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The heme oxygenase – carbon monoxide system: regulation and role in stress response and organ failure

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Abstract Heme oxygenase (HO) breaks down heme, the iron-containing, oxygen-carrying constituent of red blood cells, yielding biliverdin, iron (II) ions, and carbon monoxide (CO). Among the isoenzymes cloned to date, only HO-1 can be induced by a panoply of stimuli linked by their ability to provoke oxidative stress. HO-1 induction protects against cell death in experimental models associated with ischemia/reperfusion or inflammation, making the gene a promising target for critical care medicine. Induction of HO-1 may confer protection by controlling intracellular levels of toxic heme, or by anti-inflammatory, anti-apoptotic, and blood flow-maintaining effects of its by-products biliverdin and CO. Although protective effects of

upregulation of HO-1 have been reported for a variety of cells and tissues, evidence suggests that the protective action may be restricted to a rather narrow threshold of overexpression. In addition, there is substantial variation in gene expression depending on transcriptional control mechanisms such as a microsatellite length polymorphism. Genetic variability and the required use of cytotoxic inducers are hurdles for purposeful targeting of HO-1 gene expression in critical care, while administration of by-products of the pathway seems feasible at present.

Heme and heme oxygenase isozymes

Heme is a ubiquitous molecule with an active iron center carrying a high affinity for oxygen. The high affinity to oxygen allows for reversible binding and transport of oxygen in hemoglobin and myoglobin. Furthermore, by virtue of its cardinal function as an electron donor in oxidation/reduction cycles, the heme prosthetic moiety is of outstanding significance for electron transfer: heme groups serve as the catalytic site and act tightly bound to a variety of proteins involved in aerobic metabolism, including respiratory chain cytochromes and numerous cytochrome P450 isoenzymes [1]. “Free” cellular heme may derive from these ubiquitous heme proteins and may act as a pro-oxidant [2, 3]. Thus, free heme is poten-

tially toxic and intracellular levels are vanishingly small and tightly controlled in most cells and tissues. While regulation of heme biosynthesis is accomplished through the modulation of δ -aminolevulinic acid synthase (ALA synthase; EC 2.3.1.37) activity [4], the enzymatic degradation of heme is controlled by microsomal heme oxygenase (HO; EC 1.14.99.3) isoenzymes which catalyze the initial and rate limiting step in heme catabolism [5]. Oxidative cleavage of the α -mesocarbon bridge of b-type heme molecules by HO yields equimolar quantities of biliverdin-IX α and carbon monoxide (CO), while divalent iron is released. Activities of ALA synthase and HO are both regulated by the cellular heme content [6].

Biliverdin-IX α is subject to further degradation to bilirubin which occurs through the action of the cytosolic

enzyme biliverdin reductase (bilirubin:NAD(P)+oxidoreductase; EC 1.3.1.24) [7]. The cellular fate of CO formed during heme degradation is only incompletely understood. CO may bind to oxyhemoglobin as well as to other heme-containing proteins, thereby affecting their heme prosthetic moieties and activity, as has been previously reported for nitric oxide (NO) [8, 9]. Thus, CO may activate soluble guanylate cyclase, leading to vasodilation. However, the much less pronounced effect of CO in stimulating GC compared to NO, and the presence of a dilatory effect despite administration of blockers of the cGMP pathway, suggest cellular mechanisms others than activation of sGC [10, 11]. In particular, there is evidence for a CO-induced dilation by BK_{Ca} channel activation, as blockade of BK_{Ca} inhibits CO-mediated vasodilation [12] and HO inhibitors derogate BK_{Ca} channel activity in smooth muscle cells [13]. It is important to note that modification of an externally located histidine residue with diethyl pyrocarbonate abrogates channel activation, suggesting an essential role of this amino acid [14]. Furthermore, the α -subunit of the channel is critically involved in its activation process. This subunit contains a heme-binding pocket, and binding of heme to the channel inhibits its activity [15]. By binding to protein-bound ferrous heme as a receptor, CO activates the channel by altering the interaction of heme with the intrinsic active protein, resulting in an increase in Ca²⁺ sensitivity [16, 17]. Under physiological conditions, in smooth muscle cells, channel activity is regulated by a local and transient increase of Ca²⁺ concentration in the micromolar range, resulting in membrane hyperpolarization via K⁺ currents and subsequent reduced voltage-dependent Ca²⁺ channel activity [18]. In this context, endogenously generated or exogenously added CO elevate the amplitude and frequency of the channel dependent on varying Ca²⁺ concentrations, which may be an essential mechanism for CO-mediated vasodilatory actions [19]. Thus, the mode of action as well as the fate of endogenous CO is still a matter of debate. Ultimately, CO is exhaled by the lungs, and gas-chromatographic quantitation of exhaled CO can serve to assess HO activity in vivo [20].

