ratiometric detection, their concentration can be tightly controlled, and they can be targeted to different locations in the cell. FRET-based sensors developed by our group and others

**Fig. 7.12** Images displaying the expression of eCALWY-3 in *Arabidopsis thaliana* roots. **a** The numbers reflect sensor occupancy values calculated for each region of interest. **b** Expression pattern of the sensor in each channel for the same root: cerulean emission (*left*), citrine emission upon cerulean excitation (*middle*), and citrine emission (*right*). (Adapted from Lanquar et al. 2014)



have been instrumental to establish that the cytosolic levels of free zinc in mammalian cells are tightly regulated at around 0.5 nM. An important recent addition to the toolbox of sensors is the development of red-shifted variants, which permits the simultaneous imaging of  $Zn^{2+}$  in different cellular compartments such as the ER and the cytosol, but also provides an opportunity to study the spatiotemporal relationship between  $Zn^{2+}$  signaling and other intracellular signaling pathways. Targeting of FRET sensors to organelles has revealed conflicting results, with one sensor type (ZapCY-1) reporting extremely low levels of free  $Zn^{2+}$  in the ER, Golgi, and mitochondria, whereas much higher levels (>1,000 fold) have been observed for the eCALWY system when targeted to the ER and mitochondria in different cell lines and primary cells. These conflicting results may be resolved by the development of new FRET sensors based on different binding mechanisms. Other items on the to-do list include the development of probes that are redox

insensitive, less pH sensitive, and have affinities tuned to specific applications, such as measuring Zn<sup>2+</sup> in secretory vesicles, extracellular Zn<sup>2+</sup> in the brain, and Zn<sup>2+</sup> in blood plasma. Their genetic encoding should allow easy distribution of these probes throughout the research community and the generation of transgenic organisms to study Zn<sup>2+</sup> homeostasis and signaling in a variety of model organisms.

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# Chapter 8

## Zinc Signal in Brain Functions

Atsushi Takeda

**Abstract** Brain zinc homeostasis is strictly controlled under healthy conditions, indicating the importance of zinc for physiological functions in the brain. Zinc in the synaptic vesicles is released from glutamatergic (zincergic) neuron terminals and serves as a signal factor ( $\text{Zn}^{2+}$  signal) in the intracellular (cytosol) compartment, in addition to the extracellular compartment. The synaptic  $\text{Zn}^{2+}$  signal is dynamically linked to neurotransmission and participates in synaptic plasticity such as long-term potentiation (LTP) and cognitive function. The hypothalamic-pituitary-adrenal (HPA) axis activity, that is, glucocorticoid secretion, is linked to cognitive function and can potentiate glutamatergic neuron activity. The modification of synaptic  $\text{Zn}^{2+}$  signal by the HPA axis activity, which is enhanced by stress and aging, is likely to be linked to cognitive function. On the other hand, abnormal  $\text{Zn}^{2+}$  influx into postsynaptic neurons, which is induced by the abnormal glutamatergic (zincergic) neuron activity, induces neuronal death and is involved in neurological disorders such as stroke/ischemia, temporal lobe epilepsy, Alzheimer's disease, and amyotrophic lateral sclerosis. Therefore, the homeostasis of synaptic  $\text{Zn}^{2+}$  signal is critical in both functional and pathological aspects. This chapter summarizes the physiological significance of intracellular  $\text{Zn}^{2+}$  signaling in brain functions, especially in cognition.

**Keywords** Excitotoxicity • Glucocorticoid • Glutamate • Hippocampus • HPA axis • Memory • Synaptic  $\text{Zn}^{2+}$  • Zinc deficiency

### 8.1 Introduction

The importance of zinc in human health has been widely reported (Frederickson et al. 2005; Cole and Lifshitz 2008; Maret and Sandstead 2008). Zinc deficiency in children is a nutritional and health problem in both developing and developed countries (Black 1998; Bryan et al. 2004). Approximately 50 % of the world population is at risk of zinc deficiency (Brown et al. 2001), and 10 % of the

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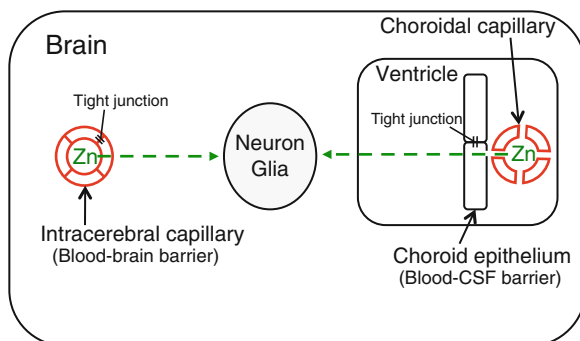
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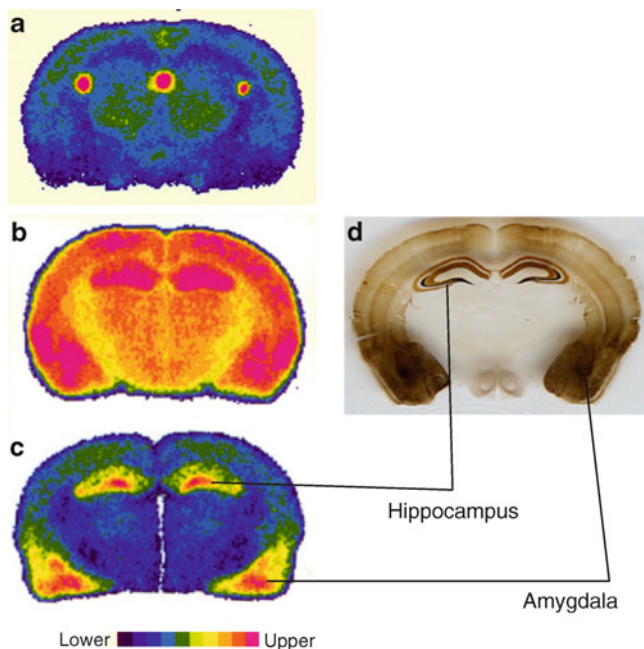
**Fig. 8.1** Zinc transport into the brain parenchyma cells through the brain barrier system. Blood–brain and the blood–cerebrospinal fluid (CSF) barriers exist in the tight junction between brain capillary endothelial cells and the tight junction between the choroidal epithelial cells, respectively



North American population consumes less than half of the recommended daily allowance for zinc (King et al. 2000).

More than 300 proteins require zinc for their functions in microorganisms, plants, and animals. Zinc powerfully influences cell division and differentiation (Vallee and Falchuk 1993; Prasad 2008). Zinc is essential for brain growth and its function. Zinc concentration in the adult brain reaches around 200  $\mu\text{M}$  (Markesbery et al. 1984). Extracellular zinc concentration in the adult brain is estimated to be much less than 1  $\mu\text{M}$  (Weiss et al. 2000). Zinc concentration in the cerebrospinal fluid (CSF) is approximately 0.15  $\mu\text{M}$  (Hershey et al. 1983), and that in the plasma is approximately 15  $\mu\text{M}$ . Zinc transport from the plasma to the brain extracellular fluid and the cerebrospinal fluid is strictly regulated by the brain barrier system, that is, the blood–brain and blood–CSF barrier (Fig. 8.1). The brain barrier system serves for zinc homeostasis in the brain (Takeda 2000, 2001). Zinc homeostasis in the brain is closely associated with neurological diseases (Capasso et al. 2005; Mocchegiani et al. 2005) and is spatiotemporally altered in the process of neurological disease (Barnham and Bush 2008).

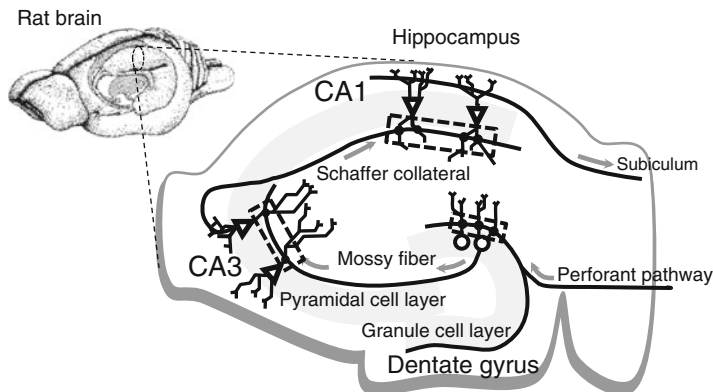
Approximately 80 % of the total brain zinc exists as zinc metalloproteins and the rest is histochemically reactive, as revealed by Timm's sulfide-silver staining method (Frederickson 1989; Frederickson and Danscher 1990), based on the data that the removal of zinc transporter (ZnT)3 protein, which is responsible for the movement of zinc from the cytoplasm into synaptic vesicles (Palmiter et al. 1996), results in a 20 % reduction of the total amount of zinc in the brain (Cole et al. 1999). Zinc is relatively concentrated in the hippocampus and amygdala (Fig. 8.2b, c) (Takeda et al. 1995). Both regions are enriched with histochemically reactive zinc, and histochemically reactive zinc predominantly exists in the presynaptic vesicles and serves as a signal factor ( $\text{Zn}^{2+}$  signal) in the cytosolic compartment as well as the extracellular compartment.  $\text{Zn}^{2+}$  is released with glutamate in a calcium- and impulse-dependent manner from glutamatergic (zincergic) neuron terminals in the hippocampus (Fig. 8.3); all the mossy fibers, and approximately 50 % of the Schaffer collateral where strong staining by Timm's method shows zinc is contained in the presynaptic vesicles (Fig. 8.2d). In contrast, the perforant pathway is minimally stained by Timm's method. Synaptic  $\text{Zn}^{2+}$  signal serves as an



**Fig. 8.2**  $^{65}\text{Zn}$  distribution and Timm's stain in the brain.  $^{65}\text{Zn}$  distribution in coronal sections 1 h (a), 12 days (b), and 30 days (c) after i.v. injection of  $^{65}\text{ZnCl}_2$  into rats. (d) Timm's stain in a mouse coronal section. Note that  $^{65}\text{Zn}$  concentrations are considerably correlated with Timm's stain intensity

endogenous neuromodulator of several important receptors including  $\alpha$ -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid (AMPA)/kainate receptor, *N*-methyl-D-aspartate (NMDA) receptors, and  $\gamma$ -amino butyric acid (GABA) receptors (Smart et al. 1994; Nakashima and Dyck 2009).

The hippocampus and amygdala participate in cognitive and emotional behavior. Synaptic plasticity such as long-term potentiation (LTP) is believed to be a cellular mechanism in learning and memory and has been widely studied at the glutamatergic synapses in the brain, especially in the hippocampus (Fig. 8.3). For processing of information in memory, glutamatergic neurons compose the neural circuit in the hippocampus and amygdala. The hypothalamic-pituitary-adrenal (HPA) axis activity, that is, glucocorticoid secretion, is linked to cognitive and emotional functions and can potentiate glutamatergic neuron activity (Sandi 2011). The modification of synaptic  $\text{Zn}^{2+}$  signal by HPA axis activity, which is enhanced by stress and aging, is likely to be linked to cognitive and emotional behavior (Takeda and Tamano 2009, 2012). On the other hand, abnormal  $\text{Zn}^{2+}$  influx into postsynaptic neurons, which is induced by the abnormal glutamatergic (zincergic) neuron activity, induces neuronal death and is involved in neurological disorders such as stroke/ischemia, temporal lobe epilepsy, Alzheimer's disease, and amyotrophic lateral sclerosis (Takeda 2011a). Therefore, the homeostasis of



**Fig. 8.3** Glutamatergic neural circuit in the hippocampus. Three synapses, i.e., the parforant pathway, mossy fiber, and Schaffer collateral synapses, where surrounded by *dotted lines* are glutamatergic. A subclass of the three synapses contains zinc in synaptic vesicles as described in the text

synaptic  $Zn^{2+}$  signal is critical for both functional and pathological aspects (Takeda 2011b; Takeda et al. 2013a). This chapter summarizes the physiological significance of intracellular  $Zn^{2+}$  signaling in brain functions, especially in cognitive and emotional behavior.

## 8.2 Zinc Homeostasis and the Brain Barrier System

Plasma zinc is largely bound to proteins such as albumin and is thought to be a major pool of zinc in the living body to transfer zinc to the tissues and organs including the brain. The regulation of zinc homeostasis in the living body is tightly controlled by both intestinal absorption and intestinal and renal excretions (King et al. 2000). Zrt-Irt-like proteins (ZIP), which are responsible for the transport of zinc into the cytoplasm, and the ZnT family, which are responsible for the transport of zinc out of the cytoplasm, are involved in the absorption and excretions of zinc to maintain zinc homeostasis in the living body (Cousins et al. 2006; Fukada and Kambe 2011). However, the absorption and excretions of zinc in the living body are synergistic, and the overall mechanism to control zinc homeostasis through the actions of ZIP and ZnT proteins is unknown.

A very stable environment via the brain barrier system is necessary for brain functions. The blood–brain barrier, which consists of the tight junction between the brain capillary endothelial cells (Fig. 8.1) (Abbott 2005), is completed around 2 weeks and 4 months after birth in rats and humans, respectively. The blood–CSF barrier, which consists of the tight junction between the choroidal epithelial cells (Fig. 8.1), is functional in early development (Johansson et al. 2008). Zinc is transported into the brain through the blood–brain and the blood–CSF barriers

(Takeda et al. 1994a). The blood–CSF barrier seems to be important for zinc transport into the hippocampus (Takeda et al. 1994b). Zinc transport into the brain is very slow (Fig. 8.2), compared to that into the peripheral tissues.

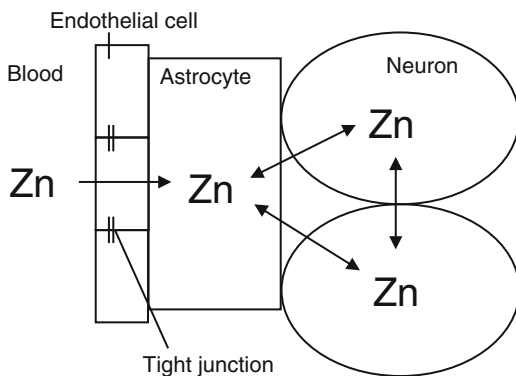
The cells forming the brain barrier system express ZIP and ZnT and maintain zinc homeostasis in the brain (Belloni-Olivi et al. 2009). These transporters have specialized functions for cellular zinc transport. However, their precise role in zinc transport across the brain barrier system is unknown (Colvin et al. 2003; Nakashima and Dyck 2009). Zinc concentration in the brain increases with development after birth and is maintained constant in the adult brain (about 200  $\mu\text{M}$ ) (Markesbery et al. 1984). It has been reported that ZIP such as ZIP1, ZIP4, ZIP6, ZIP7, ZIP10, and ZIP14, and ZnT proteins such as ZnT1, ZnT3, and ZnT10, are involved in not only brain zinc homeostasis but also brain growth (Takeda et al. 2013a). Furthermore, Timm's stain is hardly observed in the rat brain just after birth and the intensity of the stain increases with brain maturation (Valente and Auladell 2002; Valente et al. 2002), indicating that  $\text{Zn}^{2+}$  signal is involved in not only the development and maturation of neural circuits but also its function.

Zinc concentration in the brain is hardly affected by exposure to zinc. In a blood–brain barrier model, the expression of zinc transporters such as ZnT-1 and ZnT-2 and metallothioneins, zinc-binding proteins, are changed to respond to a moderately excessive zinc environment (Bobilya et al. 2008). On the other hand, dietary zinc deficiency, which readily reduces plasma zinc, facilitates zinc uptake into the brain via changes in zinc transporter expression in the brain such as ZnT-1 and LIV-1 (SLC39A6 or ZIP6) (Chowanadisai et al. 2005), resulting in the maintenance of zinc concentration in the brain. However, zinc concentration is decreased in the hippocampus when 8-week-old rats are fed a zinc-deficient diet for 12 weeks (Takeda et al. 2001). In spite of the tight regulation of the brain barrier system, hippocampal zinc is susceptible to chronic zinc deficiency. In young rats after 1-week zinc deprivation, plasma zinc concentration is less than 50 % of the control (Takeda et al. 2007a). It is possible that the decrease in plasma zinc leads to the decrease in CSF zinc, followed by decrease in hippocampal zinc.

The astrocytes directly contact the brain capillary endothelial cells and are a possible sensor to maintain zinc homeostasis in the brain (Fig. 8.4). It is possible that the astrocytes sense the decrease in plasma zinc, which serves to prevent the loss of brain zinc in cooperation with the brain capillary endothelial cells. In addition to the communication via zinc between astrocytes and capillary endothelial cells, the communication via zinc between neurons and astrocytes might be important for intracellular zinc homeostasis, which is critical for cellular function (Bertoni-Freddari et al. 2008).  $\text{Zn}^{2+}$  is a possible tool for communications; synaptic  $\text{Zn}^{2+}$  dynamically moves along with neuronal activity and modulates synaptic neurotransmission (as described next) (Ueno et al. 2002) and is potentially involved in communications. Cooperative metabolism between neurons and astrocytes is reported concerning energy metabolism (Magistretti 2006) and utilization of neurotransmitters such as glutamate (Voutsinos-Porche et al. 2003).

On the other hand, brain capillary endothelial cells also play an active part in the process of many neurological diseases. The blood–brain barrier is modified or

**Fig. 8.4** Communication via zinc between endothelial cells, astrocytes, and neurons. Endothelial cells are primarily surrounded by astrocytes. Astrocytes might be involved in zinc supply to neurons and sense the decrease in plasma zinc via communication with the brain capillary endothelial cells



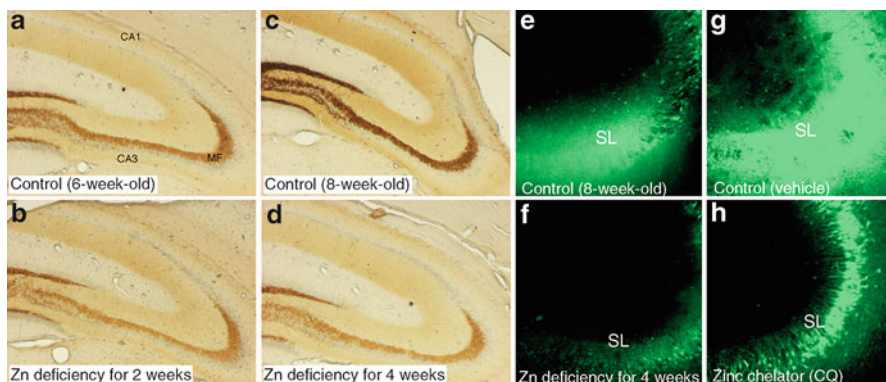
disrupted in the process of neurological diseases such as neoplasia, stroke/ischemia, epilepsy, and dementia (Ballabh et al. 2004). Increase in blood–brain barrier permeability elicits the dyshomeostasis of metals such as zinc and iron, which has been implicated in many neurodegenerative diseases (Yokel 2006).

### 8.3 Synaptic $Zn^{2+}$ Homeostasis

If zinc concentration in the brain extracellular fluid is equal to that in the cerebrospinal fluid, it is about 150 nM and approximately 1,000-fold of the total brain zinc concentration. Zinc concentration, especially  $Zn^{2+}$  concentration, in the synaptic cleft, especially in zincergic synapses, is estimated to be higher than that in the brain extracellular fluid, because the regions where zincergic synapses exist is intensely stained with ZnAF-2, a membrane-impermeable zinc indicator (Fig. 8.5e–h) (Takeda et al. 2012a). The synaptic cleft is surrounded with the processes of astrocytes and might be convenient to maintain a steady concentration of zinc and neurotransmitters.

Zinc concentration in brain extracellular fluid, as measured by the *in vivo* microdialysis, is increased with brain development (Takeda et al. 2013a). However, the increase is suppressed under chronic zinc deficiency (Takeda et al. 2006b); in the hippocampus, extracellular zinc concentration is significantly lower than that of the control rats after 4-week zinc deprivation because of the increase in extracellular zinc concentration in the control (Takeda et al. 2003a, b). The intensity of Timm's stain of zinc-deficient rats is also lower than that of the control rats after 4-week zinc deprivation (Fig. 8.5a–d) (Takeda et al. 2006a). The chronic decrease in plasma zinc concentration may suppress the increase in zinc concentration in the brain extracellular fluid, followed by suppression of the increase in the intensity of Timm's stain.

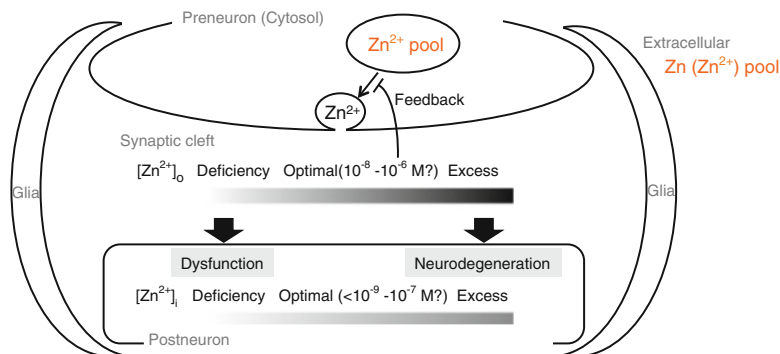
Some fractions of the total zinc in the plasma seem to be responsive to zinc deficiency. One of these is potentially free  $Zn^{2+}$  that is estimated to be as low as



**Fig. 8.5** Decrease in synaptic  $Zn^{2+}$  in the hippocampus. Rats (4-week-old) were fed a control (a, c) and zinc-deficient (b, d) diet for 2–4 weeks. The coronal sections of the brain show Timm's stain in the hippocampus. Mossy fibers (MF) from dentate granule cells are strongly stained. The increase in Timm's stain intensity is obviously suppressed in mossy fibers and other hippocampal regions after 4-week zinc deficiency (b, d). Extracellular (synaptic cleft)  $Zn^{2+}$ , which was measured with ZnAF-2, a membrane-impermeable zinc indicator, is decreased in the hippocampal CA3 region, especially in mossy fibers (stratum lucidum, SL), of rats after 4-week zinc deficiency (e, f). Extracellular (synaptic cleft)  $Zn^{2+}$  is also decreased in the hippocampal CA3 region, especially in mossy fibers of rats 6 h after i.p. injection of clioquinol (CQ, 30 mg/kg), a lipophilic zinc chelator (g, h)

$10^{-9}$ – $10^{-10}$  M (Magneson et al. 1987). The idea is supported by the data that extracellular  $Zn^{2+}$  levels detected with ZnAF-2 are lower in the hippocampus of zinc-deficient rats than that of the control rats (Fig. 8.5e, f) (Takeda et al. 2012a). Interestingly,  $Zn^{2+}$  level in the brain extracellular fluid, which is estimated to be  $10^{-8}$  M (Frederickson et al. 2006), is higher than that in the plasma. In brain extracellular fluid, the high rate of  $Zn^{2+}$  level compared to total zinc concentration seems to be associated with synaptic  $Zn^{2+}$  signal in the brain. It is possible that extracellular  $Zn^{2+}$  serves as a pool for zinc in the synaptic vesicle and is involved in synaptic  $Zn^{2+}$  homeostasis (Fig. 8.6), although the chemical form of vesicular zinc is unknown.

The basal  $Zn^{2+}$  concentrations are extremely low in the intracellular (cytosol) compartment ( $<10^{-9}$  M) (Sensi et al. 1997; Colvin et al. 2008). ZnT proteins such as ZnT1, ZnT3, and ZnT10, and ZIP such as ZIP4 and ZIP6, are involved in the control of  $Zn^{2+}$  levels in the cytosolic compartment, especially in the static (basal) circumstance (Emmetsberger et al. 2010). Some of these transporters transport cytosolic  $Zn^{2+}$  into different subcellular organelles, such as mitochondria, lysosomes, endosomes, and Golgi apparatus, probably to maintain the static  $Zn^{2+}$  levels in the cytosolic compartment (Sensi et al. 2003; Danscher and Stoltenberg 2005; Colvin et al. 2006). In contrast, it is possible that  $Zn^{2+}$  release from the subcellular organelles through synaptic neurotransmission serves as a  $Zn^{2+}$  signal that participates in synaptic function (Stork and Li 2010).  $Zn^{2+}$  levels except for vesicular  $Zn^{2+}$  are estimated to be less than 5 % of the total  $Zn^{2+}$  amount in the hippocampus

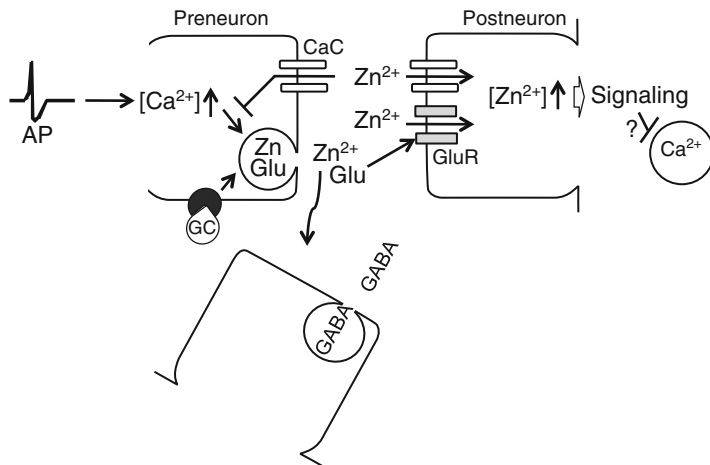


**Fig. 8.6** Synaptic Zn<sup>2+</sup> homeostasis. Zn<sup>2+</sup> released from neuron terminals serves as a signal factor in both extracellular and cytosolic compartments. It is estimated that the functional signaling occurs in the optimal ranges of extracellular Zn<sup>2+</sup> concentration [Zn<sup>2+</sup>]<sub>o</sub> and intracellular Zn<sup>2+</sup> concentration [Zn<sup>2+</sup>]<sub>i</sub>. Both the lack and excess of Zn<sup>2+</sup> signal affect synaptic neurotransmission. The synaptic vesicle and the extracellular compartment seem to be the pool of Zn<sup>2+</sup>

and cerebral cortex (Lee et al. 2011). ZnT1 is a major Zn<sup>2+</sup> transporter on the plasma membrane and may participate in cytosolic Zn<sup>2+</sup> homeostasis in neurons by transporting Zn<sup>2+</sup> from the somata to the extracellular space (Sekler et al. 2002) It has been reported that ZnT1 restricts excessive accumulation of Zn<sup>2+</sup> in the cytosolic compartment (Nolte et al. 2004), resulting in protecting neurons from Zn<sup>2+</sup> toxicity in neurological diseases such as transient forebrain ischemia (Aguilar-Alonso et al. 2008). Tissue plasminogen activator, a secreted serine protease, is excitotoxic and increases lysosomal sequestration of the increased Zn<sup>2+</sup> in the cytosolic compartment through interaction with ZIP4, which might also lead to protecting neurons from Zn<sup>2+</sup> toxicity (Emmetsberger et al. 2010). Spatiotemporal control of the Zn<sup>2+</sup> signal via ZIP and ZnT maintains the steady environment in both the extracellular and cytosolic compartments.

## 8.4 Functional and Neurotoxic Zn<sup>2+</sup> Signaling

Zn<sup>2+</sup> is released from zincergic neuron terminals and Zn<sup>2+</sup> concentration is increased in the synaptic cleft (extracellular compartment), followed by increase in the cytosol [intracellular compartment (Fig. 8.7)]. Zn<sup>2+</sup> released is quickly taken up into presynaptic and postsynaptic neurons and astrocytes. Calcium channels such as calcium-permeable AMPA/kainate receptors are involved in Zn<sup>2+</sup> influx during neuronal excitation (Weiss et al. 2000; Jia et al. 2002; Takeda et al. 2007b). On the basis of the finding that the low-affinity site (IC<sub>50</sub> ≈ 20 μM at -40 mV) of NMDA receptors is bound by Zn<sup>2+</sup> as a NMDA receptor blocker, extracellular Zn<sup>2+</sup> concentration after tetanic stimulation is estimated to range between 10 and 100 μM (Vogt et al. 2000). In contrast, Kay (2003) reports that extracellular Zn<sup>2+</sup>



**Fig. 8.7** Glutamatergic neurotransmission and  $Zn^{2+}$  signaling in the hippocampus.  $Zn^{2+}$  released from zincergic neuron terminals is immediately taken up into presynaptic and postsynaptic neurons through calcium-permeable channels (CaC and GluR).  $Zn^{2+}$  release can be enhanced by presynaptic glucocorticoid (GC) signal via mineralocorticoid or glucocorticoid receptors. Intracellular  $Zn^{2+}$  signal is critical for cognitive function, although the optimal range for intracellular  $Zn^{2+}$  signal is controversial (Fig. 8.6)

concentration after mossy fiber excitation may be nanomolar in an experiment using the fluorimetric FluoZin-3 ( $K_D$ , 15 nM) in conjunction with a zinc chelator. Hippocampal LTP modulation by exogenous  $Zn^{2+}$  suggests that endogenous  $Zn^{2+}$  reaches approximately low micromolar concentrations in the extracellular compartment after tetanic stimulation (Fig. 8.6). Therefore, the extracellular concentration of  $Zn^{2+}$  reached after depolarization, which is dependent on frequency of depolarizing stimulation (Ueno et al. 2002), is a matter of debate. The optimal range of  $Zn^{2+}$  signal in the cytosolic compartment also remains to be determined (Fig. 8.6).

In the extracellular compartment,  $Zn^{2+}$  modulates glutamatergic and GABAergic neuron activity (Fig. 8.7).  $Zn^{2+}$  potentiates AMPA/kainate receptors, while blocking  $Ca^{2+}$  current through calcium channels such as NMDA receptors and voltage-dependent calcium channels (VDCC).  $Zn^{2+}$  released from zincergic neuron terminals may serve as a negative feedback factor against glutamate release (Minami et al. 2006; Takeda et al. 2007c) (Fig. 8.7). In the cytosolic compartment,  $Zn^{2+}$  can decrease not only the basal  $Ca^{2+}$  level (Takeda et al. 2007b) but also  $Ca^{2+}$  levels increased by metabotropic glutamate receptors. Crosstalk of  $Zn^{2+}$  signaling to  $Ca^{2+}$  signaling via calcium channels may modulate presynaptic and postsynaptic neuronal activity (Takeda and Tamano 2009, 2010).

Excessive activation of glutamate receptors by excess of extracellular glutamate leads to a number of deleterious consequences, including impairment of calcium buffering, generation of free radicals, activation of the mitochondrial permeability transition, and secondary excitotoxicity (Danbolt 2001; Dong et al. 2009).



Glutamate excitotoxicity, a final common pathway for neuronal death, is observed in numerous pathological processes such as stroke/ischemia, temporal lobe epilepsy, Alzheimer's disease, and amyotrophic lateral sclerosis.  $Zn^{2+}$  plays a neuroprotective role in glutamate-induced excitotoxicity (Bancila et al. 2004; Cohen-Kfir et al. 2005; Takeda et al. 2007d). However, excess of extracellular  $Zn^{2+}$ , which is induced under glutamate excitotoxicity, is harmful; excessive  $Zn^{2+}$  influx into postsynaptic neurons is involved in neurodegeneration under pathological conditions. Calcium-permeable AMPA receptors may play a key role for  $Zn^{2+}$  influx in postsynaptic neurodegeneration (Liu et al. 2004; Noh et al. 2005; Weiss 2011). Therefore, synaptic  $Zn^{2+}$  signaling is involved in both functional and pathological aspects.

## 8.5 $Zn^{2+}$ Signal and Cognition

Synaptic  $Zn^{2+}$  signal is involved in synaptic plasticity such as LTP in the hippocampus and amygdala. Enhanced plasticity in zincergic synapses is associated with cortical modification after exposure to enriched environment. These data suggest the synaptic  $Zn^{2+}$  signal is involved in cognitive and emotional behavior through the modulation of synaptic plasticity (Takeda and Tamano 2009).

Targeted deletion of the ZnT3 prevents vesicular  $Zn^{2+}$  uptake (Cole et al. 1999) and ablates  $Zn^{2+}$  release into the extracellular space by action potentials. There are close correlations between vesicular  $Zn^{2+}$  levels and ZnT3 protein expression (Palmiter et al. 1996).  $Zn^{2+}$  transport into the synaptic vesicle is ZnT3 dependent and is important in constructing a major pool of  $Zn^{2+}$  signal (Fig. 8.6). In the initial experiment, ZnT3KO mice were able to recognize novel or displaced objects normally (Cole et al. 2001). However, Adlard et al. (2010) report that ZnT3KO mice exhibit significant cognitive deficits at 6 months of age but not at 3 months of age. Three- to 4-month-old ZnT3KO mice also exhibit significant deficits in contextual discrimination and spatial working memory (Martel et al. 2010; Sindreu et al. 2011). Furthermore, ZnT3 is also involved in associative fear memory and extinction, but not in innate fear, consistent with the role of synaptic  $Zn^{2+}$  in amygdala synaptic plasticity (Martel et al. 2011). Therefore, it is likely that  $Zn^{2+}$  signaling is involved in cognitive and emotional behavior, even in ZnT3KO. The pool of  $Zn^{2+}$  might be other subcellular organelles or zinc-binding proteins such as metallothionein in ZnT3KO mice. On the other hand, recognition memory deficit is observed in wild-type animals when the acute loss of synaptic  $Zn^{2+}$  is induced by treatment with lipophilic zinc chelators (Takeda et al. 2010a). Chelation of extracellular  $Zn^{2+}$  by CaEDTA in the amygdala increases the time of freezing behavior in the contextual recall of fear (Takeda et al. 2010b). The amount of  $Zn^{2+}$  functioning as a signal factor seems to be less available in ZnT3KO mice than in wild-type mice.

Saito et al. (2000) reported that age-dependent reduction of  $Zn^{2+}$  levels in synaptic vesicles of the mossy fibers induced by low expression of ZnT3 causes glutamatergic excitotoxicity in the hippocampal neurons and the deterioration of

learning and memory in senescence-accelerated mouse prone 10 (SAMP10). There are also age-dependent reductions in ZnT3 expression and synaptic  $Zn^{2+}$  levels in the hippocampal mossy fibers of human amyloid precursor protein-transgenic (Tg2576) mice, suggesting that extensive modifications of the brain  $Zn^{2+}$  pool, particularly synaptic (vesicular)  $Zn^{2+}$ , underlie the neuronal dysfunction characteristic of Alzheimer disease (Lee et al. 2012). Furthermore, there is a significant age-related decline in cortical ZnT3 levels from age 48 to 91 in healthy people (Adlard et al. 2010), and ZnT3 levels are more markedly decreased in Alzheimer's disease cortex. On the other hand,  $Zn^{2+}$  released from zincergic neurons is known to mediate parenchymal and cerebrovascular amyloid formation in Tg2576 mice (Lee et al. 2002; Friedlich et al. 2004; Stoltenberg et al. 2007). The transsynaptic movement of  $Zn^{2+}$  may be severely compromised in Alzheimer's disease both by the lack of ZnT3 expression and by being sequestered in amyloid. Adlard et al. (2010) reported that the genetic ablation of ZnT3 may represent a phenocopy for the synaptic and memory deficits of Alzheimer's disease. Deshpande et al. (2009) postulated that the sequestration of  $Zn^{2+}$  in oligomeric amyloid- $\beta$  (A $\beta$ )-Zn complexes may lead to a reduction in  $Zn^{2+}$  availability at the synapse, resulting in a loss of the modulatory activity by  $Zn^{2+}$  and leading to cognitive decline in Alzheimer's disease. Synaptic  $Zn^{2+}$  signal is dynamically functional for learning and memory in the healthy brain (Takeda and Tamano 2012), and also change in  $Zn^{2+}$  availability may participate in cognitive decline in dementia such as Alzheimer's disease (Bush 2013).

## 8.6 Glucocorticoid Signal and $Zn^{2+}$ Signal

The hippocampus is enriched with corticosteroid receptors and is the major target region of corticosteroids (Joëls 2008). Mineralocorticoid receptors and glucocorticoid receptors are colocalized in CA1 and CA2 pyramidal cells and in dentate gyrus granule cells. In the CA3 pyramidal cells, on the other hand, mineralocorticoid receptors are abundantly expressed and glucocorticoid receptors are much less expressed (Ozawa 2005). Mineralocorticoid receptors are extensively occupied with low levels of corticosterone, and glucocorticoid receptors are particularly activated after exposure to stress (Joëls et al. 2008; Sandi 2011). Dentate granule cells require corticosterone levels at the physiological range; a selective degeneration of dentate gyrus granule cells is observed in the hippocampus after adrenalectomy (Joëls 2007).

An increase in serum corticosterone level induces a rapid increase in corticosterone level in the hippocampus in parallel with an increase in extracellular glutamate level (Venero and Borrell 1999). Corticosterone-induced increase in extracellular glutamate levels in the hippocampus seems to be exerted through the action of membrane-associated mineralocorticoid receptors or glucocorticoid receptors, which increase glutamate release probability in synaptic activation (Fig. 8.7) (Karst et al. 2005; Musazzi et al. 2010). The rapid effects of corticosterone on

glutamatergic transmission seem to be linked to the diverse effects on synaptic plasticity and memory processes in the hippocampus. The increase in glutamate release probability through the action of corticosterone leads to increasing the amount of glutamate released during learning and increasing the activation of postsynaptic glutamate receptors. Corticosterone can contribute to increase the efficacy of glutamatergic transmission by AMPA receptor insertion at synaptic sites through both rapid and delayed (genomic) effects. These effects are the advantage in the process of synaptic plasticity such as LTP and also learning and memory (Sandi 2011). Therefore, it is estimated that corticosterone increases  $Zn^{2+}$  release probability from zincergic neuron terminals through the rapid nongenomic effect in the hippocampus (Takeda et al. 2012b) (Fig. 8.7), while requiring intracellular  $Zn^{2+}$  signal for the genomic effect (Takeda and Tamano 2012). Although the evidence is limited, it is likely that synaptic  $Zn^{2+}$  signal cooperates with corticosteroid signal in learning and memory.

In contrast, glutamate accumulates in the extracellular compartment at high levels through corticosterone-mediated blockade of glutamate transporter activity when corticosterone is abnormally secreted under severe stress circumstances. The abnormal corticosterone secretion also contributes to abnormal glutamate release from neuron terminals. These effects facilitate long-term depression (LTD), and impair LTP and memory processing (Wong et al. 2007; Howland and Wang 2008). Excess of synaptic  $Zn^{2+}$  signal induced by corticosterone or stress is also involved in impairment of LTP (Takeda et al. 2012b), possibly followed by the impairment of learning and memory (Takeda et al. 2011). Furthermore, prolonged exposure of animals to a high level of corticosterone presumably makes dentate granule cells more vulnerable to delayed cell death (Joëls 2007). Stress and corticosterone strongly inhibit adult hippocampal neurogenesis (Mirescu and Gould 2006), which participates in learning and memory, and decreased neurogenesis has been implicated in the pathogenesis of anxiety and depression. Neurogenesis-deficient mice show increased food avoidance in a novel environment after acute stress, increase behavioral despair in the forced swim test, and decrease sucrose preference, a measure of anhedonia; adult hippocampal neurogenesis buffers stress responses and depressive behavior (Snyder et al. 2011). The hippocampus provides negative control of the HPA axis (Carroll et al. 1981; Holsboer 1983; Arana et al. 1985). The HPA axis activity is disrupted in approximately 50 % of human depressives. This disruption is generally presented as a dexamethasone-mediated negative feedback resistance to cortisol secretion. It is reported that a small subset of neurons within the dentate gyrus are critical for hippocampal negative control of the HPA axis. Interestingly, zinc-deficient diet is a stressor and feeding a zinc-deficient diet induces abnormal HPA axis activity, which underlies brain dysfunction and abnormal behavior under dietary zinc deficiency, as described next.

## 8.7 Neuropsychological Symptoms in Zinc Deficiency

When young mice and rats are fed a zinc-deficient diet, reductions in total food intake are observed within approximately 3 days. The decrease in plasma zinc is also observed at this time (Ohinata et al. 2009). Zinc deficiency results in food intakes that are less than 50 % of normal. Zinc homeostasis in the brain is not easily disrupted by dietary zinc deficiency (Takeda et al. 2005a). However, zinc deficiency decreases synaptic  $Zn^{2+}$  levels in the hippocampus (Fig. 8.5e–h), followed by decrease in hippocampal zinc concentration, suggesting that  $Zn^{2+}$  is the most susceptible to zinc deficiency in zinc components. On the other hand, zinc deficiency activates the HPA axis before decreasing synaptic  $Zn^{2+}$  levels in the hippocampus. Serum corticosterone concentration is significantly increased in young mice and rats fed a zinc-deficient diet for 2 weeks (Takeda et al. 2007a, 2008). It is possible that the decrease in plasma zinc, possibly plasma  $Zn^{2+}$ , leads to abnormal corticosterone secretion through HPA axis activation, followed by reductions in total food intake.

Abnormal glucocorticoid secretion has been reported in many neuropsychiatric disorders including depression (Whiteford et al. 1987; Starkman et al. 1992; Seed et al. 2000). It is thought that exposure to chronic stress precipitates or exacerbates neuropsychiatric disorders. In human depressives, smaller volumes of the hippocampus are associated with abnormal cortisol secretion (Bremner et al. 2000). Interestingly, it is reported that human depressives are zinc deficient (Maes et al. 1994; Nowak et al. 2005). Depression-like behavior is increased in zinc-deficient animals (Takeda et al. 2011). Repeated corticosterone injections induce anxiety and depression-like behavior in mice and rats. Antiglucocorticoids, similar to conventional antidepressants, may recover depressive symptoms by boosting hippocampal neurogenesis. Zinc deficiency impairs neuronal precursor cell proliferation in the hippocampus (Corniola et al. 2008; Suh et al. 2009). It is likely that abnormal corticosterone secretion is associated with depressive symptoms in zinc deficiency through the changes in hippocampal function (Takeda and Tamano 2009).

## 8.8 Potentiation of Glutamate Excitotoxicity by Glucocorticoids

Glutamate concentration in brain extracellular fluid is estimated to be about 2  $\mu$ M and that in the synaptic vesicles of glutamatergic neuron terminals is markedly high (~100 mM) (Meldrum 2000). The hippocampus is relatively susceptible to glutamate excitotoxicity in the brain. Neuronal death in the hippocampus is observed in temporal lobe epilepsy, in which seizures frequently originate in the hippocampus. The increase in extracellular glutamate in the hippocampus may trigger spontaneous seizures in patients with complex partial epilepsy (During and Spencer 1993).

It has been reported that zinc homeostasis in the brain is associated with the etiology and manifestation of epileptic seizures (Takeda and Tamano 2009). Zinc concentration in the brain, especially in the hippocampus, is decreased by epileptic seizures (Assaf and Chung 1984; Takeda et al. 2003c). Seizure susceptibility of EI (epilepsy) mice is increased by zinc deficiency and decreased by zinc loading (Fukahori and Itoh 1990). Kainate and NMDA-induced seizures are enhanced in mice and rats after 4-week zinc deprivation, in which synaptic  $Zn^{2+}$  levels are decreased (Takeda et al. 2003b, 2005b, 2009), and hippocampal cell death is observed more after treatment with kainate in zinc deficiency (Takeda et al. 2005c). An *in vivo* microdialysis experiment indicates that an enhanced release of glutamate associated with a decrease in GABA concentration is a possible mechanism for the increased seizure susceptibility and cell death in zinc deficiency (Takeda et al. 2003b). Abnormal corticosterone secretion may also be involved in the increased seizure susceptibility in zinc-deficient epilepsy animals. Furthermore, the decrease in  $Zn^{2+}$  level, which is induced with zinc chelators, enhances susceptibility to spontaneous seizures in Noda epileptic rats (Takeda et al. 2013b), suggesting that the  $Zn^{2+}$  signal has a protective action against the development of seizures (Takeda et al. 2003d).

In global ischemia, the concentration of extracellular potassium transiently reaches 75 mM, followed by the increase in extracellular glutamate (Hansen and Zeuthen 1980). The increase in extracellular glutamate induced with 100 mM KCl is enhanced in zinc-deficient young rats (Takeda et al. 2003a, 2008). The neurological symptoms associated with glutamate excitotoxicity may be precipitated or aggravated by zinc deficiency (Stoltenberg et al. 2007). A factor of the aggravation is the increase in corticosterone secretion, which potentiates glutamate excitotoxicity (Takeda and Tamano 2012). The decrease in brain extracellular  $Zn^{2+}$  may also aggravate glutamate excitotoxicity in zinc deficiency.

Selective increase in the nocturnal levels of cortisol is observed in aged humans (Landfield and Eldridge 1994). Plasma zinc level decreases with aging in humans. The increase in the basal levels of intracellular  $Ca^{2+}$  and modification of  $Ca^{2+}$  signaling are observed in both aged (Billard 2006; Foster 2007) and zinc-deficient animals (Takeda et al. 2009; Tamano et al. 2009). Aged animals and humans seem to be more susceptible to glutamate excitotoxicity as well as zinc-deficient animals. It is likely that glucocorticoids modify the dynamics of both  $Zn^{2+}$  signal and  $Ca^{2+}$  signal and that the increased glucocorticoid secretion underlies dysfunctions in both zinc deficiency and aging, which may increase the risk of neurological diseases such as depression and Alzheimer's disease (Takeda and Tamano 2010). As a matter of fact, high levels of cortisol are found in Alzheimer's disease as well as depression. In Alzheimer's disease patients, cognitive deficits (such as memory) and psychological symptoms (such as anxiety) are associated with an early deregulation of the HPA axis (Brureau et al. 2013). Therefore, it is possible that excess of intracellular  $Zn^{2+}$  signal through abnormal cortisol secretion is involved in cognitive deficits in both normal aging and neurological diseases such as dementia.

