The "metal transcription factor" MTF-1: biological facts and medical implications

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Summary

Metallothioneins (MTs) are a class of small, cysteine-rich proteins that have an important function in heavy metal metabolism and detoxification and in the management of various forms of cell stress. Several lines of evidence suggest a role for metallothioneins in therapy resistance of malignant tumours, regulation of blood pressure and protection against some neurological diseases. Basal and heavy metal-induced expression of the stress-inducible metallothionein-I and -II genes and some other stress-regulated genes depends on the zinc-finger transcription factor MTF-1. MTF-1 acts as a cellular stress-sensor protein and, besides its crucial role in metallothionein expression, is essential for liver development since mice null mutant for MTF-1 die *in utero* due to hepatocyte degeneration. Under pathological conditions, MTF-1 seems to be involved in clinically important processes such as tumour angiogenesis and drug resistance. It thus seems generally advisable to monitor MTF-1 activity in stress-related processes including aging and carcinogenesis.

Key words: cadmium toxicity; cell stress; oxidative stress; transcription control

Introduction

Living organisms constantly need to cope with harmful environmental conditions such as heavy metal load, UV irradiation and oxidative stress. On the other hand, trace amounts of several heavy metals, notably the transition heavy metals zinc and copper, are essential for life. Zinc is crucial for the proper functioning of a large number of proteins including zinc-containing enzymes, transcription factors of the so-called zinc-finger family or other regulatory nuclear proteins containing single or multiple zinc ions as integral components. Zinc deficiency can lead to severe growth retardation, immune deficiency, impaired hair growth and fertility problems due to reduced sperm production [1-3], while a genetic defect in zinc uptake results in acrodermatitis enteropathica [4, 5]. In mammals bioavailability of zinc is controlled by a well-balanced system. Metallothioneins (MTs), a group of small, cysteine-rich proteins particularly abundant in the kidney and liver are, due to their ability to bind heavy metals (reviewed in [6]), centrally involved in the homoeostatic regulation of zinc concentrations and in detoxification of non-essential heavy metals. Under physiological conditions MTs primarily bind zinc but at the same time have a particularly high affinity for potentially toxic heavy metals [6]. For example, cadmium taken up in food is stored in a form tightly bound to metallothioneins, where it remains with a half-life of approximately 15 years [7]. Under heavy metal load, MT expression is strongly induced at the level of transcription [8]. This induction is mediated by the transcription factor MTF-1, an essential protein for liver development and cell stress response [9–11].

Glossary	MRE: "Metal-responsive element", a specific DNA-sequence motif to which MTF-1 binds and thereby activates expression of an associated gene.
Transcription factor: Protein which is necessary to start or con- trol gene expression by recruiting the transcription apparatus (RNA-polymerase and associated proteins) to gene promoters.	
	Activation domain: Protein domain of transcription factors required to recruit the transcription apparatus.
Zinc finger: Protein domain (typically for DNA-binding) with a zinc ion as a structural component.	
	Transgene: Gene that is artificially introduced and stably
Promoter: DNA sequence to which the transcription apparatus binds in order to start transcription.	integrated into the genome and transmitted to subsequent generations.

Functions of metallothionein under physiological and pathological conditions

The mouse has four genes encoding distinct metallothioneins, designated MT-I to MT-IV (reviewed in [12]), but only the expression of MT-I and MT-II is ubiquitous and stress-inducible. The human genome encodes the same four types of metallothioneins, the stress-inducible forms having been multiplied by several gene duplication events [12]. Associations have been established between MTs and a number of diseases [13]. Several lines of evidence indicate that MTs play a role in carcinogenesis and tumour cell drug resistance [14, 15]. Although the role of metallothioneins in cancer remains controversial, it is clear that at least in some malignant tumours a high expression of metallothionein genes is correlated with increased metastatic potency, resistance to therapy and a poor prognosis [16–20]. Metallothionein-I and -II

have also been shown to be neuroprotective proteins in animal models of brain trauma, familial amyotrophic lateral sclerosis (ALS) and multiple sclerosis [21–24].

Somewhat unexpectedly, mouse strains with targeted deletion of both the MT-I and MT-II genes do not exhibit an altered phenotype under normal laboratory conditions [25, 26]. Nevertheless, these mice show increased sensitivity to cadmium intoxication, a dramatically reduced myotonic reflex of mesenteric arteries and, following kainic acid-induced seizures, a higher number of convulsions as well as a prolonged convulsion time and increased hippocampal neurodegeneration [26–28]. The latter phenotype is also observed on deletion of the brain-specific metallothionein-III gene [29].