The enzyme systems regulating heme synthesis and degradation are not evenly distributed among organs and tissues, and HO activity is particularly high in spleen, testes, brain, and liver [21]. At present, cDNA of three isoenzymes, i.e. *HO-1*, -2, and -3¹, have been cloned and described to date [22–25]. While *HO-1* and -2 have been extensively characterized for several species, cDNA of *HO-3* has been cloned in rat only. It was suggested that HO-3 exhibits a substantially lower catalytic activity than

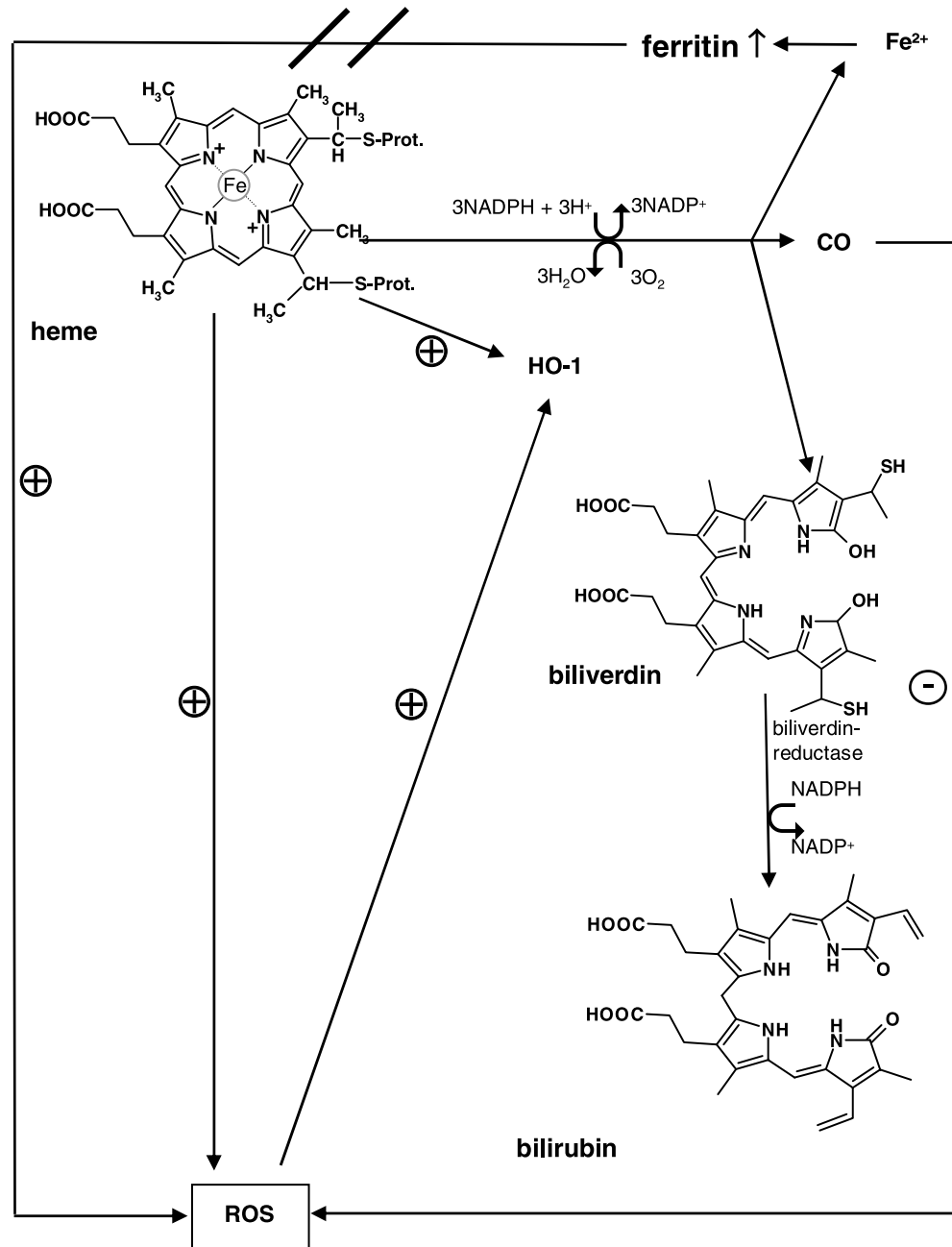
the isoenzyme 1 and 2 and plays a role in binding or transporting heme within the cell rather than degrading heme [23]. However, a recent study has questioned the existence of *HO-3*: The lack of *HO-3* transcription from two presumed genomic loci indicates that the *HO-3* gene might reflect a processed pseudo-gene of the *HO-2* locus [26]. Although HO-1 and HO-2 catalyze the same reaction and have similar cofactor requirements (NADPH, O₂), they substantially differ with respect to regulation and expression pattern. The isoenzymes are encoded by distinct genes located on chromosomes 22q12 (*HO-1*) and 16q13.3 (*HO-2*) in the human genome [27, 28]. HO-1 and -2 proteins differ in molecular weight and are immunologically distinct [29]. HO-2 – also referred to as the “constitutive” isoenzyme – does not seem to be inducible by either inflammatory or oxidative stress [30], although the promoter of the *HO-2* gene contains a glucocorticoid response element [31]. In any case, substantial increases in HO activity as observed in models pertinent to critical care are mediated by an increase in gene transcription rates for *HO-1* [30, 32]. HO-1 has been identified as the major 32-kDa heat shock (stress) protein hsp32 in the rat [33] while thermal stress did not increase HO-1 in cultured human liver cells [34]. This and other substantial differences regarding regulation of the human and rodent gene and their implications for critical care will be discussed in detail later.