## 8.9 Perspective

There are two major pools of  $Zn^{2+}$ , that is, the synaptic vesicle and the extracellular compartment, in the brain (Fig. 8.6). Synaptic  $Zn^{2+}$  homeostasis seems to be controlled by the two pools and is critical for synaptic function (Takeda et al. 2013a). The synaptic  $Zn^{2+}$  signal is involved in both cognitive function and dysfunction. On the other hand,  $Zn^{2+}$  exists in the plasma at an extremely low concentration, and plasma  $Zn^{2+}$  levels are potentially linked to HPA axis activity. HPA axis activity is increased with aging, and the increases are superimposed in neurological diseases such as depression and Alzheimer's disease. It is likely that the modification of synaptic  $Zn^{2+}$  signaling through the HPA axis activation is involved in not only cognitive function but also cognitive decline. The molecular mechanism of intracellular  $Zn^{2+}$  signaling in cognition seems to be important to understand cognitive decline in normal aging and also in neurological symptoms such as dementia. An important issue that remains to be addressed is how homeostasis of  $Zn^{2+}$  is controlled in the brain and what determines the threshold between adaptive and maladaptive  $Zn^{2+}$  signaling under diverse circumstances.

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# Chapter 9

## The Clinical Implications of Impaired Zinc Signaling in the Brain

Sara M. Hancock, Ashley I. Bush, and Paul A. Adlard

**Abstract** Zinc is an essential requirement for normal cellular processes and is involved in the function of more than 300 enzymes. Currently, it is estimated that approximately 10 % of the proteins encoded by the human genome contain zinc. Zinc is necessary for neuromodulation, synaptic transmission, intracellular signal transduction, and myriad other processes. The clinical implications of impaired zinc signaling are, therefore, far reaching, with profound central and peripheral disorders arising as a result of either an acute or a long-term dyshomeostasis in normal zinc levels. Targeting zinc as a therapy is now emerging as a tantalizing, although especially difficult, approach to a variety of diseases, including central nervous system disorders. This chapter reviews the clinical implications of impaired zinc signaling in the brain.

**Keywords** Brain • Central nervous system disorders • Zinc • Zinc homeostasis • Zinc signals • Zinc transporters

### 9.1 Introduction

Zinc, which was first described as an essential trace ion by Raulin in 1869, is now recognized as essential for life. It is a stable divalent cation that is involved in the normal function of more than 300 enzymes (being required for catalytic, co-catalytic, and structural functions of enzymes) and which is also found in approximately 10 % of all human proteins (Andreini et al. 2006). Zinc is indispensable for a multitude of normal cellular functions and organ systems, having roles in processes as diverse as DNA synthesis, cognitive function, growth, development, and immunity. As a result, zinc levels are tightly regulated throughout the body. However, when the normal homeostatic systems become impaired or fail,

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altered zinc levels can arise within different cellular compartments to then precipitate a diverse range of biological sequelae. As the body is well equipped to excrete excess zinc when required, humans are generally more likely to suffer from issues relating to zinc deficiency. Indeed, zinc deficiency, typically resulting from malnutrition, aging, or disease (e.g., cancer or diabetes), is a leading life-threatening factor in developing countries, and is becoming increasingly prevalent in developed countries, particularly in the aged population.

The human body contains 2 to 3 mg zinc, which is the second most abundant metal in mammalian tissues, second only to iron (Wang et al. 2005; Paoletti et al. 2009), with almost 90 % of that found in muscle and bone (Wastney et al. 1986). A high level of zinc has also been found in other organs including the brain, heart, kidney, liver, prostate, pancreas, lung, skin, and gastrointestinal (GI) tract. Although dietary sources of zinc come from a range of foods including vegetables and dairy products, animal flesh remains the primary source of bioavailable zinc for humans. Red meats such as beef and veal, in particular, have significantly higher zinc levels than white meats such as chicken, pork, and fish. Furthermore, phytates and dietary fibers in legumes and some vegetables actually inhibit zinc absorption in the intestine. Thus, a balanced diet is required to maintain optimal zinc nutrition.

## 9.2 Zinc Homeostatic Pathways

Before discussing the clinical implications of impaired zinc signaling, we briefly review the basic homeostatic mechanisms that control zinc levels throughout the body, as this is relevant to understanding the biological sequelae of a failure in the maintenance of normal zinc levels.

### 9.2.1 *General Zinc Handling*

Maintaining a constant state of cellular zinc nutrition is essential for normal function (King et al. 2000). In the periphery, zinc homeostasis is a highly regulated and coordinated process that involves uptake through intestinal epithelial cells and reabsorption via the kidneys; changes in the absorption/excretion of zinc in the GI tract are the primary mechanisms for maintaining zinc homeostasis in the body (King et al. 2000). Excess zinc is eliminated through excretion into the feces (Krebs 2000; Zhang et al. 2008). Research on zinc homeostasis has focused on intestinal and liver zinc transport processes (Levenson and Tassabehji 2007); however, data on zinc transport within the central nervous system (CNS) are increasingly emerging in the literature.

### 9.2.2 *Zinc in the Brain*

The brain has a large zinc content (Vasto et al. 2008), where it is essential for the correct functioning of more than 2,000 transcription factors and is a cofactor for more than 300 enzymes (Takeda 2000; Levenson and Tassabehji 2007; Jeong and Eide 2013). Here, zinc is involved in the structural conformation of about 70 % of proteins, and is present in almost half of the glutamatergic synapses in the cortex and limbic nuclei (Karol et al. 2010). Zinc is released into the synapse alongside glutamate during excitation, whereupon it interacts with ion channels, synaptic receptors, and transporters. Therefore, zinc is considered to be essential for the activity of enzymes and for modulating both synaptic transmission and plasticity.

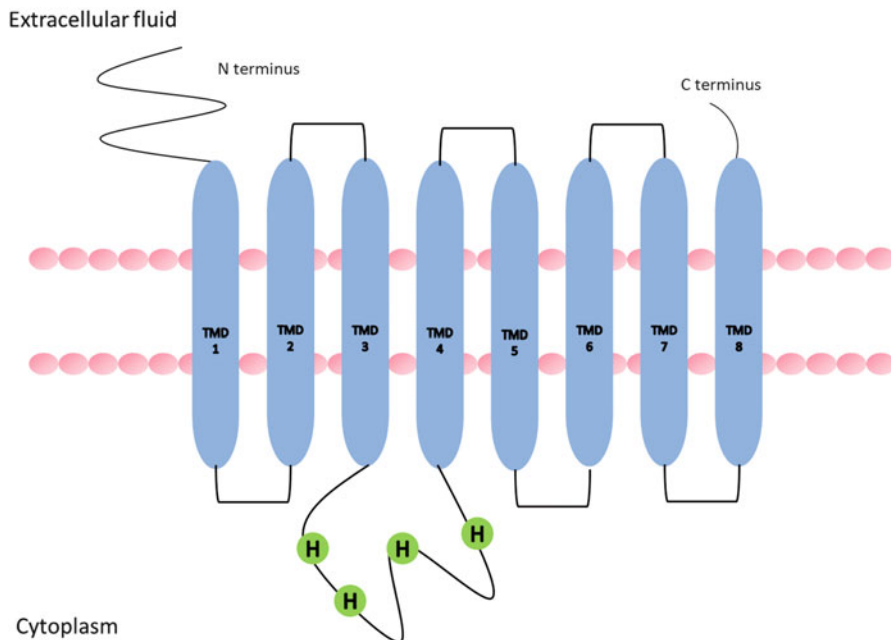
It is well known that the majority of zinc in the brain is bound to macromolecules such as enzymes and transcription factors, although a small number of zinc ions (approximately 10–15 % of total brain Zn) exists as “free” or chelatable zinc (Levenson and Tassabehji 2007). Within the brain, zinc homeostasis is controlled by three main families of proteins that each have distinct tissue- and cell-level patterns of localization and expression (Hennigar and Kelleher 2012): these are the metallothioneins (MTs), zinc- and iron-like regulatory proteins (ZIPs), and zinc transporters (ZnTs). The presenilins have also recently been demonstrated to influence zinc concentrations (Greenough et al. 2013).

### 9.2.3 *Metallothioneins*

Currently, there are four MT isoforms that control cytosolic zinc concentrations through binding and distributing  $Zn^{2+}$  (Mocchegiani et al. 2001) (they also coordinate a variety of other metal ions, including copper). Metallothioneins are composed of a single polypeptide chain of 61–68 amino acids, and there are several isoforms, named MT-1, MT-2, MT-3, and MT-4, the first three of which are synthesized in the central nervous system (CNS) (Manso et al. 2011). MT-1 and MT-2 are widely expressed in all tissues, are present throughout the brain and spinal cord, and are primarily expressed by astrocytes, although neurons and reactive microglia are capable of synthesis. MT-3 is predominantly found in the CNS, although its precise localization is still debated (Manso et al. 2011). Similar to MT-3, MT-4 is a minor MT species and is found in stratified epithelial cells (Thirumoorthy et al. 2011).

### 9.2.4 *Zinc- and Iron-Like Regulatory Proteins*

The ZIP proteins have been divided into two subfamilies. Subfamily I refers to ZIPs that are mostly present in plant species, and subfamily II contains the ZIPs that are present in mammals, of which 14 are currently known in humans (Liuzzi and



**Fig. 9.1** Proposed molecular zinc- and iron-like regulatory protein (ZIP) structure showing eight trans-membrane domains (TMDs) and a long histidine (H)-rich domain, TMDs 3 and 4

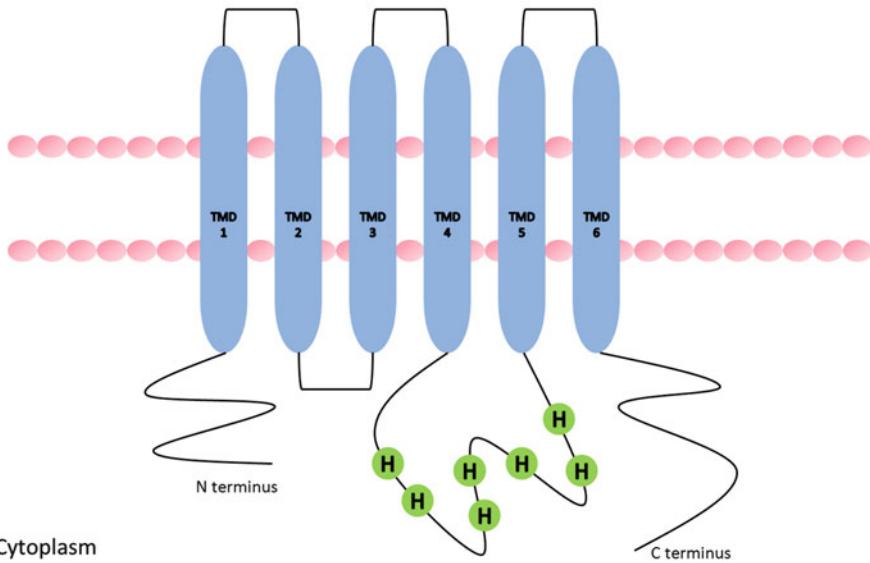
Cousins 2004). The primary role of the ZIPs is considered to be cellular zinc uptake into cells or export from vesicles or organelles (Levenson and Tassabehji 2007). Most ZIP proteins have a specific tissue-level pattern of expression and contain eight transmembrane domains and extracellular N- and C-termini, as illustrated in Fig. 9.1. Zinc transport activity has been confirmed for ZIPs 1–8 and -14 via transfection of DNA into mammalian cells (Cousins et al. 2006). Within the CNS, ZIP1 and ZIP3 appear to be the main facilitators of zinc uptake, although ZIP1 is more abundant in the brain, suggesting it is the primary neuronal zinc uptake mechanism (Levenson and Tassabehji 2007). Still, little is known about the structure, function, and localization of ZIPs 9–13, although ZIP12 is likely localized to the brain and ZIP13 is thought to be intracellular. For a summary table of tissue distributions of the ZIPs, see Eide (2004).

### 9.2.5 Zinc Transporters

There are currently ten known ZnT proteins in humans (Kambe 2012; Liuzzi and Cousins 2004), which function to regulate both the influx and efflux of zinc ions in cells and cellular compartments such as vesicles, mitochondria, and the Golgi apparatus. These transporters are predicted to have six transmembrane domains with cytoplasmic amino- and carboxy-termini (Fig. 9.2).



## Extracellular fluid

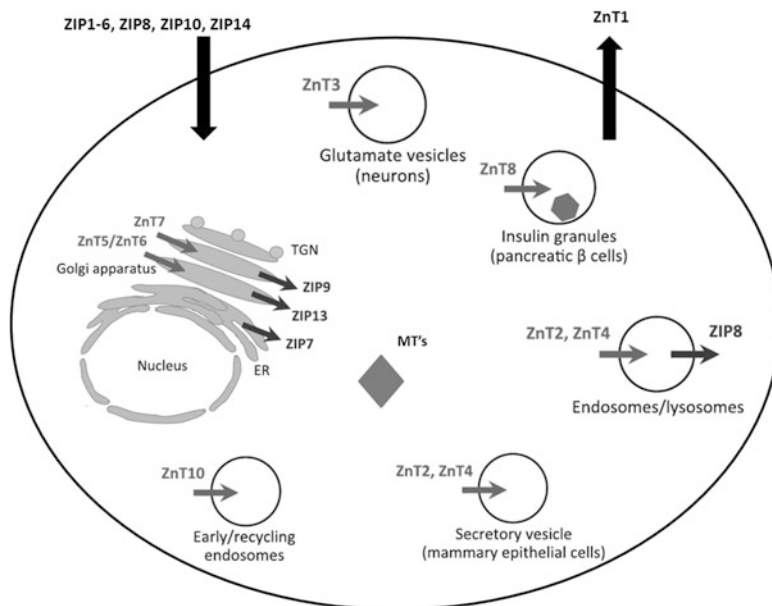


## Cytoplasm

**Fig. 9.2** Proposed molecular zinc transporter (ZnT) structure illustrating six *TMDs* and a long histidine (*H*)-rich loop between *TMDs* 4 and 5

ZnT1, which was the first mammalian zinc transporter to be identified and characterized, is ubiquitously expressed and localized to the plasma membrane. ZnT2 is specific to secretory vesicles and is upregulated by high dietary zinc intake (Lichten and Cousins 2009). ZnT3 is similar to ZnT2 in function, in its role of loading  $Zn^{2+}$  into pre-synaptic vesicles. However, ZnT3 transcripts are limited to the brain with a high abundance in the hippocampus and cortex. ZnT4 has a high expression in the mammary gland, brain, and intestinal epithelial cells, where it has been detected at the trans-Golgi network (TGN) and is involved in vesicular secretory functions. Of the ZnTs, the exception to the rule is ZnT5, which has 15 transmembrane domains; it is ubiquitously expressed and interacts with ZnT6 (found only in brain and lung) to form a complex that transports zinc into a secretory pathway. Both ZnT5 and ZnT6 are located at the TGN. ZnT7 is expressed throughout the large and small intestine (regions of zinc absorption) and is involved in transcellular zinc movement through polarized epithelial cells. ZnT8 is localized to the membrane of insulin storage granules, and a direct relationship between glucose-induced insulin secretion and ZnT8 has been suggested (Cousins and Lichten 2011). There has been little research into the localization and role of ZnT9 and ZnT10, although ZnT9 has been associated with cytosol and nuclear fractions whereas it has been suggested that ZnT10 may be restricted to fetal development.

There is low expression of ZnT 2, 5, 7, and 8 in the brain; ZnT 1, 3, 4, and 6 are more highly expressed. These latter proteins are essential for modulating intracellular cytosolic zinc (ZnT 4 and ZnT 6) as well as zinc export (ZnT1 and ZnT3).



**Fig. 9.3** Illustration of the proteins responsible for the cellular homeostasis of zinc. *MT*, metallothionein

ZnT1 and ZnT3 differ from the other ZnTs in that ZnT1 is present on the plasma membrane while ZnT3 is located on presynaptic vesicular membranes. A diagram more clearly demonstrating the homeostatic proteins is shown in Fig. 9.3. For more detailed descriptions of the ZIPs and ZnTs, see Lichten and Cousins (2009).

In summary, the regulation of zinc is tightly controlled via a range of specialized homeostatic mechanisms. When these processes are working correctly, the zinc-dependent proteins and signaling cascades present within the cell can function to maintain normal healthy tissue. However, such a large number of homeostatic proteins also provides increased opportunities for disruptions to occur. In this chapter we focus on the implications of these disruptions in the CNS. We now review the mechanisms and also the cellular and clinical outcomes of zinc dysregulation.

### 9.3 Zinc Signaling

As previously mentioned, zinc is a potent neuromodulator and has recently been suggested to have neurotransmitter qualities resulting from its role in synaptic signaling. Zinc is capable of directly influencing postsynaptic receptors and has been shown to exert effects in both neuronal and glial cells. It is able to do this via

its release into the synaptic cleft upon cellular activation, whereupon it can aid in regulating neuronal processes such as long-term potentiation (LTP) and long-term depression (LTD) by acting on *N*-methyl-D-aspartate (NMDA) receptors (Takeda and Tamano 2012). These postsynaptic actions have led to the suggestion that zinc is a signaling molecule capable of acting both intracellularly and extracellularly. Following its release alongside glutamate, zinc is taken up into adjacent cells through  $\alpha$ -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid receptor (AMPA) channels that trigger the generation of reactive oxygen species (ROS), which are known to directly contribute to oxidative stress (Fukada et al. 2011). By behaving in this manner, synaptically released zinc is able to regulate synaptic function and plasticity and has been labeled an “atypical neurotransmitter” (Haase and Rink 2011). Moreover, zinc has been identified as an endogenous G protein-coupled receptor agonist through ZIP14 regulation (Fukada et al. 2011), further supporting its identification as a neurotransmitter.

Different types of zinc signals have been observed that are thought to aid in regulating a variety of cellular functions. These zinc signals have a huge number of targets including receptors, second messengers, kinases, phosphatases, caspases, and transcription factors. The number of proteins influenced by zinc signals and the effects these signals can induce suggest there may be even more as yet unidentified proteins that zinc can affect. Previous research has defined zinc signals as a change in the concentration of intracellular free (chelatable) zinc, which then effects the transduction or processing of information at the cellular level (Haase and Rink 2011). Hirano and colleagues (2008) suggested the definitions of “transcription-independent early zinc signaling (EZS)” and “transcription-dependent late zinc signaling (LZS)” to describe signaling mechanisms also referred to as fast, intermediate (zinc wave), or slow (lasting for days). Currently, three major sources for zinc signals have been identified: zinc uptake from the extracellular environment, reversible storage of zinc in vesicles (synaptic or intracellular), and the oxidative release of zinc from storage proteins (Haase and Rink 2011). Fast signals, such as those mentioned here, occur after electrical extracellular stimulation whereas slow signals depend upon changes in the expression of proteins involved in zinc homeostasis (transporters, storage proteins, etc.). These slow signals have been predominantly observed in cell proliferation and differentiation where zinc uptake is the required signal (Li and Maret 2009). It should be noted here that uptake of zinc for signaling purposes should involve an active transport mechanism (Haase and Rink 2011).

Currently, it remains unclear how a relatively nonspecific change in intracellular free zinc can somehow regulate multiple signaling pathways. Despite advances in research techniques, the measurements used remain crude and only give average zinc concentration values for entire cells or whole populations of cells. To better understand how zinc signaling goes wrong and therefore how to specifically treat it, further improvements in research techniques are needed.

### ***9.3.1 How Does Impaired Signaling Arise and What Are the Clinical Implications?***

It is now known that there are a wide range of effectors of impaired zinc signaling, including phenomena such as mutations in key zinc transporters or homeostatic pathways. The most common cause, however, is undoubtedly diet. Although perhaps not so prevalent in wealthier countries and populations, malnutrition remains rampant throughout the developing world. First recognized as essential for humans in 1963, zinc deficiency is thought to affect approximately 40 % of the global population (Maret and Sandstead 2006). The results of nutritional zinc deficiency include growth retardation, hypogonadism in males, rough skin, and neurosensory disorders (Prasad et al 1963), as well as anorexia (Shay and Mangan 2000). This broad suite of symptoms arises from decreased zinc bioavailability throughout different tissues in the body. Although the brain has some resistance to dietary zinc deficiency through the blood–brain barrier (BBB), meaning zinc homeostasis in the brain is not easily disrupted (Takeda and Tamano 2009), it will ultimately succumb, which will be reflected by neuronal dysfunction that leads to cognitive deficits and other neuropsychiatric disturbances. Such cognitive impairments, which frequently accompany many chronic diseases (Fukada et al. 2011), are often responsive to zinc supplementation (Nyaradi et al. 2013).

One area of debate that remains in the literature is whether aging itself results in a global or tissue-specific zinc deficit. According to the current literature, brain zinc concentrations rise from birth to adulthood, then remain stable throughout life within a specific concentration range (Roberts et al. 2012). In comparison, plasma zinc levels, although constant through adulthood, decline with advancing age. Irrespective of whether there is an age-dependent change in total brain zinc, a number of reports now support an age-related decline in key zinc transporters, suggesting that there may be discrete cellular compartments that become zinc deficient with age. Although further research is essential, a study by (Wong et al 2013) showed an age-related decrease in ZIP6 that enhanced proinflammatory responses. Decreased ZnT4 and ZnT6 have been shown in individuals with mild cognitive impairment (MCI) (Smith et al. 2006), whereas in both normal aging and Alzheimer's disease (AD) there is a decline in ZnT3 protein levels (Adlard et al. 2010). In humans, it is particularly difficult to determine if changes in zinc are caused by zinc dyshomeostasis or if zinc dyshomeostasis is caused by decreased dietary zinc intake, a known problem in the elderly (Mocchegiani and Malavolta 2011). Furthermore, the neuronal uptake of zinc is dependent on a variety of factors including voltage-gated calcium ( $\text{Ca}^{2+}$ ) channels and intracellular sodium (Na) (Tapiero and Tew 2003) that could fatigue with age, although uptake via ZnT2 has been suggested to be energy independent (Gaither and Eide 2001). Thus, a decline in transporter/importer levels, in combination with decreased efficiency of remaining transporters, will foster a zinc-deficient cellular milieu that may result in a host of deficits, including impaired learning and memory and cognitive decline.

**Table 9.1** Tissue-specific expression of zinc- and iron-like regulatory proteins (ZIPs) and the related pathological conditions

Protein	Pathology/disease
<i>ZIP</i>	
ZIP4	Acrodermatitis enteropathica
ZIP6	Cancer progression markers for estrogen receptor-positive cancers (breast cancer)
ZIP7	Breast cancer
ZIP8	T-cell immune responses
ZIP10	Breast cancer
ZIP12	Schizophrenia
ZIP13	Ehlers–Danlos syndrome
ZIP14	T-cell immune responses
<i>ZnT</i>	
ZnT3	Alzheimer’s disease; cognitive decline
ZnT4	Prostate disease/cancer
ZnT5	Allergic responses
ZnT8	Diabetes

As mentioned earlier, mutations in zinc transporters/importers are also capable of damaging zinc signaling processes, resulting in a variety of disease states: these are summarized in Table 9.1. We briefly describe the most robustly described CNS-related effects of these ZnT and ZIP mutations.

Acrodermatitis enteropathica (AE) is a disease resulting from a genetic mutation in ZIP4 causing intestinal zinc malabsorption. The disease is recognizable within a few months postpartum by the distinctive skin lesions around the mouth and anus and a failure to thrive (Perafan-Riveros et al. 2002). Similar symptoms are apparent in acquired zinc deficiency. Despite the presence of other mechanisms of intestinal zinc absorption, the zinc deficiency caused by AE results in both physical and neurological deficits such as behavioral changes, depression, and irritability (Sehgal and Jain 2000). When left untreated, AE is fatal.

Various cancers have been linked to zinc transporters, with ZIP6, ZIP7, and ZIP10 suggested to have a role in breast cancer. Additionally, ZIP6 is expressed in numerous cancer cell lines, leading to the hypothesis that it is involved in cancer progression. Currently it remains unclear if and how alterations in these transporters affect cancer pathology or the neurological consequences. Downregulation of ZnT4 is associated with prostate disease and prostate cancer; however, functions related to ZnT4 have received little attention in the literature and therefore require further exploration. There is a considerable amount of epidemiological evidence supporting a relationship between diabetes, zinc, and ZnT8 in humans (Cousins and Lichten 2011), because ZnT8 is localized to the membrane of insulin storage granules in the pancreas and single-nucleotide polymorphisms (SNPs) in ZnT8 have been associated with reduced insulin secretion following glucose stimulation (Staiger et al. 2007). It is well known that diabetes can have neurological consequences, and diabetes is a risk factor for dementia and AD (Liu et al. 2009).

Reductions in motor speed, psychomotor efficiency, learning, and reasoning have been shown in diabetics from mid-life to older ages, but this has yet to be assessed in younger diabetics (Seaquist 2010). It is also unclear how changes in zinc are relevant to these deficits. Allergy and immune responses have also been linked to zinc and zinc transporters; research has focused on ZIP8 and ZIP14 (close paralogues of each other) in T-cell immune responses. The expression of ZIP8 is influenced by immune mediators whereas ZIP14 is expressed in T cells and is capable of transporting zinc. Both have been demonstrated in mouse brain to be responsive to inflammation (Galvez-Peralta et al. 2014). The spondylocheiro dysplastic form of Ehlers–Danlos syndrome is a heritable connective tissue disorder characterized by joint hypermobility, hyperelasticity of skin, as well as hypotonia of skeletal muscles, and is caused by mutations in the ZIP13 gene (Giunta et al. 2008; Jeong et al. 2012). Neurological deficits are yet to be determined as the biological characterization of ZIP13 is an ongoing process (Bin et al. 2011).

Other diseases that can influence zinc signaling include stroke, trauma, and heart attack (Nolte et al. 2004; Grabrucker et al. 2011), which can also result in zinc-dependent CNS abnormalities. For example, depression and schizophrenia (Levenson and Tassabehji 2007), AD, amyotrophic lateral sclerosis (ALS), Down's syndrome, multiple sclerosis (Grabrucker et al. 2011), normal age-related cognitive decline (Adlard et al. 2013), and anorexia have all been linked to impaired zinc homeostasis. In AD, increased expression of ZnT1, ZnT3, ZnT4, ZnT5, ZnT6, and ZnT7 has been demonstrated in A $\beta$  plaques and nearby amyloid angiopathic vessels (Zhang et al. 2008), although levels in surrounding tissues may be different. The CNS effects of zinc abnormalities are myriad: impaired signaling pathways, activation of the hypothalamic-pituitary axis (HPA), learning and memory deficits, and downregulated immune responses, to name a few. In addition, pneumonia causes abnormally low plasma zinc concentrations (Netsky et al. 1969). Alcoholism results in decreased liver zinc concentrations (McBean et al. 1972). Infectious diseases and acute myocardial infarction have also been reported to cause changes in zinc metabolism (McBean et al. 1972). For most of these disorders, the mechanisms through which zinc abnormality translates to a CNS deficit are not entirely clear and require more research.

We have discussed the human conditions that arise from impaired zinc signaling, but to gain further insights into these and the potential role of both zinc and zinc transporter mutations in the CNS, disease models are necessary. Mouse models remain the most used and perhaps most ideal tool for researching the effects of zinc deficiency. Mice with targeted disruptions in ZIP1, ZIP2, or ZIP3 are sensitive to zinc deficiency during pregnancy, and ZIP13 knockout mice experience disorganization in hard and connective tissues such as bones and teeth. A ZIP14 knockout results in retarded growth and impaired gluconeogenesis (Fukada et al. 2011). The ablation of the ZnT3 gene in mice has resulted in the most relevant CNS phenotype, as rodents develop a robust cognitive phenotype with very specific pre- and postsynaptic signaling alterations that drive deficits in learning and memory (Adlard et al. 2010; Sindreu et al. 2011; Martel et al. 2011). Other genetic modifications include loss-of-function mutations in both ZnT4 and ZnT2. This change

results in zinc deficiencies in the milk produced by the females, which in turn may result in a variety of clinical implications in both the peripheral and central nervous systems. Essentially, alterations in zinc transporters at either a genetic or molecular level, as a result of mutation or dietary deficiency, will impact the body and the brain in a multitude of ways, with many of these still to be discovered.

## 9.4 Zinc Signaling as a Therapeutic Strategy

For reasons of its prolific role throughout the nervous system, zinc signaling is an obvious therapeutic target. However, it is this extensive involvement with a multiplicity of proteins, enzymes, and signaling cascades that makes it a particularly difficult target to modulate to achieve a defined clinical outcome. Haase and Rink (2011) suggested that to regulate zinc and zinc signaling a prerequisite to treatment must be the sequestration of the zinc signal of interest. As zinc deficiency is prevalent across many diseases and physiological events, zinc supplementation should be an appropriate treatment option. However, zinc absorption is dependent on interactions with other nutrients (phytates, copper, iron, calcium) (Mocchegiani and Malavolta 2011). Hence, scientists have attempted to treat diseases with metal-modulating drugs. Two classes of interest are metal chelators and metal ionophores/chaperones, which have primarily been tested in models of age-related disorders such as AD. Chelators are compounds that bind to metal ions, decreasing their bioavailability (Ding and Lind 2009). However, currently there is little evidence for a therapeutic benefit in pathological aging. Building on the concept of metal chelators, other compounds have recently come to light that can modulate cellular metal concentrations. These compounds have been termed “metal ionophores” or “chaperones,” and the two most extensively studied, particularly in relationship to their anti-AD potential, are clioquinol and PBT2 (both belonging to the 8-OH quinolone class of compounds). Both compounds have been shown to have positive effects on both pathology and cognition in a variety of transgenic mouse models of AD (Adlard et al. 2008, 2010). One of the benefits of this latter approach is that a much more targeted modulation of zinc can be achieved, as compared to simple zinc chelation or supplementation. It should also be noted that in AE, zinc supplementation can reduce physical symptoms, but it cannot repair neurological damage. Moreover, long-term zinc supplementation may also lead to a copper deficiency, which appears to be the result of competitive absorption of zinc and copper within enterocytes (Tapiero and Tew 2003; Mocchegiani and Malavolta 2011). This absorption is regulated by MTs that have a higher binding affinity for copper. Increased dietary zinc intake results in upregulation of MT protein expression, causing increased copper binding and excretion of the MT–copper complex. This finding further highlights the need for specifically targeted zinc treatments that will allow better control of potential side effects. Hence, zinc supplementation and zinc-modulating therapies must be used within a combination of treatments that are specifically targeted to a particular deficit.

## 9.5 Conclusion

Here we have discussed the critical role of zinc in a range of physiological processes wherein it is essential for life through its ability to act as a neurotransmitter and impact molecular and cellular changes essential for cognition, growth, immunity, DNA synthesis, and cell signaling. We have also discussed the diversity of diseases and neurological disorders that have been demonstrated to involve zinc and zinc dyshomeostasis. Research has also demonstrated the differing methods of zinc signaling that result in specific cellular and protein changes. Although this signaling represents a potential therapeutic target, further research and technical advances are required to ensure specificity of treatments that can reduce potential side effects while repairing only the dysfunctional zinc signal.

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# Chapter 10

## Zinc Signals in Immunology

Lothar Rink and Martina Maywald

**Abstract** Zinc is known to be an essential trace element that is highly important for all proliferating cells in the human body, especially for the immune system. Free zinc influences several signaling pathways, such as Toll-like receptor 4 or T-cell receptor signaling, by binding reversibly to regulatory sites in signaling proteins, resulting in a change of free zinc concentrations that can affect signal transduction; thus, cellular responses can be altered. Zinc signals have been observed in cells of the innate as well as of the adaptive immune system, that is, neutrophil granulocytes, mast cells, monocytes, dendritic cells, and T cells, mostly in changes of the cytoplasmic zinc concentration. To characterize zinc signals one can distinguish them by the timescale in which they take place. First, zinc signals can occur within a few seconds to minutes, and are therefore called fast zinc signals. Second, a slightly slower type of zinc signal is known and described as “zinc wave.” Third, some zinc signals occur on a timescale significantly longer than the others. In these cases, the signals are typically involved in altered expression of proteins involved in zinc homeostasis.

Zinc signals occurring in different cell types and signaling pathways that are mentioned in this chapter are classified regarding the specific discrimination of fast zinc signal, zinc wave, and late zinc signal.

**Keywords** Adaptive and innate immunity • Signal transduction • TLR-4 • Zinc • Zinc deficiency • Zinc homeostasis

The essentiality of zinc for animals was recognized in 1934, but it was not until the early 1960s that zinc was known to be essential for humans. Compared to other metal ions with similar chemical properties, zinc is relatively harmless (Fosmire 1990). Moreover, it has been shown that only exposure to high doses has toxic effects, making acute zinc intoxication a rare event. The uptake of cytotoxic doses of exogenous zinc is prevented by systemic homeostasis and efficient regulatory mechanisms on the cellular level. Intracellular zinc has an important role in cytotoxic events in single cells and is involved in various functions in numerous

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cell and organ systems (Prasad 2009). Virtually all immune cells are modulated by zinc *in vitro* and *in vivo*.

In this chapter, we discuss the importance of zinc signals in the immune system and the interactions of zinc with major signaling pathways that are responsible for the regulation of cellular functions, as well as the influence of zinc deficiency and zinc supplementation on zinc signaling in various immune cells.

## 10.1 Zinc Homeostasis and the Immune System

Zinc is considered to be relatively nontoxic to humans, and the human body contains a total amount of 2 to 4 g zinc (Haase and Rink 2010). In general there is no specialized zinc storage system in the human body, and thus one needs a daily intake of zinc to achieve a steady state for proper immune function. The distribution of zinc in the human body differs significantly among various tissues and organs, ranging from 10  $\mu\text{g/g}$  dry weight in the brain (1.5 % of total body zinc) up to 100  $\mu\text{g/g}$  in the bones (29.0 % of total body zinc). Other organs containing estimable concentrations of zinc include liver, prostate, kidney, skin, lung, heart, pancreas, and the gastrointestinal tract. Oral uptake of zinc results in absorption throughout the small intestine, and distribution subsequently occurs via the serum, where zinc concentrations reach 10–18  $\mu\text{M}$ , comparable to around 1  $\mu\text{g/g}$  (0.1 % of total body zinc) (Mills 1989). It is abundantly bound with low affinity to albumin (60 %), with high affinity to  $\alpha_2$ -macroglobulin (30 %), and to transferrin (10 %) (Rink and Gabriel 2000). Thus, it is a predominantly intracellular ion (Haase and Maret 2009), distributed between the cell nucleus (30–40 %), cytoplasm, organelles, and vesicles (50 %) (Vallee and Falchuk 1993), including zinc-specific vesicles called “zincosomes” (Beyersmann and Haase 2001). These vesicles segregate high amounts of zinc upon stimulation, for example, with growth factors (Haase and Maret 2003). Metallothioneins (MT) play an important role in zinc homeostasis by complexing about 20 % of intracellular zinc. MTs are characterized by a low molecular weight of 6–7 kDa, high cysteine content, and their ability to complex metal ions. They are ubiquitously expressed proteins, and each MT can bind up to seven zinc ions. Although all zinc ions are bound in similar tetrathiolate coordination environments, the affinities of the sites for zinc range with a  $\log K$  from 7.7 to 11.8. Thus, MT can act as a cellular zinc buffer over several orders of magnitude that range from picomolar to nanomolar concentrations as a consequence of the different affinities of the metal ion-binding sites (Krezel and Maret 2007). The dynamic regulation of cellular zinc homeostasis results from the synthesis of the apo-form thionein (T) in response to raised intracellular zinc levels by triggering the metal-response element-binding transcription factor (MTF)-1. MTF-1 is a cellular zinc ion sensor and regulates transcription of genes, whose promoters contain metal-response elements, because at least two of its six zinc fingers are not constitutively bound to zinc, and thus these sense available free zinc by reversible binding, resulting in stabilization of the zinc-finger domains

(Radtke et al. 1993). Furthermore, oxidation of cysteine residues alters the number of metal-binding sites, thus connecting redox and zinc metabolism (Laity and Andrews 2007).

Despite the fact that the plasma zinc pool is very small, it is highly mobile and immunologically important. Similar to serum zinc, most of cellular zinc is bound to proteins, leaving only a minor part of intracellular zinc, which is also referred to as labile, mobile or “free zinc,” loosely bound or unbound. Free zinc is an operative term, used to distinguish zinc involved in signal transduction from the tightly protein-bound zinc, which is thermodynamically unavailable. The term is used in this chapter with the understanding that it is chemically incorrect, because zinc ions will never be completely without ligands, but form complexes with amino acids, glutathione, phosphate, or other low molecular weight ligands, when not bound to proteins.

So far, more than 300 enzymes and even more proteins are identified to contain zinc. Based on a screening for well-known zinc-binding sequences, it is estimated that up to 10 % of the encoded proteins in the human body may contain zinc (Andreini et al. 2006). The zinc proteome consists of two major groups of comparable size, enzymes and transcription factors. Together, these form more than 90 % of the zinc proteome, indicating that the vast majority of zinc is required for catalysis and transcriptional regulation (Andreini et al. 2009).

Tightly protein-bound zinc is required for catalytic, co-catalytic, and structural functions of enzymes (Vallee and Falchuk 1993). In some enzymes it is important for structural integrity, and in others it is the central ion for enzymatic activity, but sometimes both functions are involved. Moreover, zinc is involved in the stabilization of structural domains, such as in zinc fingers and related structures and enables interaction of proteins or nucleic acids, as for many transcription factors (Maret 2006).

First, understanding of the mechanism by which zinc uptake into the cell takes place is important. It has been shown that exogenous zinc enters the cell within minutes (Wellinghausen et al. 1996). Cellular zinc underlies an efficient homeostatic control to avoid excessive accumulation. Therefore, two families of eukaryotic zinc transporters are known to date: the Zip and ZnT proteins. The Zrt-like, Irt-like protein (Zip) family comprises 14 genes designated solute carrier family 39 (SLC39) A1 to A14 that transport zinc into the cytosol, whereas the zinc transporter (ZnT) family of 10 genes (SLC30A1 to SLC30A10) transports zinc in the opposite direction (Cousins et al. 2006; Eide 2006). The same transporter families also regulate the intracellular distribution of zinc into the endoplasmic reticulum, mitochondria, and Golgi network (see Chap. 3). In addition, different possible mechanisms for zinc uptake such as facilitated diffusion via amino acids and anionic exchange or calcium-conducting channels have been reported (Bentley 1992; Hogstrand et al. 1996). To date, additionally members of four distinct superfamilies, that is, voltage-gated calcium channels (VGCC) (Gyulhandanyan et al. 2006), glutamatergic receptors (Jia et al. 2002), nicotinic acetylcholine receptors (Ragozzino et al. 2000), and TRP channels (Dong et al. 2008) have been shown to transport zinc through the cell membrane.

However, free zinc contributes to the regulation of numerous cellular processes and influences several signaling pathways by binding reversibly to regulatory sites in signaling proteins; this results in a change of the free zinc concentration that can affect signaling pathways, and thus cellular responses can be altered (Ibs and Rink 2003). Furthermore, zinc shows intracellular fluctuation after stimulation (Haase et al. 2006a), assuming a complex interaction between zinc homeostasis and signal transduction, where zinc may have similar functions as the second messenger calcium (Williams 1984).

Free zinc is crucial for the appropriate development and function of innate as well as adaptive immunity, but the importance of zinc for proper immune function is most obvious in zinc-deficient individuals.

Although intoxication by excessive exposure is rare, zinc deficiency is widespread and has been known to have a detrimental impact on growth, neuronal development, and immunity, and in severe cases its consequences are lethal. Human zinc deficiency has been reported the first time in 1961, when Iranian males were diagnosed with symptoms including growth retardation, skin abnormalities, hypogonadism, and mental lethargy that led back to nutritional zinc deficiency (Prasad et al. 1961). Later, additional studies showed remarkably similar features and manifested zinc deficiency as a potentially widespread problem in developing countries as well as in industrial nations (Prasad et al. 1963; Sandstead 1991).

Zinc deficiency manifests itself on different levels and can be subdivided into either severe or marginal zinc deficiency. Moreover, zinc deficiency can be either inherited or acquired. On the one hand, severe zinc deficiency is caused by metabolic disorders regarding zinc uptake as well as by other sources such as parenteral nutrition without zinc.

Zinc deficiency results in complex immune defects, leading to various immune disorders (see Chap. 11). This condition is observed in its most severe form in the zinc malabsorption syndrome acrodermatitis enteropathica, an autosomal recessive disorder characterized by periorificial and acral dermatitis, mucocutaneous lesions, failure to thrive, alopecia, diarrhea, neuropsychological disturbances, weight loss, and frequent severe infections with fungi, viruses, and bacteria that is based in most cases on a mutation of the intestinal zinc uptake protein Zip 4 (Kury et al. 2002; Wang et al. 2002).

Acquired severe zinc deficiency has been observed in patients receiving total parenteral nutrition without zinc supplementation, following excessive alcohol consumption, severe malabsorption, and iatrogenic causes such as treatment with histidine or penicillamine (Prasad 1985). The arising symptoms are mostly similar to those in acrodermatitis enteropathica. Patients who become zinc deficient while receiving total parenteral nutrition without zinc supplementation develop abnormalities that include lymphopenia, decreased ratios of CD4<sup>+</sup> to CD8<sup>+</sup> T cells, decreased NK cell activity, and increased monocyte cytotoxicity, but these are readily corrected by proper zinc supplementation (Allen et al. 1983).

In another group of inherited disorders of zinc metabolism the zinc plasma level is above 3 µg/ml, more than three times the physiological level, while iron and

copper levels stay normal (Failla et al. 1982; Fessatou et al. 2005; Smith et al. 1976). Even though this exceeds the amount that can be found in serum after zinc intoxication, symptoms range from none to severe anemia, growth failure, and systemic inflammation (Fessatou et al. 2005; Smith et al. 1976; Saito et al. 2002; Sampson et al. 1997). The increased zinc levels have been attributed to excessive binding to serum proteins such as albumin (Failla et al. 1982; Smith et al. 1976) or to an overexpression of calprotectin, a zinc-binding S100 protein (Fessatou et al. 2005; Saito et al. 2002). Therefore, the large amount of zinc in the serum of these patients that is attached to proteins and thus biologically available may be depleted (Sampson et al. 1997). Furthermore, moderate zinc deficiency can also accrue as a consequence of sickle cell disease (Prasad 1981). Hyperzincuria and a high protein turnover caused by increased hemolysis lead to moderate zinc deficiency in these patients, causing clinical manifestations typical for zinc deficiency, such as growth retardation, hypogonadism in males, hyperammonemia, and cell-mediated immune disorder (Prasad 2002) connected with thymic atrophy (Dardenne et al. 1984).

Affected subjects show reduced lymphocyte proliferation response to mitogens, anergy, thymic atrophy, a selective decrease in CD4<sup>+</sup> T cells, and deficient thymic hormone activity (Prasad 2000). In general, zinc deficiency leads to an increased susceptibility to infection and parasitic disease, and is furthermore the fifth leading cause of mortality and morbidity in developing countries (WHO 2002).

Marginal zinc deficiency can be characterized by slight weight loss, oligospermia, and hyperammonemia (Prasad 1985). It may be caused by nutritional zinc deficiency consequent to high consumption levels of zinc-chelating phosphates, lignins, and phytates that counteract zinc absorption, by malabsorption syndrome, or by sickle cell anemia.

Moreover, parallels exist between the decline in immune function in the elderly and zinc deficiency even in industrialized countries. A significant percentage of elderly show reduced serum zinc levels, and zinc supplementation studies indicate that this deficiency contributes to increased susceptibility to infectious diseases. It also occurs frequently during pregnancy and lactation, because of rapid growth, in vegetarians, or in persons with renal insufficiency (Brieger and Rink 2010; Haase and Rink 2010).

The overall frequency of zinc deficiency worldwide is expected to be higher than 20 % (Wuehler et al. 2005). In developing countries, it may affect more than 2 billion people (Prasad et al. 1961, 1963; Cavdar et al. 1983). Furthermore, it has been estimated that only 42 % of the elderly ( $\geq 71$  years) in the United States have adequate zinc intake (Briefel et al. 2000). This widespread occurrence combined with the variety of clinical manifestations makes zinc deficiency a serious nutritional problem, which has a far greater impact on human health than the relatively infrequent zinc intoxication.

Detractions in zinc homeostasis affect multiple aspects of the immune system including hematopoiesis, cell-cycle progression, and immune-regulating molecules. Intracellular killing, cytokine production, and ROS (reactive oxygen species) synthesis are all affected by zinc deficiency. It also affects adversely the growth and

function of T and B cells by dysregulation of basic biological functions at the cellular level. Moreover, zinc is needed for DNA synthesis, RNA transcription, cell division, and cell activation. Programmed cell death (apoptosis) is also elevated in the absence of adequate zinc levels. Also, secretion and function of cytokines, the basic messengers of the immune system, are adversely affected by zinc deficiency. The ability of zinc to function as a pro-antioxidant and to stabilize membranes suggests that it has a role in prevention of free radical-induced injury during inflammatory processes.

All in all, zinc signals contribute to the regulation of virtually all immune cells (see Chap. 11), to numerous cellular processes, and influence several signaling pathways by binding reversibly to regulatory sites in signaling proteins. Thus, zinc is crucial for the appropriate development and function of innate as well as adaptive immunity, as is further described next.