MTF-1 directs metallothionein expression

Expression of the metallothionein-I and -II genes is induced, at the transcriptional level, by heavy metal load in particular [8]. The promoter regions of metallothionein genes contain so-called metal-responsive elements (MRE's; core consensus sequence TGCRCNC) which are responsible for induction by heavy metals [30, 31]. In 1988 the factor binding to the MRE promoter sequences was described as MTF-1 (metal-responsive element-binding transcription factor-1 or, for short, metal transcription factor-1). It required elevated zinc concentrations for optimal DNA binding [32]. Subsequently, MTF-1 was cloned and characterised [9]. MTF-1 is a ubiquitously expressed zinc finger protein that is essential for basal and

heavy metal-induced expression of metallothioneins [10]. Therefore, MTF-1 is the key regulator of metallothionein expression and recent data suggest that it is also involved in the response to oxidative and hypoxic stress, as might be expected for a stress-sensor molecule [11, 33].

Human MTF-1 is a 753 amino acid protein and its encoding gene has been mapped to the short arm of chromosome 1 (1p33) [34]. The Nterminal part of the protein is followed by six zinc fingers of the Cys₂-His₂ type that harbour the DNA-binding activity and sense the level of zinc [10]. In the C-terminus, MTF-1 contains three activation domains, each with distinct properties in transcriptional activation [35].

MTF-1 is activated under various stress conditions

When cells are treated with heavy metals MTF-1 is activated, binds to MRE's and induces transcription of target genes, notably metallothioneins [8, 9, 36]. In resting cells, most MTF-1 localises to the cytoplasm whence it is translocated from the cytoplasm to the nucleus under several different stress situations [37, 38]. The finding that MTF-1 requires an elevated concentration of zinc for strong binding to DNA suggests that MTF-1 is activated by allosteric regulation of DNA binding via binding of metals to the transcription factor itself [9, 10, 32]. Although other heavy metals readily induce metallothionein gene transcription in cultured cells, none of them can substitute for zinc in a cell-free DNA binding reaction of MTF-1 [10]. The most likely scenario is replacement of zinc by these other heavy metals in cellular and/or extracellular zinc-storage proteins, leading to concomitant activation of MTF-1 by the released zinc.

In addition, MTF-1 can be phosphorylated upon metal induction, as a result of the activation of a complex kinase signalling transduction pathway which includes protein kinase C (PKC), phosphoinositol-3 kinase (PI3K), c-Jun N-terminal kinase (JNK) and a tyrosine-specific kinase [39]. This suggests that metal ions such as cadmium could also activate MTF-1 by stimulating kinases.

However, the response of MTF-1 is not confined to heavy metals but is also activated by treatment of cells with hydrogen peroxide [40]. In line with this, MTF-1 has been reported to be greatly overexpressed in a radioresistant cervical carcinoma cell line relative to its expression in a radiosensitive cell line of the same origin [41]. These findings imply a role for MTF-1 in the regulation of genes involved in the cellular response to oxidative stress and suggest that MTF-1 might play a crucial role in therapy resistance of certain tumours.



Figure 1

Histology of wild-type (A) and MTF-1 knockout (B) embryos showing the disrupted liver phenotype in MTF-1^{+/-} embryos. Haematoxylin and eosin-stained sagittal liver sections of embryos at stage E13.5. MTF-1^{+/-} (B) embryonic livers show enlarged, congested sinusoids and dissociation of the epithelial compartment. The remaining hepatocytes are clustered to form contiguous cell patches (arrows).



MTF-1 is essential for liver development

To investigate the physiological function of MTF-1 in vivo, we generated MTF-1 null mutant mice by targeted gene disruption and found this knockout to be lethal. A closer investigation revealed that MTF-1 knockout embryos die in utero around embryonic day (E) 14, due to degeneration of the embryonic hepatocytes [11] (see fig. 1). Interestingly, loss of other proteins involved in the management of cell stress results in similar phenotypes. This raises the question whether the embryonic liver at this stage may be particularly susceptible to a lack of stress-response regulators. For example, the phenotypes of mice null mutant for c-jun and SEK-1 strongly resemble that of MTF-1 knockout mice, though they are not identical [42, 43]. Among the latter, SEK-1/MKK4 is a kinase which has been shown to participate in vitro in stress-activated cascades that terminate with the p38 and SAPK/JNK kinases, which in turn result in phosphorylation and activation of transcription factors such as c-jun [44]. C. Séguin and colleagues have shown that JNK is also involved in phosphorylation of MTF-1 [39]. Taken together, activation of MTF-1 may overlap with activation of c-jun and thereby result in transcriptional activation of some common target genes needed for correct hepatocyte differentiation. Furthermore, the fact that MTF-1 levels in c-jun knockout fibroblasts are not changed (and vice versa [11]) speaks in favour of a parallel rather than epistatic relationship between these two essential transcription factors.