HO-1 gene expression under stress conditions: heme-dependent and independent pathways

Formation of reactive oxygen intermediates is a hallmark of ischemia/reperfusion injury, and inflammatory conditions substantially contribute to organ failure in the critically ill. *HO-1* is highly inducible under these conditions and reflects one of the most prominent lines of defense of the cell against oxidative stress (Fig. 1). Moreover, deliberate induction of the gene prior to the stress event seems to be a promising stratagem to increase tolerance under conditions with anticipated formation of reactive oxygen species, e.g. in organ transplantation [35]. Similarly induction of the gene upon an insult confers protection in a variety of injury models pertinent to critical care medicine, as described in detail below. Thus, in-depth understanding of regulation of the *HO-1* gene is of outstanding importance if this pathway is to be utilized deliberately in critical care medicine. Unfortunately, there are substantial differences with respect to regulation of the gene in rodents and man, so that caution should be exercised in extrapolating promissory results from rodent models to the critical care setting [36]. Nevertheless, genetic variability in the human *HO-1* gene exists and geno- or haplotypes with higher transcription rates seem to favorably affect outcome (see below; for review [35, 37]). The *HO-1* gene – and thus presumably CO – is induced in critically ill patients in

¹The HGNC approved gene symbols for the two isoenzymes are *HMOX1* (alias *HO-1* and *bK286B10*) and *HMOX2* (alias *HO-2*) respectively, thus we use *HO-1* and *HO-2* for convenience throughout the manuscript.

Fig. 1 Mutual interaction of the heme oxygenase pathway and the cellular response to oxidative stress (ROS, reactive oxygen species)



a broad range of conditions, as mentioned above, although the molecular mode of action will differ between inhaled and endogenously formed CO [36].

The different inducers of *HO-1* act either via a metalloporphyrin-dependent (heme, the heme precursor ALA, phenobarbital, or other metalloporphyrins) or a metalloporphyrin/heme-independent (e.g. transition metals, heat shock, oxygen radicals) mechanism. Despite the differences, the effects of the diverse factors on hepatic *HO-1* gene expression appear to be mainly controlled at the transcriptional level [30, 32], and induction via classical stress

pathways involves mitogen-activated protein kinases. The broad spectrum of inducing agents essentially reflects the presence of a variety of transcriptional enhancer elements including binding sites for activator protein-1 (AP-1) and nuclear factor κ B (NF κ B) as well as hypoxia response, cadmium response, heat shock response, metal response, and IL-6 response elements within the *HO-1* promoter (Fig. 2) [6]. Nevertheless, there is recent evidence to suggest that de-repression of the BACH-1 repressor (a bZip protein that forms heterodimers with small Maf proteins) is functionally significant to enhance *HO-1* transcription