## 10.2 Types of Zinc Signals

Free zinc influences several signaling pathways by binding reversibly to regulatory sites in signaling proteins, resulting in a change of free zinc concentrations that can affect signaling pathways. Thus, cellular responses can be altered (Haase and Rink 2009a).

It has been shown that activation of T cells causes an intracellular redistribution of zinc and an activation of protein kinase C (PKC) (Csermely et al. 1987, 1988). Since that time, zinc signals have been observed in different immune cells, that is, T cells (Kaltenberg et al. 2010; Yu et al. 2011; Lee et al. 2008; Aydemir et al. 2009), dendritic cells (Kitamura et al. 2006), monocytes (Haase et al. 2008), neutrophil granulocytes (Hasan et al. 2013), and mast cells (Yamasaki et al. 2007), mostly in changes of cytoplasmic zinc concentration (Haase and Rink 2009a).

One way to characterize zinc signals is by the timescale in which they take place. First, zinc signals can occur within a few seconds to minutes by triggering receptors such as Toll-like receptor (TLR)-4. Zinc acts as second messenger, comparable to calcium, and influences several signaling pathways directly. Therefore, the zinc signal is independent from the synthesis of proteins such as Zips and ZnTs and is thus called the fast zinc signal.

Second, a slightly slower type of zinc signal is known that is described as “zinc wave” and investigated in mast cells. Here, crosslinking of FcεRI induces a release of free zinc from the perinuclear area, including the endoplasmic reticulum. Comparable to the fast zinc signal, zinc acts also as a second messenger but is induced indirectly depending on calcium influx (see Chap. 5). However, zinc signals and the zinc wave also have a function as second messenger; the altered cytoplasmic zinc concentration influences other signaling pathways also, comparable to the role of late zinc signals.

Third, some zinc signals occur on a significantly longer timescale. In these cases, the late signals are typically involved in altered expression of proteins involved in



**Table 10.1** Characterization of zinc signals concerning the timescale during which they take place

Zinc signal	Duration	Effect
Fast zinc signal	Seconds to minutes	Influence of cGMP by inhibition of PDE in monocytes/macrophages
		MKP inhibition in monocytes/macrophages
		PMA-induced NET-formation in PMN
		Expression of IL-8 in epithelial cells
		Lck recruitment to TCR-activating complex
		Zinc release from lysosomes in T cells
		T-cell activation by APC
		Homodimerization and activation of Lck in T cells
		Redistribution of zinc from nucleus/mitochondria to cytosol/microsomes in T cells
		IL-2-mediated zinc signal
Zinc wave	Minutes	Zinc release from perinuclear area in mast cells
Altered zinc homeostasis (late zinc signal)	Hours	Adherence of monocytes to endothelial cells
		Influence of mRNA transcription, e.g., IL-2, A20 in T cells, monocytes/macrophages
		MAPK activation in airway epithelial cells and monocytes/macrophages
		Negative regulation of TRIF pathway in macrophages
		Change of Zip/ZnT expression in DCs and T cells
		Inhibition of adenylate cyclase transcription in T cells
		Influence of cytokine production, e.g. IL-2 in T cells
		Upregulation of Akt phosphorylation in T cells
		PTEN inhibition in T cells
		Stat 3/6 phosphorylation in B and T cells
		Induction/stabilization of regulatory T cells
Reduced cytokine production, e.g., IFN- $\gamma$ in T cells		

Zinc signals occurring within a few seconds to minutes are called fast zinc signals and are independent of the synthesis of proteins such as Zips and ZnTs. A slightly slower type of zinc signal, described as a “zinc wave,” occurs after a few minutes. Zinc signals that take place on a timescale significantly longer (hours) are typically involved in altered expression of proteins involved in zinc homeostasis

zinc homeostasis, such as maturation of monocytes and DCs or cytokine expression (Dubben et al. 2010; Kitamura et al. 2006). Furthermore, the altered zinc homeostasis results in an influence of several signaling pathways, but zinc itself does not function as a second messenger.

Examples for each classification of zinc signals occurring in different cell types and signaling pathways are mentioned in the following section and are summarized in Table 10.1.

### 10.3 Zinc Signal and Innate Immunity

Innate immunity as the first line of defense is a highly important natural protection system against harmful substances, consisting of different cell types such as monocytes/macrophages, granulocytes, dendritic cells (DC), mast cells, and natural killer (NK) cells, as well as countless soluble proteins such as complement proteins, acute-phase proteins, cytokines, and chemokines. It is not highly specific, as is adaptive immunity, but reacts on different antigens in the same way. Its cells are activated by conserved structures in pathogens, called pathogen-associated molecular patterns (PAMPs), that are recognized by conserved receptor-triggering processes such as cytokine production, killing of target cells, or antigen presentation to cells of the adaptive immune system. Compared to the number of processes regulated on the cellular level, only limited numbers of signaling pathways exist. These pathways, depending on the cell type, are induced by different receptors and lead to the expression of cell type-specific genes. Immune cells as well as a myriad of other cell types share these identical pathways, as discussed next.

In an infection, polymorphonuclear leukocytes (PMNs) are the first cells actively entering the infected tissue by following a concentration gradient of chemical messengers, a mechanism known as chemotaxis. It is reported that this and other cellular functions are disturbed by altered zinc levels. Zinc deficiency leads to reduced PMN chemotaxis (Ibs and Rink 2003; Shankar and Prasad 1998), whereas elevated zinc concentrations, about 500  $\mu\text{M}$ , are reported to induce chemotactic activity directly *in vitro* (Hujanen et al. 1995). PMNs are phagocytes that are essential to destroy pathogens by phagocytosis and generation of the respiratory burst. Zinc deficiency leads to a decreased phagocytosis that can be restored by zinc supplementation (Sheikh et al. 2010). These effects depend on an altered zinc homeostasis.

PMNs kill phagocytosed pathogens through the rapid production and release of reactive oxygen species (ROS), including superoxide anion, hydrogen peroxide, and hypochlorous acid. Superoxide anions are produced by NADPH oxidase, which can be inhibited by zinc deficiency as well as by zinc excess (DeCoursey et al. 2003; Chasapis et al. 2012; Hasegawa et al. 2000). Another neutrophil granulocyte function is influenced by altered zinc concentrations, namely, NETosis. NETosis is described as the release of a matrix composed of DNA, chromatin, and granule proteins to capture extracellular bacteria within so-called neutrophil extracellular traps (NETs). NETosis can be induced by protein kinase C (PKC) activator 12-myristate 13-acetate (PMA) and depends on the production of ROS by NADPH oxidase. PMA treatment leads to a fast zinc signal in neutrophil granulocytes that is an essential component of the ROS-dependent signal transduction leading to NET formation. Recently, it was shown that zinc chelation abrogates NET formation *in vitro* (Hasan et al. 2013).

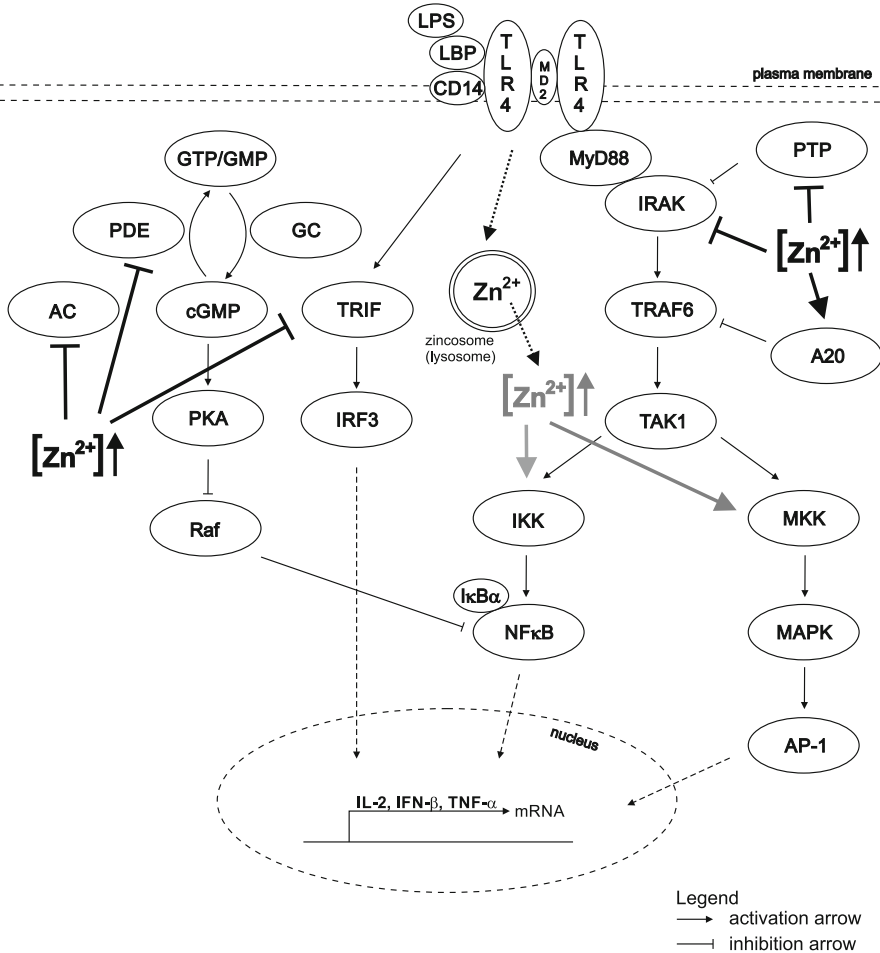
Similar to PMNs, macrophages also take up pathogens or cellular debris by phagocytosis and kill pathogens by oxidative burst, both of which are zinc dependent. Monocytes produce various cytokines, for example, pro-inflammatory

cytokines such as interleukin (IL)-1 $\beta$ , IL-6, and tumor necrosis factor (TNF)- $\alpha$ . Therefore, zinc signals are essential and can also be directly induced by stimulation with high extracellular zinc concentrations (Wellinghausen and Rink 1998; Wellinghausen et al. 1997a). Monocytes develop from myeloid precursor cells and can move quickly to sites of infection in the tissues and differentiate into macrophages and dendritic cells to elicit an immune response. The differentiation of monocytes is calcitriol dependent and can be enhanced by zinc sequestration, which indicates a negative regulatory role for this ion (Dubben et al. 2010), depending on an altered zinc homeostasis. After their development, monocytes circulate in the bloodstream, from which they start to migrate into the tissue where the maturation into resident macrophages takes place. Migration from blood into tissues starts by adherence to endothelial cells, which can be augmented by zinc, and stimulation of monocytes with chemoattractant protein-1 (MCP)-1 or PMA induces an intracellular zinc signal promoting adhesion to endothelial cells (Chavakis et al. 1999; Kojima et al. 2007). These effects depend on altered zinc homeostasis.

Monocytes/macrophages and dendritic cells (DC) take up and present antigens to T cells. They coordinate the immune response by producing cytokines in response to a sufficient stimulation that leads to an activation of both cell types, such as lipopolysaccharide (LPS), which is sensed by Toll-like receptor (TLR)-4. Thus, TLR-4 signaling leads to secretion of pro-inflammatory cytokines and maturation and antigen presentation in dendritic cells and macrophages.

In TLR-4 signaling, zinc has a double-edged effect on the cytokine secretion in monocytes (see Fig. 10.1). Herein fast zinc signals that are moderately increased are involved in TLR-4 signal transduction, whereas long-term higher concentrations are inhibitory. A fast zinc signal has been observed within less than 2 min by binding of bacterial LPS to TLR-4 that is involved in the activation of mitogen-activated protein kinase (MAPK) signaling. MAPK activation via zinc can be observed in many cell types. The MAPK extracellular-regulated kinase (ERK) is shown to be activated by zinc treatment of fibroblasts (Hansson 1996), as well as of neurons or neuroblastoma cells (An et al. 2005; Park and Koh 1999). In addition, this effect is also described in the activation of further MAPKs such as p38 and Jun N-terminal kinase (JNK) (An et al. 2005; LaRochelle et al. 2001). Similar observations have been made with other TLR ligands, such as pam3CSK4, insulin, and TNF- $\alpha$ .

Although no direct effect of zinc on MAPK activity has been reported, a fast zinc signal is reported to lead to an inhibition of MAP kinase phosphatases (MKP) that dephosphorylate both tyrosine and threonine residues in activated MAPKs. Thus, indirectly zinc causes inhibition of ERK1/2 and dephosphorylation of p38 in human macrophages (Haase et al. 2008). The zinc-dependent inhibition of MKP is involved in ERK activation during oxidative stress in neurons (Ho et al. 2008) and is one mechanism by which zinc stimulates expression of IL-8 in epithelial cells (Kitamura et al. 2006). However, not all the effects of zinc on MAPK phosphorylation and activation can be explained simply by zinc inhibition of MKP because zinc also affects targets upstream of the MAPKs. For instance, MAPK activation in



**Fig. 10.1** Zinc and Toll-like receptor 4 (*TLR-4*) signaling. Triggering of *TLR-4* induces fast zinc release (highlighted in *dotted arrows*) from zinosomes. These physiological fast zinc signals (highlighted in *dark grey*) are required for activation of nuclear factor kappa B (*NF-κB*) and mitogen-activated protein kinase (*MAPK*) signaling (*activation arrow*) leading to translocation (*dashed arrows*) into the nucleus. Long-term higher concentrations of zinc, resulting from the use of ionophores in experimental procedures (highlighted in *bold black*), inhibit *TLR-4* signaling (*inhibition arrow*). Suggested mechanisms are a direct inhibition of interleukin-1 receptor-associated kinase (*IRAK*), an upregulation of *A20* that removes the activating ubiquitination of tumor necrosis factor receptor-associated factor 6 (*TRAF6*), an inhibition of cyclic nucleotide phosphodiesterases (*PDE*) or an inhibition of TIR-domain-containing adapter-inducing interferon-β (*TRIF*). Inhibition of *PDE* leads to a rise in cyclic guanosine monophosphate (*cGMP*) and cross-activation of protein kinase A (*PKA*), resulting in *Raf* inhibition and thereby *TLR*-mediated *NF-κB* activation. Furthermore, increased intracellular zinc concentrations inhibit adenylate cyclase (*AC*). *IKK* I kappa B kinase, *IRF3* interferon regulatory factor 3, *MKK* MAPK kinase, *PKA* protein kinase A, *PTP* protein tyrosine phosphatases, *AP-1* activator protein 1, *GMP* guanosine monophosphate, *GTP* guanosine triphosphate

airway epithelial cells also depends on a long-time zinc effect on tyrosine phosphorylation upstream of ERK (Wu et al. 2002).

However, the effect of zinc on MAPKs is not always agonistic. Low concentrations of zinc are shown to activate ERK in rat glioma cells, whereas higher concentrations reduced the activating phosphorylation (Haase and Maret 2005). One potent molecular mechanism could be that the zinc transporter (ZnT)-1 homologue CDF-1 mediates zinc efflux, leading to an activation of Ras/Raf/MEK/ERK pathway (Bruinsma et al. 2002). Here zinc may promote the inhibitory phosphorylation of kinase suppressor of Ras (KSR). KSR works as a scaffolding protein that stabilizes the interaction of Ras, Raf, and MEK (Yoder et al. 2004). Another molecular mechanism could be CDF/ZnT-1 binding to Raf-1, promoting its biological activity, which is inhibited by zinc (Jirakulaporn and Muslin 2004). Therefore, an altered zinc homeostasis influences the signaling pathways and the threshold of activation.

Also, extended concentrations of zinc inhibit TLR-4 signaling. In this connection the first suggested mechanism is a direct inhibition of the interleukin-1 receptor-associated kinase (IRAK). Second, the late zinc signal leads to upregulation of mRNA of the cytoplasmatic zinc-finger protein A20 (Prasad et al. 2004) that removes the activating ubiquitination of tumor necrosis factor receptor-associated factor 6 (TRAF6), which could result in disturbed TLR-4 signaling. In TLR signaling, TRAF6 ubiquitination leads to proteasome-independent activation of the transforming growth factor beta-activated kinase (TAK)1, which in turn phosphorylates I $\kappa$ B kinases (IKKs) and MAPK kinases (MKKs) (Deng et al. 2000; Wang et al. 2001). A20 is induced by pro-inflammatory stimuli and is involved in the termination of TLR-induced activity of NF- $\kappa$ B and pro-inflammatory gene expression in macrophages (Boone et al. 2004). Moreover, it deubiquitinates TRAF6, inactivating this protein. Therefore, upregulation of A20 by zinc leads to diminished NF- $\kappa$ B and MAPK activation in response to TLR stimulation. Third, the inhibition of the cyclic nucleotide phosphodiesterases (PDE) via a fast zinc signal is named, which results in an increase in cyclic guanosine monophosphate (cGMP) synthesized by guanylate cyclases (GCs). This effect is caused by cross-activation of protein kinase A (PKA) by elevated cGMP concentrations. In human monocytes, degradation of cyclic nucleotides is mediated by PDEs 1, 3, and 4, that are all inhibited by zinc (von Bulow et al. 2005), which leads to inhibitory phosphorylation of Raf-1, resulting in its inactivation. Because Raf-1 is necessary for TLR-4 mediated NF- $\kappa$ B activation, however, the zinc/cGMP/PKA/Raf pathway blocks the activation of this transcription factor and thereby transcription of genes for pro-inflammatory cytokines (von Bulow et al. 2007). In addition to PDEs, adenylate cyclase (AC) is inhibited by the late zinc signal, leading to a reduced cAMP level, whereas the synthesis of cGMP by soluble GC is unaffected. So far, two different mechanism for zinc inhibition of AC have been presented: zinc may influence enzymatic activity by altering the conformation of AC (Klein et al. 2004) or, alternatively, by inhibiting the activation of AC via the heterotrimeric G-protein alpha-subunit (Gao et al. 2005).

Moreover, during a longer timescale zinc affects the response of DCs to LPS. Treatment of murine DCs with LPS leads to a reduction of free intracellular zinc, based on a TIR-domain-containing adaptor protein inducing IFN- $\beta$  (TRIF)-dependent change in the expression pattern of several zinc transporters. This step involves a reduction of Zrt-like, Irt-like Protein (Zip) 6 and 10 gene expression, and upregulates expression of zinc transporter (ZnT)-1, -4, and -6. The reduction in free zinc is important for maturation of DCs (Kitamura et al. 2006), but also chelation of zinc influences TLR-4 signaling in macrophages. Stimulation with the zinc chelator TPEN augments TLR-4-mediated production of IFN- $\beta$  and subsequent synthesis of inducible NO synthase and production of NO. The effect is based on zinc acting as a negative regulator of the TRIF pathway via reducing IFN regulatory factor 3 activation (Brieger et al. 2013).

Zinc is involved in the regulation of LPS signaling in cells of the innate immune system, but effects depending on zinc are not limited to the response to LPS. Also, a role for free zinc in regulation of protein kinase C (PKC) activity during monocyte chemoattractant protein (MCP)-1-induced adhesion is known (Kojima et al. 2007). In this context, which other receptors depend on zinc for cellular signaling need investigation. *In vivo*, zinc deficiency will impair the function of monocytes, in particular their ability to mount an adequate cytokine response during infection, but because zinc is equally involved in negative regulation of the same pathways, a disturbance of zinc homeostasis could also affect the limitation of pro-inflammatory cytokine production, leading to overproduction. Although this seems contradictory, it is supported by experimental evidence. For instance, in the elderly reduced spontaneous cytokine production is observed by long-term zinc supplementation, but simultaneously an improved cytokine response to PAMPs occurs (Kahmann et al. 2008).

NK cells play also a major role in immunity against infections and tumor development. This subset of lymphocytes mediates the killing of either infected or transformed cells, using a variety of different receptors. They act mainly by two different mechanisms: the first is based on the availability of major histocompatibility complex class I (MHC-I) molecules or other cell-surface proteins on target cells screened by NK cells. The absence of those molecules indicates an attempted evasion of T-cell immune surveillance. The second mechanism is antibody-dependent cell-mediated cytotoxicity (ADCC), which is based on the recognition of antibodies that are bound to the target cell surface. In both cases, target cells are killed by release of the content of cytotoxic granules, such as perforin and granzyme B.

Here, zinc is involved in the recognition of MHC-I on target cells, mainly human leukocyte antigen C, by p58 killer cell inhibitory receptors on NK cells for inhibition of the killing activity (Rajagopalan et al. 1995; Rajagopalan and Long 1998). In general, the NK cell number as well as activity is dependent on the serum zinc level. The lytic activity of NK cells is decreased by zinc deficiency, probably because of decreased stimulation from T cells via the cytokine IL-2. Furthermore, the relative number of precursors of cytolytic cells is decreased during zinc deficiency as well as the lytic activity of NK cells itself (Prasad 2000), but moderate

zinc supplementation increases differentiation of CD34<sup>+</sup> progenitors toward NK cells and their cytotoxic activity (Muzzioli et al. 2007). However, merely the inhibitory signal is zinc dependent, whereas the human leukocyte antigen C interaction and positive signals do not require zinc. Thus, zinc is needed to maintain the normal function of NK cells, and zinc deficiency may result in functional loss and evoke nonspecific killing.

To date intracellular zinc signals have not been investigated in NK cells. However, lines of evidence connect major signaling pathways in NK cells to zinc. A multitude of different receptors are required for fine-tuning of NK cell activity (Yokoyama and Plougastel 2003). A common feature of many of these receptors is the presence of characteristic tyrosine phosphorylation sites that either activate (immunoreceptor tyrosine-based activation motif, ITAM) or inhibit (immunoreceptor tyrosine-based inhibitory motif, ITIM) NK cell function. In this respect, one feature of zinc is of particular importance: its ability to inhibit protein tyrosine phosphatases (PTPs) by a fast zinc signal (Brautigam et al. 1981). This inhibition seems to be a common feature of PTPs, in which zinc interacts with the highly conserved catalytic domain, possibly by binding to the active site cysteine (Haase and Maret 2005). Notably, a nucleophile attack by the catalytically active cysteine residue is a shared feature of PTPs and MKPs, another target of zinc that has already been mentioned. On the other hand, serine/threonine phosphatases have a dinuclear metal center in which water acts as the nucleophile (Barford et al. 1998), and so far there are no reports about a specific inhibition of these enzymes by zinc. Several PTPs are inhibited by low concentrations of zinc, including T-cell PTP with an half-maximal inhibitory concentration (IC<sub>50</sub>) of 200 nM (Maret et al. 1999), and PTP1B and SHP-1, with an IC<sub>50</sub> of 17 and 93 nM, respectively (Haase and Maret 2003). These values are close to the concentration range of physiological levels of free zinc and presume a partial inhibition of PTPs by free zinc even at basal levels. These effects therefore depend on the extracellular zinc concentrations and are not zinc signals.

Cell-surface antibody receptors, called Fc receptors, allow different immune cells to utilize antibodies for pathogen recognition, as in mast cells. The triggering of the high-affinity IgE-specific FcεR in mast cells induces degranulation. Notably, the secretory mast cell granules are rich in zinc that is released into the cellular environment together with a variety of immunological mediators (Gustafson 1967; Ho et al. 2004). The relationship between activation of FcRs and zinc status has been investigated in mast cells, but so far the results are undetermined. Measurements with fluorescent probes show a reduction of free zinc in response to treatments that induce degranulation, including the triggering of FcεRs (Ho et al. 2004). Another study (Yamasaki et al. 2007) reports that the crosslinking of FcεRI induces a release of free zinc from the perinuclear area, including the endoplasmic reticulum in mast cells. This phenomenon is known as zinc wave (see Chap. 5), which depends on calcium influx and MAPK.

This discrepancy might be the result of the use of different fluorophores in the two studies, detecting different pools of cellular zinc. Although the decrease of zinc is attributed to a loss of granule zinc, the increase seems to be cytosolic, originating

from the perinuclear region (Yamasaki et al. 2007). Furthermore, treatment with the membrane-permeable zinc chelator TPEN (*N,N,N',N'*-tetrakis-(2-pyridyl-methyl) ethylenediamine) activates NF- $\kappa$ B. TNF- $\alpha$ -induced NF- $\kappa$ B activation is blocked by treatment with zinc/pyrithione (Ho et al. 2004). A later study states a blockade of NF- $\kappa$ B activation in response to Fc $\epsilon$ R crosslinking by TPEN administration, and this effect can be reversed by zinc treatment (Kabu et al. 2006). Thus, it remains to be analyzed under which circumstances zinc inhibits NF- $\kappa$ B and caspase-3 activity, or is involved in the activation of NF- $\kappa$ B, ERK, JNK, and PKC $\beta$ I, and is thereby required for degranulation and cytokine production in mast cells in vitro as well as allergic reactions in vivo (Yamasaki et al. 2007).

Despite the fact that the innate immunity is the first stage in response of the immune system, observations relating to the influence of zinc signals are also associated with the function of the adaptive immunity.

## 10.4 Zinc Signals and Adaptive Immunity

The influence of zinc has also been identified regarding the two parts of adaptive immunity, humoral (B cells) and cellular immunity (T cells). B and T cells are produced as precursors and educated to recognize their specific antigen in the thymus (T cells) or bone marrow (B cells). The resulting naïve lymphocytes differentiate after antigen contact into effector cells and memory cells, in which the latter are the basis for immunological memory and the stronger reaction to a known antigen as a secondary response. Zinc is highly important, especially concerning the development of T cells and B cells (Osati-Ashtiani et al. 1998).

T cells are effector cells as well as important cells for the regulation of the specific immune system. Zinc not only influences NK cell-mediated killing, as already mentioned, it also affects the activity of cytolytic T cells (Mingari et al. 1998). Here the relative amount of CD8<sup>+</sup> CD73<sup>+</sup> T cells is decreased during zinc deficiency (Prasad 2000). These cells are predominantly precursors of cytotoxic T cells (CD8<sup>+</sup>), and CD73 is needed for antigen recognition and proliferation as well as cytolytic process generation (Beck et al. 1997). Furthermore, zinc is involved in the development of T cells, because zinc deficiency results in various T-cell defects manifested in thymus atrophy and lymphopenia (King et al. 2005).

Zinc acts as an essential cofactor for various enzymes, such as the thymic hormone thymulin (a nonapeptide). Thymulin is a hormone that is produced by the thymus, released by thymic epithelial cells (Dardenne et al. 1984), and induces markers of differentiation in immature T cells (Saha et al. 1995). Besides these intrathymic functions on thymocytes and immature T cells, thymulin acts on mature T cells in the periphery. It also modulates cytokine release by peripheral blood mononuclear cells (PBMC) and proliferation of CD8<sup>+</sup> T cells in combination with interleukin (IL)-2 (Coto et al. 1992). Therefore, zinc influences immature and mature T cells through the activation of thymulin. As a consequence of zinc deficiency, T-cell proliferation decreases after mitogen stimulation (Dowd



et al. 1986), whereas zinc supplementation is able to reverse zinc deficiency-induced changes in the thymus and on peripheral cells; this can also be observed in patients with acquired immunodeficiency syndrome (Mocchegiani et al. 1995). In contrast to other lymphocyte populations, a direct effect of zinc on T cells can be observed. For instance, zinc induces blast transformation in human lymphocytes (Berger and Skinner 1974; Sood et al. 1999), and ensures the expression of the high-affinity receptor for IL-2 on mature T cells (Tanaka 1989), one effect resulting in decreased proliferation of T cells in zinc deficiency (Crea 1990). Moreover, IL-2, the soluble IL-2 receptor (sIL-2R), and IFN- $\gamma$  can be induced by high concentrations of zinc in human PBMC (Driessen et al. 1994; Wellinghausen et al. 1997b).

In addition, zinc deficiency results in disturbed polarization of mature T cells. Zinc deprivation inhibits the polarization into Th1 cells and therefore changes the Th1/Th2 ratio toward Th2 cells, leading to unbalanced cell-mediated immune responses (Prasad 2000). It is observed that the production of IFN- $\gamma$  and IL-2 (products of Th1 cells) is decreased during zinc deficiency, whereas production of IL-4, IL-6, and IL-10 (products of Th2 cells) is not affected. Accordingly, the risk for infections and Th2-driven allergies is increased. Furthermore, the functional impairment of T cell-mediated responses during zinc deficiency favors the development of autoimmune diseases (Honscheid et al. 2009). Consistently, both zinc deficiency, and increased zinc levels influence T-cell function. Increasing zinc levels during T-cell activation are postulated to calibrate T-cell receptor (TCR) signaling, leading to T-cell responses following suboptimal stimuli (Yu et al. 2011). This effect depends on a fast zinc signal. In contrast, physiological zinc levels exceeding zinc concentrations, ranging from 50 to 100  $\mu$ M, inhibit T-cell activity as demonstrated by suppressed IL-1 $\beta$ -stimulated IFN- $\gamma$  expression (Wellinghausen et al. 1997b). Furthermore, induction and stabilization of regulatory T cells (Treg) can be observed in zinc-supplemented mixed lymphocyte cultures (MLC), leading to a reduced secretion of IFN- $\gamma$  (Rosenkranz et al., unpublished data), as a result of altered zinc homeostasis.

In contrast to T-cell stimulation, T-cell inhibition by an excess of zinc can also be observed *in vivo*, leading to the assumption that T-cell activity is critically regulated by the zinc concentration. This criticality may be a reason why some autoimmune diseases with a T-cell pathology, such as rheumatoid arthritis, are associated with moderate zinc deficiency. Some clinical trials show a reduction of the pain score with zinc supplementation, leading to a presumption that zinc deficiency increases allo- or autoreactivity, whereas it is inhibited by high zinc dosages.

Important molecular zinc targets responsible for the aforementioned zinc effects comprise receptor proteins, kinases, phosphatases, caspases, and transcription factors, which can be activated or inactivated by zinc (Haase and Rink 2009b). Furthermore, it functions as a second messenger in signal transduction, contributing to its immunomodulating capacity (Haase et al. 2008).

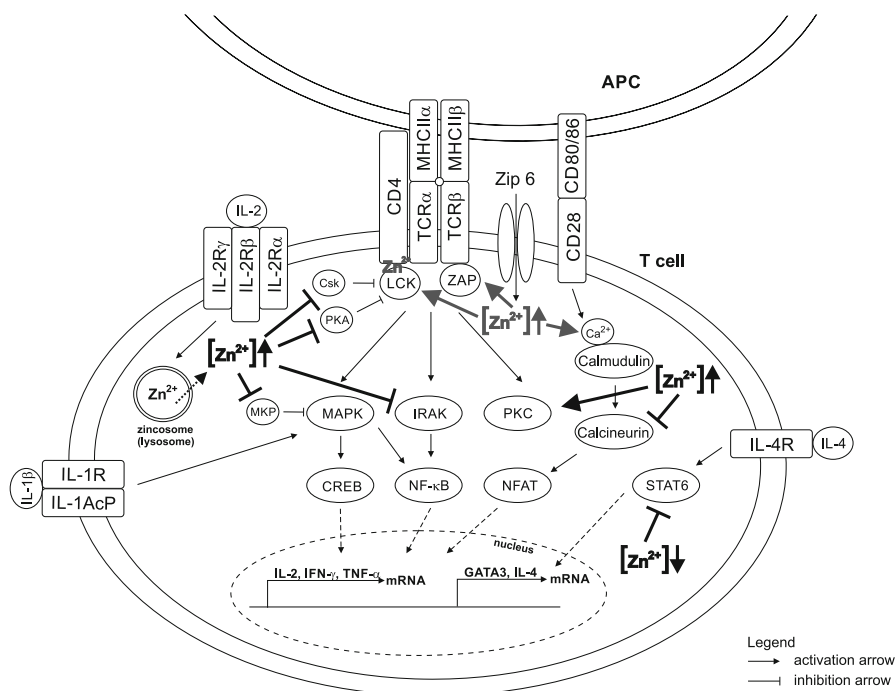
In T cells, fast zinc signals have been observed in response to TCR or interleukin-2 receptor (IL-2R) stimulation (Kaltenberg et al. 2010; Yu et al. 2011). Regarding the TCR, the signal seems not to be dependent on direct

activation of this receptor. Initiation of signaling from the TCR occurs by specific interaction with an antigen-loaded MHC molecule on the surface of a neighboring antigen-presenting cell (APC) by formation of a functional immunological synapse (see Fig. 10.2), and this results in an immediate influx of zinc from the extracellular environment through the transporter Zip 6 after T-cell stimulation (Yu et al. 2011). In contrast, triggering of IL-2R results in a release of zinc from lysosomes within 2 min after T-cell stimulation (Kaltenberg et al. 2010). Thus, an altered intracellular zinc level is induced, leading to an influence of dual-specificity phosphatases (DUSP) or protein phosphatase 2 (PP2A), for example, by a fast zinc signal, as well as signal transduction and protein expression by late zinc signals, such as diminished dephosphorylation of MEK and ERK or elevated transcription of Zip 6, leading to an increased MT expression, which supports T-cell proliferation and is of particular importance for T-cell survival and expansion in the elderly (Kaltenberg et al. 2010; Yu et al. 2011; Lee et al. 2008).

Concerning the TCR, the zinc signal influences assembly of the TCR-activating complex by reduced recruitment of SHP-1 to the TCR activation complex and thus increased activation of the lymphocyte protein tyrosine kinase (Lck). TCR has no intrinsic kinase activity and depends on the Src-family tyrosine kinase, Lck, for signal transduction. Lck is one of the first kinases activated, is essential for phosphorylation of the ten ITAM motifs of the T-cell antigen receptor-signaling complex, and augments phosphorylation of the kinase ZAP70 (Palacios and Weiss 2004). The activation of ZAP70 phosphorylates downstream targets that activate MAPK pathways and cause T-cell activation.

Lck expression is upregulated in T cells of zinc-deficient mice (Lepage et al. 1999; Moore et al. 2001), and additional evidence also suggests direct regulation of Lck and sustained calcium influx (Yu et al. 2011). Zinc-provoked Lck activation occurs by linking two distinct protein interface sites. The N-terminal region of Lck is bound to the intracellular domains of the membrane proteins CD4 and CD8 (Huse et al. 1998; Lin et al. 1998). In a so-called “zinc clasp structure,” this interaction is stabilized by a zinc ion that is bound to two cysteine residues from each protein at the interface site between Lck and CD4/CD8 (Kim et al. 2003). Because CD4 and CD8 also bind to MHC with their extracellular domains, they are thus recruited in close proximity of the TCR-signaling complex, and this brings Lck close to its substrates.

Another zinc-dependent interface site is necessary for the homodimerization of Lck. Therefore, two zinc ions at the dimer interface of the SH3 domains stabilize the complex (Romir et al. 2007). The activation of Lck is a complex event, depending on two tyrosine phosphorylation sites. The first is tyrosine 394 situated in the so-called activation loop. It is transphosphorylated between Lck molecules upon activation, increasing kinase activity (Palacios and Weiss 2004; Brautigan et al. 1981). Lck activation is caused by the zinc-induced homodimerization by a fast zinc signal, bringing two Lck molecules into close proximity. The second phosphorylation occurs in the C-terminal negative regulatory site at tyrosine 505. According to phosphorylation, the kinase assumes a closed, inactive conformation. The transmembrane PTP CD45 selectively dephosphorylates tyrosine 505, thus



**Fig. 10.2** Zinc and T-cell signaling. Overview of T-cell receptor (TCR) signaling, interleukin-1 receptor (*IL-1R*), *IL-2R*, and *IL-4R* signaling in T cells. A direct induced zinc signal via Zip 6, by APC-mediated T-cell activation (highlighted in *dark grey*), is known to activate TCR signaling, by augmented ZAP phosphorylation, sustained  $Ca^{2+}$  influx, and inducing the active TCR signaling complex by binding of lymphocyte-specific protein tyrosine kinase *LCK*. *IL-2R* triggering in experiments leads to a zinc release (*dotted arrows*) from zinosomes, resulting in an increased intracellular zinc concentration (highlighted in *bold black*). Zinc mediates the inhibition (*inhibition arrow*) of signaling via interleukin-1 receptor-associated kinase (*IRAK*), or c-src tyrosine kinase (*Csk*)/protein kinase A (*PKA*)-mediated inhibition *LCK* in TCR signaling, but induces (*activation arrow*) zeta-chain (TCR)-associated protein kinase (*ZAP*), and protein kinase C (*PKC*) activity, mitogen-activated protein kinase (*MAPK*) signaling, and nuclear factor kappa B (*NF-κB*) phosphorylation. Increased intracellular zinc concentrations lead to an inhibition of calcineurin (*CN*) and avoid translocation into the nucleus (*dashed arrows*) of nuclear factor of activated T cells (*NFAT*). Besides zinc signals, zinc deficiency also influences T-cell signaling, i.e., *IL-4R* signaling. Zinc deficiency leads to a decreased phosphorylation of signal transducer and activator of transcription 6 (*STAT6*). *MKP* MAP kinase phosphatase, *CREB* cyclic adenosine monophosphate response element-binding protein

keeping *Lck* in a primed state. TCR signaling and *Lck* phosphorylation are regulated by numerous PTPs (Mustelin and Tasken 2003) that are all potential targets for zinc inhibition. Consequently, it cannot be predicted if this would result in preferential dephosphorylation of an activating or inactivating tyrosine by zinc in vivo. Zinc can activate *Lck* directly in the absence of phosphatases, most likely as a result of dimerization. Zinc-dependent homodimerization as well as

heterodimerization are specific for Lck, because the cysteine residues that form both intermolecular zinc-binding sites are not present in other Src kinase family members but are unique for this kinase (Romir et al. 2007; Kim et al. 2003).

An inhibition of TCR signaling and T-cell activation results from phosphorylation of the inactivating tyrosine 505 of Lck via c-src tyrosine kinase COOH-terminal Src kinase (Csk) (Chow et al. 1993). Zinc can interfere with these events in several ways. First, the fast zinc signal leads to an inhibition of Csk by reversible binding of zinc that is mediated by substituting for  $Mg^{2+}$  at one of its binding sites (Klein et al. 2002). Second, the activation of Csk in T cells can be observed via phosphorylation by PKA (Vang et al. 2001). Although zinc has no direct influence on PKA activity, it can inhibit AC transcription by a late zinc signal and thereby the formation of the PKA activator cAMP. Furthermore, also fast zinc signals influence cAMP by inhibition of PDE that can block degradation of cyclic nucleotides, leading to activation of PKA (von Bulow et al. 2007). Inhibition of Csk and AC promotes TCR signaling whereas PDE inhibition antagonizes it. The outcome on TCR signaling resulting from the modulation of this pathway by zinc in vivo remains to be investigated, however.

In response to TCR stimulation, another transcription factor, nuclear factor of activated T cells (NFAT), mediates the expression of many genes, such as IL-2. In resting cells, NFAT proteins are constitutively phosphorylated and are found in the cytoplasm. In response to TCR/CD28-mediated calcium signaling, NFAT is dephosphorylated by calcineurin (CN), a  $Ca^{2+}$ /calmodulin-dependent serine/threonine phosphatase, and translocates into the nucleus (Macian 2005). Iron and zinc are essential cofactors for the catalytic domain of CN, containing a  $Fe^{2+}$ - $Zn^{2+}$  binuclear center, but merely an inhibition of CN by zinc is described. Also, in vitro experiments show an inhibition at physiologically relevant zinc concentrations, ranging from 10 nM to 10  $\mu$ M (Huang et al. 2008; Takahashi et al. 2003). One of the kinases that keeps CN in its phosphorylated, inactive state in resting cells is phosphatidylinositol-3-kinase (PI3K) which is a negative regulator of glycogen synthase kinase-3-beta (GSK-3 $\beta$ ). Therefore, augmented PI3K activity can abrogate NFAT activity (Macian 2005).

Increased GSK-3 $\beta$  phosphorylation via a pathway involving PI3K is known wherein zinc acts through the PI3K pathway in various cell types (Eom et al. 2001; LaRochelle et al. 2001; Tang and Shay 2001). One possible explanation for this mechanism is increased enzyme degradation of phosphatase and tensin homologue deleted on chromosome 10 (PTEN) (Wu et al. 2003). A later study examining the IL-2-induced PI3K/Akt signaling pathway could not verify these results but showed an inhibition of PTEN (Plum et al. 2014). Here it has been indicated that late zinc signals seem to be necessary for the regulation the PI3K/Akt pathway, because under zinc deficiency the IL-2-induced Akt phosphorylation is diminished. Late zinc signals are known to upregulate phosphorylation of Akt at Ser473 and inhibit PTEN at sub-nanomolar concentrations ( $IC_{50}$  0.59 nM). This inhibition seems to be mediated by binding of zinc ions at its cysteine thiol at position 124 (cys124), which is essential for the catalytic activity of PTEN (Plum et al.). Thus, a modulation of this pathway occurs upstream of Akt, but

downstream of Jak1, because Stat5 signaling, which is also downstream of Jak1, is not influenced by zinc.

PTEN in general function as a dephosphorylase of phosphatidylinositol 3,4,5-trisphosphate, which is a product of PI3K, mediating the activation of PDK-1/Akt/GSK-3 $\beta$ . These results suggest a comparable activation of PI3K via zinc occurring in T cells. Inhibition of CN by zinc results in NFAT inactivation and reduction of TCR-mediated transcription simultaneously, whereas activation of PI3K signaling acts agonistically.

In addition to TCR signaling, zinc signals also affects signals originating from the IL-1 receptor. High zinc concentrations of about 100  $\mu$ M inhibit IL-1 $\beta$ -stimulated IFN- $\gamma$  production in primary human T cells and IL-1-dependent proliferation of murine T cells. Zinc incubation leads to reduced activity of IL-1 receptor-associated kinase (IRAK), which is a central kinase in the signaling pathways downstream of the IL-1 receptor. Zinc supplementation to zinc-deficient T cells has also regulatory effects on cytokine production. Zinc supplementation leads to a fast rise in intracellular zinc levels, that is, zinc flux, resulting from increased expression of cell membrane-located zinc transporters Zip 10 and Zip 12 because of the former zinc deficiency condition. Thus, IL-2 production and IL-2 mRNA expression are highly increased after IL-1 $\beta$  stimulation, concerning phosphorylation of MAPK p38, and NF- $\kappa$ B subunit p65 (Daaboul et al. 2012).

Moreover, the IRAK family of serine/threonine kinases is also involved in other pathways. IRAK4 participates in TCR-mediated NF- $\kappa$ B activation (Suzuki et al. 2006), although this observation is debated (Kawagoe et al. 2007). Thus, zinc can inhibit two central signaling pathways (TCR and IL-1 receptor) that are essential in the activation of T cells, by its effect on IRAK, making this a major target for negative regulation of T cells by zinc supplementation. However, the role of IRAK is not limited to merely T cells. The high rate of similarity between TLR-4 and IL-1 receptor signal transduction suggests IRAK inhibition for another mechanism by which zinc negatively influences TLR-4 signaling.

Zinc as a mediator of T-cell signal transduction has been known since the first reports of a potential role of this ion in signaling. Its interaction with PKC is identified as the biochemical basis of these observations (Csermely and Somogyi 1989). The PKC family are serine/threonine kinases that comprise several isoforms. They are differentiated into classical PKCs, which are activated by cofactors such as Ca<sup>2+</sup> and diacylglycerol, novel PKCs, which bind diacylglycerol but no Ca<sup>2+</sup>, and atypical PKCs, which do not interact with either cofactor. Each isoform has specific roles in the regulation of cellular functions; for example, in T cells, PKC $\theta$  is involved in the activation of several transcription factors in response to TCR/CD28 stimulation. In addition, a role for PKC $\alpha$  in proliferation and IL-2 production of T cells is known. Furthermore, several PKC isoforms are involved in survival of B cells, pre-B cell development, and induction of tolerance toward self-antigens (Tan and Parker 2003).

PKCs have four conserved domains (C1–C4) in common. The diacylglycerol binding C1 domain in the N-terminal regulatory part of PKC $\beta$ 1 contains two homologous regions with six cysteines and two histidines, forming a total of four

Cys<sub>3</sub>His zinc-binding motifs (Hubbard et al. 1991). No information about a differential effect of zinc on the different isoforms is available, and varying forms of C1 domains are present in conventional, novel, and atypical PKCs, indicating zinc binding to all known PKC isoforms (Tan and Parker 2003).

Late zinc signals affect multiple steps during PKC activation, for example, augmented PKC kinase activity, increased affinity to phorbol esters, and enhanced binding to the cytoskeleton and plasma membrane (Forbes et al. 1990; Wellinghausen et al. 1997b). Inhibition of these events can be mediated by membrane-permeable zinc chelators, such as TPEN. PKC itself can be a source for zinc release; thus, interaction between PKC and zinc is not limited to an effect of zinc on the PKC activation. PKC activation by lipid second messengers or thiol oxidation leads to measurable zinc release from the regulatory domain (Knapp and Klann 2000; Korichneva et al. 2002). In addition, PKC regulates the intracellular free zinc concentration and distribution. In T cells, phorbol ester treatment leads to a fast zinc signal, resulting in redistribution of zinc from the nucleus and mitochondria to the cytosol and microsomes (Csermely et al. 1987). Furthermore, treatment with phorbol esters such as PMA leads to an increase of free zinc in human T cells, whereas PHA stimulation, for example, leads to calcium increase (Haase et al. 2008), and the phorbol ester-induced differentiation of HL-60 cells into macrophages comprises a transitional increase of nuclear zinc depending on PKC $\beta$  (Glesne et al. 2006).