The lethal embryonic phenotype of MTF-1 knockout mice initially prevented investigations at stages later than E14. Nevertheless, fibroblasts taken into culture and neural tissue grafted into wild-type recipient mice survived [11, 45]. For a more thorough analysis, we generated so-called conditional knockout mice in order to study the role of MTF-1 in the development and functioning of tissues other than the liver. These studies are based on generation of transgenic mouse strains in which MTF-1 expression can be eliminated at a chosen time point or in a chosen tissue, using the so-called cre/lox system [46]. Indeed, preliminary data using such mice indicate that MTF-1 can be eliminated in adulthood, but that these mice are more susceptible to heavy metal stress. Hence MTF-1 probably plays a dual role in being essential for liver development and thereafter required to cope with cell stress (Ying Wang, P.L., W.S, unpublished results).

MTF-1 target genes and medical implications

The observation that the double knockout of metallothionein-I and -II genes was viable, while the knockout of the control protein MTF-1 was lethal, suggested that MTF-1 activates other important genes besides those encoding metallothioneins (fig. 2). Gamma glutamyl-cysteine synthetase heavy chain (YGCShc), a key enzyme for glutathione synthesis, was the first additional putative candidate gene identified [11]. Nevertheless, we recently found glutathione levels in E12.5 embryonic MTF-1 knockout livers to be at least as high as in wild-type littermates, questioning the contribution of yGCS_{hc} for the MTF-1 knockout phenotype [47]. In the same study we presented C/EBP α and α -foetoprotein (AFP) as likely in vivo target genes of MTF-1. Both genes provide new clues to the molecular pathogenesis of the knockout phenotype: C/EBP α , another transcription factor, is required to maintain the differentiated, non-proliferating state of hepatocytes [48]. In addition, it plays a role in cellular energy metabolism and, interestingly, is also involved in the cellular stress response, as indicated by its induction during acute phase response [49, 50]. AFP is expressed during embryogenesis, and its expression is turned off after birth [51]. It is clinically important as a tumour marker for primary hepatocellular carcinoma and for prenatal diagnosis of spina bifida. Physiologically it is responsible for maintenance of embryonic colloid-osmotic pressure, and hence its down-regulation in MTF-1 knockout embryos could explain the late stages of the knockout phenotype, which are marked by generalised oedema [11]. In addition, AFP acts as a scavenger for heavy metals and reactive oxygen intermediates (ROI) [51]. The zinc transporter ZnT-1 was shown to be yet another *in vivo* target gene of MTF-1 [52]. It is expressed in the liver and also plays an important role in zinc metabolism in the brain [53].

In sum, MTF-1 is a crucial transcriptional regulator for basal expression of at least three important genes (MT-I, MT-II, ZnT-1) involved in zinc metabolism. The toxicity of zinc for neurons [53] would warrant studies with neural cell-specific conditional MTF-1 knockout mice. Such studies might also cast more light on the recent findings that the gene encoding the prion protein Prp, whose scrapie form causes Creutzfeldt-Jacob disease, contains MRE's in the promoter region (Ying Wang and W.S., unpublished results) and its gene product is a copper-binding protein [54].

Solid tumours usually grow under hypoxic conditions and must induce angiogenesis in order to grow. Of particular interest in this context is the recent finding that under hypoxic conditions expression of placenta growth factor (PlGF), encoding a member of the VEGF family of angiogenic factors, is induced in an MTF-1-dependent manner in fibroblasts [33]. Furthermore, preliminary results of xenograft studies suggest that MTF-1 deficiency retards the formation of ras-transformed fibrosarcomas, resulting in significantly reduced tumour masses when compared to MTF-1-expressing tumours at two weeks after injection of the cells into nude mice (Brian Murphy, P.L., W.S., unpublished data).

As is typical of higher eukaryotes, different forms of stress response produce overlapping patterns of gene activity. Thus, it would not be surprising to find new roles for MTF-1 in a variety of stress conditions other than those evoked by heavy metal, hypoxia, xenobiotic components and reactive oxygen intermediates. The downside of this ability of cells to cope with various forms of stress, however, might be a propensity to malignant growth and therapy resistance of tumours, as a result of MTF-1 boosting expression of metallothioneins and other cytoprotective proteins. Given the multiple facets of MTF-1 activity, it certainly seems advisable to monitor changes in MTF-1 expression and activity in studies involving cell stress, aging and cancer.

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