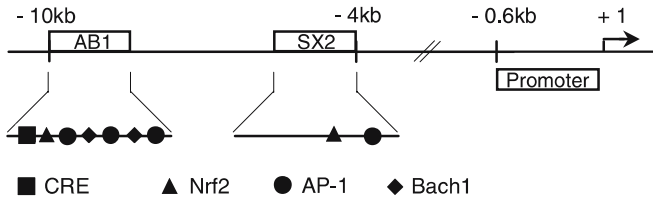


Fig. 2 Model of the human HO-1 gene and potential regulatory elements (AB1, distal enhancer element AB1; SX2, distal enhancer element SX2; CRE, cAMP responsive element; Nrf2, nuclear factor erythroid 2-related transcription factor 2; AP-1, activator protein-1)

in human cell lines: small interfering (si)RNAs targeted to *BACH-1* mRNA by itself induce upregulation of *HO-1* and further enhance dose-dependent upregulation by the prototypic inducer heme [38]. It is noteworthy that a wide variety of drugs used in the ICU setting, such as steroids [39], statins [40], and β 1-agonists [41], can interfere with regulation of *HO-1* and this might contribute to the salutary actions of these compounds [42].

Biological functions of by-products of HO-1: “The good, the bad, and the ugly”

Due to the potential toxic effects of free heme, a meticulous balance between its synthesis and catabolism is crucial to ensure cellular homeostasis. Thus, heme oxygenase has classically been viewed exclusively as a heme-degrading enzyme system, and heme itself has long been recognized as a potent inducer of *HO-1* [43]. On the other hand, two products of this pathway, i.e. biliverdin and CO, received little attention until the finding that they exert biological functions under physiological conditions [44, 45]. These functions are even more pertinent after induction of *HO-1*, e.g. after resuscitation from shock [46]. The observation that almost all of the stimuli for *HO-1* induction including the substrate heme are linked by their ability to provoke oxidative stress, in concert with the observation that bile pigments can function as endogenous antioxidants, has supported a role for *HO-1* and its products biliverdin/bilirubin in the adaptive response to oxidative stress [47]. Among the stimuli pertinent to critical care medicine, (low-flow) ischemia and reperfusion secondary to shock and resuscitation is a particularly frequent clinical problem. Previous work from our laboratory regarding the role of *HO-1/hsp32* in the hepatic stress response in experimental models of hemorrhagic shock and subsequent resuscitation indicated that induction of *HO-1* reflects an adaptive response to reactive oxygen species (ROS) formation [48, 49], and confers delayed protection against tissue injury [50, 51].

Although the protective actions of CO and the bile pigments in vitro and in vivo during heme degradation are meanwhile well documented (see review by Scott

et al. in this issue; [44, 52–54]), it is obvious that the long-known potential toxic effects of iron, CO, and the bile pigments [55, 56] are likely to limit the beneficial actions to a rather narrow threshold of overexpression. Iron is released in equimolar amounts when heme is degraded to yield biliverdin and carbon monoxide. Since iron catalyzes the formation of reactive oxygen intermediates, most notably the hydroxyl radical, it is obvious that this by-product may offset the anti-oxidative properties of the bile pigments if it is formed in significant amounts. Thus, *HO-1* expression as part of the cellular stress response may exhibit pro- and antioxidant properties [4]. Ferrous iron is rather effective as a strong oxidant; however, it stimulates the synthesis of ferritin through its regulatory protein binding and activation of iron response elements [57]. Ferritin is an intracellular iron-storage protein ensuring safe sequestration of free iron ions, thereby serving as an additional antioxidant [58]. However, the mechanisms that are involved in co-expression of *HO* and ferritin genes may involve additional pathways. For instance, in *HO-2* knock-out mice ROS may initiate transcriptional activation of the *HO-1* gene, but these animals fail to induce ferritin transcripts simultaneously [59]. Furthermore, there is evidence to suggest that iron ions can synergize with ROS to regulate the expression of oxidative stress response genes, including *HO-1* itself [60]. In any case, *HO-1* seems to be of outstanding importance for iron reutilization in rodents [61] and humans [62] even under physiologic conditions, and *HO-1* deficiency has been shown to result in iron deposition with inflammatory sequelae secondary to impaired reutilization. While *HO-1*-targeted mice exhibit a phenotype characterized by iron metabolic disorders with long survival, the first human autopsy case of *HO-1* deficiency in a 6-year-old boy revealed predominant intravascular hemolysis, coagulation, and amyloidosis with substantially reduced life expectancy [63]. Whether increased release/deposition of free iron ions due to acute overexpression and increased *HO* activity may result from induction of the *HO-1* gene in vivo (as has been suggested in cultured cells [55]) has not been studied specifically.