In general, a forecast of zinc effects on T cells is impossible because of the high number of zinc-related signaling pathways. Several studies concerning zinc status and T-cell function *in vivo* stated an increase of the delayed-type hypersensitivity reaction upon correction of zinc deficiency (Haase et al. 2006b). On the other hand, zinc supplementation diminishes the allogeneic reaction in the MLCs (Faber et al. 2004) and stabilizes regulatory T-cell function (Rosenkranz et al., unpublished data), indicating that zinc may have multiple, opposing functions, depending on its concentration and certainly also on the interaction with multiple other environmental factors.

B cells represent the main cells of humoral immunity and differentiate to antibody-producing plasma cells after stimulation. Nearly all the zinc-regulated signaling pathways already discussed are also important in B cells, such as tyrosine phosphorylation, PKC, MAPK, and activation of the transcription factors NFAT and NF- $\kappa$ B. In contrast to many of the cell types discussed earlier, mature B-cell proliferation and function are not as dependent on the organisms' zinc status as it is in T cells. Therefore, the influence of zinc deficiency on B cells is not comparable to the situation of T cells (Fraker and Telford 1997). Zinc itself seems to have no direct influence on the activity of B cells (Crea 1990). However, zinc-deficient patients, such as elderly and hemodialysis patients, show a reduced response to vaccination (Cakman et al. 1996; Bonomini et al. 1993). Rather, lymphopoiesis and pre-B-cell development are mainly affected by zinc deprivation *in vivo* (Fraker and King 2004). Zinc deficiency causes a greater loss of lymphoid tissue compared to other tissues, and thus T-cell development is impaired as well as that of B cells (Keen and Gershwin 1990). B cells and their precursors (especially pre-B cells and

immature B cells) are reduced in absolute number during zinc deficiency, but changes among mature B cells are only slight.

During development, lymphocytes are sensitive for apoptosis signals because of positive and negative selection mechanisms in the primary lymphoid organs, whereas mature B and T cells are apoptosis resistant, and therefore inactivated (known as “anergy”) in case of autoreactivity. A strict selection guarantees functionality and avoids autoreactive cells by eliminating the majority of newly formed cells by apoptosis. Zinc deficiency increases the rate of apoptosis within the B-cell population (Fraker et al. 2000) and leads to cell depletion. In contrast to zinc deficiency, low zinc levels have no influence on the cell-cycle status of precursor B cells and only modest influence on cycling pro-B cells (King and Fraker 2000). Thus, there are fewer naïve B cells during zinc deficiency that can react on neoantigens. Taking into account that the number of T cells is reduced during zinc deficiency also, and that most antigens are T-cell dependent, it is probable that in a state of zinc deficiency the body is unable to respond with antibody production in response to neoantigens. This assumption is consistent with findings showing a disturbed antibody production by B cells during zinc depletion (DePasquale-Jardieu and Fraker 1984). In accordance with this, a late zinc signal is essential for Stat6 phosphorylation via IL-4 induction, because Stat6 phosphorylation is diminished by zinc deficiency in B cells as well as in T cells (Gruber et al. 2013). Thus, T-cell reactivity is impaired, and B-cell activity and antibody production are affected as well, because IL-4 promotes the activation of early B cells and the immunoglobulin class switch toward IgE, and thereby further antibody specification, leading to a higher risk of parasitic infection (Kopf et al. 1993). Furthermore, zinc signals are important for IL-6-induced Stat3 phosphorylation, increased by zinc deficiency. IL-6 is responsible for the activation and final differentiation of B cells into plasma cells, and IL-6 overproduction is associated with autoantibody production. Many diseases, such as rheumatoid arthritis (RA) and plasma cell neoplasias, accompany reduced serum zinc levels, indicating potential co-effects of IL-6 overproduction and enhanced susceptibility of B cells because of zinc deficiency. This finding indicates that strict regulation is necessary to keep the immune system balanced (Gruber et al. 2013).

In addition, studies reveal that antibodies as a response to T-cell-dependent antigens are more sensitive to zinc deficiency than antibody production in response to T-cell-independent antigens (Moulder and Steward 1989). For example, zinc-deficient mice show reduced antibody recall responses to antigens for which they were previously immunized. This effect has been observed in T-cell-independent as well as in T-cell-dependent systems. Thus, immunological memory also seems to be influenced by zinc (Fraker et al. 1986). However, mature B cells are more resistant to zinc deficiency because of the high Bcl2 level. B-cell memory is less affected than the primary response (Fraker et al. 2000).

Late zinc signals influence several regulatory proteins, such as those from the Bcl/Bax family (Truong-Tran et al. 2001) and furthermore several aspects of apoptotic signal transduction. In this connection, zinc directly regulates the acidity of enzymes in the apoptotic cascade. First, the calcium-dependent endonuclease,

which mediates DNA fragmentation, is inhibited by zinc. However, this target is beyond the point of no return for programmed cell death, and inhibition could explain suppression of DNA fragmentation during apoptosis but not the effect on cellular survival.

Another important group of enzymes in apoptosis are cysteine-aspartic acid proteases, also known as caspases. They form a cascade to transduce initial apoptotic signals to the effector enzymes that mediate the organized cellular destruction which is characteristic of programmed cell death. In this process, inactive pro-caspases are activated by proteolytic cleavage. An additional regulatory mechanism is shown by inhibition of caspases-3, -6, and -8 by application of low micromolar zinc concentrations (Stennicke and Salvesen 1997). A half-maximal inhibitory concentration for caspase-3 was found below 10 nM (Maret et al. 1999). This value is clearly in the physiological range of free intracellular zinc, leading to the suggestion that endogenous zinc can inhibit caspase-3. Furthermore, recent studies showed a blockade of caspase-3-dependent apoptosis occurring in a rat heterotrophic heart transplant model, leading to increased allograft survival (Kown et al. 2000, 2002).

It is interesting that the function of mature B cells, which utilize the same signaling pathway as other immune cells, seems to be affected by zinc to a lesser magnitude. Even the reduced antibody production during zinc deficiency is based on reduced B-cell numbers whereas it is unaffected on a per-cell basis (Cook-Mills and Fraker 1993), which indicates an effect on cellular development rather than on function. One reason might be a difference in zinc homeostasis, making mature B cells less susceptible to conditions of limited zinc availability. Although B cells are highly susceptible to apoptosis during development, and zinc is one factor that influences these signals, mature B cells can tolerate comparable conditions by changes in zinc-regulating proteins, but also by changing the expression patterns of several other factors that regulate the cellular responsiveness to apoptotic signals.

In summary, nearly all immune cells are directly affected by zinc, especially by zinc deficiency, indicating that zinc is a main regulator of cellular function and signal transduction. However, the majority of these effects are characterized by investigations at isolated signaling pathways *in vitro*. Thus, further efforts must elucidate the *in vivo* situation, that is, which effects are actually physiologically relevant.

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# Chapter 11

## Zinc Signal in Inflammation

Ming-Jie Liu and Daren L. Knoell

**Abstract** Zinc (Zn) is essential to maintain normal health, to protect the host from damage, and to repair damage once it has occurred. Inflammation is typically defined as a response to cellular injury that is marked by capillary dilatation, leukocytic infiltration, redness, heat, and pain. Inflammation is designed to ultimately eliminate noxious agents, such as bacterial and viral pathogens, and to repair damaged tissue. The extent of inflammation that occurs following cellular injury must be tightly regulated so that danger is localized, damage is minimized, and recovery occurs expeditiously. Recent advances have established Zn as a critical component of the inflammatory response that is directly coupled to regulation of immune function. Importantly, Zn intake and the capacity to maintain normal Zn levels within the body are critical for proper regulation of immune function, host defense, and the extent of inflammation that occurs. Insufficient Zn levels within the body and particularly within key cells that are involved in host defense increase susceptibility to improper immune function, excessive inflammation, tissue damage, and failure to repair properly. As one leading example, Zn has been shown to directly regulate the extent of inflammation through interaction with the NF- $\kappa$ B signaling pathway, a pathway that is essential for normal immune function. In addition, Zn deficiency promotes chronic, systemic, low-grade inflammation associated with obesity and aging. It is anticipated that continued discovery of the many roles that Zn plays in controlling inflammation will yield meaningful insight for nutritional strategies that prevent or significantly reduce the morbidity and mortality associated with inflammation-based diseases.

**Keywords** Adipose tissue inflammation • Host defense • Infection • Inflammation • Innate immunity • NF- $\kappa$ B • Obesity • Sepsis • Zinc • Zinc deficiency

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## 11.1 Zinc and Inflammation-Based Disorders

The word *inflammation* comes from the Latin word “inflammo,” meaning “I set alight, I ignite.” Inflammation is a programmed biological response to harmful stimuli. For example, infection is caused by virulent pathogens that gain access within our body and inflammation is the ensuing response to the infection. It is an essential component of host defense and considered to be part of our innate immune system that is required for full recovery. Inflammation that occurs subsequent to cellular injury is marked by capillary dilatation, leukocytic infiltration, redness, heat, and pain. The extent of inflammation that occurs following cellular injury must be tightly regulated so that danger is localized, damage is minimized, and recovery occurs expeditiously. If left unchecked, inflammation can become self-perpetuating such that more inflammation is created in response to the existing inflammation, leading to chronic imbalance.

The trace element Zinc (Zn) is one of the most important and second most abundant trace elements in the human body. It has established roles in facilitating some of the most fundamental molecular functions that include catalyzing biochemical reactions, maintaining proper protein structure, and regulating cell signaling. In doing so, it is involved in governing required cellular operations that include transcription, translation, replication, and repair. Zn is essential for proper innate immune function and plays an indispensable role in modulating the host inflammatory response to noxious stimuli. The concomitant presence of low-grade systemic chronic inflammation that is associated with mild Zn deficiency further underscores the importance of Zn in the context of chronic inflammatory diseases. A strong correlation exists between low Zn levels and chronic diseases that include, but are not limited to, cardiometabolic disease, diabetes, Alzheimer’s disease, aging, and chronic obesity. Accordingly, Zn status in humans is important in the context of how the host responds to both acute and chronic stimuli that can provoke inflammation.

## 11.2 Zn and Acute Inflammation-Based Disorders

Nutritional Zn deficiency, which commonly occurs in socioeconomically challenged populations, is a leading cause of newly acquired bacterial pneumonia and diarrhea in children and the elderly (Caulfield et al. 2004). Many of these infections are caused by pathogens that, under normal circumstances, would not cause significant problems to the host. Upon pathogen exposure, Zn deficiency can increase susceptibility to acquiring infection and increase the duration and extent of infection once it has occurred (Black 2003). Importantly, Zn supplementation in these at-risk populations can significantly reduce the risk of developing newly acquired infections and can also improve morbidity and mortality if infection has already occurred (Yakoob et al. 2011).

The long-standing paradigm for understanding the pathophysiology of septic shock, often the result of bacteremia, is centered on a dysfunctional innate immune system, wherein excessive and uncontrolled inflammation leads to direct tissue and organ injury (Cornell et al. 2010; Wynn et al. 2010). Multiple gene expression studies have consistently shown that septic shock is characterized by widespread repression of gene families that either directly participate in Zn homeostasis or directly depend on Zn homeostasis for normal function (Cvijanovich et al. 2008, 2009; Shanley et al. 2007; Wong et al. 2007, 2010). These observations suggest that altered Zn homeostasis may contribute to the pathogenesis associated with septic shock. Indeed, low serum Zn concentrations have been documented in pediatric septic shock, and nonsurvivors have lower serum Zn concentrations compared with survivors (Wong et al. 2007). Low serum Zn concentrations have also been reported in other forms of critical illness in both adults and children (Besecker et al. 2011; Cvijanovich et al. 2009; Heyland et al. 2008). These observations support the notion that Zn supplementation may be a low-cost and effective therapeutic strategy for septic shock (Knoell and Liu 2010). In animal models of sepsis, Zn supplementation confers a survival benefit, and the survival benefit correlates with enhanced bacterial clearance as well as modulation of excessive inflammation (Bao et al. 2010b; Knoell et al. 2009; Nowak et al. 2012). Two recent studies that involve children with either pneumonia or bacteremia in developing countries demonstrated that Zn supplementation significantly reduced infection-related complications, including mortality (Srinivasan et al. 2012; Bhatnagar et al. 2012). A study involving critically ill children in the United States tested the efficacy of oral Zn supplementation, in combination with oral selenium, glutamine, and metoclopramide, as a means of preventing nosocomial infection or sepsis (Carcillo et al. 2012). There was no efficacy in the overall study population for the primary study endpoint (time to development of nosocomial infection/sepsis), but a secondary analysis restricted to patients with baseline immune dysfunction suggested a beneficial effect in reducing nosocomial infections. Clinical trials demonstrate that antioxidant cocktails administered either enterally or parenterally improve patient survival (when evaluated in aggregate: relative risk 0.72, 95 % confidence interval 0.62–0.85,  $P < 0.0001$ ). Zn is one component of the cocktail administered in most of these trials. Importantly, all published trials are limited in scope because of substantial patient heterogeneity. In fact, very few study subjects had sepsis. Further complicating interpretation of findings, Zn was exclusively studied in combination with other micronutrients thereby making it impossible to distinguish its individual impact. In addition, Zn status before critical illness was not determined, so that it was unclear whether Zn deficiency existed as a premorbid condition. Accordingly, Zn supplementation as an adjunctive therapeutic strategy for septic shock remains an intriguing concept that requires further testing.

The common cold, which is caused by a constellation of more than 20 viruses, occurs throughout the world and across all populations. The morbidity and corresponding cost associated with the cold are substantial. Zn is now commonly marketed as a “cure” for the common cold and sold over the counter. The use of Zn is predicated on past studies that have demonstrated that when Zn supplements,

typically in the form of lozenges, are administered within the first 24 h of symptoms, the severity and duration of cold symptoms are significantly reduced (Prasad et al. 2000, 2008; Eby et al. 1984). Further analysis in study subjects revealed a significant decrease in soluble interleukin (IL) receptor antagonist and soluble ICAM-1 plasma levels that indicated a reduction in the extent of inflammation associated with cold symptoms. Similar studies that also aimed at determining whether Zn indeed does prevent the occurrence of a cold have yielded contradictory findings, which may in part be explained by the design of these studies that varied significantly. Taking all studies into consideration, a recent meta-analysis that evaluated only randomized, double-blind, placebo-controlled trials concluded that Zn supplementation can reduce the duration and severity of the common cold when therapy is started within the first 24 h of the onset of a cold (Singh and Das 2011).

### 11.3 Zn and Chronic Inflammation-Based Disorders

Alcohol use and abuse are highly prevalent within both developed and underdeveloped countries and impose a substantial health burden to society. Alcohol abuse is the third leading cause of preventable death in the United States and is associated with numerous chronic disease states (Mokdad et al. 2000). Importantly, alcohol abuse is also a cause of nutritional deficits, including Zn deficiency. Zn deficiency caused by alcoholism has been shown to increase oxidative stress within vital organs including the lung, thereby causing dysregulation of inflammation, innate immune function, and macrophage phagocytosis, and, hence, bacterial clearance (Joshi et al. 2009). This point is important because alcoholics have a higher incidence of acquiring pneumonia, resulting in increased lung injury and mortality (Mehta et al. 2013). Based on these findings, which are strongly supported by animal models, future studies that involve Zn supplementation in patients that suffer from alcoholism and are prone to life-threatening infection, are warranted.

Aging, and particularly deficits in Zn deficiency in the elderly, is now recognized as a potential cause of the chronic inflammation that is observed in a substantial proportion of the elderly population (Mocchegiani et al. 2012; Kanoni et al. 2010). Aging is associated with gradual impairment of immune function and a corresponding systemic low-grade chronic inflammation (Wilcock and Griffin 2013). Remarkable similarities between the hallmarks of Zn deficiency and aging-related immune dysfunction have been observed. Zn supplementation may improve age-related immune dysfunction and chronic inflammation (Wong and Ho 2012). Further, many age-related diseases, including cancer, cardiovascular disease, type 2 diabetes, osteoporosis, and Alzheimer's disease, are associated with low-grade chronic inflammation. Alzheimer's disease (AD) is a progressive neurodegenerative disease, and chronic inflammation has been shown to be a pathological hallmark of the most vulnerable regions of the AD brain (Griffin 2013). Compared to other vital organs, the brain is highest in Zn content. An evolving

paradigm is that bioavailable pools of Zn, or a lack thereof, may regulate the immune response and inflammation in the brain: this is based on previous studies that have revealed abnormally low Zn levels within key compartments of the brain (Molina et al. 1998; Kapaki et al. 1989). In support of this concept, a placebo-controlled clinical trial revealed that Zn supplementation stabilized cognitive function whereas the placebo group continued to deteriorate (Maylor et al. 2006). Although it is plausible that alterations in Zn homeostasis in the brain may contribute to AD pathogenesis, the molecular mechanisms that account for these disturbances remain to be identified (Vasto et al. 2008).

Obesity is recognized as a worldwide public health problem (Finucane et al. 2011). In the United States, obesity has become epidemic, and the proportion of obese people is among the highest (more than 30 %) in the world (Flegal et al. 2010). Obesity is a prevalent risk factor for multiple disorders, including insulin resistance, type 2 diabetes, and cardiovascular diseases (Berrington de Gonzalez et al. 2010; Zheng et al. 2011; Lumeng and Saltiel 2011; Ferrante 2007). The obese population chronically consumes energy-dense foods that are rich in fats but lacking in vitamins and micronutrients (Finucane et al. 2011). As a result, these individuals commonly experience micronutrient deficiencies (Garcia et al. 2009). In obese people, decreased dietary Zn intake has been shown to inappropriately alter immune function, lipid metabolism, and insulin production (Costarelli et al. 2010). In contrast, weight loss has been shown to significantly improve metabolic function and increase circulating Zn levels (Voruganti et al. 2010). Adipose tissue has emerged as an active participant in regulating endocrine function through the secretion of adipokines, especially leptin (Ouchi et al. 2011). Accumulating evidence suggests that chronic inflammation, which originates in adipose tissue, plays a crucial role in the pathogenesis of obesity-related metabolic dysfunction (Hotamisligil 2006). Activated M1 macrophages are recruited into adipose tissue and have a central etiological role in the development of chronic tissue inflammation, leading to the secretion of adipokines and cytokines (Chawla et al. 2011; Xu et al. 2003; Weisberg et al. 2003; Ouchi et al. 2011). This secretion is in part the result of liberation of saturated free fatty acids from adipocytes, which bind to macrophage Toll-like receptor-4 (TLR-4) and activate inhibitor of  $\kappa$ B kinase- $\beta$  (IKK- $\beta$ ) and nuclear factor- $\kappa$ B (NF- $\kappa$ B) (Suganami et al. 2007; Arkan et al. 2005). Inhibition of IKK and NF- $\kappa$ B has been proposed as the mechanism whereby antiinflammatory agents such as salicylates reverse insulin resistance (Yin et al. 1998; Yuan et al. 2001). Obese people have lower circulating Zn levels, but it is unknown how and why this happens. Further, their plasma Zn levels are inversely correlated with systemic inflammatory markers (Costarelli et al. 2010; Voruganti et al. 2010). Based on these observations, our group recently reported that Zn deficiency may be a factor that contributes to the development of systemic chronic inflammation associated with obesity through immune dysregulation (Liu et al. 2013a). C57BL/6 mice were randomly assigned to receive either a 60 % high-fat diet or control diet for 6 weeks, followed by further subdivision into Zn-deficient and matched Zn-sufficient groups for 3 additional weeks. Although Zn deficiency did not influence the extent of visceral adiposity,

insulin resistance, or systemic inflammation in the obese mice, Zn deficiency significantly augmented circulating leptin levels and leptin signaling in the liver. Furthermore, Zn deficiency increased the expression of the macrophage-specific markers ADAM8 and CD68, indicating an increase in adipose macrophage infiltration and the exacerbation of tissue inflammation. These findings demonstrate that Zn deficiency contributes to metabolic and immune dysregulation in obesity *in vivo*.

Obesity is also a significant risk factor for developing diabetes. Zn metabolism is altered in diabetic patients, and the Zn transporter ZnT-8 has recently been identified as an etiological cause. A single-nucleotide polymorphism (SNP) located within the SLC30A8 gene that codes for the protein ZnT-8 in conjunction with SNPs within metallothioneins (MT) have been implicated as a cause of type 2 diabetes (Jansen et al. 2009). Similarly, recent advances using  $\beta$ -cell-specific *Slc30a8* deficiency (ZnT8KO mice) demonstrated that SLC30A8 regulates hepatic insulin clearance and that its genetic defect contributes to the pathogenesis of type 2 diabetes (Tamaki et al. 2013). The pathogenesis of diabetes mellitus is multifactorial, but establishment of this novel pathway through alteration of Zn metabolism and corresponding inflammation has fostered new approaches to the treatment of this disease.

## 11.4 Zn Deficiency and Immune Disorders

Zn deficiency was first recognized in humans more than 50 years ago and was originally observed in adult males in developing areas of the Middle East (Prasad et al. 1963). Nutritional Zn deficiency results in complex immune disorders, as perhaps best exemplified by a rare autosomal recessive disease called acrodermatitis enteropathica (AE) that is a cause of severe Zn deficiency. It is now known that mutations harbored within the Zn transporter gene *SLC39A4* (ZIP4), which is abundantly expressed in the intestine and is responsible for Zn uptake from the gut, is centrally involved in the pathogenesis of this condition (Kury et al. 2002). Treatment of AE requires lifelong Zn supplementation. Typically, 1 to 3 mg/kg Zn gluconate or sulfate is administered orally each day. Clinical improvement, including restoration of proper immune function, occurs before any significant change in the plasma Zn levels, usually within days to weeks of initiating treatment. Clinically, the serum Zn levels and alkaline phosphatase levels are monitored every 3 to 6 months. As already discussed, Zn deficiency is a leading contributing factor to immune dysfunction, thereby increasing susceptibility to acquiring infectious-based pneumonia, diarrhea, and malaria (Caulfield et al. 2004). Zn supplementation has been reported to prevent or reduce the burden of these infectious diseases. In addition to bacterial infection, Zn is also important in regulating the extent of inflammation in the setting of viral infection. Zn supplementation has been shown to enhance the response to interferon therapy in the setting of intractable chronic hepatitis C (Takagi et al. 2001) and also to

decrease the extent of common debilitating adverse side effects associated with treatment in chronic hepatitis C patients (Ko et al. 2005).

## 11.5 The Impact of Inflammation on Zn Metabolism

The acute-phase response (APR) to stress, trauma, and infection results in the robust induction of APR proteins in the blood as part of the inflammatory response. The purpose of this response is to help inhibit the growth of pathogens, modulate the extent of inflammation, and activate coagulation. There are also a number of proteins whose concentration is significantly reduced. This group of “negative” acute-phase response proteins includes (but is not limited to) albumin, antithrombin, and transferrin. The rationale for reduced synthesis of these proteins is to divert critical amino acids toward the synthesis of positive APRs. As previously stated, Zn is required for gene transcription and translation of new proteins. Zn homeostasis rapidly and dynamically changes in humans in response to inflammation as an extension of the acute-phase response. The primary and most apparent alteration observed is the rapid decline in blood Zn levels, which is commonly referred to as hypozincemia. Previously it has been shown in a human endotoxemia model that blood cytokine levels increase [tumor necrosis factor (TNF)- $\alpha$  and IL-6] with a concomitant precipitous decrease in blood Zn levels within the first hour following systemic endotoxin injection. Importantly, in these subjects the decrease in Zn levels could not be explained by changes in circulating albumin levels, plasma protein binding, or urinary excretion (Gaetke et al. 1997). Based on this seminal work and that of others, it is now clear that the ensuing APR results in redistribution of Zn into vital organs, such as the liver and lung, as well as immune cells (Liuzzi et al. 2005; Beker Aydemir et al. 2012; Liu et al. 2013b). The rationale behind Zn redistribution during the host response supports the concept of “nutritional immunity,” akin to iron deprivation, whereby the body shunts micronutrients away from pathogens following infection, thereby affording a competitive host advantage (Kehl-Fie and Skaar 2010; Liuzzi et al. 2005). Zn redistribution into the liver also facilitates the reprogramming of hepatic protein synthesis in a manner that is beneficial to the host. Our group recently discovered a novel negative feedback loop whereby extracellular Zn, in addition to enhancing protein synthesis, is deliberately shunted into leukocytes and parenchymal cells for Zn to specifically decrease the extent of inflammation as part of the resolution process following systemic infection (Bao et al. 2010b; Knoell et al. 2009; Liu et al. 2013b). Importantly, deficient Zn levels before the onset of infection result in exuberant inflammation, excessive collateral damage in vital organs, and increased mortality. Collectively, these findings indicate that Zn plays multiple pivotal roles during the early stages of the host inflammatory response to potentially overwhelming challenges.

Zn is an essential structural component of many proteins, as perhaps best exemplified by zinc-finger motifs, that is required for normal molecular function

of proteins within and outside cells. Cellular Zn homeostasis is regulated by two families of Zn transporters and also by the Zn-binding proteins known as metallothioneins (MT), a family of cysteine-rich proteins that bind up to seven Zn molecules per protein. In mammals, the Zn transporter proteins are encoded by two solute-linked carrier (SLC) gene families that include 14 SLC39 (aka ZIP) family members and 10 SLC30 (aka ZnT) family members. SLC39 transporters increase cytosolic Zn content by promoting extracellular uptake or release from subcellular organelles, whereas SLC30 transporters function as counter-regulators that decrease intracellular Zn levels (Lichten and Cousins 2009). The MT protein family serves as an intracellular buffer that helps to maintain intracellular Zn levels and participates in the regulation of labile Zn content (Maret 2006).

Protein-bound Zn, which largely includes a pool that is avidly bound to zinc-finger motifs, is typically believed to be less exchangeable, especially during stress and inflammation. In sharp contrast the labile Zn pool, also referred to as bioavailable Zn, is defined as the Zn that is loosely bound and easily exchanged within and outside of the cell, as well as between subcellular organelles. Using Zn-specific intracellular probes it has been shown that the labile Zn pool is observed as a speck-like pattern that is contained within intracellular vesicles, which have been referred to as zincosomes (Haase and Rink 2007). Consistent with the hypozincemia observed following systemic infection or endotoxin challenge, the concentration of labile Zn within cells rapidly increases in response to inflammatory mediators. As one example, it has been shown that labile Zn rapidly accumulates in hepatocytes in an IL-6-dependent manner following a systemic endotoxin challenge. Similarly, our group observed a rapid increase of labile Zn within monocytes in response to endotoxin and bacterial sepsis (Liu et al. 2013b). Other groups observed a similar sequestration of Zn within macrophages in response to intracellular bacteria and fungi (Botella et al. 2011; Subramanian Vignesh et al. 2013). Collectively, these findings indicate that Zn is naturally sequestered in key cells by a variety of diverse pathogens and danger signals as the host mounts a defense response. The labile pool that is rapidly sequestered following systemic insult then becomes critical in transmitting essential signals within the cell through direct and indirect interaction with key signal transduction pathways. In the context of Zn fluctuations or intracellular translocation, mobilization of labile Zn is viewed as a “Zn signal.” Numerous examples have recently emerged demonstrating that Zn signals are propagated through Zn binding with regulatory sites on proteins that possess enzymatic activity. Indeed, labile Zn has been shown to regulate the function of many proteins, including kinases and phosphatases, many of which are instrumental in orchestrating the inflammatory response. Depending upon the protein and the environment wherein it resides, Zn has the potential to either inhibit or activate protein function. Direct inhibition of catalytic activity by Zn is often through transient binding to specific amino acids (cysteines or histidines) that reside within reactive sites, as perhaps best exemplified by protein tyrosine phosphatases (PTP) (Haase and Maret 2003), PKC (Nishida et al. 2009), and IKK $\beta$  (Liu et al. 2013b).



Changes in cellular labile Zn content are primarily navigated by Zn transporter proteins. A clearer picture has emerged in recent years suggesting two broad classifications of Zn transporters, those that are constitutively expressed for house-keeping functions and those which are induced for specialized function. Clearly it requires an orchestrated effort of both types, working in concert, to maintain balance, particularly in the setting of stress and inflammation. ZIP4 perhaps provides the best example of a constitutively abundant transporter that is required to maintain normal homeostatic function through its capacity to continuously absorb dietary Zn from the intestinal tract. In contrast, other Zn transporters, for example, ZIP8 and ZIP14, are not naturally abundant but are rapidly induced at the onset of danger signals (Besecker et al. 2008; Liuzzi et al. 2005). The function of these Zn transporter proteins is often transcriptionally regulated following insult and subsequent activation of transcription factors and corresponding upstream kinase pathways (Liu et al. 2013b; Haase and Rink 2009). In addition to modulation of gene expression, Zn transporters can be controlled through posttranscriptional regulation. The best example of this has been shown through CK2-dependent phosphorylation of ZIP7, thereby allowing Zn release from the endoplasmic reticulum as a key component of cell proliferation (Taylor et al. 2012). How subsequent downstream Zn-dependent signaling occurs in this setting remains to be resolved. In the setting of inflammation, Zn metabolism can also be modulated through alternative mechanisms. For example, the metal-response element-binding transcription factor-1 (MTF-1) functions as a cellular Zn sensor that coordinates the expression of genes involved in Zn homeostasis as well as protection against metal toxicity and oxidative stress (Laity and Andrews 2007). When Zn begins to accumulate in the cytosol, MTF-1 senses increased metal load because the Zn-finger domain of MTF-1 directly (and reversibly) binds to Zn. This metalloregulatory protein then adopts a DNA-binding conformation and translocates into the nucleus, where it binds to metal-response elements in specific gene promoter regions of target genes that lead to transcriptional activation. MTF-1 function is believed to be essential in regulating Zn homeostasis (Botella et al. 2011). Although substantial progress has been made, a full account of the dynamic redistribution of Zn that occurs particularly at the subcellular level in response to danger signals requires further investigation. With the continued development of new and improved Zn sensors, it is anticipated that many new discoveries in this emerging area will become possible.

## 11.6 Zn Signaling in Response to Systemic Infection

Inflammation is a primordial response designed to protect the host against pathogen invasion or body injury (Takeuchi and Akira 2010). Upon recognition of pathogen-associated molecular patterns, the Toll-like receptor (TLR) pathway becomes activated in immune cells that include monocytes, macrophages, and dendritic cells (Kawai and Akira 2010). TLR signaling initiates recruitment of adaptor molecules such as TRIF, TIRAP, and MyD88 (Takeuchi and Akira 2010). In

turn, the inflammatory signal is transmitted coordinately through a series of molecular events that involve the IRAK family, TRAF6 and TAK1, leading to activation of I $\kappa$ B kinase (IKK) and mitogen-activated protein kinases (MAPKs) (Johnson and Lapadat 2002; Hayden and Ghosh 2008). Activation of the IKK complex, which includes IKK $\alpha$ , IKK $\beta$ , and NEMO, results in I $\kappa$ B phosphorylation and degradation, thereby allowing phosphorylated NF- $\kappa$ B dimers to translocate into the nucleus and bind  $\kappa$ B sites located within target gene promoters to activate transcription (Hayden and Ghosh 2008). NF- $\kappa$ B regulates an array of inflammatory genes, including cytokines, chemokines, and adhesion molecules, and plays a central role in inflammation.

Coordination of the initial host response to infection through regulation of the NF- $\kappa$ B pathway must be tightly regulated to maintain proper immune balance, thereby maximizing host defense while simultaneously minimizing collateral damage (Liew et al. 2005). To achieve this precise balance, multiple counter-regulatory elements have evolved within these pathways, including but not limited to I $\kappa$ B $\alpha$  (Chiao et al. 1994), MyD88s (Burns et al. 2003), IRAKM (Kobayashi et al. 2002), and A20 (Boone et al. 2004). The expression and function of many of these negative regulators, including I $\kappa$ B $\alpha$ , A20, MyD88s, and IRAKM, are themselves activated by TLR ligands and thus constitute classic negative regulatory feedback loops that ensure attenuation of the TLR response in a threshold-dependent manner (Ruland 2011). The negative feedback pathways have evolved to control the extent of innate immune activation and the resolution of inflammation (Ruland 2011).

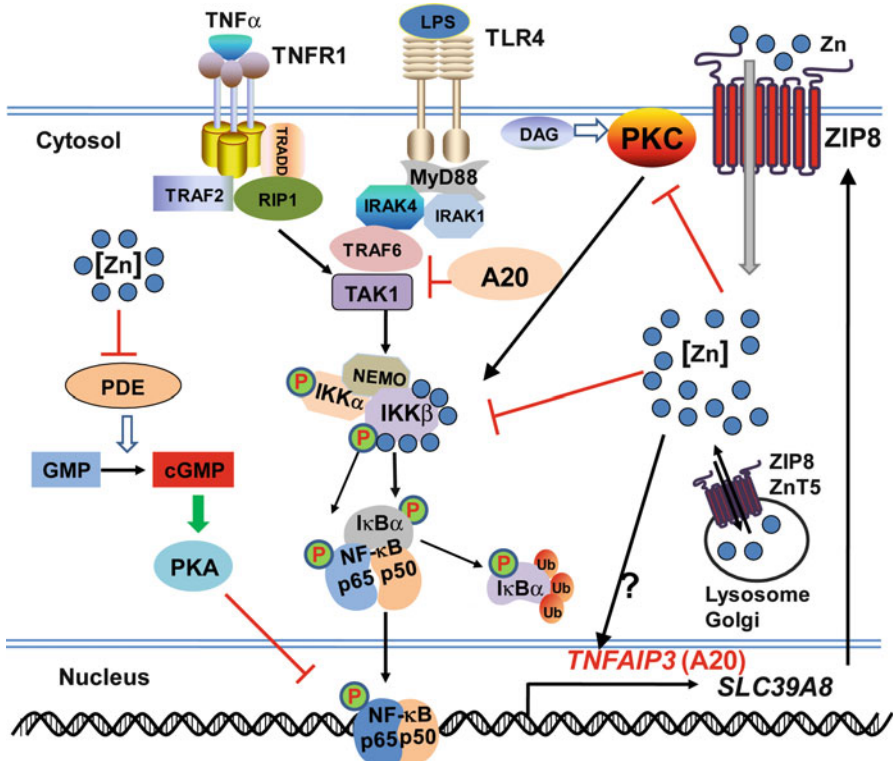
Nutritional Zn deficiency in a mouse model of multibacterial sepsis (using a technique called cecal ligation and puncture) results in augmentation of the initial pro-inflammatory response, increased bacterial burden, increased vital organ damage, and higher mortality (Liu et al. 2013b; Bao et al. 2010b; Knoell et al. 2009). Further, prophylactic Zn supplementation reduces bacterial load and improves survival (Nowak et al. 2012). These studies that use relevant animal models are consistent with clinical studies conducted on critically ill and septic humans. (Wong et al. 2007; Heyland et al. 2008; Besecker et al. 2011; Cvijanovich et al. 2009). Collectively, these findings strongly support the hypothesis that Zn intake, Zn metabolism, and Zn signaling are essential for proper host defense and innate immune function.

Although much remains to be learned regarding the key signaling pathways and molecules at play with Zn in the setting of sepsis, new findings have emerged indicating that Zn metabolism and immune function are directly coupled to Zn transporter function. In particular, it was discovered that ZIP8 functions as a critical negative feedback regulator that directly couples Zn metabolism to the regulation of innate immunity (Fig. 11.1). At the onset of inflammation, NF- $\kappa$ B directly activates the expression of ZIP8, which then localizes to the plasma membrane, thereby mediating Zn uptake. The new pool of Zn that enters the cytosol via ZIP8 then goes on to inhibit IKK $\beta$  kinase activity by binding to a specific coordination site located within the kinase domain of this protein, thereby attenuating the pro-inflammatory response. This concept is also supported by past observations demonstrating that Zn has the capacity to directly interact with IKK (Jeon et al. 2000). Consistent with

these findings, fetal fibroblasts obtained from ZIP8 transgenic hypomorphic mice exhibit decreased Zn uptake and an increased inflammatory response in response to TNF- $\alpha$  or IL-1 $\beta$ , thereby confirming the role of ZIP8 as a negative regulator of the NF- $\kappa$ B pathway (Liu et al. 2013b) (Galvez-Peralta et al. 2012). Consistent with this, the redistribution of Zn into the liver during the acute-phase response was significantly decreased in ZIP14 (*Slc39a14*<sup>-/-</sup>) knockout mice in response to lipopolysaccharide (LPS)-induced endotoxemia (Beker Aydemir et al. 2012). This finding is intriguing when taking into account that ZIP8 and ZIP14 genes emerged in land animals from a single gene in sea animals approximately 420 million years ago. This evolutionary divergence supports the notion that specialized Zn transporter function(s) may have evolved as a consequence of new environmental pressures capable of provoking inflammation (Girijashanker et al. 2008). These findings also provide novel mechanistic insight that links Zn metabolism via specialized Zn transporters to innate immune function, and in so doing enriches the list of regulatory mechanisms that control NF- $\kappa$ B and TLR signaling. Three other mechanisms have been reported that may also explain the inhibitory effects of Zn on inflammation (Fig. 11.1). A hypothetical model suggests that increased expression of A20, which is a de-ubiquitinase and negative regulator of NF- $\kappa$ B, is modulated by Zn (Prasad et al. 2011). Although provocative, there is yet no direct experimental evidence demonstrating that Zn directly regulates the activity of A20. A second mechanism demonstrating the inhibitory effect of Zn on NF- $\kappa$ B has shown that Zn is an inhibitor of cyclic nucleotide phosphodiesterase (PDE). The inhibition of PDE leads to elevation of the cyclic nucleotide cGMP, which activates PKA and subsequently inhibits NF- $\kappa$ B (von Bulow et al. 2007). In a similar fashion, Zn has also been shown to inhibit PMA-mediated PKC translocation to the plasma membrane through binding to a Zn finger-like motif found in PKC. When this occurs, NF- $\kappa$ B activity is indirectly inhibited in mast cells (Nishida et al. 2009). Although some of the latter findings require confirmation in validated in vivo settings, taken together these findings demonstrate that Zn-mediated regulation of the host response to inflammation is complex and that Zn may possess the capacity to interact at multiple points within individual pathways.

The capacity for Zn, in concert with ZIP8, to inhibit NF- $\kappa$ B activation is conserved across different cell types that directly control the innate immune response and include both immune (monocytes and macrophages) and nonimmune cells (lung epithelia). However, ZIP8 is not expressed by every cell in the body. The regulatory function of Zn in coordinating the inflammatory response across all cells within the body is presumed to be broad in scope, requiring the activity of many proteins. Further, there exist an impressive number of conserved Zn transporter proteins in mammals, which would imply that there are many yet to be identified specialized functions for Zn transporters in human health and disease. Consistent with this, loss of the Zn exporter *Slc30a5* (*Znt5*) in mast cells resulted in increased labile Zn and suppressed NF- $\kappa$ B signaling in response to Fc $\epsilon$ RI stimulation (Nishida et al. 2009).

Additional pathways have been shown to be modulated by Zn and therefore may also play important roles in controlling inflammation. As one example, Zn has been



**Fig. 11.1** Zn signaling pathways in the Toll-like receptor (*TLR*)-mediated inflammatory response. Zn inhibits the *TLR* and *NF-κB* pathway through interaction with *IKK*, *A20*, *PDE*-*cGMP*-*PKA*, and *PKC*. *IKK* I kappa B kinase, *PDE* phosphodiesterase, *PKA* protein kinase A, *cGMP* cyclic guanosine monophosphate, *PKC* protein kinase C, *[Zn]* labile Zn pool

shown to be involved in the activation of multiple signaling pathways that are important in cell activation following Toll-like receptor (*TLR*) stimulation. *TLRs* constitute a family of proteins with a key role in the innate immune system. *TLRs* are single, membrane-spanning, noncatalytic receptors, usually expressed in sentinel cells such as macrophages and dendritic cells, that recognize structurally conserved molecules derived from microbes. Once these microbes have breached physical barriers they are recognized by *TLRs*, which activate immune cell responses. In particular, activation of *TLR4* triggers Zn-mediated signaling in a *MyD88*-dependent manner in monocytes. This signal is transmitted through the *MAPK* pathway signaling and ultimately results in phosphorylation of *IKKα/β*, thereby modulating *NF-κB* signaling (Haase et al. 2008). In contrast, the same Zn signal also results in inhibition of *TRIF*-mediated activation of *IRF3*. Based on these observations, one can conclude that labile Zn can simultaneously affect *TLR* signaling at multiple levels and within different pathways (Brieger et al. 2013). In addition to *TLR*-mediated *MAPK* signaling, Zn, or a lack thereof, has recently

been shown to modify the JAK-STAT3 pathway, thereby modulating the acute-phase response (work from our group, in review). In the setting of sepsis, Zn deficiency increased the acute-phase response through alteration of JAK-STAT signaling in the liver and significantly enhanced the production of acute-phase reactants including serum amyloid A. Upon inspection of whole exome expression profiles and subsequent computational pathway analysis, we identified that Zn deficiency significantly increased JAK-STAT3 signaling in hepatocytes whereas Zn supplementation reversed this effect. The detailed molecular mechanism(s) that fully account for these observations remain under investigation.

Oxygen radicals are important mediators of the inflammatory response, and excessive radical production is known to be a cause of multiple inflammatory-based disorders. Reactive oxygen species (ROS) are produced within cells as part of the host defense and are vital to maintain proper immune function to eliminate invading pathogens (Fang 1997), with an essential role in the intracellular killing of microorganisms by macrophages (Subramanian Vignesh et al. 2013). Increased cellular accumulation of ROS is counterbalanced by antioxidant molecules, thereby preventing excessive damage to the host. The ability of Zn to inhibit oxidative processes and reduce ROS formation is well established (Puertollano et al. 2011). Although Zn is not considered a direct antioxidant molecule, it possesses antioxidant properties through its ability to protect protein sulfhydryl groups or reduce hydroxide formation from  $H_2O_2$  through the antagonism of redox-active transition metals, such as iron and copper (Powell 2000). Zn sequestration from eukaryotic cells or subcellular organelles results in the increased production of ROS. For example, Zn deprivation from phagosomes in activated macrophages elevated intraphagosomal ROS generation by NADPH oxidase and enhanced the clearance of the intracellular pathogen *Histoplasma capsulatum* (Subramanian Vignesh et al. 2013). In a clinical trial involving the impact of Zn supplementation in healthy elderly subjects, those taking supplemental Zn exhibited a higher plasma antioxidant index (represented by ascorbate equivalent units) with a corresponding decrease in oxidative stress markers, as well as the cytokine concentrations in plasma, including CRP, IL-6, macrophage chemo-attractant protein 1 (MCP-1), and vascular endothelial cell adhesion molecule 1 (VCAM-1) (Bao et al. 2010a). Based on these findings and many others, the role of Zn as an antioxidant has great potential to prevent or treat inflammatory-based diseases and warrants considerably more study.

## 11.7 Zn Signals in Immune Cells

Zn deficiency compromises the function of immune cells that are directly involved in regulating the extent of inflammation, including leukocytes (Haase and Rink 2009). It is also important to recognize that Zn deficiency also alters the phenotype of nonimmune cell types (for example, epithelia, endothelia, hepatocytes, and fibroblasts) that are also integral components of the inflammatory response. Zn

deficiency alters the function of multiple immune cells, including monocytes, neutrophil granulocytes, natural killer (NK), and T- and B cells, and therefore Zn is critical to the function of both the innate and adaptive immune systems. It is important to recognize that Zn signaling and trafficking are highly dependent on the cell type and the specific environment in which cell activation occurs. In recent years, new data have emerged that have increasingly proven that Zn transporters have very specific functions within cells that comprise both the innate and adaptive immune systems. In the setting of inflammation, there remains much to be known when considering the similarities and differences in Zn metabolism that exist between different immune cell types.

As one example, Zn supplementation has been shown to inhibit the secretion of pro-inflammatory cytokines by primary human monocytes in response to stimulation with LPS (von Bulow et al. 2005). Similarly, Zn protects animals from LPS-induced liver injury (Zhou et al. 2004). Diverse results have been observed in other cell types whereby LPS-mediated TLR4 stimulation of dendritic cells decreased cytosolic free Zn through the suppression of ZIP6. The downmodulation of intracellular labile Zn was an instrumental component of dendritic cell activation. Accordingly, Zn supplementation or overexpression of the Zn transporter ZIP6 inhibited LPS-induced upregulation of major histocompatibility complex class II and costimulatory molecules (Kitamura et al. 2006). In T cells, it was revealed that ZIP8 possesses alternative functions when compared to monocytes and macrophages. In particular, T-cell (CD3<sup>+</sup>) activation upregulated ZIP8, which then translocated to the lysosome membrane, promoting labile Zn release, which resulted in the increase of IFN- $\gamma$  production (Aydemir et al. 2009). TCR activation in CD4<sup>+</sup> T cells is also known to induce Zn influx through ZIP6, resulting in augmentation of TCR signaling (Yu et al. 2011). In mast cells, FcR-mediated activation induced a burst of free Zn in the cytosol, which then enhanced cytokine secretion (Yamasaki et al. 2007); and in macrophages, a robust increase of free Zn following release from MT during *Mycobacterium tuberculosis* infection resulted in Zn accumulation within the mycobacterial phagosome to presumably toxify this compartment to prevent bacterial growth (Botella et al. 2011). Similarly, recent advances that involve Zn function in macrophages in response to the fungus *H. capsulatum* have revealed the importance of intracellular Zn trafficking in this setting. In particular, Zn trafficking and sequestration are regulated by the Zn transporters *Slc30a4* (ZnT4) and *Slc30a7* (ZnT7) within the Golgi apparatus (Subramanian Vignesh et al. 2013). Fewer studies have examined the sustained effects of Zn or Zn deficiency in vivo. In a ground-breaking study conducted years ago it was revealed that the thymus is the most sensitive primary tissue to chronic Zn deficiency. By day 50 of suboptimal Zn intake, the thymus had atrophied by 36 % with significant loss of pre-T cells via apoptosis such that T-cell lymphopoiesis was disrupted. Significant reductions were also noted in the erythropoietic population by day 50. Conversely, the marrow maintained myelopoiesis and B cell lymphopoiesis during this time. Importantly, the changes observed in gene expression for cytokines, DNA repair enzymes, Zn transporters, and signaling

molecules indicated that cells of the immune system attempt to adapt to the stress of suboptimal Zn (Fraker and King 2004; King et al. 2005).