Carbon monoxide has received much attention as a messenger molecule and as a potential therapeutic target [13]. *HO* as a potential endogenous source of CO co-localizes with soluble guanylate cyclase – as a potential target of CO actions – primarily in neuronal tissues, and inhibition of *HO* by false substrates or gene knock-out may adversely affect functions of the central and peripheral nervous system [65–68].

Although CO and NO display some similarities, there are substantial differences between these two gaseous monoxides with respect to their mode of action. NO synthesis by the constitutive NOS isoforms is tightly regulated by physiological stimuli (coupled to Ca^{2+} release), and its half-life is highly limited due to an unpaired electron leading to rapid reactions with metal ions, ROS, or sulfhydryl groups in the cell. Thus, stimulation of the

constitutively expressed NOS isoenzymes (NOS1, NOS3) leads to a short-lived burst of NO production, which in turn results in a rapid and transient rise in local cGMP levels reflecting an approximately 100- to 400-fold activation of soluble guanylate cyclase (sGC). The substantial increase in sGC activity is due to binding of NO to the prosthetic heme moiety of sGC, leading to breaking of the proximal His-Fe bond and formation of a 5-coordinated nitrosyl heme complex [68, 69].

In contrast, CO is not a radical and its production by HO-1 is not tightly regulated in an "on-off" manner. Furthermore, binding of CO to the prosthetic heme group of sGC – at least under *in vitro* conditions – leads to formation of a 6-coordinated heme complex interacting with His-Fe bonds with only a fivefold increase in activity of the $\alpha_1\beta_1$ heterodimeric isoform of sGC [70]. However, mechanisms such as 'sensitization' of sGC to CO in biological systems [71] as well as control of NO production by HO [72] may result in a substantial increase in the impact of the HO pathway in the control of cGMP levels. Heme prosthetic moieties are abundantly present in enzymes catalyzing single electron-transferring reactions. Thus, CO might interfere with the activity of a variety of enzymes others than sGC. Evidence in this respect has been provided for a panel of enzymes including xanthine oxidase [73], NADPH oxidase [74, 75], and prostaglandin-H-synthase [76], underlining the significance of the HO system for modulation of the oxidative stress response.

Similar to the NOS system, which comprises constitutive and inducible isoforms, the HO system is characterized by constitutive and stress-inducible isoenzymes. The stress-induced production of NO by the inducible NOS isoform (NOS2) is independent of Ca^{2+} /calmodulin, which control NO production by the constitutive NOS isoforms. Thus, substantially higher amounts of NO are produced in a tonic fashion. Work from our laboratory suggests that similarities exist between the stress-inducible NOS/NO and the HO-1/CO pathway, at least for the portal circulation of the liver under conditions of septic and hemorrhagic shock [46, 51]. Blockade of HO activity with false substrates of the HO pathway produced a moderate, selective, and transient increase in portal vascular resistance but no decrease in portal blood flow in the normal rat liver. In contrast, a substantial, selective, and lasting increase in portal resistance was observed upon administration of Sn-protoporphyrin-IX, a false substrate leading to a long-lasting blockade of HO activity, after transcriptional activation of the *HO-1* gene by hemorrhage and resuscitation [46]. This augmented pressor response of false substrates of HO in the liver is paralleled by a decrease in portal blood flow and reflects unmasking of a parallel induction of vasoconstrictors, such as endothelin-1 [77]. Due to similarities between the gaseous monoxides CO and NO, sGC has been traditionally considered as the target of cellular actions of CO, although

alternative modes of action of CO have been suggested. In addition, CO might regulate expression of *NOS2* in lung and liver, which is another important aspect regarding critical care in general and specifically sepsis [78]. These cGMP-independent effects may include activation of vascular 238pS K_{Ca} [79] and 105pS K_{Ca} channels, rendering smooth muscle cells less responsive to the actions of vasoconstrictors [80]. The protective effect of *HO-1* overexpression, e.g. in the lung, has been ascribed to CO-induced elevation of cGMP and/or activation of p38 MAPK [81]. Recently, it was shown that the expression and activity of the matrix metalloproteinases MMP-1 and MMP-2, which are regulated in a MAPK-dependent manner, are inhibited in the human lung epithelial cell line A549, implicating a crucial role of CO in the pathophysiology of emphysema and other diseases involving a protease/antiprotease imbalance [82]. In addition, CO at physiological concentrations inhibits the production of proinflammatory cytokines such as TNF- α , MIF, and IL-1 from macrophages and the secretion of interleukin-2 from activated T-cells via selective activation of the MAPK pathway [83, 84].

Induction of *HO-1* – a double-edged sword

Studies using *HO-1* knock-out mice, as well as the report of the first human case of HO-1 deficiency [63], suggest an important role for the inducible HO isoenzyme already under physiological conditions. Mice lacking *HO-1* were unable to modulate body iron stores properly and were more susceptible to tissue injury [61, 85]. In addition, stress conditioning including *HO-1* gene expression as well as *HO-1* gene transfer can render cells, tissues, and organisms less susceptible to subsequent stress [86, 87]. Although the bulk of literature available to date would suggest that *HO-1* gene expression confers protection in a variety of injury models pertinent to critical care medicine [88–91], there is evidence to suggest that the protective properties of this pathway are restricted to a rather narrow threshold of overexpression [55]. Thus, evidence available to date would suggest that HO-1 is neither exclusively cytoprotective nor exclusively cytotoxic. While most of the animal data were obtained after stress conditioning using cytotoxic inducers, e.g. heavy metal ions, this is not an intriguing option in the critical care setting. Nevertheless, these studies were conducted almost exclusively in rodent species and, thus, a fairly homogeneous induction of the gene in these animals can be assumed.

Differences between rodent and human *HO-1* genes – a plea for caution

Data from a flurry of studies mostly conducted in rodents provided evidence that antioxidant properties (presumably via biliverdin formation) and improved blood flow

(presumably via CO formation) contribute to the salutary effects of *HO-1* gene expression under conditions of shock and inflammation [46, 51, 92]. Thus, CO may confer additional protective effects via anti-inflammatory mechanisms [87, 93] particularly in models pertinent to surgical conditions, such as transplantation or infection.

In this light, alternative regulatory features of the human as compared to the mouse/rat gene give rise presumably to substantial variability in *HO-1* expression in humans, with potential implications for critical care medicine. One striking difference in the genomic organization of the genes in the species is the presence of a (GT)_n repeat microsatellite in the human *HO-1* gene. Several lines of evidence point to a regulatory function of this motif. (1) Systematic analysis shows that rat and mouse genes completely lack the microsatellite (the same is true for the dog genome, while in the chimpanzee draft genomic sequence only a low-number repeat is present). (2) The non-inducible *HO-2* gene is not associated with such a (GT)_n microsatellite [94]. (3) The length of this polymorphic repeat has been associated with a different outcome in a variety of diseased states. Interestingly, this has also been demonstrated for *NOS1*, where a similar genomic element at a similar position around the first exon is found and the repeat length influences the decline in lung function in patients with cystic fibrosis [95].

Whether this repeat influences gene transcription, for instance by spacing apart interacting binding sites for transcription factors, or may influence translation of the protein by forming a (GU)_n stem-loop structure in the 5'-UTR of the mRNA has to be elucidated. There is at least evidence by two spliced ESTs (expressed sequence tags,

BE407102, DA903962) from the EST database that this repeat region can be part of the *HO-1* transcript. If transcribed, such a structure may hinder the ribosome scanning and therefore efficient translation. A similar translational control mechanism has been described for glutamate receptor 2 [96].

In line with this concept, genotypes associated with higher transcriptional activity, such as a short GT repeat in the well-characterized microsatellite length polymorphism between -198 and -256, are associated with a better outcome in a variety of diseases pertinent to intensive care [97-102]. These include conditions associated with ischemia and reperfusion as well as inflammatory conditions, such as kidney transplantation and myocardial infarction but also lung emphysema. On the other hand, these differences would imply that strategies to induce the gene in humans deliberately, e.g. prior to ischemia/reperfusion associated with transplantation, will vary greatly with respect to the genetic background of the patient. Thus, assessment of the genotype prior to such interventions seems mandatory. Strategies to apply the by-products of the pathway, such as biliverdin or CO, directly to the patient seem more promising. It is noteworthy that - unlike data obtained in experimental models - the *HO-1* gene is induced in brain-dead organ donors as a result of the underlying trauma/injury [35, 37]. Thus deliberate induction of the gene prior to organ harvest is less likely to lead to substantial increases in activity. In any case, if the promising data from preclinical studies in rodents prove to be applicable to man, this pathway bears outstanding potential for medicine in general and in particular for the care of the critically ill.

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