From this constellation of observations, a clearer picture has emerged that supports the concept that Zn trafficking and metabolism are unique to specific immune cell types, guided by specific Zn transporters reserved for specialized function. Further, Zn-mediated responses to diverse danger signals that provoke the primordial inflammatory response occur through distinct mechanisms which are not shared by all cell types. In other words, Zn metabolism, in response to danger signals, does not adhere to a “one size fits all” policy but rather is customized to accommodate unique circumstances under a variety of conditions, presumably to better serve the host.

## 11.8 Concluding Remarks

Exciting advances in the field of Zn biology have substantially improved our understanding of the role of Zn and its metabolism with respect to immune function and the inflammatory response to danger signals. Clearly, Zn is absolutely required to support normal immune function. Changes in Zn concentration, particularly suboptimal concentrations, have profound influence on how the host responds to danger signals that provoke inflammation through activation of the innate immune system. Similarly, substantial progress has been made in demonstrating that Zn supplementation, particularly within Zn-deficient populations, improves immune function and helps to prevent the incidence and extent of inflammatory-based disease. For many years it was not clear exactly how Zn mediates its beneficial effects; however, it is now becoming much better defined that adequate amounts of Zn are required to help “buffer” the host inflammatory response in virtually all cells involved in immune function. When sufficient amounts of Zn are present, the host response is optimal and danger is minimized, affording a greater chance for full recovery from the insult. When Zn content within and outside of cells is insufficient, alteration of the host response occurs through numerous changes in vital cell-signaling pathways. These effects are in large part the result of changes in Zn metabolism, via transporters, which subsequently alter the manner by which Zn can directly interact with target proteins that alter cellular phenotype. The impact of these changes can be quite substantial because these subtle molecular events influence virtually all the most fundamentally important cellular processes, which include transcription, translation, replication, and cellular repair. Importantly, prolonged Zn deficiency, caused by insufficient intake or inherent deficits in Zn metabolism, alters the acute inflammatory response but also creates an environment that prevents normal repair, thereby paving a pathway for chronic inflammation. Multiple examples whereby Zn deficiency perpetuates a viscous cycle of unresolved inflammation leading to chronic disease states have now emerged. The implications of these consequences are enormous when considering that Zn deficiency is highly frequent within undeveloped and developed countries.

Continued advances in state-of-the-art technologies will help to further establish the role of Zn in inflammatory-based disease. Clearly, the mosaic created so far has revealed that Zn metabolism in mammals is highly sophisticated. Continued effort must be placed on translational studies that bridge basic and clinical science so that fundamental discoveries can have meaningful impact for patients who may benefit from Zn supplementation. The cost of Zn treatment is highly affordable, and its safety profile is very favorable. Based on this, one can envision an expansion of Zn supplementation strategies whereby we prevent the incidence of acute and chronic inflammatory diseases across a broader range of susceptible populations.

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# Chapter 12

## Zinc Signal in Growth Control and Bone Diseases

Toshiyuki Fukada, Shintaro Hojyo, and Bum-Ho Bin

**Abstract** Zinc (Zn) deficiency syndrome, discovered only half a century ago, first showed the physiological significance of this trace mineral. More recent studies have shown that a disturbance in Zn homeostasis in mammals is primarily characterized by growth retardation, accompanied by impaired bone metabolism, and Zn is now recognized as an indispensable metal required for systemic growth. Zn homeostasis is controlled by a family of Zn transporters, transmembrane proteins that regulate the intracellular availability of Zn. Recent studies using Zn transporter knockout mice and human genetic data have revealed a novel role for Zn as a signaling factor that affects multiple cellular processes, impacting numerous biological and physiological functions. These studies have also shed light on the mechanisms by which Zn regulates mammalian systemic growth. In this chapter, we present an overview of the roles of Zn and Zn transporters in regulating systemic growth and bone metabolism, focusing on the role of Zn as a signaling molecule that fine-tunes multiple intracellular signaling pathways.

**Keywords** Bone • Ehlers–Danlos syndrome • Growth • Osteogenesis imperfecta • Signal transduction • Transporter • Zinc

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## 12.1 Zinc and Systemic Growth

Zinc (Zn) is an essential micronutrient that is indispensable for the cellular activities of all organisms (Broadley et al. 2007; Prasad 2008; Sugarman 1983). The total human body content of Zn, 2 to 4 g (Rink and Gabriel 2000), is primarily located in the bone, muscle, brain, and liver (Wapnir and Chemical Rubber Company 1990), where it supports the structural conformation and catalytic functions of enzymes and transcription factors. Recent *in silico* studies predicted that approximately 2,800 proteins (corresponding to 10 % of the human proteome) are potential Zn-binding proteins (Andreini et al. 2006), consistent with an important role for Zn in human biological functions. Zn deficiency occurs when Zn levels are insufficient to meet the physiological requirements of organisms, resulting in their abnormal growth. An estimated 2 billion people in the developing world suffer from various diseases associated with Zn deficiency (Prasad 1995). In children, it causes growth retardation, delayed sexual maturation, increased susceptibility to infection, and diarrhea, resulting in the death of approximately 800,000 children per year in the world (Hambidge and Krebs 2007).

Somatic growth is primarily regulated by the endocrine factors growth hormone (GH) and insulin-like growth factor-I (IGF-I), whose main sources are the pituitary gland and liver, respectively (MacDonald 2000; Nilsson et al. 2005; Procter et al. 1998). Circulating GH stimulates the liver to produce IGF-I, which in turn binds to the IGF receptor (IGFR) to promote somatogenic cell proliferation via IGFR-mediated tyrosine kinase activation (De Meyts et al. 1994). GH and IGF-I also regulate longitudinal bone growth by controlling the endochondral ossification process, a well-organized sequence of events involving chondrocyte differentiation at the growth plate (Kronenberg 2003). Thus, the GH-IGF axis plays a critical role in systemic growth.

Zn deficiency causes a marked reduction in circulating GH and IGF-I concentrations (MacDonald 2000; Roth and Kirchgessner 1994; Underwood 1996), leading to dwarfism, shortened growth plate width (Rossi et al. 2001), and decreased food intake (Giugliano and Millward 1984). The pituitary gland has a relatively high Zn content, which has been shown to promote hormone function (Henkin 1976). Several studies have demonstrated that Zn deficiency leads to impaired GH secretion, resulting in low concentrations of circulating GH (Root et al. 1979; Roth and Kirchgessner 1994). Interestingly, when Zn-deprived rats are treated with exogenous GH, the stunted growth is not corrected despite the increased circulating levels of GH, whereas Zn treatment effectively reverses the growth impairment (Prasad et al. 1969). Similar findings are obtained in Zn-deficient animals treated with IGF-I, in which the growth retardation phenotype persists despite increased serum IGF-I levels (MacDonald 2000). Intriguingly, Zn deficiency leads to reduced food intake, suggesting that inadequate dietary protein or energy intake could contribute to the reduced growth. However, the decreased levels of IGF-I in Zn-deficient rats are not overcome with a high protein-containing diet but are corrected with a low-protein plus Zn-containing diet (Cossack 1986). Furthermore,



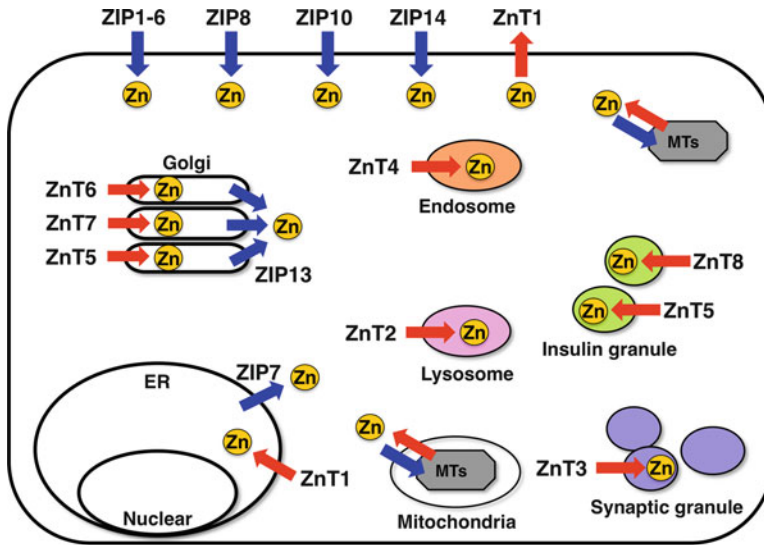
force-feeding rats a Zn-depleted diet results in decreased circulating IGF-I levels, whereas a Zn-adequate diet containing a similar level of dietary energy intake promotes normal growth (Roth and Kirchgessner 1994). Moreover, in humans, Zn deficiency-induced serum IGF-I reduction was shown to occur independently of the total energy intake (Cossack 1991). Thus, Zn deficiency affects circulating GH and IGF levels, although the administration of exogenous GH or IGF-I does not correct Zn deficiency-associated growth defects.

The GH-IGF axis is also known to positively regulate bone growth (Ohlsson et al. 1998). Similar results to those just described were observed in the bone growth of Zn-deficient rats (Cha and Rojhani 1997). Hypophysectomized Zn-deficient rats implanted with GH-containing miniosmotic pumps in the hindlimb were found to be hyporesponsive to exogenous GH, resulting in poor growth of the tibial epiphyseal cartilage. This finding indicated that the impaired bone growth in Zn-deficient rats is resistant to GH treatment, and was consistent with an earlier report indicating that Zn-deficient rats are hyporesponsive to GH, resulting in reduced levels of circulating IGF-I (Oner et al. 1984). Thus, it is likely that the failure of GH to stimulate somatic growth under Zn-deficient conditions is caused by the limited availability of intracellular Zn, which is independent of the GH-IGF status. Given that Zn increases IGF-I synthesis (Yamaguchi and Hashizume 1994) and potentiates IGF-I-mediated actions (Matsui and Yamaguchi 1995), these findings collectively suggest that intracellular Zn affects the hormone- or growth factor-mediated signaling cascade(s) required for somatic growth.

## 12.2 Zn Transporters in Growth and Bone Homeostasis

Zn homeostasis is tightly controlled by the coordinated actions of Zn transporters and metallothioneins (Fig. 12.1) (Fukada and Kambe 2011; Gaither and Eide 2001; Kambe et al. 2004). Mammalian Zn transporters are divided into two major families, SLC39s/ZIPs and SLC30s/ZnTs, which have opposing roles in the regulation of intracellular Zn levels. ZIPs increase cytoplasmic Zn by promoting Zn transport from extracellular fluid or intracellular organelles into the cytoplasm; ZnTs reduce cytoplasmic Zn by promoting Zn transport from the cytoplasm into the extracellular space or intracellular organelles (Fukada and Kambe 2011). Although the molecular mechanisms by which Zn transporter's functions are largely unknown, sequence analysis of these transporters does not suggest that they transport Zn using ATP-dependent processes. Instead they are postulated to promote Zn transport by facilitated diffusion, secondary active transport, or by symport (see Chap. 3).

Molecular and genetic studies in rodents and humans have revealed important roles of Zn transporters in physiological regulatory mechanisms, including growth control (Table 12.1). Mice with a targeted disruption of ZIP1, ZIP2, or ZIP3 show no overt abnormalities under dietary Zn-adequate conditions, but under Zn-limited conditions during pregnancy, the embryos from single (*Zip1*, *Zip2*, or *Zip3*)- and double (*Zip1/Zip2* or *Zip1/Zip3*)-knockout mice display abnormal development



**Fig. 12.1** Subcellular localization of Zn transporters and metallothioneins. Localization and potential functions of Zn transporters from the SLC39/ZIP (blue) and SLC30/ZnT (red) families, and intracellular metallothioneins (MTs), based on currently available information. *Arrows* show the predicted direction of Zn mobilization. *ER* endoplasmic reticulum

compared to those from wild-type mice. In addition, *Zip8* hypomorphic and *ZnT1*-null mice exhibit embryonic lethality (Andrews et al. 2004; Galvez-Peralta et al. 2012; Wang et al. 2011). These studies suggest that Zn is a critical nutritional factor for normal embryonic development. Furthermore, *Lethal milk* mutant mice, which have a loss-of-function mutation of *ZnT4*, produce Zn-deficient milk (Huang and Gitschier 1997), and a similar abnormality is observed in patients with a *ZNT2* loss-of-function mutation (Chowanadisai et al. 2006). These findings clearly demonstrate that Zn is crucial for postnatal growth, indicating that Zn transporters in the mammary gland are required for the transfer of Zn into milk for lactation (Fig. 12.2a). Similarly, Zn ingested through dietary intake or breast milk is absorbed through the action of several intestinal Zn transporters (Wang and Zhou 2010). Human ZIP4, encoded by the *SLC39A4* gene, is expressed on the apical membrane of polarized enterocytes in the intestine and plays a crucial role in intestinal Zn transport (Fig. 12.2b). Loss-of-function mutations in this gene cause a rare and fatal recessive disorder called acrodermatitis enteropathica (AE) (Kury et al. 2002; Wang et al. 2002). Mouse ZIP4 is essential for early embryonic development, in which it is postulated to transfer Zn via the visceral yolk sac into the embryo, and is later required for the uptake of dietary Zn (Dufner-Beattie et al. 2007). Once absorbed, Zn is transported through the blood to cells in various tissues. Zn transporters on the cell surface such as ZIP14 play crucial roles in intracellular Zn accumulation (Fig. 12.2c), and Zn transporters on the membranes of intracellular organelles, such as ZIP13, contribute to Zn distribution within cells

**Table 12.1** Genetic evidence for the biological significance of Zn transporters

Gene symbol	Protein name	Mutation type	Phenotypes and disorders	References
SLC39A1	ZIP1	KO	Abnormal embryonic development	Dufner-Beattie et al. (2006)
SLC39A2	ZIP2	KO	Abnormal embryonic development	Peters et al. (2007)
SLC39A3	ZIP3	KO	Abnormal embryonic and T-cell development	Dufner-Beattie et al. (2005)
SLC39A4	ZIP4	KO	Embryonic lethal	Dufner-Beattie et al. (2007), Kury et al. (2002), Wang et al. (2002)
		Mutation	Acrodermatitis enteropathica	
SLC39A5	ZIP5	Mutation	Autosome dominant non-syndromic high myopia	Guo et al. (2014)
SLC39A8	ZIP8	Mutation	Impaired multiorgan organogenesis and hematopoiesis	Galvez-Peralta et al. (2012), Kim et al. (2014), Liu et al. (2013)
		KO	Abnormal innate immune function Osteoarthritis	
SLC39A10	ZIP10	KO	Abnormal early B-cell development	Miyai et al (2014), Hojyo et al (2014)
			Impaired humoral immune response	
SLC39A13	ZIP13	KO	Connective tissue dysplasia	Fukada et al. (2008), Giunta et al. (2008)
		Mutation	Spondylocheiro dysplastic Ehlers–Danlos syndrome	
SLC39A14	ZnT14	KO	Growth retardation and impaired gluconeogenesis	Hojyo et al. (2011)
SLC30A1	ZnT1	KO	Embryonic lethal	(Andrews et al. 2004; Bruinsma et al. 2002)
			Abnormal vulva formation	
SLC30A2	ZnT2	Mutation	Low Zn in milk	Chowanadisai et al. (2006), Itsumura et al. (2013)
SLC30A3	ZnT3	KO	Prone to seizures	Adlard et al. (2010), Cole et al. (1999)
			Alzheimer's disease-like	
SLC30A4	ZnT4	Mutation	<i>lethal milk: lm</i>	Huang and Gitschier (1997)
			Low Zn in milk	
SLC30A5	ZnT5	KO	Growth retardation, osteopenia, hypodontia, and male-specific cardiac death	Inoue et al. (2002), Nishida et al. (2009)
			Impaired mast cell functions	

(continued)

**Table 12.1** (continued)

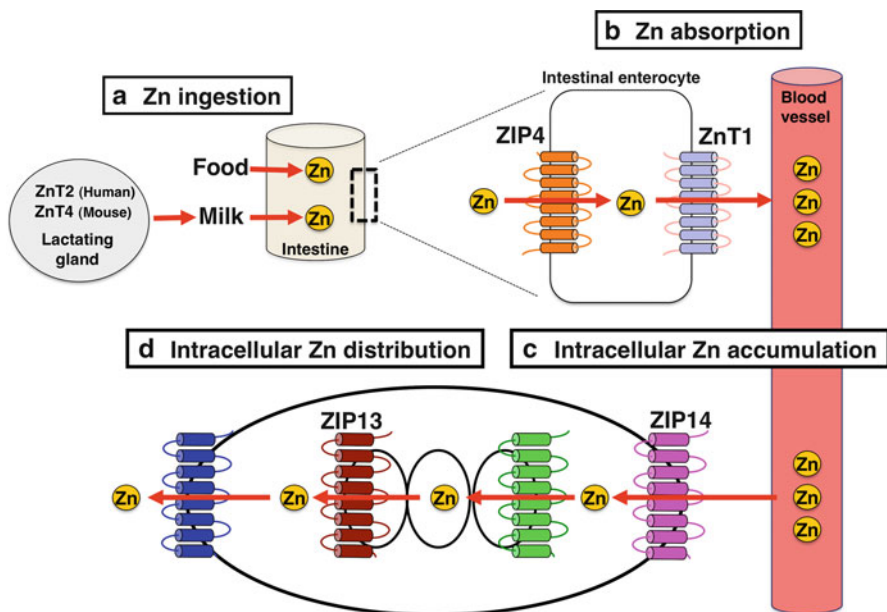
Gene symbol	Protein name	Mutation type	Phenotypes and disorders	References
SLC30A7	ZnT7	KO	Reduced body fat accumulation	Huang et al. (2012), Huang et al. (2007)
			Susceptible to diet-induced glucose intolerance and insulin resistance	
SLC30A8	ZnT8	KO	Type 2 diabetes mellitus	Lemaire et al. (2009), Nicolson et al. (2009), Tamaki et al. (2013), Wenzlau et al. (2007)
		SNP	Type 1 and 2 diabetes mellitus	
SLC30A10	ZnT10	Mutation	Parkinsonism, Dystonia, Hypermanganesemia, Polycythemia, Chronic Liver Disease	Quadri et al. (2012), Tuschl et al. (2012)

(Fig. 12.2d). Thus, the coordinated actions of the various Zn transporters are important for Zn uptake and maintenance throughout the body (Wang and Zhou 2010), and are indispensable for normal growth control in mammals.

### 12.3 Zn Signaling and the Zn Signal Axis

Zn has been known to primarily function as a cofactor for cellular proteins, nucleic acids, carbohydrates, and lipids. Enzymes with a Zn atom in their reactive center are widespread in metabolism, such as alcohol dehydrogenase in humans (Maret 2013). More than 300 proteins contain Zn-interacting regions such as zinc-finger motifs, RING fingers, or LIM domains, which influence cellular responses by coordinating ions. However, several reports have recently demonstrated that the Zn mobilized by Zn transporters acts as a signaling molecule similar to calcium and cAMP. This “Zn signal” (see Chaps. 2 and 3) regulates a variety of intracellular signaling pathways (Fukada et al. 2011b; Maret 2011), including growth factor- (Haase and Maret 2003), antigen receptor- (Hojyo et al. 2014; Nishida et al. 2009), apoptotic pathway (Miyai et al. 2014), and JAK-STAT-mediated pathways (Kitabayashi et al. 2010; Yamashita et al. 2004).

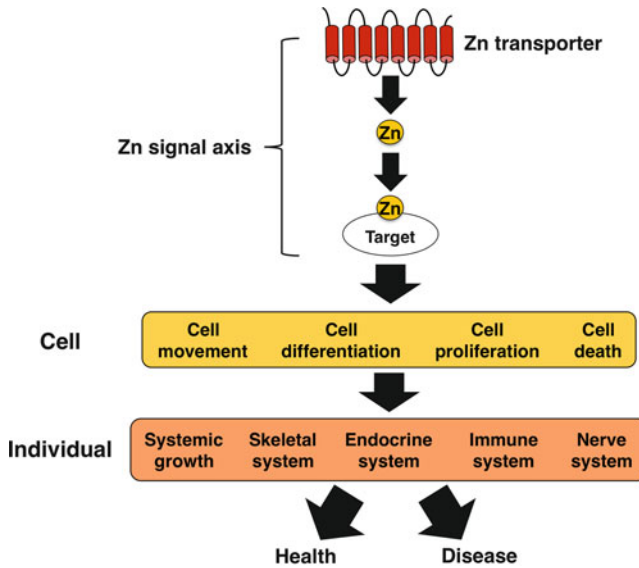
These recent reports have also led to an increased understanding of the physiological significance of Zn. For example, the Zn transporter ZIP6 induces the epithelial mesenchymal transition (EMT) in the zebrafish gastrula organizer by regulating the nuclear translocation of SNAIL, a transcriptional suppressor of *E-cadherin*. This finding suggests that the Zn signal depends on the induction of Zn transporter expression to regulate the early developmental process. In addition, mice deficient in *Zip13*, *Zip14*, *ZnT5*, or *ZnT7* exhibit impaired growth (Fukada et al. 2008; Hojyo et al. 2011; Huang et al. 2007; Inoue et al. 2002), and *ZnT5* is



**Fig. 12.2** Zn homeostasis mediated by Zn transporters is essential for the control of normal mammalian physiology. Appropriate levels of Zn are ingested from the daily diet by adults, or from breast milk during lactation. **a** ZnT2 (Chowanadisai et al. 2006) or ZnT4 (Huang and Gitschier 1997) in the mammary gland transports Zn into milk for lactation in both humans and mice, respectively. **b** Zn absorption through intestinal Zn transporters such as ZIP4 (Dufner-Beattie et al. 2007; Wang et al. 2002; Weaver et al. 2007) and ZnT1 (Wang et al. 2009) is the critical event determining Zn levels in the body. **c** Zn is transported into peripheral or somatic cells by ZIP14 (Hojo et al. 2011) or other ZIPs to maintain intracellular Zn levels. **d** Intracellular Zn is then delivered to organelles by intracellular Zn transporters such as ZIP13 (Fukada et al. 2008) and ZnT5 (Inoue et al. 2002), which fine-tune the intracellular distribution of Zn. Each step is critical for the maintenance of mammalian health; a disruption in any one of them can cause disorders associated with Zn deficiency, including growth retardation, even in the presence of normal serum Zn levels (Fukada et al. 2008; Hojo et al. 2011)

also involved in the allergic response through mast cell activation (Nishida et al. 2009) (See Chap. 5). Collectively, these reports strongly suggest that Zn transporters act not only to maintain Zn homeostasis but also to provide signaling factors to control a variety of cellular functions. Importantly, each individual Zn transporter defines a signal transduction cascade that regulates specific target molecules to elicit cellular effects. Within these pathways, the Zn regulatory system is referred to as the “Zn signal axis” (Fukada et al. 2013) (Fig. 12.3).

In the following section, we introduce the physiological significance of Zn signaling and two Zn signal axes that are involved in systemic growth and bone metabolism.



**Fig. 12.3** Different “Zn signal axes” affect distinct signaling pathways to promote and control cellular functions. Each Zn signal axis targets a specific molecule. This mode of Zn action exerts a variety of cellular functions by selectively regulating distinct signaling molecules. Therefore, the disruption of a Zn signal axis can lead to pathogenesis in the absence of redundant machinery

## 12.4 Zn Signals in Growth and Bone Metabolism

The Zn concentration is relatively high in bone, cartilage, and teeth (Bergman and Soremark 1968), and Zn has been proposed to stimulate bone formation and mineralization (Yamaguchi and Gao 1998). As just described, Zn is absorbed in the intestine, circulates in the blood, and is transported to cells in the peripheral tissues. However, the mechanism by which the Zn signal regulates systemic growth and bone metabolism is currently unclear. Because systemic growth is controlled by the endocrine system, it is hypothesized that the Zn signal plays pivotal roles in the regulation of endocrine signaling.

The analysis of ZIP13 and ZIP14 knockout mice (Fukada et al. 2008; Hojyo et al. 2011) revealed that these transporters control Zn signal axes that selectively regulate the intracellular signaling cascades required for bone metabolism and systemic growth. Defects in either the ZIP13 or ZIP14-mediated axis lead to impaired bone homeostasis or growth, and the specific signaling cascades of both axes are nonredundant.

### ***12.4.1 ZIP13-Mediated Zn Signaling Controls Bone and Connective Tissue Formation***

ZIP13, encoded by the *Slc39a13* gene, is a homodimeric intracellular Zn transporter that plays a critical role in the development of hard and connective tissues (Bin et al. 2011, 2014; Fukada and Kambe 2011; Fukada et al. 2008).

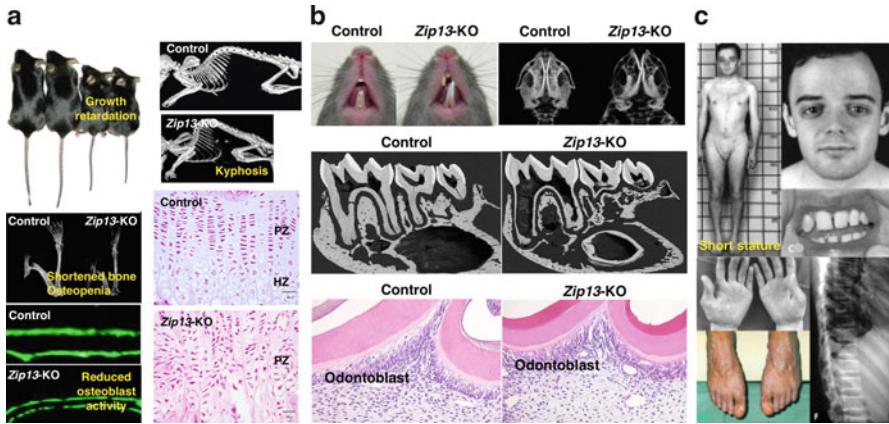
#### **12.4.1.1 Abnormal Formation of Bone, Skin, and Teeth in *Zip13*-KO Mice**

*Zip13*-KO mice exhibit multiple phenotypes, including growth retardation, progressive kyphosis, abnormal bone and teeth formation, increased skin fragility, and reduced levels of corneal stromal collagen at 3 to 4 weeks of age (Fig. 12.4a). Endochondral ossification is a process required for the proper development of long bones and vertebrate growth (Kronenberg 2003). At the growth plate of long bones, resting chondrocytes differentiate into proliferative chondrocytes with a columnar morphology, and then stop dividing, followed by maturation into pre-hypertrophic and then hypertrophic chondrocytes. *Zip13*-KO mice also exhibit a significant reduction in the length of their long bones. The hypertrophic chondrocytes in their growth plates are rarely observed; instead, irregularly organized proliferative chondrocytes are present (Fig. 12.4a). Furthermore, *Zip13*-KO mice exhibit reduced osteoblast activity, consistent with the observed osteopenia (Fig. 12.4a), whereas the osteoclast activity appears normal. These findings indicate that ZIP13 controls the normal differentiation and function of chondrocytes and osteoblasts during the growth phase of long bones.

*Zip13*-KO mice also display odontological morphological aberrations, including the abnormal development of incisor teeth, including deformity, malocclusion, and breakage, the reduced formation of molar root dentine, and the reduced volume of both the mandible and the alveolar bone, although the molar crowns are morphologically unchanged (Fig. 12.4b). Thus, the *Zip13*-KO-associated abnormalities appear to occur selectively in tissues of mesenchymal origin (Fukada et al. 2011a; Fukada et al. 2008). Collectively, ZIP13 has indispensable roles for the proper development of both hard and connective tissues such as bone, teeth, and skin.

#### **12.4.1.2 ZIP13 and Human Disease**

The phenotypes of *Zip13*-KO mice are reminiscent of human Ehlers–Danlos syndrome (EDS), a group of genetic recessive disorders that affect connective tissue development (Steinmann and Royce 2002; Steinmann et al. 2002), and of osteogenesis imperfecta (OI), which affects bone and teeth formation (Rauch and Glorieux 2004) (Fig. 12.4c). Patients with spondylocheiro dysplastic EDS (SCD-EDS) display short stature, downslanting palpebral fissures, hypodontia, fragile skin, osteopenia,



**Fig. 12.4** ZIP13 plays a role in regulating systemic growth and bone homeostasis. **a** Growth retardation, kyphosis, osteopenia, shortened long bones, reduced osteoblast activity, and abnormal cartilage development in the *Zip13*-KO mouse. *PZ* proliferative zone; *HZ* hypertrophic zone. **b** Abnormal teeth and craniofacial development in the *Zip13*-KO mouse. *Zip13*-KO mice develop abnormal incisor teeth, and exhibit reduced molar root dentin and mandible bone volume. Abnormal arrangement of odontoblasts is observed. **c** Clinical features of an SCD-EDS patient possessing the ZIP13/SLC39A13 mutation, including short stature, anti-mongoloid eye slant with lack of periorbital tissue, missing upper lateral incisors, wrinkled skin, severe varicosity, and vertebral flattening with sclerosis of the vertebral endplates

flattened or biconcave vertebral bodies with flaky irregularity of the endplates, mild dysplastic changes at the metaphyses of the long bones and phalanges, bluish or greyish sclerae, and varicose veins (Fig. 12.4c). DNA analysis revealed that these patients possess a homozygous loss-of-function point mutation in *ZIP13* involving a G-to-A transition at nucleotide 221, resulting in a mutant ZIP13 with a G64D substitution (Fukada et al. 2008; Bin et al. 2014). Furthermore, another EDS-associated loss-of-function mutation in *ZIP13* was identified as a deletion encompassing nucleotides 483 to 491 (FLA amino acids deletion: *ZIP13*  $\Delta$ FLA) by a genome-wide SNP scan and sequence analysis (Giunta et al. 2008), clearly confirming the importance of ZIP13 for growth and bone homeostasis in humans.

### 12.4.1.3 Regulation of the BMP/TGF- $\beta$ Signaling Pathway by ZIP13

Consistent with the multiple defects observed in *Zip13*-KO mice, ZIP13 was found to be expressed in osteoblasts, proliferative chondrocytes, odontoblasts, and skin fibroblasts. Both primary osteoblasts and chondrocytes isolated from *Zip13*-KO mice show impaired gene marker expression, indicating that ZIP13 affects their differentiation and function. Microarray analysis indicated that the BMP/TGF- $\beta$  signaling cascade is significantly dysregulated in *Zip13*-KO cells. Indeed, BMP4-induced *Msx2* gene transcription is reduced in ZIP13-deficient primary osteoblasts, and this phenotype is reversed by the introduction of wild-type ZIP13, but not by



the G64D mutant ZIP13, demonstrating that the G64D substitution results in loss of function. Further analysis revealed that the SMAD phosphorylation levels are unchanged, but the nuclear translocation of SMAD is disrupted in BMP4-treated *Zip13*-KO osteoblasts (Fukada et al. 2008). BMP and TGF- $\beta$  are coordinated local paracrine regulators of bone formation and elongation, and of systemic growth (Akhurst 2004; Cao and Chen 2005; Cobourne and Sharpe 2003). Human genetic studies also support the pivotal role of these regulators in hard and connective tissue development (Akhurst 2004; Mizuguchi et al. 2004). Collectively, these findings provide evidence of a functional link between ZIP13-mediated Zn signaling and BMP/TGF- $\beta$ -mediated growth regulation.

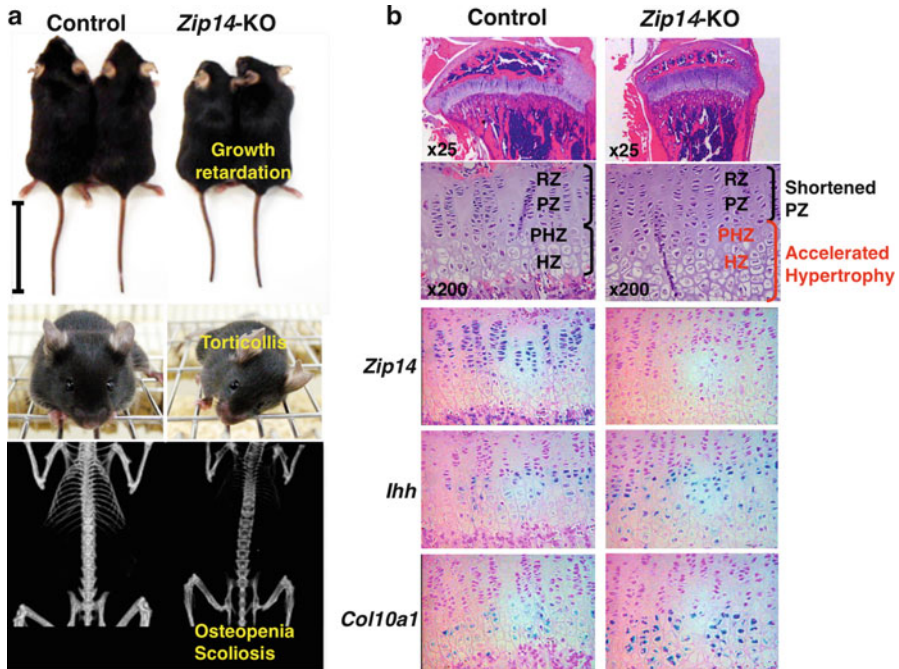
A series of biochemical analyses revealed that ZIP13 possesses eight putative transmembrane domains and unique hydrophilic regions at both its N- and C-termini, which face the luminal side of the Golgi, and that ZIP13 forms a homodimer and contributes to Zn influx from the Golgi to the cytosol (Bin et al. 2011). We also demonstrated the molecular pathogenic mechanism of SCD-EDS caused by two different mutant ZIP13 proteins, G64D and  $\Delta$ FLA. Both mutant proteins are susceptible to rapid degradation via the valosin-containing protein (VCP)-linked ubiquitin proteasome pathway without the effects on dimer-formation (Bin et al. 2014). The inhibition of degradation pathways rescued the protein expression levels, resulting in improved intracellular Zn homeostasis. Together, these findings suggest that intracellular Zn levels and its distribution regulated by ZIP13 are critical for the normal control of mammalian bone and connective tissue development as well as systemic growth control.

## 12.4.2 ZIP14-Mediated Zn Signaling Controls Bone Formation

ZIP14, encoded by the *Slc39a14* gene, is a cell membrane-localized Zn transporter that plays a critical role in regulating systemic growth and bone metabolism (Hojyo et al. 2011).

### 12.4.2.1 Abnormal Bone Formation in *Zip14*-KO Mice

*Zip14*-KO mice exhibit dwarfism, torticollis (wry neck), scoliosis, osteopenia, and shortened long bones (Fig. 12.5a). The finding that *Zip14* mRNA is highly expressed in bone tissues (Fig. 12.5b) is consistent with the *Zip14*-KO phenotype and suggests that ZIP14 plays a role in bone formation. In particular, ZIP14 was found to be expressed in each of the zones of the epiphyseal growth plate during endochondral ossification, at relatively high levels in the proliferative zone (PZ), and at minimal levels in the hypertrophic zone (HZ) (Fig. 12.5b). *Zip14*-deficient mice exhibit growth retardation accompanied by a shortened proliferative zone and



**Fig. 12.5** ZIP14 has a role in regulating systemic growth and bone homeostasis. **a** Dwarfism, torticollis, osteopenia, and scoliosis in *Zip14*-KO mice. Bar 5 cm. **b** Abnormal chondrocyte differentiation in the growth plate of *Zip14*-KO mice. Hematoxylin and eosin (H&E) staining and in situ hybridization analysis for *Zip14*, *Ihh*, and *Col10a1* in the growth plates from control and *Zip14*-KO mice

an extended hypertrophic zone, resulting in impaired bone elongation. Consistent with this observation, expression of *type II Collagen (Col2a1)*, an RZ and PZ marker, was decreased, whereas the expressions of *Indian hedgehog (Ihh)*, a pre-hypertrophic zone (PHZ) marker, and *type X Collagen (Col10a1)*, an HZ marker, were both enhanced, indicating accelerated hypertrophy at the *Zip14*-KO growth plate (Fig. 12.5b).

The morphology of the *Zip14*-KO growth plate is a partial phenocopy of that in mice with a chondrocyte-specific deletion of *parathyroid hormone 1 receptor (Pth1r)* (Chung et al. 1998; Kobayashi et al. 2002; Kronenberg 2006). Parathyroid hormone-related peptide (PTHrP) binds to PTH1R and stimulates the phosphorylation of cAMP response element-binding protein (CREB) by the nuclear-translocated catalytic alpha-subunit of protein kinase A (PKA-C $\alpha$ ), followed by the phosphorylated CREB (p-CREB)-mediated induction of *c-fos* (Guo et al. 1995). Interestingly, PTHrP-induced *c-fos* transcription is significantly reduced in the *Zip14*-KO chondrocytes. The level of p-CREB and the nuclear translocation of PKA-C $\alpha$  in response to PTHrP treatment are also reduced in the *Zip14*-KO chondrocytes (Hojyo et al. 2011), suggesting a functional interaction between ZIP14- and PTHrP-regulated signal transduction.

#### 12.4.2.2 Regulation of the PTHrP Signaling Pathway by ZIP14

PTHrP binding to PTH1R, a G protein-coupled receptor, leads to adenylyl cyclase (AC) activation, resulting in high levels of cAMP that in turn activate PKA by binding to its regulatory subunit (Ionescu et al. 2001). To identify the defective component in PTH1R signaling in *Zip14*-KO cells, we evaluated AC activity by measuring cAMP levels. The basal cAMP level was significantly reduced in *Zip14*-KO chondrocytes, and even after treatment with either PTHrP or the AC activator forskolin (FSK), the cAMP levels were lower than in control chondrocytes, while the treatment-induced fold increase in cAMP levels was comparable between the control and *Zip14*-KO chondrocytes. These findings indicated that ligand-mediated AC activation was intact in the *Zip14*-KO cells, and that ZIP14 is required to maintain the basal level of cAMP in chondrocytes. Phosphodiesterase (PDE), a critical regulator of cyclic nucleotide signaling, degrades cAMP and cyclic guanosine monophosphate (cGMP) (Jeon et al. 2005). *Zip14*-KO chondrocytes show enhanced PDE activity and reduced cAMP levels, both of which are corrected by treatment with a PDE inhibitor, 3-isobutyl-1-methylxanthine (IBMX), consistent with an earlier finding that Zn inhibits cAMP-specific PDE activity (Percival et al. 1997; von Bulow et al. 2005). Taken together, these results suggest that ZIP14 regulates the PTH1R-cAMP-CREB pathway by affecting Zn homeostasis.

In fact, the Zn levels are significantly decreased in proliferative but not in hypertrophic chondrocytes at the *Zip14*-KO growth plate, consistent with the high *Zip14* expression levels in the PZ. We confirmed that ZIP14 is localized to the plasma membrane, as previously reported (Liuzzi et al. 2005). Furthermore, we found that Zn treatment reduces the cAMP-specific PDE activity and elevates the cAMP levels in *Zip14*-KO chondrocytes, and that the ectopic expression of ZIP14 in KO cells rescues the intracellular Zn and cAMP levels.

#### 12.4.2.3 Regulation of the GH-IGF-I Axis by ZIP14

*Zip14*-KO mice show phenotypic similarity to GH-mutant mice and human cases of GH deficiency (Procter et al. 1998). The GPCR growth hormone-releasing hormone receptor (GHRHR) acts on pituitary somatotroph cells to produce GH through the cAMP-CREB pathway (Mayo et al. 1995; Struthers et al. 1991), suggesting that ZIP14 may be involved in GHRHR-mediated GH production. Indeed, we found that the pituitary gland expresses *Zip14*, and that the levels of pituitary cAMP and Zn are decreased in *Zip14*-KO mice. Intriguingly, bolus administration of GHRH increases the plasma GH levels in control mice but has little effect in the *Zip14*-KO mice. In addition, a similar defect in *Gh* induction is observed in the *Zip14*-KO mice in response to fasting, during which GHRHR-mediated GH induction is known to occur (Sakharova et al. 2008). *Zip14*-KO mice show reduced serum IGF-I and hepatic *Igf-I* expression levels, which may be explained by impaired GH production, because their *growth hormone receptor* (*Ghr*) expression levels are

similar to wild-type levels. These observations suggest that ZIP14 is involved in the signaling of GHRHR, a GPCR in the pituitary gland. Collectively, these results clearly demonstrate that ZIP14 not only acts as a positive GPCR regulator in the endochondral ossification process, but also functions to regulate GH production, resulting in the concomitant regulation of vertebrate systemic growth. This conclusion may explain why Zn deficiency causes reductions in serum GH and IGF-I levels (MacDonald 2000).

## 12.5 Conclusions and Future Perspectives

Zn transporter-mediated Zn signaling plays essential roles in the control of mammalian growth. Mice lacking ZIP13 or ZIP14 exhibit stunted growth, accompanied by impaired bone growth. Both transporters are preferentially expressed in the PZ of the growth plate during endochondral ossification (Fukada et al. 2008; Hojyo et al. 2011; Inoue et al. 2002), and the absence of either transporter alters the morphology of the PZ and HZ. However, it should be noted that the *Zip13*- and *Zip14*-KO mice exhibit opposing alterations in growth plate morphologies; the loss of ZIP13 results in the formation of an elongated PZ and a shortened HZ, whereas the loss of ZIP14 leads to a shortened PZ and an elongated HZ. Consistent with these morphological differences, ZIP13 and ZIP14 play distinct roles in the regulation of growth-related signaling cascades. For example, ZIP13 regulates SMAD nuclear translocation during BMP/TGF- $\beta$  signaling, whereas ZIP14 regulates PDE activity, to alter GPCR-mediated signaling. These transporters also exhibit different localizations: ZIP13 is localized to the Golgi and controls intracellular Zn distribution, whereas ZIP14 is expressed on the cell membrane and controls intracellular Zn accumulation (Fukada et al. 2008; Fukada and Kambe 2011; Hojyo et al. 2011; Inoue et al. 2002). Thus, the intracellular Zn status is controlled by the localization of each Zn transporter, and their coordinated functions ultimately impact mammalian growth. These findings support the concept that various “Zn signal axes” act in different signaling pathways to promote systemic growth (Fig. 12.3).

Currently, a four-step model of Zn homeostasis is postulated for the mediation of mammalian growth: (1) ZnT2 (Chowanadisai et al. 2006) and ZnT4 (Huang and Gitschier 1997) contribute to Zn ingestion into the body through breast milk and daily diet (Fig. 12.2a); (2) Zn is absorbed by intestinal transporters such as ZIP4 (Dufner-Beattie et al. 2007) and ZnT1 (Wang et al. 2009) (Fig. 12.2b); (3) intracellular Zn accumulates and is maintained through Zn influx via cell-surface Zn transporters such as ZIP14 (Hojyo et al. 2011) (Fig. 12.2c); and (4) intracellular Zn is distributed by intracellular Zn transporters such as ZIP13 (Fukada et al. 2008) and ZnT5 (Inoue et al. 2002) (Fig. 12.2d), leading to the fine-tuning of cellular functions. Thus, the unique Zn signal axes generated by the coordinated Zn transporter functions are essential for the proper control of mammalian systemic growth and regeneration. The disruption of each Zn signaling axis can affect pathogenesis in the absence of redundant machinery.

Many aspects of Zn signaling and its effects on growth regulation and bone homeostasis remain to be investigated. Zn may also have additional uncharacterized functions and interactions with other involved signaling factors (Akhurst 2004; Cao and Chen 2005; Nilsson et al. 2005; Procter et al. 1998) that impact bone homeostasis and body growth. Other areas of interest include the molecular basis of the specificity of the Zn signal axes (Fig. 12.3) and the downstream functions of Zn as a signaling molecule, following its mobilization by Zn transporters, as discussed in other chapters. Further molecular and genetics-based studies on Zn transporters are required to address these issues and to expand our knowledge about Zn signaling.

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# Chapter 13

## Zinc and Its Role in the Pathogenesis of Type 2 Diabetes

**Yoshio Fujitani, Motoyuki Tamaki, Ayako Fukunaka, and Hirotaka Watada**

**Abstract** Although zinc ions have important roles in the biosynthesis and storage of insulin, many previous studies have reported the possible involvement of zinc deficiency in the pathogenesis of diabetes. Zinc may counteract the deleterious effects of oxidative stress, which contributes to increased insulin sensitivity, and may also protect pancreatic  $\beta$  cells from glucolipotoxicity. The recent discovery that loss of SLC30A8/ZnT8 function may increase the susceptibility to type 2 diabetes provides novel insights into the role of zinc in diabetes. Here, we discuss the roles of zinc in glucose homeostasis, particularly in relationship to ZnT8 function, based on our knowledge of mice and humans with ZnT8 loss-of-function mutations.

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**Keywords** Diabetes • Insulin • Insulin clearance • Insulin metabolism • Insulin secretion • SLC30A8 • Zinc • Zinc transporter • ZnT8

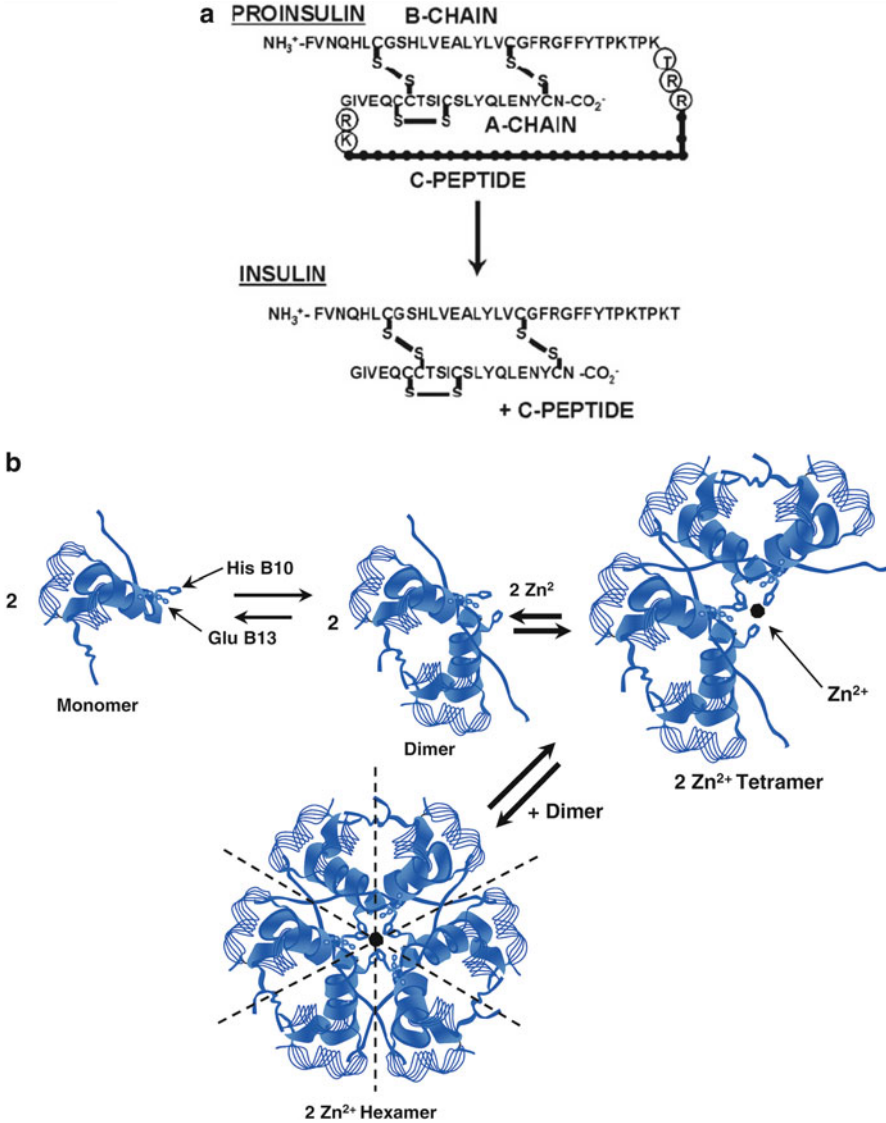
### 13.1 Zinc and Pancreatic $\beta$ Cells

Zinc was reported as an essential factor for insulin crystal formation in the 1930s (Scott 1934), and zinc content in the pancreas of diabetic patients was shown to be reduced by 50 % (Scott and Fisher 1938). These findings suggested a close relationship between zinc and diabetes. Follow-up studies have shown that insulin exists as a hexamer consisting of six insulin and two zinc molecules (Dodson et al. 1979; Dunn 2005) (Fig. 13.1). Crystallized insulin in insulin secretory granules is observed as “dense-core granules” upon electron microscopic analysis (Hou et al. 2009; Tamaki et al. 2013) (Fig. 13.2; ZnT8-KO mice).

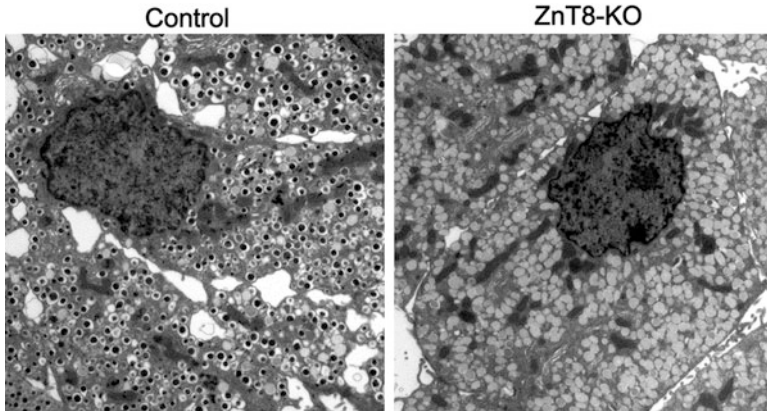
After folding, the proinsulin protein forms dimers via electrostatic interactions. The residues B24–B26 (amino acids 24–26 of the B-chain) are thought to be important for this dimer formation (Zoete et al. 2005). In fact, amino acid substitutions of these residues yielded a series of ultra-rapid-acting insulin analogues that are now widely used in clinical practice (Brange et al. 1990; Kang et al. 1991). The electrostatically coupled proinsulin dimers and zinc bind with B10 histidine, resulting in proinsulin hexamer formation (Havu et al. 1977) (Fig. 13.1). This insulin hexamer formation is accomplished by prohormone convertase-mediated c-peptide dissociation (Steiner et al. 1996). Because the c-peptide portion of proinsulin is located outside the proinsulin hexamer, it has been considered that the formation of the hexamer contributes to c-peptide dissociation (Dunn 2005). Insulin crystals are formed under specific conditions within insulin granules in which both insulin and zinc exist in high concentrations and acid pH is maintained (Emdin et al. 1980; Hutton 1989). Given that the addition of zinc to commercial insulin products improves its stability, hexamer formation and crystallization are thought to similarly contribute to insulin stabilization in vivo. Once insulin crystals are secreted from pancreatic  $\beta$  cells, they are believed to rapidly dissociate into monomers and flow into the bloodstream.

### 13.2 Zinc Deficiency and Diabetes

The relationship between zinc deficiency and diabetes has been extensively examined in mouse models. Mice with zinc deficiency demonstrated decreased insulin granules in their pancreatic  $\beta$  cells (Boquist and Lernmark 1969), as well as impaired glucose-stimulated insulin secretion (GSIS) (Huber and Gershoff 1973). Because pancreatic  $\beta$  cells actively synthesize a large amount of ATP, they are prone to exposure to and damage by oxidative stress (Donath et al. 2005). Because zinc is an essential component of antioxidative enzymes, including Cu–Zn-SOD



**Fig. 13.1** The biosynthesis of insulin. **a** The insulin precursor preproinsulin contains a signal sequence that is proteolytically cleaved to yield proinsulin, in which the C-peptide links the future A- and B-chains of mature insulin. Cleavage of the C-peptide converts proinsulin to insulin. **b** Association of insulin monomers in the presence of zinc. Insulin readily associates into dimers, and then aggregates into hexameric forms in the presence of zinc. His B10 is implicated in the zinc-mediated insulin hexamer formation



**Fig. 13.2** Electron microscopic images of pancreatic  $\beta$  cells from a control and a ZnT8-KO mouse. Numerous dense-core granules are observed in the control  $\beta$  cells. ZnT8-KO  $\beta$  cells are devoid of dense-core granules, suggesting a deficiency in insulin crystal formation

(superoxide dismutase) (Mysore et al. 2005) or catalase (Marklund et al. 1982), zinc deficiency could worsen the condition of pancreatic  $\beta$  cells under oxidative stress. These findings support the idea that zinc deficiency may result in impaired pancreatic  $\beta$ -cell function and survival. The supplementation of zinc also improved insulin sensitivity in obese diabetic *db/db* or *ob/ob* mice (Begin-Heick et al. 1985; Simon and Taylor 2001). A recent study by Adachi et al. reported that oral administration of zinc (II) complex for 4 weeks to obese diabetic KKA<sup>y</sup> mice significantly improved their glucose tolerance and insulin sensitivity, which was accompanied by increased plasma adiponectin levels (Adachi et al. 2006). The insulin-sensitizing effect of zinc has been explained by the inhibition of the tyrosine phosphatase activity of PTP1B (protein tyrosine phosphatase-1B) (Haase and Maret 2005). The enzymatic activity of PTP1B is inhibited by zinc ions. The concentration of available cellular zinc is in the nanomolar or picomolar range, and hence inhibition of PTPs by zinc occurs within this low range of available zinc (Haase and Maret 2003). Experiments in cell culture provided evidence for a physiological role of zinc in modulating PTP activity. Incubation of cells with zinc increases tyrosine phosphorylation of the insulin receptor, and its effects are mediated by the inhibition of dephosphorylation rather than enhanced phosphorylation. The concentration of cellular available zinc is not constant but fluctuates under various conditions. Zinc fluctuations are controlled by zinc-buffering systems, and one of these systems involves metallothionein (MT) (Maret 2009). Metallothionein and zinc have been implicated in cellular defense mechanisms against oxidative stress (Eibl et al. 2010). This finding is consistent with the observation that zinc administration to streptozotocin-induced diabetic rats reduced their glucose levels through robust induction of MT in the pancreas and liver (Yang and Cherian 1994). Thus, zinc appears to show antidiabetic activity not only through potentiating  $\beta$ -cell function

but also through insulin-sensitizing effects on the liver and other insulin-sensitive tissues.

In humans, a prospective cohort study employing 82,000 women in the United States revealed that women with low zinc intake have a 17 % increased risk of onset of diabetes compared to women who take adequate amounts of zinc (Sun et al. 2009). In a Brazilian study, 30 mg/day of zinc supplementation to obese women improved insulin sensitivity (Marreiro et al. 2006), and another cross-sectional study in North India reported that lower consumption of dietary zinc and low serum zinc levels are associated with an increased prevalence of coronary artery disease (CAD) and diabetes, as well as several of their associated risk factors including hypertension and hypertriglyceridemia (Singh et al. 1998). Recently, a negative correlation between plasma zinc concentrations and diabetes onset has been reported in China (Shan et al. 2014). Interestingly, this report describes the possible interaction of SLC30A8 [zinc transporter 8 (ZnT8)] dysfunction and decreased plasma zinc concentrations in regulating glucose tolerance and diabetes. According to this report, lower plasma zinc concentrations and decreased ZnT8 function coordinately increase the risk of diabetes. Although these data suggest that zinc supplementation can prevent the deterioration of glucose homeostasis, particularly in people with zinc deficiency, prospective interventional studies are necessary to confirm the efficacy of zinc supplementation in preventing diabetes onset.

### 13.3 Structure and Function of ZnT8

ZnT8 is a member of the ZnT family, which has a predicted membrane topology of six membrane-spanning domains with both N- and C-terminal ends, four conserved amino acid residues within transmembrane domains (TMDs) II and V, and a cytoplasmic His-rich loop between TMDs IV and V (Kambe 2012). ZnT8 is closely related to ZnT2, ZnT3, and ZnT4, which are members of a subfamily of ZnT proteins that is involved in secretory/synaptic vesicle transport and lysosomal/endosomal zinc storage (Chimienti et al. 2004). The expression of ZnT8 is two to three orders of magnitude higher in the islet than in all other tissues examined (Nicolson et al. 2009). Thus, ZnT8 is responsible for transporting zinc into insulin-containing granules in islet  $\beta$  cells, where insulin is stored as a hexamer bound with two zinc ions before secretion (Fig. 13.1b). ZnT8 is also expressed in other tissues, including islet  $\alpha$  cells, pancreatic polypeptide (PP) cells, and a subset of endocrine cells in the thyroid and adrenal glands (Tamaki et al. 2009). The islet-specific expression of ZnT8 was shown to be regulated by the  $\beta$ -cell-enriched transcriptional factor Pdx-1 through an intronic enhancer (Pound et al. 2011).

Several studies have shown that ZnT8 is a bona fide zinc transporter by using ZnT8-overexpressed cells (Lefebvre et al. 2012), ZnT8-knockdown cells (Fu et al. 2009), or ZnT8-KO mice (Nicolson et al. 2009). The mechanism of zinc transport is still incompletely understood. However, experiments using fluorescence-based functional measurements have shown that ZnT transporters

function as  $\text{Zn}^{2+}/\text{H}^{+}$  exchangers (Ohana et al. 2009). The zinc transport activity of ZnT3 in neurons has been reported to be potentiated by chloride channels and vesicular glutamate transporters (Salazar et al. 2005; Salazar et al. 2004a). Similar mechanisms may also operate in ZnT8. Furthermore, similarly to ZnT3 in which synaptic localization is controlled by AP-3 (Salazar et al. 2004b), ZnT8 localization in the insulin granule might be controlled by other molecules, because the sorting signal of ZnT8 to the insulin granule has not been identified.

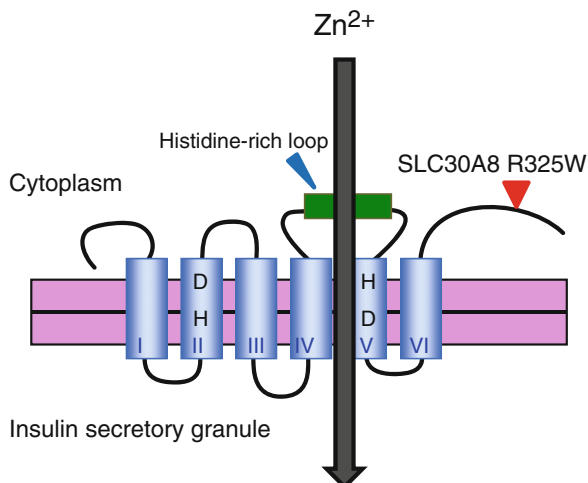
The expression of ZnT transporters is transcriptionally regulated by various stimuli. In  $\beta$  cells, it has been shown that glucose and cytokines play roles in the regulation of zinc transporter expression. Cytokines [interleukin (IL-1 $\beta$ ), tumor necrosis factor (TNF- $\alpha$ )] decrease the expression of zinc transporters, particularly ZnT8 (El Muayed et al. 2010), suggesting that the expression of ZnT8 may be decreased during diabetes that accompanies pancreatitis. Moreover, ZnT8 expression was found to be remarkably downregulated in the early stages of diabetes in diabetic model mice, such as *db/db* and *Akita* (Tamaki et al. 2009). These findings demonstrated that the expression of ZnT8 is reduced during the course of hyperglycemia and inflammation in type 2 diabetes. Further analyses are required to determine the factors that might regulate ZnT8 expression in such situations.

Homology modeling studies based on the bacterial zinc transporter and ZnT homologue YiiP have shown that ZnT8 forms homodimers held together by four zinc ions located at the interface of the cytoplasmic domains, with two transmembrane domains swinging out to yield a Y-shaped structure (Nicolson et al. 2009). Recent genome-wide association studies demonstrated that the nonsynonymous single-nucleotide polymorphism rs1326634 in the *SLC30A8* gene, resulting in the replacement of tryptophan-325 with arginine, increases the risk of type 2 diabetes (Fig. 13.3) (Diabetes Genetics Initiative of Broad Institute of Harvard and MIT, Lund University, and Novartis Institutes of BioMedical Research et al. 2007; Scott et al. 2007; Sladek et al. 2007). To examine the potential physiological differences between the low-risk and increased-risk variants of ZnT8, Guy Rutter's group showed, using fluorescent dyes to monitor the vacuolar accumulation of zinc, that the increased-risk R-form of ZnT8 is less active as a zinc transporter (Nicolson et al. 2009).

### 13.4 The Role of ZnT8 in Glucose Homeostasis

In pancreatic  $\beta$  cells, ZnT8 is located within the plasma membrane of insulin secretory granules and is implicated in zinc transport into insulin secretory granules (Fig. 13.3) (Murgia et al. 2009). How is the transport of zinc into insulin granules related to the increased risk of diabetes onset? To address this question, we examined the physiological role of ZnT8 by generating pancreatic  $\beta$ -cell-specific *Slc30a8*-deficient mice (ZnT8-KO) (Tamaki et al. 2013).

As expected, immunohistochemical analysis demonstrated that ZnT8 expression is largely absent from ZnT8-KO islets. Furthermore, dense-core granules, a



**Fig. 13.3** Zinc transporter 8 encoded by SLC30A8 is localized on the membranes of insulin secretory granules. Like other ZnT family members, it contains six transmembrane domains (TMDs) and a histidine-rich loop between TMDs IV and V (thick green line). Four conserved amino acid residues (two histidine (H) and two aspartic acid (D)) are located within TMDs II and V. A nonsynonymous single nucleotide polymorphism affecting amino acids 325 on ZnT8 is implicated in type 2 diabetes from genome-wide association studies

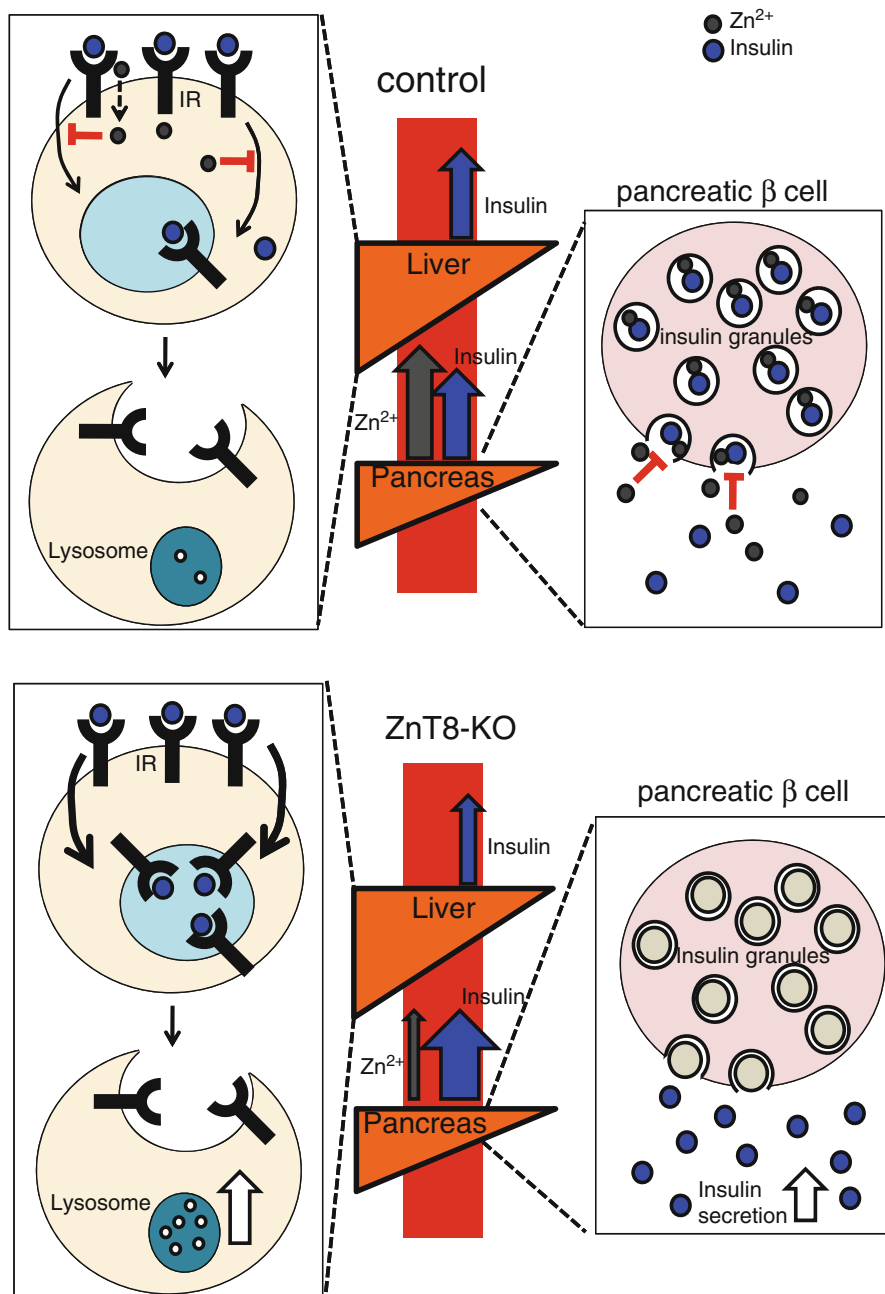
hallmark of crystallized insulin usually seen in normal  $\beta$  cells, were absent in the ZnT8-KO  $\beta$  cells (Fig. 13.2). In agreement with these observations, intra-islet zinc content was severely depleted in ZnT8-KO mice. Because ZnT8-KO mice showed mildly impaired glucose tolerance, we expected insulin secretion from the ZnT8-KO islets to be decreased. Indeed, after glucose challenge, lower peripheral blood insulin levels were detected in ZnT8 mice compared with control mice (Tamaki et al. 2013). Glucose-stimulated insulin secretion (GSIS) from the isolated ZnT8-KO islets was, in contrast to our expectations, almost twice that from the control islets. Enhanced GSIS from islets usually results in increased blood insulin levels. Although enhanced insulin secretion from the ZnT8-KO islets was observed, insulin concentrations in the blood circulation of ZnT8-KO mice were lower than those in control mice, for some unknown reason. To explain this discrepancy, the pancreas perfusion experiment was performed. In this experiment, pancreata were perfused with a glucose solution, so that more physiologically relevant insulin secretion profiles can be assessed compared with experiments using isolated islets. Enhanced insulin secretion was still noted in ZnT8-KO islets upon pancreas perfusion, further supporting that insulin secretion is actually increased in vivo in ZnT8-KO islets. Next, to examine insulin metabolism, pancreas–liver dual perfusion was performed (Tamaki et al. 2013). A comparison of the results obtained by pancreas perfusion versus pancreas–liver perfusion revealed that a large proportion of the secreted insulin was degraded during the first liver passage.



The idea that ZnT8 regulates hepatic insulin clearance is intriguing. It has been reported that insulin clearance is dynamically altered before and after meals (Caumo et al. 2007). In the fasting state, clearance of unnecessary insulin by the liver plays a major role in preventing inappropriate hyperinsulinemia, which may otherwise cause hypoglycemia and obesity (Poy et al. 2002). In the postprandial state, on the other hand, hepatic insulin degradation is inhibited to ensure a sufficient supply of insulin to the peripheral target tissues. Although previous studies proposed that incretin hormones, such as glucagon-like peptide-1 (GLP-1) and gastric inhibitory polypeptide (GIP), that are secreted with food intake regulate hepatic insulin clearance (Ahren et al. 2005; Rudovich et al. 2004), a later study argued against such a possibility (Meier et al. 2007). Another report suggested that the insulin pulse mass from pulsatile insulin secretion into the portal vein is involved in suppressing the hepatic insulin clearance rate (Meier et al. 2005), but the mechanism underlying this process remains largely unknown. As it was reported that zinc secretion is absent in ZnT8-KO islets because of the loss of zinc storage within secretory granules (Lemaire et al. 2009), we then speculated the possibility that the zinc co-secreted with insulin from  $\beta$  cells may have some regulatory roles in insulin clearance. A set of *in vivo* and *in vitro* experiments revealed that zinc inhibits hepatic insulin uptake by counteracting clathrin-mediated endocytosis of the insulin receptor (Ceresa et al. 1998). Because of the suppressive role of zinc in hepatic insulin clearance, glucose tolerance can be maintained by optimizing hepatic insulin degradation (Fig. 13.4).

The next question is this: Why is insulin secretion from ZnT8-KO islets enhanced? It was reported that zinc secreted from  $\beta$  cells can affect neighboring endocrine cells (Ishihara et al. 2003) (Kim et al. 2000). Previous studies showed that zinc binds to specific histidine residues of the K-ATP channel and thus hyperpolarizes pancreatic  $\beta$  cells by enhancing the outward current of the K-ATP channel (Bancila et al. 2005; Prost et al. 2004). Therefore, we hypothesized that the absence of zinc secretion from  $\beta$  cells causes derepression of insulin hypersecretion from ZnT8-KO islets. As expected, addition of zinc (30  $\mu$ M) to the perfusate during pancreas perfusion markedly suppressed insulin hypersecretion in ZnT8-KO mice, almost to control levels. These results indicated that the zinc co-secreted with insulin from  $\beta$  cells acts to decrease the insulin secretion of neighboring  $\beta$  cells (Fig. 13.3). These findings are consistent with a previous report by Nicolson et al. in which similar hypersecretion of insulin from ZnT8-deficient islets was observed (Nicolson et al. 2009).

There is increasing evidence that glucagon secretion is regulated by various stimuli, including insulin, glucose (Gylfe and Gilon 2014), amino acids (Cabrera et al. 2008), amylin (Young 2005), GLP-1 (Meier and Nauck 2005), and zinc (Egefjord et al. 2010). Whether zinc can suppress glucagon secretion (Ishihara et al. 2003) (Slucca et al. 2010) or cannot (Ravier and Rutter 2005) is currently an active topic of debate. As two independent studies reported that there was no alteration in glucagon secretion in ZnT8 global KO mice (Nicolson et al. 2009), we measured glucagon secretion from islets isolated from pancreatic  $\beta$ -cell-specific ZnT8-KO mice and controls. The average glucagon secretion from ZnT8-KO islets



**Fig. 13.4** Schematic representation of insulin clearance in control and ZnT8-KO mice. Zinc co-secreted with insulin suppresses insulin secretion from pancreatic  $\beta$  cells (*upper right*) and inhibits hepatic insulin clearance (*upper left*) in *control* mice. Although the reduced zinc secretion allows enhanced insulin secretion from  $\beta$  cells in ZnT8-KO mice (*lower right*), hepatic insulin clearance is not suppressed (*lower left*). Thus, peripheral insulin levels in ZnT8-KO mice are maintained at lower levels than in control mice IR: insulin receptor

under a low glucose condition appeared to be larger than that from control islets, but there was no statistically significant difference. We also measured blood glucagon concentrations to test whether glucose-stimulated insulin plus zinc secretion can suppress glucagon secretion *in vivo*. However, there were no differences in the levels of glucagon suppression between ZnT8-KO and control mice after glucose challenge. In conclusion, consistent with the reports by Nicolson et al. (2009) and Hardy et al. (2011), glucagon secretion was not changed in ZnT8-KO mice.

### 13.5 Insulin Metabolism and Hepatic Insulin Clearance

Insulin secreted from the islets of Langerhans flows directly into the portal vein (PV). About half the insulin that enters the liver is cleared; the rest flows into the systemic circulation (Eaton et al. 1983). Thus, the rate of hepatic insulin clearance is an important regulator of peripheral insulin levels. In the postprandial state, hepatic insulin clearance is estimated to be suppressed by 20 % (Caumo et al. 2007). Insulin clearance by the liver involves the following three steps: (i) binding of insulin to the insulin receptor (IR) on the cell surface of hepatocytes, (ii) internalization of insulin via IR-mediated endocytosis, and (iii) degradation of insulin by insulin-degrading enzyme (IDE) within endosomes (Authier et al. 1996). We found that zinc does not affect either steps (i) or (iii) and that step (ii) is the zinc-sensitive process. It was reported that endocytosis of the transferrin receptor in hepatocytes is inhibited by zinc in a clathrin-dependent manner (Liu et al. 2010; McAbee and Jiang 1999). The same mechanism appears to be involved in endocytosis of the insulin receptor (IR). Blockade of IR endocytosis was enhanced by pyrithione, a zinc ionophore, suggesting that internalized zinc is responsible for the inhibitory effects. However, the effect was independent of the zinc transporter ZIP14 (Hojyo et al. 2011).

As already discussed, ZnT8 has a pivotal role in determining the levels of insulin to be delivered to the liver versus other peripheral organs, and thus optimizes the effect of insulin on whole-body glucose metabolism. Insulin and c-peptide are generated from proinsulin at a 1:1 ratio by prohormone convertase-mediated digestion (Fig. 13.1a). Although c-peptide, which is not degraded by the liver, represents insulin secretion per se from pancreatic  $\beta$  cells, insulin is dynamically degraded during liver passage. Accordingly, the c-peptide/insulin ratio can be used as a marker for assessing insulin clearance *in vivo* (Meier et al. 2007; Poy et al. 2002). In wild-type animals, the released  $\text{Zn}^{2+}$  inhibited further insulin release whereas loss of ZnT8 resulted in sustained insulin secretion (Tamaki et al. 2013). Intriguingly, despite increased insulin secretion, peripheral insulin levels were lower and the c-peptide/insulin ratios were increased in KO mice (Tamaki et al. 2013). These data are in agreement with the idea that lower insulin levels might result from increased insulin clearance from the bloodstream, rather than

decreased insulin secretion from  $\beta$  cells. Studies of c-peptide/insulin ratios and rates of insulin clearance in humans with the SLC30A8 R325W polymorphism were also consistent with this idea (Tamaki et al. 2013).

### 13.6 Clinical Significance of Zinc-Mediated Pancreas–Liver Communication

In the Eugene study, human homozygous carriers of the *SLC30A8* risk allele had low peripheral insulin levels in the early phase of intravenous glucose tolerance test (i.v. GTT) (Boesgaard et al. 2008). However, in previous studies that characterized the ZnT8-deficient mice, there was no agreement on the underlying mechanism by which *SLC30A8* regulates the susceptibility to type 2 diabetes (Lemaire et al. 2009; Nicolson et al. 2009; Pound et al. 2009; Wijesekara et al. 2010). Furthermore, there is a lack of consensus on the effect of *Slc30a8* deletion on insulin secretion and circulation in mice, as summarized in the recent mini-review by O'Halloran et al. (2013). Although some studies reported that deletion of SLC30A8/ZnT8 results in impaired glucose tolerance (Nicolson et al. 2009; Wijesekara et al. 2010), others reported that loss of ZnT8 exhibits essentially no change in glucose tolerance (Lemaire et al. 2009; Pound et al. 2009). These differences might have been caused by differences in the study designs or the genetic backgrounds of the mice generated (Pound et al. 2012; Tamaki et al. 2013). We demonstrated that SLC30A8/ZnT8 regulates hepatic insulin clearance, by extensive examination of  $\beta$ -cell-specific ZnT8-KO mice, and importantly, the same mechanism appears to be conserved also in humans (Tamaki et al. 2013). In general clinical practice, hypoinsulinemia is usually interpreted to result from low insulin secretion by pancreatic  $\beta$  cells. However, this cannot be confirmed without measuring insulin secretion from the pancreas, because insulin levels in the systemic circulation are determined by a balance between insulin secretion and insulin clearance. Our study highlighted a zinc-mediated, novel inter-organ communication between the pancreas and liver; together with the pancreas, the liver is actively involved in the regulation of postprandial plasma insulin levels by modulating insulin clearance (Fig. 13.4). Indeed, inhibition of hepatic insulin clearance has been a target for the pharmacological intervention of diabetes. A previous study reported the therapeutic potential of designed small molecule inhibitors of insulin-degrading enzyme (IDE) that regulate the catabolism of insulin (Leissring et al. 2010). Our findings provide a novel insight into the molecular pathology of diabetes: dysregulated hepatic insulin clearance, which could be an attractive future therapeutic target for diabetes.

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**Note added in the proof** During the author's proofreading of this manuscript, Flannick et al. report 12 rare protein-truncating mutations in *SLC30A8*, which collectively explain a 65% reduction in diabetes risk (Flannick et al. 2014 *Nat Genet* 46(4):357–363). They report a study including genotyping and sequencing of ~150,000 individuals that concludes that rare loss-of-function mutations in *SLC30A8* are protective against the development of diabetes. This finding challenges the recent studies suggesting the reverse relationship in this disease association.

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# Chapter 14

## Zinc Signaling and Cancer

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**Abstract** The intracellular level of zinc is tightly controlled by ZnT (SLC30A) and ZIP (SLC39A) zinc transport proteins, as well as zinc-binding proteins such as metallothioneins. The ZIP channels are responsible for zinc influx into the cytoplasm, either from the extracellular space or intracellular storage compartments, such as the endoplasmic reticulum and the Golgi, whereas the ZnT transporters transport zinc in the opposite direction. Malfunctions of some zinc transport proteins, resulting in cellular zinc dyshomeostasis and subsequent effects on zinc signaling pathways, have been associated with cancer in a tissue-specific manner. In this chapter we detail what is known about the association between zinc channel and transporter dysregulations and the impact that this has on zinc signaling in different cancers. A particular emphasis is placed on the types of cancer in which the role of zinc dyshomeostasis on carcinogenesis or cancer progression has been most thoroughly investigated, including cancers of the breast, prostate, liver, pancreas, and colorectum. Posttranslational modification by phosphorylation as a novel regulatory mechanism of ZIP channels is also discussed as an important mechanism that may provide a clinical biomarker or target mechanism.

**Keywords** Cancer • SLC30A • SLC39A • Zinc channel • Zinc transport • ZIP6 • ZIP7

### 14.1 Introduction

As has already been described in previous chapters, zinc is clearly an essential trace element of extraordinary biological and public health significance (Hambidge and Krebs 2007). It is the only metal that can be found in all six enzyme classes, according to the IUPAC system of enzyme classification (Food and Nutrition Board of Institute of Medicine 2001). Recent bioinformatic analysis has revealed that 2,800 to 3,200 human proteins, or approximately 10 % of the proteome, are predicted to be zinc-binding proteins (Andreini et al. 2006; Passerini et al. 2007),

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and more than 1,000, or 3 %, of all 32,000 identified genes in the human genome encode proteins with zinc-finger domains (Maret 2001). Not surprisingly, zinc is known to play an important role in various biological processes that are essential for both cell survival and cell death (John et al. 2010), including signal transduction, gene expression, and apoptosis (Hambidge and Krebs 2007). Zinc not only protects the body from invaders by promoting the functions of immune cells (John et al. 2010), but it also protects cells from free radical damage by modulating the free radical scavenging system (Oteiza 2012). Through its functional and structural association with enzymes, zinc is also involved in the metabolism of carbohydrates, lipids, proteins, nucleic acids, and other micronutrients, as well as control of cellular proliferation, growth, and differentiation (World Health Organization and Food and Agriculture Organization of the United Nations 2002). Mechanistically, intracellular zinc is suggested to exert its functions in three interrelated biological activities, consisting of catalysis, structural arrangement of proteins, and regulation of cellular events (Swinkels et al. 1994).

Furthermore, zinc has recently been classified as an intracellular second messenger, because it is capable of transducing an extracellular stimulus into intracellular signaling cascades, which was first experimentally demonstrated in mast cells (Yamasaki et al. 2007). In this study, the intracellular zinc was shown to be increased by release from intracellular storage compartments, such as the endoplasmic reticulum (ER), which was termed a zinc wave (Yamasaki et al. 2007). This intracellular store release of zinc in the form of a zinc wave results in activation of multiple intracellular signaling pathways and subsequent stimulation of the growth potential of cells (Taylor et al. 2008). Thereafter, the role of zinc as a second messenger has been further confirmed in other types of immune cells, such as lymphocytes (Yu et al. 2011), as well as breast cancer cells (Taylor et al. 2012a). These data confirm that an extracellular stimulus of cells can produce a store release of zinc inside the cell with dramatic effects on cellular signaling, manifesting a response on the time scale of minutes, independently of the much slower transcriptional and DNA-binding effects of zinc, which require hours or days to attain. This demonstration of zinc as a second messenger has elevated zinc signaling to an intracellular role potentially as important as that of calcium, yet relatively little is known about the mechanism of how zinc is released within cells and its relevance to disease.

## 14.2 Control of Intracellular Zinc Level

Both zinc deficiency and excess result in detrimental cellular consequences (Plum et al. 2010). For example, zinc deficiency abrogates cell proliferation (MacDonald 2000) and induces programmed cell death or apoptosis (Fraker 2005), whereas zinc excess results in apoptosis and necrosis (Kim et al. 1999). Therefore, it is necessary for a cell to tightly regulate the cellular level of free zinc. This control is contributed by three groups of proteins, consisting of ZnT transporters (formerly called cation

diffusion family, SLC30A), ZIP channels (Zrt- and Irt-like proteins, SLC39A), and cytosolic zinc-binding proteins, particularly metallothioneins (Cousins et al. 2006; Lichten and Cousins 2009). The ZnT transporters reduce cytosolic zinc concentration by promoting zinc efflux from the cytoplasm to the extracellular space or intracellular compartments depending on their cellular location, whereas the ZIP channels increase cytosolic zinc bioavailability by mobilizing zinc in the opposite direction (Fukada and Kambe 2011; Lichten and Cousins 2009). Additionally, the cysteine-rich metallothioneins also play a crucial role in intracellular zinc homeostasis by orchestrating the zinc buffering and muffling reactions and serving as an intracellular zinc supply for redox signaling (Colvin et al. 2010). The buffering reaction occurs under steady-state conditions to regulate a cytosolic free zinc concentration within picomolar levels, whereas the muffling reaction modulates the cytosolic free zinc concentration that transiently changes under a non-steady-state situation (Colvin et al. 2010). According to the muffler model, the increase in intracellular free zinc level, which results from either zinc uptake from the extracellular space or zinc release from the intracellular stores after activation, is tightly regulated by the binding of the zinc ion to the muffler metallothioneins before delivery into the internal storage compartments or by removal from the cells (Colvin et al. 2010). A further detailed description of this mechanism has already been provided in Chap. 2.

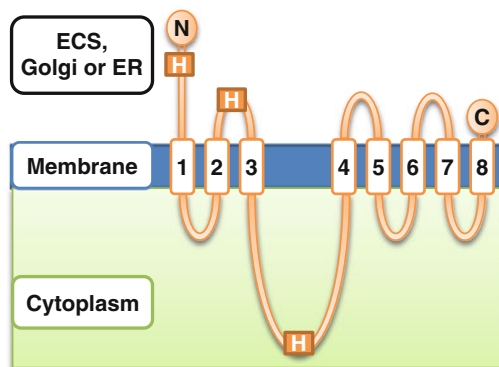
### 14.3 Classification and Predicted Membrane Topology of Zinc Transport Proteins

Most zinc transport proteins that have been associated with cancer belong to the LIV-1 subfamily of the ZIP channels, which constitute the main focus of this chapter. However some information on ZnT transporters and cancer does exist and is also mentioned.

#### 14.3.1 ZIP Channels

The ZIP channels (SLC39A) are zinc influx transport proteins mobilizing zinc into the cytoplasm, either from the extracellular space or intracellular stores, such as the ER or the Golgi, depending on their cellular location. There are 14 human members of this family, ZIP1 to ZIP14 (Cousins et al. 2006; Eide 2004). Phylogenetically, the ZIP channels can be classified into four subfamilies: subfamily I (ZIP9), subfamily II (ZIP1, ZIP2, ZIP3), *gufA* subfamily (ZIP11), and the most recently characterized LIV-1 subfamily (ZIP4–ZIP8, ZIP10, ZIP12–ZIP14, previously called LZT) (Taylor and Nicholson 2003).

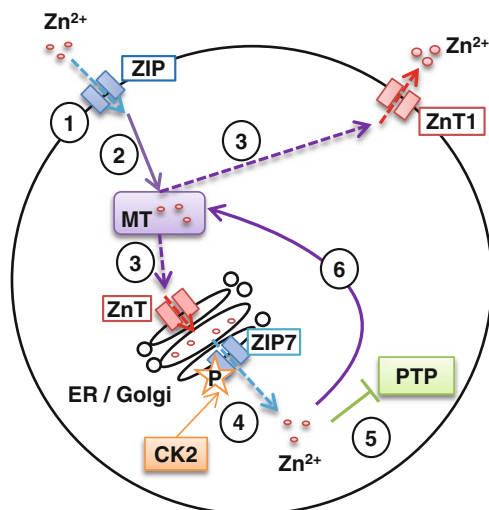
Structurally, the ZIP channels are predicted to have eight transmembrane (TM) domains with extracellular or extracytoplasmic amino- and carboxyl-termini,



**Fig. 14.1** Topological model of Zrt- and Irt-like protein (ZIP) channels. The predicted structure of the ZIP channels proposes they have eight transmembrane (TM) domains, with a long amino-terminus, a long histidine-rich intracytoplasmic loop between TM III and TM IV, and a short carboxyl-terminus. *ECS* extracellular space, *ER* endoplasmic reticulum, *H* histidine

and a long variable histidine-rich intracytoplasmic loop between TM III and IV, which is predicted to be a metal-binding site (Fig. 14.1) (Taylor and Nicholson 2003). In contrast to the other subfamilies of ZIP channels, those belonging to the LIV-1 subfamily have some unique features, including additional histidine-rich regions in the extracellular amino-terminus and the extracellular loop between TM II and III. They also have a unique motif HEXPEHXGD (where H = histidine, E = glutamate, P = proline, D = aspartate, G = glycine and X = any amino acid) in TM V (Taylor and Nicholson 2003) which is the consensus motif for this subfamily of zinc channels and fits the catalytic zinc-binding site of the zinc in PDF metalloproteases (Taylor and Nicholson 2003).

All the ZIP channels are localized to the plasma membrane, being responsible for zinc uptake from the extracellular space, except ZIP7, which has been demonstrated on the intracellular membranes of the ER (Taylor et al. 2004) and the Golgi (Huang et al. 2005), and ZIP13, which is found in the Golgi (Bin et al. 2011). The unique locations of ZIP7 and ZIP13 suggest that they have a role in mobilization of zinc from the intracellular stores into the cytoplasm. As a result of its unique location in the cells, ubiquitous expression throughout the body (Taylor et al. 2004), and the recently discovered posttranslational activation mechanism by phosphorylation by protein kinase CK2 (Taylor et al. 2012a), ZIP7 is proposed to be a gatekeeper for intracellular zinc release (Hogstrand et al. 2009), which may be a prerequisite for zinc-mediated signaling cascades via the well-known zinc inhibitory effect on protein tyrosine phosphatases (PTP) (Haase and Maret 2005). This discovery, that CK2 phosphorylation of ZIP7 is the stimulus to open the ZIP7 gate and cause release of zinc from stores into the cytoplasm (Taylor et al. 2012a), presumably down a concentration gradient, now allows the SLC39A family of zinc transporters to be redesignated as zinc channels rather than transporters. This crucial role of ZIP7 in release of zinc from stores has been confirmed by a study conducted by our group in which ZIP7-mediated zinc release is shown to be



**Fig. 14.2** Intracellular zinc homeostasis and regulation of ZIP7 shown in a schematic representation of the muffler model (Colvin et al. 2010). (1) Zinc influxes from the extracellular space into a cell via a ZIP channel. (2) Cytosolic free zinc is immediately muffled by the cysteine-rich metallothioneins (MT). (3) The muffled zinc is either shuttled directly to the intracellular stores, such as the endoplasmic reticulum (ER) or the Golgi, or eliminated from the cells via ZnT1, the only ZnT transporter located on the plasma membrane (Palmiter and Findley 1995). (4) Upon activation by an appropriate extracellular stimulus, protein kinase CK2 triggers ZIP7-mediated zinc release from the stores, resulting in a zinc wave (Taylor et al. 2012a). (5) The released zinc ions activate intracellular signaling molecules via an inhibitory effect on protein tyrosine phosphatases (PTP) (Taylor et al. 2012a). (6) The excess cytoplasmic zinc ions are tightly regulated by the muffling reaction. Eventually, the muffled zinc ion is either delivered back to intracellular stores or removed from the cell via ZnT1 (step 3)

triggered by protein kinase CK2 phosphorylation on serine residues S<sup>275</sup> and S<sup>276</sup>, resulting in activation of mitogen-activated protein kinases and tyrosine kinases (Taylor et al. 2012a), which are known substrates of the PTPs (Haase and Maret 2005). A simplified schematic of zinc homeostasis according to the muffler model with ZIP7 regulation is illustrated in Fig. 14.2.

Interestingly, the activation of ZIP9, which is located on the Golgi membrane (Matsuura et al. 2009), is also demonstrated to decrease PTP activity, resulting in activation of the same kinases in the chicken DT40 B cell line (Taniguchi et al. 2013). Given that ZIP7 expression is not detectable in chickens (Kambe et al. 2006), this further highlights the important role of the gatekeepers of zinc release from the stores, such as ZIP7 for mammalian cells and ZIP9 for chicken cells, in zinc signaling.

### ***14.3.2 ZnT Transporters***

The ZnT transporters (SLC30A), functioning as Zn<sup>2+</sup>/H<sup>+</sup> exchangers (Ohana et al. 2009), are responsible for zinc efflux from the cytoplasm. This family of zinc efflux transporters contains ten members, ZnT1 to ZnT10, which can be grouped into subfamilies I, II, and III (Huang and Tepasamorndech 2013). The majority of ZnT transporters have six TM domains, with intracytoplasmic amino- and carboxyl-termini and a long intracytoplasmic loop between TM IV and V, which includes the histidine-rich region, except for ZnT6, which has a serine-rich region instead (Seve et al. 2004). All ZnT transporters are located on intracellular membranes, except ZnT1, which is the only ZnT transporter on the plasma membrane, thereby being essential for zinc efflux from the cell (Palmiter and Findley 1995).

## **14.4 Zinc and Cancer**

Zinc has been widely studied for its potential involvement in human diseases. Because of its antioxidant properties and beneficial influences on the immune system and cell growth, zinc has been believed to protect the body against age-related diseases such as age-related macular degeneration (Age-Related Eye Disease Study Research Group 2001), to accelerate wound healing (Lansdown et al. 2007), and to reduce morbidities of the common cold (Science et al. 2012) and gastroenteritis (Walker and Black 2010).

The beneficial effects of zinc should generally help decrease the risk of cancer development and can be a potential dietary cancer-chemopreventive agent (Dhawan and Chadha 2010; Ho 2004; Prasad 2009). This hypothesis is supported by the epidemiological evidence that serum zinc levels are significantly decreased in patients with most types of cancers, including carcinomas of the head and neck (Buntzel et al. 2007), the breast (Arinola and Charles-Davies 2008), the gastrointestinal tract (Boz et al. 2005), the gallbladder (Gupta et al. 2005), and the female genital tract (Martin-Lagos et al. 1997; Naidu et al. 2007). Zinc levels in hair samples, which are likely to provide less variable results, confirm the decrease in zinc levels for cancers of the lung (Piccinini et al. 1996), breast (Memon et al. 2007), and ovary (Memon et al. 2007).

### ***14.4.1 Cancer-Preventive Role of Zinc***

Theoretically, the cancer-preventive effects of zinc are mainly attributed to its crucial role in both prevention of oxidative DNA damage, via its involvement in the free radical scavenging system, and response and repair of damaged DNA

(Ho et al. 2003). The involvement of zinc in DNA repair is supported by downregulation of some DNA repair genes in zinc-depleted cells (Ho et al. 2003). Interestingly, even though p53 expression, one of the most important tumor suppressor and DNA-repair genes, is increased by cellular zinc deficiency, its ability to induce an effective DNA repair is impaired in the absence of zinc, resulting from the loss of its binding capability to DNA sequences (Ho and Ames 2002). Zinc supplementation has also been suggested to help control the growth of cancers by inhibiting angiogenesis, inducing inflammatory cytokines, and promoting apoptosis in cancer cells (Prasad et al. 2009). Furthermore, in vivo studies have demonstrated that zinc supplementation prevents the development of *cis*-platinum- and melphalan-induced lung cancers in mice (Satoh et al. 1993), 1,2-dimethylhydrazine-induced colonic cancer in rats (Dani et al. 2007), and *N*-nitrosomethylbenzylamine (NMBA)-induced esophageal cancer in zinc-deficient rats (Fong et al. 2001).

Regardless of these anti-cancer properties of zinc, it is noteworthy that clinical studies have reported conflicting results. For instance, instead of preventing prostate carcinogenesis (Kristal et al. 1999), the use of zinc supplementation was instead shown to either increase the risk of prostate cancer (Kolonel et al. 1988; Leitzmann 2003) or have no association at all (Chang et al. 2004). Nevertheless, the cancer-promoting effect of zinc was possibly confounded by cadmium in some zinc supplements (Krone and Harms 2003). Collectively, the data from many studies to date have suggested that zinc has some cancer chemopreventive or even chemotherapeutic properties, at least for some types of cancers, even though the effectiveness and risk of zinc supplementation are yet to be proved.

Notwithstanding, some other studies have also reported contradictory results of zinc levels in patients with cancers of the breast, lung, stomach, and prostate (Navarro Silvera and Rohan 2007). Moreover, zinc levels in individual malignant tissues are not always well correlated with body zinc status: rather, they vary in a cancer type-specific manner. For example, zinc levels are significantly reduced in prostate cancer, but, regardless of the decrease in serum zinc levels, they are elevated in most other types of cancers, including cancers of the breast (Margalioth et al. 1983; Mulay et al. 1971) and the lung (Mulay et al. 1971). Therefore, the alterations in zinc levels in cancerous tissues may not necessarily be affected by systemic zinc status.

#### ***14.4.2 Cancer Tissue Zinc Levels with Aberrant Expressions of Zinc Transport Proteins***

Many studies support the fact that the changes in tumor tissue zinc levels are actually attributed to tissue-specific zinc dysregulation, resulting mainly from aberrant expressions of various ZIP channels. The uniquely decreased zinc level in prostatic cancer tissue directly corresponds to the decrease in the expression of

zinc channels ZIP1 (Huang et al. 2006), ZIP2, and ZIP3 (Desouki et al. 2007), as well as ZIP4 (Chen 2012). In contrast, the increased tissue zinc levels in various types of cancers are reasonably related to the increase in the expression of particular ZIP channels, such as ZIP6 (Taylor et al. 2003) and ZIP10 (Kagara et al. 2007) in breast cancer cells, ZIP7 in both tamoxifen-resistant and fulvestrant-resistant breast cancer models, and ZIP8 in a fulvestrant-resistant breast cancer model (Taylor et al. 2007).

Although no relevant data of tissue zinc levels are available to our knowledge, ZIP6 is known to increase in adenocarcinomas of the cervix and the lung (Taylor and Nicholson 2003). Parenthetically, even though bronchogenic carcinoma of the lung has been reported to have increased tissue zinc level, the tumor demonstrated squamous phenotypes, suggesting the diagnosis of squamous cell carcinoma, rather than adenocarcinoma (Mulay et al. 1971). Similarly, cervical cancer tissue is found to have no difference in zinc content from corresponding normal tissue, but no histological subtype was indicated (Margalioth et al. 1983). According to the much higher incidence of squamous cell carcinoma before the use of the Papanicolaou smear test as a screening method (Wang et al. 2004), it is more likely to be this histological type rather than adenocarcinoma, for which the increase in zinc channel ZIP6 is known.

Additionally, ZIP4 is shown to be overexpressed in 94 % of pancreatic adenocarcinoma specimens, and the experimentally induced ZIP4 overexpression results in zinc accumulation and cancer progression (Li et al. 2007). The zinc levels and zinc transport protein expression in tumor tissues or models are summarized in Table 14.1.

## 14.5 Zinc Signaling and Cancer

Currently available data suggest that zinc dysregulation resulting from aberrant expression of zinc transport proteins is associated with particular types of cancers in a cancer-specific manner. We therefore discuss each type of cancer individually in the remainder of this chapter. The roles of zinc transport proteins in carcinogenesis and cancer progression have been investigated most thoroughly for breast cancer and prostate cancer, which are the main focus of this review. However, we also discuss recent discoveries in other types of cancers.

### 14.5.1 Zinc Signaling in Breast Cancer

As all relevant studies have been performed in invasive ductal carcinoma of no special type, which is the most common type of breast cancer, comprising up to 79 % of breast carcinoma (Lester 2010), breast cancer in this chapter refers to this particular cancer type.



**Table 14.1** Zinc levels and zinc transport protein expression in tumor tissues or models

Cancer	Tissue zinc level	Aberrant expression of zinc transport proteins
Prostate adenocarcinoma	Decreased (Desouki et al. 2007)	Decreased <ul style="list-style-type: none"> <li>• ZIP1 (Huang et al. 2006)</li> <li>• ZIP2 (Desouki et al. 2007)</li> <li>• ZIP3 (Desouki et al. 2007)</li> <li>• ZIP4 (Chen 2012)</li> </ul>
Breast cancer (invasive ductal carcinoma)	Increased (Margalioth et al. 1983; Mulay et al. 1971)	Increased <ul style="list-style-type: none"> <li>• ZIP6 (Taylor et al. 2003)</li> <li>• ZIP10 (Kagara et al. 2007)</li> </ul>
Anti-hormone-resistant breast cancer	Increased in tamoxifen-resistant breast cancer model (Taylor et al. 2007)	Increased <ul style="list-style-type: none"> <li>• ZIP7 (Taylor et al. 2007) (tamoxifen-resistant and fulvestrant-resistant breast cancer model)</li> <li>• ZIP8 (Taylor et al. 2007) (fulvestrant-resistant breast cancer model)</li> </ul>
Pancreatic adenocarcinoma	N/A	Increased <ul style="list-style-type: none"> <li>• ZIP4 (Li et al. 2007)</li> </ul>

### 14.5.1.1 Zinc Status in Breast Cancer

Physiologically, the intact functions of particular zinc transporters are important during lactation, as impairment in zinc secretion into breast milk can result in zinc deficiency in a nursing infant (Kelleher et al. 2011). Pathologically, epidemiological data have long implicated zinc dysregulation in breast cancer, because significant elevation in zinc level has been consistently reported in cancerous tissue when compared with noncancerous breast tissue (Margalioth et al. 1983; Mulay et al. 1971). Zinc content in breast cancer tissue is demonstrated to be twice as high as the adjacent nonneoplastic tissue, and increase in metallothionein expression consistent with an elevation in zinc content is also observed (Jin et al. 1999).

The robustly increased zinc content in breast cancer and the role of zinc dysregulation in breast carcinogenesis have further been reinforced by experimental *in vivo* studies employing the *N*-methyl-*N*-nitrosourea (MNU)-induced mammary tumorigenesis model in rats, which is one of the most widely used animal models for investigating human breast carcinogenesis because of the biological similarities between MNU-induced mammary tumours and human breast cancer (Welsch 1985). These studies demonstrated the accumulation of zinc in the MNU-induced mammary tumors, with an increase in zinc concentration up to 19 fold when compared with nontumorous mammary glands (Lee et al. 2003; Woo and Xu 2002). Interestingly, the increase in zinc content was consistently observed, regardless of various dietary zinc intake levels (Woo and Xu 2002). In humans, the increase in zinc content in benign breast tissue has also been confirmed to be associated with a modestly increased risk of subsequent breast cancer (Cui

et al. 2007). Collectively, these data further support the role of zinc in breast cancer carcinogenesis and confirm the local, rather than systemic, zinc dysregulations, most likely resulting from malfunctions of zinc transport proteins and irrespective of dietary zinc consumption.

#### 14.5.1.2 Zinc Transport Proteins in Breast Cancer

The elevation in zinc content in breast cancer tissue has been attributed to aberrantly increased expressions of ZIP6 (Taylor et al. 2003) and ZIP10 (Kagara et al. 2007). ZIP6 has been linked to positive immunohistochemical staining for estrogen receptor (Manning et al. 1993) and breast cancers with lymph node involvement (Manning et al. 1994). It has been established to be an estrogen-regulated gene (Manning et al. 1994) and as such has become a reliable biomarker of estrogen receptor-positive luminal type A breast cancer (Perou et al. 2000; Tozlu et al. 2006). Using polymerase chain reaction (PCR) analysis, our group has confirmed the relationship between ZIP6 expression and estrogen-positive breast cancer both in cell lines and in clinical material (Taylor et al. 2007). Recently, using our unique ZIP6 antibodies, ZIP6 protein has been experimentally proved to be involved in epithelial-mesenchymal transition (EMT) and anoikis resistance, indicating ZIP6 as a cause of cell motility, migration, and metastasis (Hogstrand et al. 2013).

Furthermore, another ZIP channel, ZIP10, has also been connected to the increased invasiveness of cancer cells (Kagara et al. 2007). ZIP7, which increases in both tamoxifen-resistant and fulvestrant-resistant breast cancer models, has been implicated as a contributory factor in the development of anti-hormone resistance (Taylor et al. 2008), and additionally associated with poor clinical outcome in human breast cancer, according to the Oncomine database (Taylor et al. 2007). Recently, in association with protein kinase CK2, ZIP7 has also been shown to promote cell proliferation and migration (Taylor et al. 2012a). Therefore, there appear to be increasing data available to suggest that in the context of breast cancer, zinc and a number of ZIP channels are considered to be cancer promoting. The association between ZIP channels and breast cancer biology is summarized in Table 14.2. The mechanisms whereby these zinc channels contribute to particular malignant behaviors are discussed in detail next.

#### 14.5.1.3 Zinc Channel ZIP6 in Breast Cancer

Epithelial-mesenchymal transition (EMT) is crucial for embryonic development, as well as various pathological processes, including tissue repair and tumor metastasis (Thiery et al. 2009). As the name implies, it is the process whereby the cells lose their epithelial markers, such as adhesion molecule E-cadherin, and adopt a mesenchymal phenotype, promoting cell detachment and migration. Among the metastatic oncogenes, the transcription factor Snail plays an important role in EMT after

**Table 14.2** Association between ZIP channels and breast cancer biology

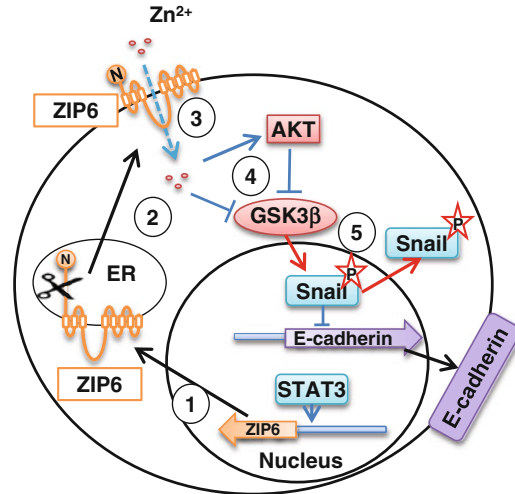
ZIP channel	Association with breast cancer biology
ZIP6	<ul style="list-style-type: none"> <li>• Reliable marker of estrogen-positive disease (Perou et al. 2000; Taylor et al. 2007; Tozlu et al. 2006)</li> <li>• Lymph node involvement (Manning et al. 1994; Taylor et al. 2007)</li> <li>• Cell motility, migration, and metastasis (Hogstrand et al. 2013)</li> <li>• Part of a five-gene molecular signature of outcome (Andres et al. 2013)</li> </ul>
ZIP10	<ul style="list-style-type: none"> <li>• Migration and metastasis (Kagara et al. 2007)</li> </ul>
ZIP7	<ul style="list-style-type: none"> <li>• Development of anti-hormone resistance (Taylor et al. 2008)</li> <li>• Proliferation and migration (Taylor et al. 2012a)</li> </ul>

its nuclear localization by repressing the transcription of E-cadherin (Peinado et al. 2007). Snail has been demonstrated to be negatively regulated by glycogen synthase kinase-3-beta (GSK-3 $\beta$ )-mediated phosphorylation, which promotes its nuclear export, ubiquitination, and consequential degradation (Zhou et al. 2004).

Importantly, with its molecular link to signal transducer and activator of transcription 3 (STAT3), ZIP6 is known to be essential for EMT in zebrafish gastrulation, by promoting the nuclear localization of Snail, resulting in the repression of E-cadherin and increased cell migration (Yamashita et al. 2004). Given that the roles of both STAT3 (Pakala et al. 2013) and Snail (Zhang et al. 2013) in metastasis have been well documented in breast cancer, with an additional strongly positive correlation between the expression of ZIP6 and STAT3 (Taylor et al. 2007), the potential mechanistic link between the role of ZIP6 in gastrulation and breast cancer metastasis has come to light.

Recently, the mechanism of action of zinc channel ZIP6 in breast cancer migration has been unraveled by a study in which ZIP6 was demonstrated to be transcriptionally transactivated by STAT3, resulting in its expression as a pro-protein (Hogstrand et al. 2013). The ZIP6 pro-protein resides on the endoplasmic reticulum membrane until the appropriate stimulus triggers cleavage at the N-terminus between residues 155 and 237, which causes it to relocate to the plasma membrane where it can influx zinc into the cell. This posttranslational processing of ZIP6 was discovered using a panel of anti-peptide antibodies with different epitopes (Hogstrand et al. 2013) and observing that the ZIP6 antibody epitope near the far N-terminus and upstream of residue 155 never recognized plasma membrane-located ZIP6, but only ZIP6 located in the endoplasmic reticulum. These data now explain some apparently conflicting results in the literature suggesting that ZIP6 was a good indicator of favorable breast cancer outcome (Kasper et al. 2005). The antibody epitope used in this latter study was upstream of the N-terminal cleavage site of ZIP6 and would only be able to recognize endoplasmic reticulum-located ZIP6. This study therefore agrees with new data, provided the endoplasmic reticulum-located ZIP6 is considered to be the inactive pro-protein form of ZIP6.

After ZIP6 had been activated by N-terminal cleavage and relocated to the plasma membrane (Hogstrand et al. 2013), it was able to mediate zinc influx into



**Fig. 14.3** Schematic illustration of ZIP6 involvement in epithelial-mesenchymal transition (EMT) demonstrates the ZIP6 signaling pathway associated with EMT, as proposed by a recent study (Hogstrand et al. 2013). (1) After transcriptional activation by STAT3, ZIP6 protein is produced as a pro-protein and located on the endoplasmic reticulum. (2) Upon activation by N-terminal cleavage, the ZIP6 channel is translocated to the plasma membrane. (3) The plasma membrane-located ZIP6 mediates zinc influx into the cytoplasm. (4) Glycogen synthase kinase-3-beta (*GSK-3β*) is inhibited by phosphorylation, mediated either directly by zinc or indirectly by zinc-activated AKT. (5) Normally, GSK-3β negatively regulates Snail by phosphorylation, resulting in nuclear export, ubiquitination, and degradation of Snail. Inhibition of GSK-3β therefore causes nuclear retention of Snail, leading to repression of the adhesion molecule E-cadherin, and consequential cell migration and metastasis

the cytoplasm, resulting in inhibitory phosphorylation of GSK-3β, either directly by zinc (Ilouz et al. 2002) or indirectly by zinc-activated AKT (Lee et al. 2009), with subsequent nuclear retention of Snail, transcriptional repression of E-cadherin, and increased cell detachment (Hogstrand et al. 2013). Interestingly, being resistant to anoikis, the detached cells retained their capability to proliferate even after detachment (Hogstrand et al. 2013), thereby having a high potential to migrate and metastasize. A simplified schematic illustration of this mechanism is depicted in Fig. 14.3.

#### 14.5.1.4 Zinc Channel ZIP10 in Breast Cancer

ZIP10 is known to be the closest paralogue to ZIP6 (Taylor and Nicholson 2003). ZIP6, an estrogen-regulated gene, and ZIP10 have a positive correlation with estrogen receptor in breast cancer tissue, even though the latter does not have such potential clinical relevance because of its low expression (Taylor et al. 2007). Similar to ZIP6, ZIP10 is also demonstrated to be involved in migration and metastasis of breast cancer (Kagara et al. 2007). Furthermore, among all the

members of the LIV-1 subfamily, ZIP10 is the only zinc channel other than ZIP6 that contains a potential PEST cleavage site (Taylor and Nicholson 2003), and it has been shown to be proteolytically modified at its ectodomain (Ehsani et al. 2012). However, it is yet to be determined whether it is posttranslationally processed in the same manner as ZIP6 and whether it synergistically participates with ZIP6 in the process of migration and metastasis in breast cancer.

#### 14.5.1.5 Zinc Channel ZIP7 in Breast Cancer

In routine clinical practice, patients with both early and late estrogen receptor-positive breast cancers, pathologically diagnosed by tissue biopsies, are treated with anti-hormonal drugs, such as tamoxifen (Osborne 1998). Unfortunately, as many as 40 % of patients who initially respond to the adjuvant tamoxifen therapy eventually acquire drug resistance, resulting in relapse and death from the disease (Ring and Dowsett 2004). To investigate the mechanisms of acquired resistance, our group has developed a tamoxifen-resistant breast cancer cell line (TamR), which was derived from estrogen receptor-positive tamoxifen-responsive MCF-7 breast cancer cells (Knowlden et al. 2003). Interestingly, not only are the TamR cells able to continue growing in the presence of the drug, but they also exhibit an even more aggressive phenotype, such as increased cell motility and invasiveness (Hiscox et al. 2004). The aggressive phenotype was attained by hyperactivation of alternative pathways, including those mediated by epidermal growth factor receptor (EGFR) (Knowlden et al. 2003), insulin-like growth factor-1 receptor (IGF-1R) (Jones et al. 2004), and non-receptor tyrosine kinase Src (Hiscox et al. 2006), all of which are included among the known substrates of PTP1B (Bourdeau et al. 2005).

Given that ZIP7 is the only ZIP channel to be overexpressed in TamR cells, which have been demonstrated to have twice as much zinc as the responsive MCF-7 cells (Taylor et al. 2007), the potential role of ZIP7 in the development of anti-hormone resistance and the associated aggressive behaviour cannot be overstated. We have investigated this in TamR cells and proved that ZIP7-mediated zinc release from the stores was responsible for activation of tyrosine kinase receptor signaling pathways as well as Src-dependent pathways (Taylor et al. 2008), which was likely mediated by the zinc inhibitory effect on PTP1B (Haase and Maret 2005). The stimulation of these signaling pathways resulted in activation of their downstream effectors, including mitogen-activated protein kinase (MAPK) such as extracellular signal-regulated protein kinases 1 and 2 (ERK1/2) and AKT, with consequential increases in cell growth and motility (Taylor et al. 2008). It is noteworthy that Src not only activates the tyrosine kinase receptor signaling pathways itself, but it also contributes to cell proliferation, cell survival, invasiveness, and angiogenesis (Summy and Gallick 2006), all of which result in increased aggressiveness of the malignancy. Moreover, we demonstrated that concentrations of zinc as low as 20  $\mu\text{M}$  could overcome the effects of Src inhibitor on cancer invasiveness, conveying the efficiency of the intracellular zinc ions to activate this oncogenic tyrosine kinase (Taylor et al. 2008). Altogether, these data introduce the

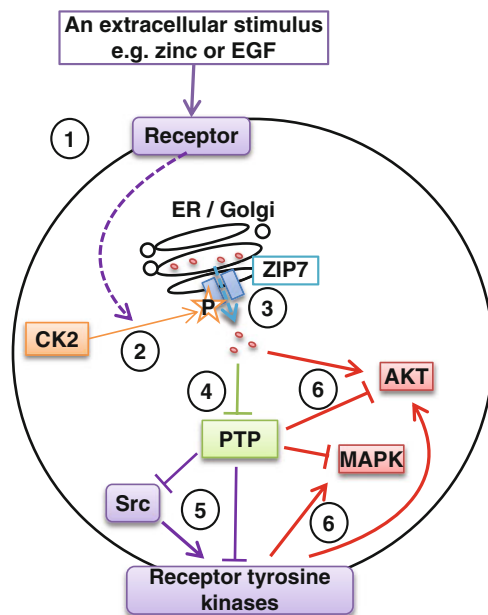
concept that blocking ZIP7-mediated zinc release could be a new and worthwhile strategy for the treatment of anti-endocrine-resistant breast cancer.

Regardless of the well-established involvement of ZIP7 in cancer, little is known of its molecular regulatory mechanisms. Remarkably, posttranslational regulation by phosphorylation of ZIP7 has been demonstrated in a recent study, in which CK2 phosphorylated serine residues S<sup>275</sup> and S<sup>276</sup>, which reside within the long histidine-rich intracytoplasmic loop between TM III and TM IV. This phosphorylation triggered the ZIP7-mediated release of zinc from internal stores (Taylor et al. 2012a), and the released zinc in turn activated downstream signaling pathways, including phosphorylation of ERK1/2 and AKT, and promoted cell migration. This information now provides new insight into how the ZIP channels are regulated. Furthermore, the protein kinase that phosphorylates ZIP7, CK2, is itself involved in cell growth and proliferation, as well as oncogenesis and pathobiological features of neoplasms, with numerous possible substrates that may be responsible for these effects (Tawfic et al. 2001). Therefore, these findings also suggest a possibility that CK2 may cause a number of these cancer-promoting effects by mediating the phosphorylation of zinc channel ZIP7 (Taylor et al. 2012b). A simplified schematic demonstrating ZIP7-mediated zinc release from the stores with activations of downstream effectors is shown in Fig. 14.4.

According to the phosphorylation prediction databases, there are at least four residues in the cytoplasmic loop between TM III and IV of zinc channel ZIP7 that have been experimentally confirmed by mass spectrometry (Daub et al. 2008; Kim et al. 2005; Zahedi et al. 2008) to be phosphorylated in mammalian cells (Fig. 14.5). Serine residues S<sup>275</sup> and S<sup>276</sup> (Kim et al. 2005) are the only two sites that have to date been confirmed by site-specific methods to be phosphorylated by CK2 (Taylor et al. 2012a). Interestingly, the kinases predicted according to the consensus sequences for the other two sites, S<sup>293</sup> and T<sup>394</sup> (Olsen et al. 2010), have some cancer-promoting properties. The kinases MAPKAPK2 and MAPKAPK3, predicted for S<sup>293</sup>, are involved in cell migration (Menon et al. 2009), while the kinases PIM1, PIM2, and PIM3, predicted for T<sup>394</sup>, promote cell proliferation (Chen et al. 2005) and survival (Amaravadi and Thompson 2005). It is yet to be investigated whether these two sites also orchestrate the regulation of ZIP7, whether they are phosphorylated by the particular predicted kinases, and whether ZIP7-mediated zinc release is responsible for the cancer-promoting properties of these predicted kinases. Given that ZIP7 is activated by phosphorylation, it is also to be questioned if other ZIP transporters can be activated in the same manner.

### ***14.5.2 Zinc Signaling in Prostate Cancer***

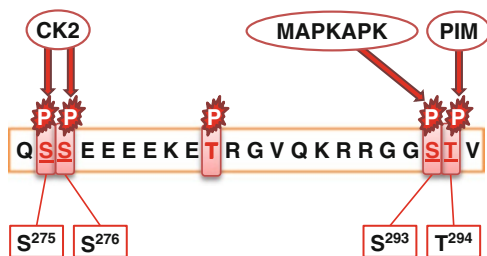
A role for zinc and zinc signaling has also been demonstrated for prostate cancer. However, in contrast to that observed for breast cancer, the level of zinc appears to decrease in prostate cancer compared to normal prostate.



**Fig. 14.4** ZIP7-mediated zinc release from stores and the downstream cascades. (1) ZIP7-mediated zinc release from stores can be activated by an extracellular stimulus, such as zinc or epidermal growth factor (*EGF*) (Taylor et al. 2012a). (2) This activation results in association between protein kinase CK2 and ZIP7 and consequential phosphorylation on S<sup>275</sup> and S<sup>276</sup> of ZIP7 (Taylor et al. 2012a). The connection between the extracellular stimulus and ZIP7 activation is as yet unknown. (3) The phosphorylation of ZIP7 activates zinc release from the stores on which ZIP7 resides, such as the endoplasmic reticulum (*ER*) or the *Golgi*, thereby producing a zinc wave (Taylor et al. 2008, 2012a). (4) The released zinc in turn inhibits PTPs (Haase and Maret 2005). (5) The inhibition of PTPs, such as PTP1B, results in sustained activation of tyrosine kinases, including EGFR, IGF-1R, and nonreceptor tyrosine kinase *Src* (Taylor et al. 2008). (6) Eventually, this zinc release results in activation of various kinases downstream of these tyrosine kinases such as *MAPK* and *AKT*, either via *Src*-dependent receptor tyrosine kinase activation (Taylor et al. 2008) or via the zinc inhibitory effect on PTPs (Haase and Maret 2005). Additionally, *AKT* is directly activated by zinc (Lee et al. 2009)

#### 14.5.2.1 Zinc Status in Prostate Cancer

Along with the choroid of the eye, the prostate gland has the highest concentration of zinc in the body (World Health Organization and Food and Agriculture Organization of the United Nations 2002). Zinc is known to be involved in male fertility, as it is required for sperm release and motility (Yoshida et al. 2008). Physiologically, high zinc levels in the prostate gland spare citrate from the citric acid cycle by inhibiting the enzyme m-aconitase, thereby helping supply high amounts of citrate into prostatic fluid (Costello et al. 2005). In pathological conditions, prostate tissue zinc levels increase in nonneoplastic prostate disease, whereas they dramatically decrease in prostate cancer (Zaichick et al. 1997). These epidemiological data introduce zinc decrease as a cancer-promoting condition and zinc supplementation



**Fig. 14.5** Phosphorylation sites for ZIP7 with kinase prediction. The amino acid sequence of ZIP7 between residues 274 and 295 is located on the intracytoplasmic loop between TM III and TM IV. We show the predicted phosphorylation sites that have been experimentally confirmed in mammalian cells for ZIP7 (Daub et al. 2008; Kim et al. 2005; Zahedi et al. 2008), and the predicted kinases with the highest scores for these sites using PhosphoNET (Kinexus Bioinformatics Corp.), PhosphoSitePlus (Hornbeck et al. 2012), and Phosida (Gnad et al. 2007)

as a promising cancer-preventive strategy, even though clinical studies have failed to show consistent results, as mentioned earlier in Sect. 14.4.1.

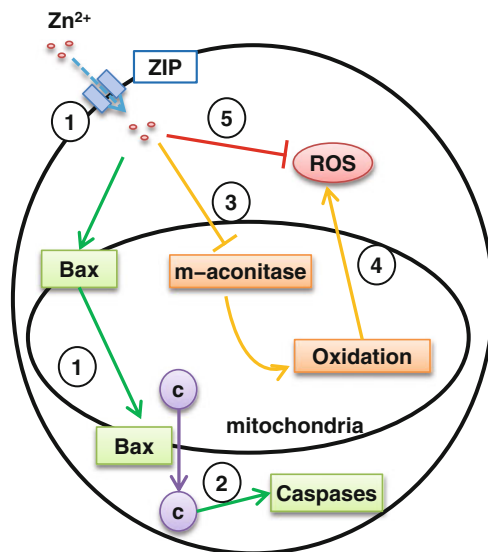
#### 14.5.2.2 Zinc and Prostate Carcinogenesis

Mechanistically, the role of zinc in prostate cancer prevention or suppression is at least twofold: it prevents prostate epithelial cells from oxidative DNA damage, and it induces apoptosis. A simplified schematic is shown in Fig. 14.6.

Zinc-deficient prostate epithelial cells have been reported to have increased DNA damage (Yan et al. 2008), which suggests that high zinc content is essential for prevention of oxidative DNA damage in the prostate gland. This beneficial effect of zinc can be linked to its physiological action of m-aconitase inhibition (Costello et al. 1997). Loss of any zinc inhibitory effect on the enzyme encourages citrate to enter into the citric acid cycle and the subsequent oxidative phosphorylation. Even though this ATP-producing process is vital for life, it also results in the production of reactive oxygen species, a major cause of DNA damage. Furthermore, the decrease in zinc with its antioxidant properties (Oteiza 2012) results in uncontrolled generation of free radicals. It therefore can be concluded that decrease in the zinc content of prostate glands may eventually cause excessive production of free radicals and consequential DNA damage.

Moreover, high zinc concentration also produces pro-apoptotic conditions in the prostate gland (Feng et al. 2002), supported by the finding that zinc directly induces bax-mediated mitochondrial cytochrome *c* release, which in turn activates the caspase cascade, ultimately leading to apoptotic cell death (Feng et al. 2008). Therefore, the cellular zinc deficiency observed in the prostate promotes cell survival by inhibiting apoptosis in prostate epithelial cells.





**Fig. 14.6** Role of zinc in prostate cancer prevention or suppression. Schematic illustrates the mechanism whereby zinc suppresses prostate cancer. (1) In the normal prostate, ZIP channels, including ZIP1, ZIP2, ZIP3, and ZIP4, assure high zinc levels. Zinc directly causes *Bax*-mediated cytochrome *c* release from the mitochondria (Feng et al. 2008). (2) The released cytochrome *c* activates a caspase cascade, resulting in apoptotic cell death. (3) To spare citrate for secretion into prostatic fluid, zinc inhibits *m-aconitase* (Costello et al. 1997), preventing citrate from entering into the citric acid cycle and oxidation. (4) As normal oxidative phosphorylation produces free radicals, the inhibitory effect of zinc on *m-aconitase* results in a decrease in free radical production. (5) Moreover, zinc itself has anti-oxidant properties (Oteiza 2012), thereby preventing oxidative DNA damage

### 14.5.2.3 Zinc Signaling in Prostate Cancer

The reduced zinc level in prostate cancer is associated with decreased expression of ZIP channels, including ZIP1 (Huang et al. 2006), ZIP2, and ZIP3 (Desouki et al. 2007), as well as ZIP4 (Chen 2012). Among these zinc channels, ZIP1 is demonstrated to be highly expressed in the peripheral zone, the most common site of cancer, and its gene expression is massively downregulated at an early stage of the cancer (Franklin et al. 2005), explaining why it is known as a tumor suppressor gene in prostate cancer (Costello and Franklin 2006; Franklin and Costello 2007).

Surprisingly, zinc transporters ZnT1 (Hasumi et al. 2003) and ZnT4 (Beck et al. 2004) are found to decrease in prostate cancer tissue, but their involvement in prostate carcinogenesis is rather obscure and is yet to be unraveled.

### ***14.5.3 Zinc Signaling in Other Cancers***

In the past few years a number of studies have implicated aberrant zinc transporter expression in other cancers. For example, ZIP4 has been implicated in the acquisition of zinc by hepatocellular carcinomas (Weaver et al. 2010). In these cancers, ZIP4 was present in increased amounts and as such able to repress apoptosis, enhance growth rate, and enhance the invasive capacity of the cancers. Moreover, ZIP6 mRNA was increased in liver cancer cells compared to normal cells and demonstrated an inverse relationship with E-cadherin (Shen et al. 2013), agreeing with the role for ZIP6 in EMT and migration of breast cancer cells (Hogstrand et al. 2013). A decrease in another ZIP channel, ZIP14, in contrast to ZIP1, ZIP2, and ZIP3, has also been associated with hepatocellular cancer and thought to be involved with the depletion of zinc observed in these cells (Franklin et al. 2012).

Although the exact role for zinc in pancreatic cancer has not yet been elucidated, there is certainly new evidence emerging that zinc may have a role. Levels of ZIP transporters appear considerably decreased in the disease (Costello and Franklin 2013; Yang et al. 2013), especially levels of ZIP3, which has also been implicated in the early development of pancreatic adenocarcinoma (Costello et al. 2011, 2012). Additionally, ZIP4 has been demonstrated to regulate pancreatic cell growth and does not show the decrease in cancerous tissue observed with other family members (Yang et al. 2013). Furthermore, the pathway of action of ZIP4 was elucidated to involve increases of IL-6, activating STAT3 and leading to increased cell proliferation by increases of cyclinD1 (Zhang et al. 2010). As the zinc-associated events appear to take place in the early phase of oncogenesis, this would suggest a worthy area for future investigation.

Recently, three independent groups have implicated ZIP14 as having a role in colorectal cancer, encompassing ZIP14 splice variants in the disease (Thorsen et al. 2011) and their use as a potential biomarker (Sveen et al. 2012) or therapeutic target (Miura et al. 2012). Furthermore, ZIP10, a molecule with a recognized role in breast cancer (Kagara et al. 2007), is one of seven genes upregulated in activated colon tumor cells.

It seems increasingly obvious that aberrant expression of a variety of zinc transporters, depending on the tissue in question, may be involved in providing more zinc to tumor cells than is required for normal growth and thus encouraging excessive or cancerous growth. Further examination of these molecules is now required, as well as investigation of their phosphorylation status, to understand their influence on zinc signaling pathways in tumors.

## 14.6 Use of Zinc Signaling as a Target or Cancer Biomarker

This is an exciting time in zinc biology with respect to targeting cancer growth, as the mechanisms of action of zinc transporters and channels within cells are just beginning to emerge with the hope of delivering new potential biological targets that could impact greatly on clinical disease. Furthermore, the proven involvement of certain zinc channels and transporters could also provide new biomarkers for this type of treatment. Moreover, the realization that zinc channels require phosphorylation to release zinc opens the door for biomarkers using antibodies that only recognize the phosphorylated, and therefore active, forms of these molecules.

### 14.6.1 Zinc Signaling as a Cancer Target

As more information is discovered defining the mechanism of action of zinc transporters in intracellular zinc release, more opportunities are made available for producing agents that may be useful new inhibitors of the signaling pathways known to drive the aggressive growth of tumors. Two particular examples are discussed in the following sections.

#### 14.6.1.1 Targeting ZIP7 Using Protein Kinase CK2 Inhibitors

The discovery that zinc channel ZIP7 requires phosphorylation by protein kinase CK2 to open the channel gate and release zinc from intracellular stores (Taylor et al. 2012a) has provided a means for targeting this mechanism of zinc release by using CK2 inhibitors. Interestingly, Cylene Pharmaceuticals has developed a CK2 inhibitor that is currently under evaluation in clinical cancer trials (Siddiqui-Jain et al. 2010). This inhibitor, called CX-4945, has not only shown promise in combination with EGFR inhibitors in killing cancer cells (Bliesath et al. 2012), but also and more recently has been demonstrated as a potential new treatment for glioblastoma (Zheng et al. 2013) and leukemia (Martins et al. 2013).

Protein kinase CK2 is a ubiquitously expressed threonine/serine kinase composed of two catalytic  $\alpha$ -subunits and two regulatory  $\beta$ -subunits (Niefind et al. 2009) that has a multitude of cellular targets. Protein kinase CK2 has a proven role in cell survival and proliferation (St.-Denis and Litchfield 2009) and shuttles between the cytosol and nuclei of cells to support apoptosis or mitosis, respectively. Furthermore, CK2 levels are known to be increased in many different cancer types, suggesting deregulation and a potential target. Importantly, the ZIP7-mediated zinc release from the ER and the subsequent activation of multiple downstream pathways that enhance cell proliferation and migration rely on phosphorylation of zinc channel ZIP7 by protein kinase CK2 (Taylor et al. 2012b).

ZIP7 abundance is increased in tumors, being one of the top 10 % of genes overexpressed in many poor prognostic cancer states, and shows a statistically significant positive correlation of mRNA expression with known indicators of poor outcome in breast cancer, such as the proliferation marker Ki67 (Taylor et al. 2007). This finding, together with current thinking that CK2 is essential for the neoplastic phenotype and can also act as an oncogene when overexpressed (Duncan and Litchfield 2008), suggests that these two molecules may have a common role in cell survival. The fact that CK2 inhibitors decrease the viability of various cancer cells, including prostate cancer cells and tamoxifen-resistant MCF-7 breast cancer cells (Yde et al. 2007), adds further weight to this view, supporting the possibility that CK2 and ZIP7 may function together to mediate intracellular zinc release.

Targeting ZIP7-mediated release of zinc in breast cancers leads to loss of growth, invasion, and signaling (Taylor et al. 2008). The identification here of a CK2-mediated phosphorylation switch for activating ZIP7 to release zinc opens the door to the use of CK2 inhibitors, which are well tolerated by cancer patients (Solares et al. 2009), to treat breast cancer. Furthermore, because intracellular zinc signals inhibit protein tyrosine phosphatases (Haase and Maret 2005), targeting zinc release could prevent activation of multiple tyrosine kinases and their associated signaling pathways, thereby benefiting cancer patients (Taylor et al. 2008, 2011).

ZIP7 has a recognized role in driving the growth of tamoxifen-resistant breast cancers (Taylor et al. 2008). Therefore, targeting zinc release, in conjunction with anti-hormones such as tamoxifen, the usual treatment for these types of cancer, is likely to provide a successful method of inhibiting multiple signaling pathways because of the ability of intracellular zinc to inhibit multiple phosphatases (Haase and Maret 2005). This method should prevent the cancer from harnessing alternative pathways and ensure a continual response to current anti-hormone treatment.

#### **14.6.1.2 Targeting ZIP6**

ZIP6 is an estrogen-regulated gene and as such used as a marker of luminal A breast cancer (Perou et al. 2000). We have also shown that ZIP6, after N-terminal cleavage, is enriched on the plasma membrane of migratory cancer cells (Hogstrand et al. 2013) as part of an EMT mechanism. Evidence that ZIP6 associates with ER-positive and triple-negative breast cancers has been used to generate a new therapeutic for breast cancer (Sussman et al. 2013). SGN-LIV1A is an antibody drug-conjugate targeting ZIP6 in metastatic breast cancer that consists of a humanized ZIP6 antibody conjugated to the microtubule-disrupting agent, monomethyl auristatin E, via a protease-cleavable linker. Clinical trials using this agent are currently in the initiation phase by Seattle Genetics, with the hope that the ZIP6 antibody would attach to cancer cells and the toxin would destroy them.

### ***14.6.2 Zinc Signaling as a Cancer Biomarker***

ZIP7 associates with STAT3 and cancer spread in anti-hormone-resistant breast cancer (Taylor et al. 2007). The level of ZIP7 may be indicative of the potential for zinc release, although the level of the phosphorylated form may be a better indicator of the activated ZIP7 than the total. There is existing evidence from Affymetrix analysis of a variety of anti-hormone-resistant breast cancer cell models (Taylor et al. 2007) that ZIP7 expression is not only increased but that the zinc level in these cells is also increased. Furthermore, it has also been suggested that this increased zinc, as a direct result of increased ZIP7-mediated zinc release into the cytoplasm (Taylor et al. 2008), is responsible for the activation of multiple signaling pathways that promote aggressive growth and migration of the cancers. All these data collectively suggest that levels of ZIP7 or phosphorylated ZIP7 may, together or individually, be useful markers of cancers that are likely to become resistant to anti-hormones. Our group are currently testing an antibody that detects only the phosphorylated form of ZIP7 as such a biomarker in breast cancer disease states.

ZIP6 also has a significant association with STAT3 in breast cancer samples (Taylor et al. 2007) and has been demonstrated recently to have a causative role in cell detachment (Hogstrand et al. 2013). This mechanism requires N-terminal cleavage of ZIP6 to cause relocation of ZIP6 from the endoplasmic reticulum to the plasma membrane where it can influx zinc into cells. These data suggest that ZIP6 could be present on the plasma membrane of cancer cells and also those cancer cells that have detached from the original tumor. This mechanism could be harnessed to deliver a novel biomarker for metastatic cells, provided the ZIP6 antibody was directed to the correct extracellular location of ZIP6.

## **14.7 Conclusions and Perspectives**

From the foregoing discussions, there appears to be an emerging role for zinc in driving the excessive growth of cancer cells. Most cancer tissues examined to date, with the exception of prostate cancer, have elevated intracellular zinc, which could easily cause tyrosine kinase-driven growth by the known ability of zinc to inhibit tyrosine phosphatases. The realization that zinc channel ZIP7 requires phosphorylation to transport zinc (Hogstrand et al. 2013) now raises the question of whether other zinc channels also require phosphorylation. If this is true, then much work is needed to examine which kinases are involved in activating which zinc channels. Further discoveries in this area should shed light on this and open the door for new and novel small kinase inhibitors that can be used to inhibit the effects of excessive zinc in cancer cells.

The knowledge of the three-dimensional structure of the bacterial ZnT family member, YiiP (Lu and Fu 2007), has provided much insight into the workings of these transporters. There is now a need for the complementary structure of the ZIP

family to be discovered, which would enable the design of specific inhibitory small molecules to target the phosphorylation of individual zinc channels. The hope would be that these small molecules would be more specific than broad kinase inhibitors and prevent the often unwanted side effects observed with these types of drugs in the clinic.

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# Chapter 15

## Zinc as a Key Meiotic Cell-Cycle Regulator in the Mammalian Oocyte

Ru Ya, Emily L. Que, Thomas V. O'Halloran, and Teresa K. Woodruff

**Abstract** Mammalian oogenesis is a discontinuous process that begins during fetal development, arrests at birth, and then resumes on a cyclical basis from puberty to menopause to produce fully mature oocytes that are competent for fertilization. Females are born with a fixed number of oocytes arrested at the prophase I stage of meiosis. This arrest is maintained until oocytes are selected to resume growth by gonadotropins, which are released from the pituitary upon entering puberty. At the time of ovulation, a fully grown oocyte completes maturation and arrests again at metaphase of meiosis II until fertilization occurs. Sperm binding triggers egg activation and release from metaphase II arrest. This entire process is tightly controlled, as it has a significant impact on egg quality and the developmental potential of the resulting embryo. The underlying mechanisms regulating oocyte meiotic entry, arrest, and exit—which can occur over a span of decades—have always been of great interest in the reproductive biology field, and many groundbreaking discoveries have revealed the existence of a dynamic network of hormones, receptors, kinases, and second messengers that control this process. Recent work has expanded this regulatory network to include the transition metal zinc, which adds a new level of complexity and fine-tuning to the regulation of the oocyte meiotic cell cycle. Dynamic accrual, sequestration, and exocytosis of zinc through controlled pathways are crucial for appropriate timing of the meiotic cell cycle as oocytes progress through maturation and activation. This work is important to our general understanding of oocytes and will have implications for reproductive interventions in the future.

**Keywords** Egg • Fertilization • Meiosis • Oocyte • Zinc spark • Zinc

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## 15.1 Introduction

Zinc is the second most abundant transition metal, after iron, in living organisms, and its roles in enzymatic catalysis, in protein structure, and in signal transduction have been well characterized (Berg and Shi 1996; Vallee and Falchuk 1993). Zinc may also have second messenger roles in a number of physiological and pathological processes such as glucose-responsive insulin secretion, diabetes, and immune cell function (Mocchegiani et al. 2008; O'Halloran et al. 2013; Yamasaki et al. 2007). Excessive levels of zinc are toxic to cells whereas zinc deficiency is associated with a number of abnormal developmental conditions, including neuronal and immune system defects (Fukada et al. 2011). A number of proteins have known functions in regulating the total cellular zinc concentration and subcellular distribution, including zinc-responsive transcription factors, a wide array of zinc transporters, and zinc-sequestering proteins including the metallothioneins (MT) (Blindauer and Leszczyszyn 2010; Finney and O'Halloran 2003; Fukada and Kambe 2011; Guerra and Giedroc 2012; Kambe et al. 2004; Outten and O'Halloran 2001; Vallee 1995; Waldron et al. 2009). Recent studies reveal that changes in zinc content and subcellular distribution are essential for the maturing oocyte to move through reductive division, known as meiosis, and to later successfully navigate fertilization and early embryogenesis. This chapter reviews the emerging role of zinc in female oocyte biology, where zinc plays a necessary role in completing meiosis and providing the key signal to convert from the meiotic cell cycle in the egg to the mitotic cell cycle of the embryo.

## 15.2 Oocyte Growth, Maturation, Activation, and Fertilization

To put several of the emerging roles of zinc fluxes in meiotic progression into a biological context, we begin with a brief review of mammalian oogenesis. In mammals, oogenesis begins during embryogenesis and continues until just before birth, when germ cells stop dividing and enter meiosis. Females are born with a fixed number of oocytes, which are enclosed by a single layer of somatic cells called granulosa cells to form follicles, the functional unit of the ovary. The smallest follicles, primordial follicles, form around the time of birth, and each follicle contains a prophase I-arrested (PI) immature oocyte. Primordial follicles remain dormant until they are activated and recruited into the growing follicle pool with each reproductive cycle (McGee and Hsueh 2000). A single primordial follicle and its meiotically arrested oocyte may remain dormant for years, even decades, from the time of birth to the time of activation. Following activation, the follicle grows as the granulosa cell layer proliferates and expands. Growth completes upon formation of the antral follicle, which is characterized by the appearance of the fluid-filled cavity (Rodgers and Irving-Rodgers 2010). As the follicle is growing, so

does its enclosed oocyte, expanding from a diameter of 10  $\mu\text{m}$  in a primordial follicle to 70–80  $\mu\text{m}$  at its final stage in mice (Griffin et al. 2006). The coordinated growth of the follicle and its oocyte is critical for production of a fully mature, meiotically competent oocyte that can be successfully fertilized following ovulation and develop into a viable embryo (Erickson and Sorensen 1974).

During early stages of follicle growth, the oocyte remains arrested in prophase I, displaying an enlarged nuclear envelope called the germinal vesicle (GV). In the antral follicle stage, the PI-arrested oocyte is fully grown and becomes transcriptionally quiescent. At this point, a surge in luteinizing hormone (LH) from the pituitary initiates meiotic resumption in the oocyte, inducing germinal vesicle breakdown (GVBD), concurrent with the condensation of the chromosomes, and promoting the expansion of the surrounding cumulus granulosa cells. After GVBD, the oocyte progresses through meiosis I and undergoes asymmetrical cell division by extruding the first polar body. It then enters meiosis II without interphase and arrests again at metaphase II (MII), at which point the oocyte is now called an egg. In mice, the MII egg ovulates approximately 12 h after the LH surge. This entire process (from PI to MII) is called oocyte maturation, and results in a mature egg that is ready for fertilization.

Upon fertilization, the MII egg completes meiosis II. Binding of sperm to the egg triggers a series of reactions referred to as egg activation, which includes calcium oscillations, exocytosis of cortical granules that block polyspermy, and release of the second polar body to reduce the maternal genome by half (Horner and Wolfner 2008; Wakai et al. 2011). The events of MII egg activation can be induced by artificial means in the absence of sperm in a process called parthenogenesis. Soon after fertilization, paternal and maternal pronuclei form separately and then eventually fuse together before initiating embryonic cell division. Transcription ceases before the oocyte resumes meiosis until zygotic genome activation occurs around the two-cell stage in mice; thus, the entire oocyte maturation and the initial embryonic division are under the influence of the maternally stored transcripts (Moore and Lintern-Moore 1974, 1978; Schultz 2002). Although much is known about oocyte maturation, the meiotic cell cycle, and the egg-to-embryo transition, nothing was known about zinc biology in this process, which is reviewed next.

### **15.3 Massive Zinc Fluxes Are Integral to Oocyte Development and Activation**

The role of calcium in egg activation had been recognized for some time, but little was known about the role of other ions or inorganic metals in oocyte biology. Our first clue that zinc was an integral part to this whole process came from our studies using advanced elemental detection technologies, namely synchrotron-based X-ray fluorescence microscopy (XFM) (de Jonge and Vogt 2010). Using XFM, we discovered quantitative dynamic changes in the inorganic signature of the oocyte



during maturation, activation, and fertilization. More specifically, the elemental makeup at three key stages was determined: the PI oocyte, the MII egg, and the two-cell embryo (Kim et al. 2010). Indeed, XFM data showed that zinc is the most abundant transition metal in the mouse oocyte and that its quota is an order of magnitude higher than those of iron or copper. During maturation, the oocyte rapidly acquires 20 billion zinc atoms, an increase of about 50 % in total zinc content that occurs with minimal change in total cell volume. Following fertilization, approximately 12 billion zinc atoms are lost by the time the newly fertilized embryo reaches the two-cell stage (~20 % decrease) (Kim et al. 2010). These large fluxes in zinc content suggested a larger role for zinc during oocyte maturation and egg activation and motivated a number of further studies regarding the possible cellular functions of zinc during these transitions. What is known regarding the role of zinc in the regulation of oocyte maturation, activation, and fertilization is discussed in detail next.

### ***15.3.1 Roles for Zinc in Maintenance of Prophase I Arrest and Meiotic Resumption***

The follicle environment inhibits oocyte maturation until the LH surge, as the oocyte undergoes spontaneous maturation once released from the antral follicle in vitro. Prophase I arrest of the follicle-enclosed oocyte is primarily enforced in part by high cAMP levels within the oocyte. This level is maintained by adenylyl cyclase activity, and release from PI arrest is initiated by oocyte-specific cAMP phosphodiesterase-3A (PDE3A) activity, which leads to cAMP turnover (Masciarelli et al. 2004). PI arrest of isolated oocytes can be maintained in vitro by addition of the cAMP analogue dibutyryl cAMP (dbcAMP), as well as phosphodiesterase inhibitors such as milrinone and 3-isobutyl-1-methylxanthine (IBMX). As the oocyte develops in a complex dynamic follicular environment, it is not surprising that more than one signaling molecule participates in maintaining meiotic arrest.

Recently, we showed that zinc depletion through treatment with a chelator could release oocytes from the meiotic PI arrest. Tetrakis-(2-pyridylmethyl) ethylenediamine (TPEN) is a heavy metal chelator with high affinity for zinc ( $K_d = 2.6 \times 10^{-16}$  M), in addition to other metals including iron ( $K_d = 2.5 \times 10^{-15}$  M) and copper ( $K_d = 3 \times 10^{-20}$  M) (Sigdel et al. 2006). Disruption of intracellular zinc homeostasis in in vitro cultured oocytes using low, nontoxic levels of TPEN (10  $\mu$ M) induces meiotic resumption even in the presence of the meiotic inhibitor milrinone (Kong et al. 2012; Tian and Diaz 2012). TPEN acts as a specific zinc chelator, as supplementation of the culture medium with zinc reversed the TPEN-induced meiotic resumption, with oocytes remaining at prophase I. These results can be recapitulated using an in vivo model. Fully grown oocytes from mice fed a zinc-deficient diet for 10 days underwent premature

GVBD, before the LH surge (Tian and Diaz 2012). Thus, both small-molecule zinc chelation *in vitro* and systemic zinc deficiency *in vivo* are capable of inducing premature GVBD. We noted that PI oocytes treated transiently with TPEN resumed meiosis normally and proceeded to the MII arrest stage if they were transferred, after completion of GVBD, to TPEN-free medium.

The rapid decrease in cAMP after the LH surge permits meiotic resumption (Norris et al. 2009). A complex bidirectional talk exists between oocytes and its surrounding somatic compartments (Sugiura et al. 2008; Wigglesworth et al. 2013; Zhang et al. 2010). The signaling cascades that mediate meiotic arrest and resumption have been reviewed in great detail elsewhere (Conti et al. 2012; Downs 2010). In brief, the release from prophase I arrest in the oocyte is accompanied by an increase in the activity of maturation-promoting factor (MPF), the activity of which is indirectly inhibited by a high level of cAMP that activates protein kinase A (PKA) during meiotic arrest (Duncan et al. 2006; Han et al. 2005; Oh et al. 2010). Similar to its role in mitotic cell-cycle regulation, MPF is composed of cyclin B1 and cyclin-dependent kinase 1 (CDK1), which drives cell-cycle progression in oocytes. In fact, oocyte growth and gain of meiotic competency are positively correlated with accumulation of MPF (Mitra and Schultz 1996). The kinetics of GVBD induced by TPEN in the presence of milrinone was prolonged, occurring 9 h later in the pulsed TPEN-treated oocytes compared to spontaneously maturing oocytes *in vitro* (Kong et al. 2012; Tian and Diaz 2012). Accordingly, MPF activity in TPEN-treated oocytes was similarly delayed, which was consistent with the slow GVBD kinetics (Tian and Diaz 2012). The relationship between MPF activity and oocyte zinc levels is not limited to the time of GVBD, as is discussed in the following section.

Surprisingly, in contrast to the decline of cAMP levels before GVBD as one would expect, cAMP levels initially increased in TPEN-treated oocytes and then dropped back down to the baseline around the time of GVBD (Tian and Diaz 2012). This finding is consistent with work by Salustri et al., who reported a transient rise in cAMP level in mouse cumulus-enclosed oocytes cultured *in vitro* after treatment with a maturation-stimulating dose of follicle-stimulating hormone (FSH) (Salustri et al. 1985). Indeed, short-term incubation of mouse oocytes with cAMP analogues induced meiotic resumption (Chen et al. 2009), likely because of the activation of AMP-activated protein kinase (AMPK), which has been shown to mediate hormone-induced maturation in mouse oocytes (Chen and Downs 2008). Exactly how zinc deficiency leads to cAMP elevation remains elusive. We note that PDE4A hydrolyase activity is enhanced by zinc and that a high concentration of zinc is inhibitory to purified PDE3A protein (Percival et al. 1997; Zhang and Colman 2000). Although we are not sure whether this is the case for oocyte-specific PDE3A *in vivo*, it still remains possible that TPEN treatment may inactivate some fraction of the PDE3A pool. Altogether, it is likely that TPEN induces meiotic resumption by stimulating more than one pathway.

Further analysis of the mechanisms underlying TPEN-induced GVBD by Kong et al. (2012) suggested that meiotic resumption in zinc-insufficient oocytes is mediated through premature activation of the Mos-mitogen-activated protein

kinase (Mos-MAPK) pathway. The meiosis-inducing action of LH is conveyed to the oocyte through the participation of somatic compartments (Park et al. 2004), as the oocyte does not express LH receptors (Lawrence et al. 1980). Granulosa cell MAPK activation is required for LH signaling in the follicle (Fan et al. 2009; Norris et al. 2008; Su et al. 2003), as mice lacking MAPK3/1 signaling specifically in granulosa cells are infertile and show no signs of GVBD or ovulation (Fan et al. 2009). Although activation of MAPK3/1 in somatic cells is indispensable for oocyte meiotic resumption (Fan et al. 2009; Su et al. 2003), activation of this pathway within the oocyte itself is not required for maturation, which is supported by two lines of evidence. First, both MAPK protein and phosphorylation levels increase in oocytes only after GVBD (Kubiak et al. 1993; Verlhac et al. 1996). Second, *mos*-null oocytes are able to undergo maturation with similar kinetics as wild-type control oocytes (Hashimoto et al. 1994). It therefore appears that mammalian oocytes have evolved to limit Mos-MAPK pathway signaling to later meiotic events. Interestingly, ectopic expression of Mos in bovine oocytes accelerates GVBD (Fissore et al. 1996), and microinjection of *mos*, or MAPK kinase RNA induces GVBD in mouse oocytes maintained in prophase I arrest by IBMX (Choi et al. 1996), suggesting that premature activation of this pathway can trigger meiotic cell-cycle resumption. Indeed, both Mos and phospho-MAPK3/1 protein levels were elevated before MPF activation and GVBD in TPEN-treated oocytes (Kong et al. 2012). Inhibition of protein synthesis and knockdown of Mos-MAPK pathway components abolished the effect of TPEN on delaying meiotic induction, suggesting that premature activation of the Mos-MAPK pathway drives the maturation defect in TPEN-treated oocytes, and that increased zinc availability suppresses the Mos-MAPK pathway to maintain meiotic arrest (Kong et al. 2012).

### ***15.3.2 Zinc Fluxes Regulating Meiotic Progression and Metaphase II Arrest***

Following release from PI arrest, we find that the next stage of meiotic progression is dependent on fluctuations in zinc availability in a completely different manner: the choreography of chromosomal movement and cytoskeletal dynamics as the oocyte proceeds from GVBD and into metaphase II (MII) arrest shows a striking requirement for elevated zinc availability (Bernhardt et al. 2011; Kim et al. 2010).

Shortly after GVBD, spindle microtubules nucleated from centriole-lacking microtubule-organizing centers (MTOCs) start polymerizing around the condensed chromosomes. The initial meiotic spindle forms slightly off center in the region of the ooplasm that corresponds to the location of the original GV, and then migrates to the cortex before extrusion of the first polar body, along with half of its chromosomal complement (Li and Albertini 2013). Metaphase II arrest is established following completion of this process. During this same maturation period, the total zinc concentration in oocytes increases by about 50 %, with zinc

levels peaking at the MII stage (Kim et al. 2010). This dramatic change is remarkable and has not been reported in any other cell type investigated thus far (Krężel and Maret 2006). As already discussed, a transient TPEN-induced zinc deficiency at the PI oocyte stage induces meiotic resumption and produces a mature MII egg. However, chronic zinc depletion by TPEN impairs meiotic progression. We found that when oocytes were exposed to 10  $\mu$ M TPEN during the entire maturation period, a significant number of TPEN-treated oocytes generated unusually large polar bodies (PBs). Further investigation into the spindle morphology of these cells revealed that instead of progressing completely to the metaphase II arrest stage, these cells stalled at a telophase I-like stage and retained a persistent midbody at the site of cytokinesis (Bernhardt et al. 2011; Kim et al. 2010). Subsequent studies reveal that exposure of oocytes to TPEN only after the formation of the MI spindle was sufficient to induce maturation defects (Bernhardt et al. 2012), indicating that premature meiotic arrest is largely caused by zinc insufficiency after the MI stage. In addition to spindle defects, TPEN-treated oocytes exhibited defects in cortical reorganization as an incomplete clearance of cortical granules close to the meiotic spindle region was observed (Bernhardt et al. 2011).

The phenotypes of TPEN-treated oocytes, that is, defects in spindle formation, spindle migration, and cortical reorganization, suggested disruption of the Mos-MAPK pathway. Spindle migration is dependent on an actin filament network, which ensures asymmetrical division so that the majority of the oocyte content is preserved (Azoury et al. 2008). In oocytes, the Mos-MAPK pathway and additional proteins, such as formin-2 and Cdc42, mediate spindle formation and positioning. For instance, *mos*-null oocytes often undergo symmetrical oocyte division and generate a large polar body (Choi et al. 1996; Deng et al. 2005; Verlhac et al. 1996), similar to TPEN-treated oocytes. They also exhibit defects in cortical reorganization, a process that normally includes thickening of actin filaments and loss of microvilli in the region that has close contact with the translocated meiotic spindle (Choi et al. 1996; Longo and Chen 1985; Nicosia et al. 1977). However, *mos*-null oocytes and wild-type oocytes treated with TPEN during the entire maturation period arrest at different developmental stages. *Mos*-null oocytes were able to complete maturation, whereas zinc-insufficient oocytes stalled at telophase I (Bernhardt et al. 2011; Choi et al. 1996). Interrogation of the potential link between zinc insufficiency and disruption of the Mos-MAPK pathway indicated that TPEN treatment did not affect the Mos-MAPK pathway during the MI to MII transition (Bernhardt et al. 2011). Briefly, zinc-insufficient oocytes had phospho-MAPK3/1 levels comparable to those of controls, despite the decreases in Mos protein levels and MAP2K1/2 phosphorylation in TPEN-treated oocytes; however, this decrease happened later than telophase I arrest, and microinjection of *mos* RNA did not rescue the zinc-insufficient phenotypes (Bernhardt et al. 2011).

Having found that the Mos-MAPK pathway is unlikely to play a role in premature meiotic arrest, Bernhardt et al. explored a potential role for zinc in the regulation of MPF activity (Bernhardt et al. 2011, 2012). To put these observations into context, it is important to consider the cell-cycle regulators controlling oocyte

meiotic progression. MPF levels accumulate until metaphase I (MI), remain high before each meiotic cell division, and then quickly decline afterward (Hashimoto and Kishimoto 1988; Ledan et al. 2001). Similar to mitotic cell division, the onset of anaphase is initiated by Cdc20-containing anaphase-promoting complex/cyclosome (APC/C), an E3 ubiquitin ligase that triggers degradation of substrates including cyclin B1 and securin. Proteasomal degradation of securin liberates separase, which cleaves cohesin and allows the segregation of homologous chromosomes (Terret et al. 2003). APC/C activity is tightly controlled, as premature activation before correct chromosome alignment would cause aneuploidy that compromises later development. Oocytes enter meiosis II without undergoing the S phase and arrest again at MII with fully aligned chromosomes. MPF levels rise quickly after anaphase II and peak during MII arrest; this increase in MPF is caused by active translation as fully grown oocytes are transcriptionally quiescent (Moore and Lintern-Moore 1974, 1978). Meanwhile, APC/C activity is inhibited by the cytosolic factor (CSF), which is essential for maintaining high MPF levels during MII arrest (Madgwick and Jones 2007).

Bernhardt et al. have provided evidence supporting the model that elevated zinc in the GV–MII transition leads to zinc loading of the oocyte-specific APC/C inhibitor, early mitotic inhibitor 2 (Emi2), and that the zinc–Emi2 complex constitutes active CSF (Madgwick and Jones 2007; Shoji et al. 2006). Emi2 contains a zinc-binding region (ZBR) in the C-terminus that is indispensable for blocking the ability of Cdc20 to activate APC/C (Schmidt et al. 2005; Tung et al. 2005). This region resembles an in-between ring (IBR) zinc-finger structural motif and contains eight putative zinc-binding residues, which are composed of seven cysteine residues and one histidine residue (Suzuki et al. 2010a, b). Most importantly, Emi2 not only participates in cytosolic factor (CSF) maintenance, it also establishes CSF activity. Several lines of evidence support the role of Emi2 as a CSF component. First, Emi2 protein levels rise immediately after MI (Liu et al. 2006; Ohe et al. 2007). This timing allows reaccumulation of cyclin B1 and presumably allows the oocyte to proceed through MI, because premature expression of Emi2 induces MI arrest (Madgwick et al. 2006; Suzuki et al. 2010a). Second, the MII spindle fails to assemble in Emi2 morpholino knockdown oocytes after PB extrusion and chromosomes quickly become decondensed; this phenotype can be rescued by nondegradable cyclin B1 (Madgwick et al. 2006), indicating a role of Emi2 in establishment of CSF. Third, Emi2 is rapidly degraded before cyclin B1 destruction upon fertilization, which is consistent with the relief of inhibition on APC/C, thereby allowing the resumption of the meiotic cell cycle (Madgwick et al. 2006). Emi2 was identified in *Xenopus* oocytes as a downstream substrate of polo-like kinase 1 (Plk1) that is important for mediating calcium-dependent activation of APC/C during fertilization (Schmidt et al. 2005; Shoji et al. 2006). Taken together, these data suggest an indispensable and conserved role for Emi2 in maintaining MII arrest in vertebrate oocytes.

Given the importance of the ZBR of Emi2 and the zinc quota change during oocyte maturation, we hypothesize that zinc levels within the oocytes regulate the proper inhibitory functioning of Emi2. We observed that MPF failed to accumulate

after the first meiotic division in TPEN-treated oocytes. Restoration of MPF activity by either expressing nondegradable cyclin B1 or incubating oocytes with protease inhibitor significantly increased the percentage of zinc-insufficient oocytes that progressed to MII (Bernhardt et al. 2011, 2012). This finding implied that inappropriate degradation of cyclin B1, most likely by premature activation of APC/C, accounts for the zinc-insufficient oocyte phenotype. Indeed, oocytes with morpholino knockdown of Emi2, the zinc-binding domain containing APC/C inhibitor, phenocopied zinc-insufficient oocytes, with the formation of large PB and an inability to establish the MII spindle (Shoji et al. 2006). The proper functioning of Emi2 is dependent on zinc availability, as TPEN perturbed the ability of Emi2 to induce metaphase arrest and expression of Emi2 mutated in the zinc-binding region did not completely rescue Emi2-knockdown oocytes (Bernhardt et al. 2012). Based on the data and zinc accumulation profile, we speculate that zinc binding to Emi2 constitutes the active CSF complex, making the zinc flux which leads to loading of Emi2 a critical step in regulating meiotic progression and establishing MII arrest.

### 15.3.3 Fertilization and Egg Activation

Upon fusion of the sperm with the ooplasmic membrane, the mammalian oocyte goes through a process known as activation. A hallmark of activation is the exit of the oocyte from MII arrest and resumption of meiosis II upon downregulation of CSF activity. Calcium signaling is a remarkably conserved pathway in fertilization in the animal kingdom (Stricker 1999). During fertilization, intracellular calcium is elevated by repetitive calcium rises, referred to as calcium oscillations (Cuthbertson et al. 1981; Ducibella and Fissore 2008). A novel member of the PLC family, PLC $\zeta$ , is a sperm factor capable of inducing calcium oscillations and triggering egg activation (Saunders et al. 2002). Egg activation can also be achieved artificially without sperm fertilization by chemical treatment (parthenogenesis) such as calcium ionophores (Nakagawa et al. 2001), strontium chloride (Ma et al. 2005; O'Neill et al. 1991), ethanol (Cuthbertson 1983; Kaufman 1982), and phorbol ester (Cuthbertson and Cobbold 1985; Sun et al. 1999). All methods lead to egg activation by increasing intracellular calcium levels.

Zinc chelation can also result in parthenogenetic egg activation, as treatment of MII eggs with 10  $\mu$ M TPEN results in exit from MII and formation of a single pronucleus (Kim et al. 2010). This TPEN-induced activation is accompanied by reduction in both MPF and MAPK activity, which normally occur when oocytes exit MII arrest (Suzuki et al. 2010b). Furthermore, TPEN treatment successfully induced MII exit in eggs injected with heat-inactivated sperm heads, resulting in live birth of mice following embryo transfer. This result suggested the depletion of zinc at the time of fertilization could also act as an egg-activating method, as heat-inactivated sperm heads alone fail to activate. Strikingly, calcium oscillations did not occur after TPEN treatment in these experiments, arguing against the absolute

requirement for calcium oscillations during egg activation (Suzuki et al. 2010b). The action of TPEN has been attributed in part to its ability to modulate the activity of the ZBR of Emi2 as overexpression of Emi2 in mouse oocytes reduces the ability of TPEN to promote egg activation (Suzuki et al. 2010a). Mutation of putative zinc-binding residues abrogated this effect. These experiments further supported the importance of zinc as a gatekeeping switch for eggs exiting MII by regulating Emi2 and thus as a key component of egg activation.

In a complementary set of experiments, the effect of increasing intracellular zinc levels on egg activation was investigated. The ability of TPEN to activate eggs, and XFM results that indicate a decrease in zinc levels is a characteristic of the egg to embryo transition, suggested that inducing higher than normal zinc levels in MII eggs should prevent activation. Indeed, artificially increasing the zinc level in eggs using the ionophore zinc pyrithione (ZnPT) abolished strontium-induced activation (Bernhardt et al. 2012). Furthermore, ZnPT administration 90 min after strontium-induced egg activation produced eggs with a metaphase-like spindle and suppressed pronucleus formation (Kim et al. 2011). These experiments further emphasize how the oocyte exploits precise cellular zinc levels to control its meiotic cell cycle.

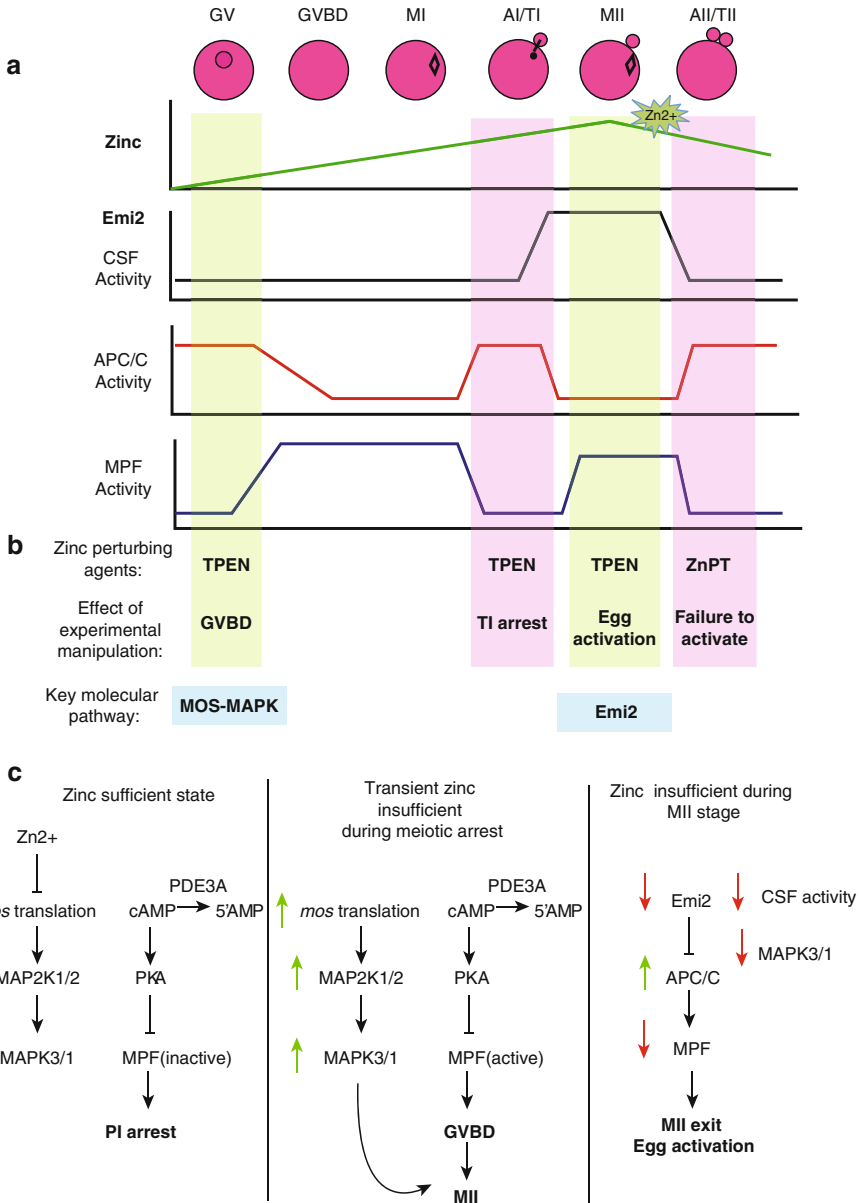
### ***15.3.4 Zinc Sparks: A Novel Facet of the Egg–Embryo Transition***

Zinc fluxes not only control resumption and completion of oocyte maturation, but also play a striking role upon fertilization. In contrast to the previous stages where zinc uptake and trafficking plays a central role, zinc efflux is essential in the first several hours of the egg-to-embryo transition. Soon after fertilization, zinc is rapidly expelled from the egg through a series of exocytosis events called zinc sparks (Kim et al. 2011). These concentrated, periodic releases of zinc from the female gamete were detected using live cell fluorescence microscopy and the extracellular zinc dye FluoZin-3. Individual mouse eggs display one to five sparks following  $\text{SrCl}_2$  activation, with the majority of eggs displaying between two and three sparks. Zinc sparks were also observed upon in vitro fertilization. The cell biology of the coordinated zinc spark events remains uncertain but it is clear that they originate from regions of the egg cortex centered at the microvilli region, that is, distal to the meiotic spindle (Kim et al. 2011). The asymmetrical localization of both total and labile zinc has been established using X-ray fluorescence microscopy (XFM) and in fluorescence microscopy experiments using zinc-selective fluorophores. Z-stack confocal imaging reveals a pattern similar to that observed for the cortical granules that are released at fertilization (Kim et al. 2011). As the cortical granules contain enzymes that are important for zona pellucida hardening and the prevention of polyspermy (Barros and Yanagimachi 1971; Burkart et al. 2012), it is possible that zinc sparks have additional roles during egg activation that have yet to be explored.

Further observation suggested a relationship between intracellular calcium signaling and the release of the zinc sparks. Each zinc spark is preceded by an intracellular rise in calcium, shown using calcium-sensitive and zinc-sensitive dyes simultaneously. The sequestration of intracellular calcium by a calcium chelator, 1,2-bis (*o*-aminophenoxy) ethane-*N,N,N',N'*-tetraacetic acid (BAPTA), inhibited the zinc sparks. In addition, the number of zinc sparks in mouse oocytes positively correlates with the pattern of calcium oscillations triggered by different parthenogenetic activation agents. Strontium chloride induces multiple calcium oscillations in eggs that mimic the effect of sperm contact, whereas ionomycin only triggers a single calcium transient in this organism (Alberio et al. 2001; Bos-Mikich et al. 1995; Kline and Kline 1992; Whittingham and Siracusa 1978). Consistent with these effects, no more than one spark was observed when eggs from either mice (unpublished results) or nonhuman primates (Kim et al. 2011) were activated with ionomycin.

Even after egg activation and fertilization, zinc continues to influence subsequent embryonic development. Maternal zinc deficiency is associated with poor pregnancy outcomes and developmental abnormalities (King 2000). Female rats fed a zinc-deficient diet exhibited reduced litter size and slower growth rate of pups (Hurley and Swenerton 1966). Pregnant patients with acrodermatitis enteropathica, a genetic disorder that affects zinc absorption, are at higher risk of severe abnormalities in fetal development (Hambidge et al. 1975). The negative effect of zinc deficiency traced back to its impact on oocyte quality, as oocytes from zinc-deficient animals underwent premature meiotic resumption and did not ovulate, and also showed abnormal epigenetic programming and aberrant gene expression in oocytes (Tian and Diaz 2013). Of course we cannot negate the systemic effect of zinc deficiency, which might have changed the follicle microenvironment in a way that impairs the ability of follicles to maintain oocyte meiotic arrest, suggesting a negative effect on normal ovarian function as well. Although cultured oocytes treated transiently with TPEN can be fertilized *in vitro* and proceed through to live birth, the blastocyst rate is significantly reduced (Suzuki et al. 2010b). Similarly, a reduction in fertilization rate and blastocyst formation was observed in the eggs that were collected from the animals on a zinc-deficient diet, and few expanded blastocysts were recovered from the reproductive tract of zinc-deficient animals (Tian and Diaz 2013). Abnormal imprinting of embryos from these zinc-deficient animals was also observed. Embryonic development initiated after transient TPEN activation as just described involved a brief exposure to TPEN that was followed by somatic nuclear transfer. However, compared to traditional strontium activation methods, both the activation rate and embryonic development were lower in the TPEN-treated group (Suzuki et al. 2010b). Whether this is caused by general embryo toxicity or lack of calcium oscillations remains to be investigated. Taken together, these results indicate that zinc availability to the developing oocyte is extremely important to generation of both high-quality gametes and subsequent normal, viable embryos.





**Fig. 15.1** Summary of zinc dynamics throughout meiotic maturation. **a** Total cellular zinc increases by 50 % during meiotic maturation from the prophase I-arrested oocyte to the metaphase II (MII)-arrested egg, and then drops upon fertilization in events described as zinc sparks. The fluctuations of cytotostatic factor (CSF), anaphase-promoting complex/cyclosome (APC/C), and maturation-promoting factor (MPF) activity during oocyte maturation and egg activation are also depicted. **b** Perturbation of zinc availability using the heavy metal chelator tetrakis-(2-pyridylmethyl)ethylenediamine (TPEN) or the zinc ionophore zinc pyrithione (ZnPT) at critical windows of meiotic maturation and fertilization interferes with specific zinc-dependent pathways,

## 15.4 Concluding Remarks and Future Directions

Zinc has a central role in many physiological processes. Acute or chronic zinc deficiency causes endoplasmic reticulum stress that could contribute to neuron toxicity (Homma et al. 2013) and is linked to thymic atrophy and lack of cytokine production (Fraker et al. 1986). Zinc is also critical for immune system function (Fraker and King 2004). In this review we have summarized studies of mammalian oocytes in which zinc fluxes play a series of specific and unrelated roles in regulating sequential steps in the meiotic cell cycle. Zinc availability is tightly regulated in the developing oocyte, and its disposition is critical for meiotic cell-cycle progression. First, zinc is required for maintaining prophase I arrest before the LH surge. Second, rapid accumulation of zinc over a short period of time is absolutely necessary for establishing and maintaining metaphase II arrest. Consequently, lowering intracellular zinc content via a series of zinc sparks initiates the second meiotic cell-cycle resumption (summarized in Fig. 15.1). Thus, zinc acts as both a permissive and maintenance factor throughout oocyte maturation and egg activation. These discoveries have opened up a new window onto the role of inorganic elements in egg physiology, adding another layer of complexity to oocyte maturation and egg activation.

The rapid zinc accrual during oocyte maturation is particularly intriguing, and the mechanism by which it occurs is an active area of research. It will be important to identify the specific zinc transporters involved and their temporal and spatial relationships to localization of zinc during oocyte maturation and early embryonic development. Two conserved zinc transporter family proteins mediate cellular zinc transport: ZIP family proteins (Zrt- and Irt-like proteins, e.g., SLC39) and ZnT family proteins (SLC30) (Kambe et al. 2004). ZIP family zinc transporters regulate zinc uptake from the extracellular environment or zinc storage, whereas ZnT family



**Fig. 15.1** (continued) resulting in premature arrest or progression through the maturation pathway. Decreasing zinc availability using TPEN at the two crucial arrest points, namely, prophase I and metaphase II, results in premature meiotic progression. Oocytes that undergo germinal vesicle breakdown (GVBD) because of zinc insufficiency have the capacity to develop to MII eggs on return to zinc-replete medium and form blastocysts upon egg activation. This effect of zinc insufficiency in causing meiotic resumption from prophase I arrest is mediated via the MOS-MAPK pathway. As described, experimental manipulation of zinc levels before or after MII arrest, when zinc is actively being acquired or released, respectively, results in meiotic arrest. **c** Model showing proposed action of a zinc-mediated pathway during the first meiotic arrest at prophase I. In a zinc-sufficient state, the MOS-MAPK pathway is maintained in a quiescent state, MPF activity remains low and the oocyte remains arrested at the prophase I-arrested (PI) stage. Transient zinc insufficiency as induced by chelation relieves the inhibition on the MOS-MAPK pathway, allowing meiotic resumption, GVBD, and progression toward MII. Chronic zinc insufficiency or zinc insufficiency during MI–MII transition causes telophase I arrest. Zinc insufficiency during the MII stage induces egg activation by decreasing CSF activity and alleviates APC/C inhibition, which ultimately leads to MII exit. [Figure adapted from Kong et al. (2012) and Bernhardt et al. (2012)]

proteins are responsible for mediating zinc efflux (Fukada and Kambe 2011). Compartmentalization of labile zinc has functional significance; for example, zinc sequestration in macrophages enhances intracellular pathogen clearance (Subramanian Vignesh et al. 2013). Furthermore, zinc compartmentalization by ZnT8 along with insulin in the secretory compartments of pancreatic beta cells is essential to normal systemic glucose utilization (Chimienti et al. 2006). Metallothionein proteins also regulate labile intracellular zinc levels (Blindauer and Leszczyszyn 2010; Vallee 1995). These are but a few examples wherein cell-specific zinc trafficking machinery has a key role in highly differentiated cells. Many zinc transporters are differentially expressed in mouse oocytes and cumulus cells, suggesting the regulation of zinc uptake and sequestration in oocytes by its somatic compartment (Lisle et al. 2013).

The zinc spark phenomenon is striking and raises a myriad of questions. Is the zinc spark a conserved mechanism? What is the function of the zinc spark? If it is as well conserved as calcium oscillations, why do zinc sparks adopt a redundant pathway? The zinc spark is not unique to the mouse egg; it seems to be a conserved biological event in mammals and has been observed in nonhuman primates (Kim et al. 2011). Future studies will clarify whether the zinc spark is conserved in other mammalian species and when it appeared during animal evolution. Current data support the idea that accumulation of zinc during maturation is a component of the gatekeeping mechanisms maintaining MII arrest, as premature parthenogenetic activation is undesired. This role of zinc is supported by the fact that the zinc accumulation profile overlaps with Emi2 expression during oocyte maturation. To resume the meiotic cell cycle upon fertilization, cyclin B1 needs to be degraded by APC/C, which can be accomplished by quick exocytosis of zinc that subsequently reduces the function of Emi2. Therefore, zinc sparks could have a dual effect of maintaining MII arrest in the absence of activation stimuli and facilitating robust meiotic cell-cycle resumption when cued.

Ultimately, it is important to examine the translational value of these findings in a clinical setting. Infertility affects one of every ten couples in the United States, and it is well recognized that decreasing egg quality is associated with increasing maternal age and metabolic dysfunction (Qiao et al. 2013). The insights that we gain from studies of zinc biology in the regulation of oocyte maturation and egg activation may inform improvements in assisted reproductive technologies (ART). In most cases, women who are treated with human chorionic gonadotropin (hCG) to induce *in vivo* oocyte maturation and ovulation experience mood swings and other adverse effects, and the procedure is associated with a high incidence of multiple births; these outcomes can be circumvented by controlled *in vitro* oocyte maturation (IVM) (Heijnen et al. 2004). Monitoring and controlling zinc dynamics may ultimately have an impact on IVM outcomes and yield a higher proportion of high-quality fertilizable eggs in several ways. For instance, pharmacological alteration of zinc levels may make it possible to rescue eggs that fail to activate after intracytoplasmic sperm injection (ICSI) (Lu et al. 2006), which is a method of treating male patients with a PLC mutation (Eldar-Geva et al. 2003; Taylor et al. 2010). The discovery of a new hallmark of egg activation—that is, the zinc

spark—holds promise as a noninvasive method to predict embryo developmental potential, giving embryologists a way to select the best quality embryos to implant, thereby reducing the risk of multiple births and other complications.

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# Future Perspectives

Toshiyuki Fukada

During the past decade, our understanding of the role of zinc as an intracellular and extracellular “zinc signal” has increased dramatically. Advances in molecular, biochemical, genetic, and computational methodologies have undoubtedly contributed to the recent insights into the biological roles of zinc as well as the novel mechanisms by which it functions. At the same time, zinc signaling is still an emerging field, in need of continued sustained efforts to fully understand the impact of zinc on biological processes. Here, I discuss the significant issues that should be addressed in the next decade to facilitate our understanding of this enigmatic molecule.

More than 50 years have passed since zinc was recognized as an essential trace element required for human health. Although we now appreciate the various roles zinc plays in maintaining human health, the molecular basis of the requirement for zinc remains a question. The necessity of zinc for life has been analyzed and accounted for in different ways, invoking a variety of mechanisms. One reasonable answer to this question is that approximately 10 % of human genes encode zinc-binding motifs that may be necessary for protein function or regulation. Thus, the requirement for zinc may, in actuality, be readily comprehensible. Nevertheless, more experimental data are needed to fully validate this observation at the molecular level. At present, a growing body of evidence indicates that zinc acts as both an intracellular and extracellular signaling factor, contributing to our understanding not only of the chemical and biological features of zinc, but also of the zinc-dependent physiological events in human health and disease, which are well described in this book.

The 15 chapters in this volume outline the cutting-edge insights on zinc, ranging from a basic introduction (Chap. 1) to clinical points of view, and identify

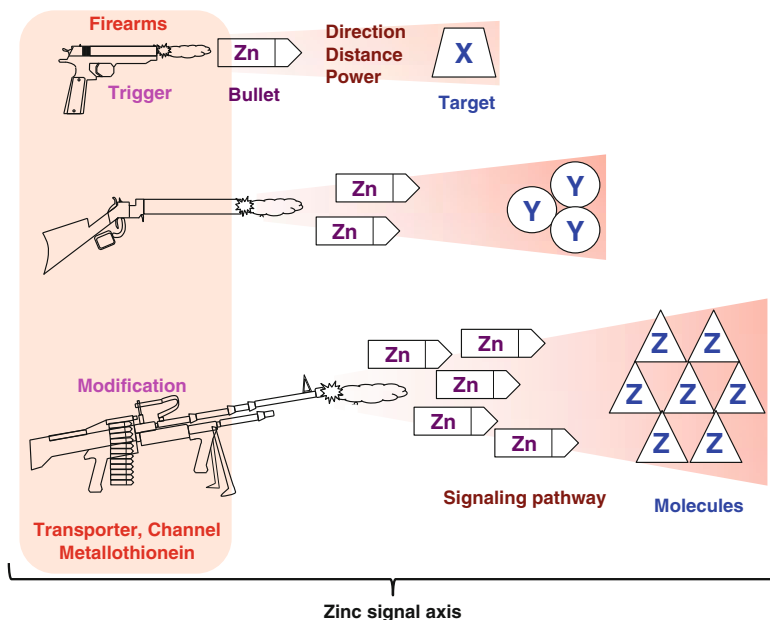
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remaining mechanistic questions in the area of zinc signaling. For example, to understand further the mechanisms by which zinc homeostasis is regulated and impacts cell signaling, the various functions of cytosolic zinc-binding proteins involved in zinc “buffering and muffling” in specific cellular locations is needed. The interaction between zinc signaling and other essential or nonessential metal ions is another intriguing subject (Chap. 2). Zinc transporters are the main gatekeepers controlling zinc signaling. Thus, investigation into their activation and inactivation, modification, and three-dimensional structures will provide key insights into the regulation of zinc signaling and may shed light on the molecular basis of their biological specificity (Chap. 3). Oxidative stress activates multiple signaling pathways and induces the elevation of intracellular zinc levels. The complexity of zinc biology will be further clarified by exploring its interaction with other intracellular and extracellular signaling pathways, such as stress responses toward reactive oxygen species (Chap. 4). The development of techniques for detecting zinc signaling *in vitro* and *in vivo* will certainly improve our mechanistic understanding of zinc signaling and its interaction with other signaling pathways (Chap. 7). The zinc receptor GPR39, a zinc sensor that converts the extracellular zinc signal to intracellular signaling, is an excellent example of this phenomenon. Because GPR39 is a G protein-coupled receptor (GPCR), the development of GPR39-specific agonists may modulate zinc-signaling processes linked to disease (Chap. 6).

Recent genetic and clinical investigations have advanced our knowledge about zinc signaling and its relationship to various diseases. One of the leading areas is the field of neuroscience. Synaptic zinc homeostasis is involved in both cognitive function and dysfunction including memory loss, depression, and Alzheimer’s disease; however, the regulation of zinc homeostasis in the brain is currently unclear. Further investigation into this area may contribute to improved outcomes for patients with zinc-related neurodegenerative diseases (Chaps. 8 and 9). Allergy and immunology, as well as diabetes are also emerging as areas in which zinc signaling is important; zinc has been thought to be required for normal immunity and inflammatory responses since zinc deficiency was discovered. The regulation of zinc signaling in lymphocytes and monocytes (Chaps. 10 and 11), the “zinc wave” in mast cells (Chap. 5), and the “zinc stream” from pancreatic beta cells (Chap. 13) appear to play roles in immunological and inflammatory diseases and diabetes mellitus. It is well established that abnormal zinc homeostasis causes growth retardation and dwarfism; therefore, the proper regulation of zinc homeostasis is indispensable for mammalian growth. Zinc signaling machineries orchestrate other pathways involved in bone homeostasis and elongation (Chap. 12) and in early development (Chap. 15). Therefore, it will be important to define the molecular mechanisms by which zinc signaling regulates the cellular events before and after oocyte fertilization, during growth, in aged individuals, and in a variety of diseases. In particular, zinc signaling appears to be involved in cancer malignancy; thus, further studies dissecting the regulatory mechanisms of zinc transporters may lead to the development of new anti-cancer therapies (Chap. 14).



**Fig. 1** Each zinc signal from an individual zinc transporter, channel, or metallothionein selectively controls the target molecules and zinc-mediated effects on cellular functions. This situation may be analogous to the relationship between a bullet and a firearm. Even with use of the same bullet and gunpowder (zinc), the use of different firearms (zinc gatekeepers such as transporters, channels, and metallothioneins) will result in hitting different targets (signaling molecules). Each firearm has different triggers and safety devices (modifications or unique motifs), which may influence its efficiency. The objects around the targets (such as chaperons), location of targets and firearms in the field (intracellular distribution), and firearm numbers (expression level of zinc transporters in differential cells and tissues) may affect the results. These complexes form “zinc signal axes” to achieve specific cellular responses and physiological outcomes

The chapters written for this book represent a diverse range of approaches but together raise a simple and common query: How does zinc signaling possess the necessary specificity to correctly regulate the relevant target molecules and biological processes? Although this question undoubtedly requires additional exploration, I would propose that “a bullet and firearm” analogy might provide some mechanistic insight into the specificity of zinc signaling (Fig. 1). Even if the same bullets and gunpowder (zinc in this case) are used, different targets will be hit by using different firearms (i.e., zinc gatekeepers including transporters, channels, and metallothioneins) because the characteristics of an individual firearm affect the distance, direction, speed, and relative timing of the bullets they fire. A machine gun might be likened to a fully open zinc transporter in a constitutively active state, whereas a single-loader gun with safety devices might be more similar to a zinc transporter regulated by negative feedback systems. Similar to firearms, the transporters respond to different triggers (e.g., modification by phosphorylation or oxidation), which also exert profound downstream effects. The aiming of a firearm

may encounter interference by objects around the targets (e.g., intermediate proteins such as chaperones). Even when using the same firearm, the targets hit will depend on their location (i.e., intracellular distribution, differential cell and tissue expression). As of today, many aspects of zinc signaling remain unknown. As we enter the next phase of work in this area, we remain convinced that further studies on zinc signaling will manifest the answers to these key questions in molecular terms, which will shed light on the role of zinc signaling in both normal and disease conditions.

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