

The HMGB1-RAGE Inflammatory Pathway: Implications for Brain Injury-Induced Pulmonary Dysfunction

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Abstract

Significance: Deceased patients who have suffered severe traumatic brain injury (TBI) are the largest source of organs for lung transplantation. However, due to severely compromised pulmonary lung function, only one-third of these patients are eligible organ donors, with far fewer capable of donating lungs (~20%). As a result of this organ scarcity, understanding and controlling the pulmonary pathophysiology of potential donors are key to improving the health and long-term success of transplanted lungs. **Recent Advances:** Although the exact mechanism by which TBI produces pulmonary pathophysiology remains unclear, it may be related to the release of damage-associated molecular patterns (DAMPs) from the injured tissue. These heterogeneous, endogenous host molecules can be rapidly released from damaged or dying cells and mediate sterile inflammation following trauma. In this review, we highlight the interaction of the DAMP, high-mobility group box protein 1 (HMGB1) with the receptor for advanced glycation end-products (RAGE), and toll-like receptor 4 (TLR4). **Critical Issues:** Recently published studies are reviewed, implicating the release of HMGB1 as producing marked changes in pulmonary inflammation and physiology following trauma, followed by an overview of the experimental evidence demonstrating the benefits of blocking the HMGB1-RAGE axis. **Future Directions:** Targeting the HMGB1 signaling axis may increase the number of lungs available for transplantation and improve long-term benefits for organ recipient patient outcomes. *Antioxid. Redox Signal.* 23, 1316–1328.

Introduction

SEVERE NEUROLOGIC INJURY due to trauma often results in numerous cells that are killed in a nonspecific manner as well as displacement of physical structures of the brain, including damage to blood vessels, axonal shearing, alterations in the blood–brain barrier, and intracranial hemorrhaging. Subsequent to the initial traumatic brain injury (TBI) is a secondary injury cycle, which includes ischemia, cerebral hypoxia, hypotension, cerebral edema, and raised intracranial pressure. This array of events is also accompanied by the release of excitotoxic neurotransmitters, which damage both neural and non-neural cell types and further amplify the induction of numerous biochemical cascades and initiate neurodegeneration (61). Depending on the severity of the trauma,

TBI patients may also be subjected to complications of non-neurologic organ dysfunction (NNOD).

The pathophysiology of NNOD following TBI is unclear. Apart from the direct nervous system involvement, including the hypothalamus–pituitary axis and sympathetic nervous system efferent limbs and resultant massive release of catecholamines (31), there is also systemic release of inflammatory mediators, such as pro- and anti-inflammatory cytokines, chemokines, complement factors, and reactive oxygen species, which can produce direct injury within the heart and lungs (43, 48, 54, 65). Although the concentrations of many of these factors may be highest within the brain extracellular compartment due to decreased cerebral blood flow (18, 102), release into venous drainage can occur rapidly following disturbances of the blood–brain barrier (48, 118),

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propagating tissue damage in susceptible organ systems, leading to further inflammation, tissue damage, and mortality (29). By some analyses, NNOD produces mortality that is proportionally similar to initiating neurological complications (91).

Pulmonary Complications Related to TBI

Pulmonary complications are among the most prevalent NNODs encountered in the TBI population (95). Although intensive care units (ICUs) strive to optimize oxygen delivery following severe brain injury, little is known regarding the pathophysiology of pulmonary dysfunction secondary to the neurologic insult. The most frequent NNODs present in the pulmonary system include the acute respiratory distress syndrome (ARDS) and neurogenic pulmonary edema (NPE). Clinical recognition of ARDS is classically associated with inflammatory processes, including the onset of hypoxemia, reduction in pulmonary compliance, and presence of cellular infiltrates (14). In contrast, NPE often occurs in the absence of direct lung injury and is marked by pulmonary interstitial and alveolar fluid accumulation likely due to disruptions in the integrity of the alveolar capillary membrane (9, 10). Although exploration of either condition can be justified based upon its own specific merits and mechanisms, one must also consider that the temporal elements may potentially act as a continuum; one condition may essentially contribute to the onset of the other. This common pathway may exhibit characteristics of both hemodynamic and inflammatory responses (Fig. 1). The hemodynamic attribute may serve to increase in pulmonary vascular pressure, resulting in hydrostatic edema, while the inflammatory mechanism of brain cytokine and chemokine release causes an increase in the permeability of pulmonary capillaries causing both exudative edema and leukocytic infiltration of the tissue.

Numerous inflammatory mediators are thought to contribute to the latter response and include interleukin (IL)-1 beta, IL-6, and tumor necrosis factor (TNF)-alpha (43, 48, 54, 65). In addition to these factors are damage-associated molecular patterns (DAMPs) (80). Extracellular DAMPs are released from injured or stressed cells and trigger an immune response to injury or trauma. Damaged cells of all types release DAMPs and can influence the inflammatory reactions that follow sterile traumatic injury, such as TBI.

The exact mechanism by which TBI causes pulmonary dysfunction remains unclear, but it may be related specifically to nervous system release of the DAMP, high-mobility group box protein 1 (HMGB1). This review focuses on the numerous inflammatory roles of HMGB1 and its respective receptors, receptor for advanced glycation end-products (RAGE) and toll-like receptor 4 (TLR4), and how they contribute to lung injury, and then specifically addresses the role of this pathway in acute lung injury (ALI) caused by TBI.

High-Mobility Group Box Protein 1

HMGB1, formerly known as amphoterin, was originally discovered as an important protein in neurite outgrowth. HMGB1 was rediscovered and identified as a nuclear factor to enhance DNA transcription (30, 73). HMGB1 has also been called HMG-1, p30, sulfoglucuronyl carbohydrate-binding protein-1 (SBP1), and differentiation-enhancing factor (56). The nomenclature was eventually revised to HMGB1 (21).

HMGB1 belongs to a family of nonhistone chromosomal proteins, including HMGB2-4 (107). The structure of HMGB1 is very important to its function as post-translational modifications of the molecule can result in not only a difference in functionality but also a change in the localization of the ligand entirely. Expressed as a single polypeptide chain

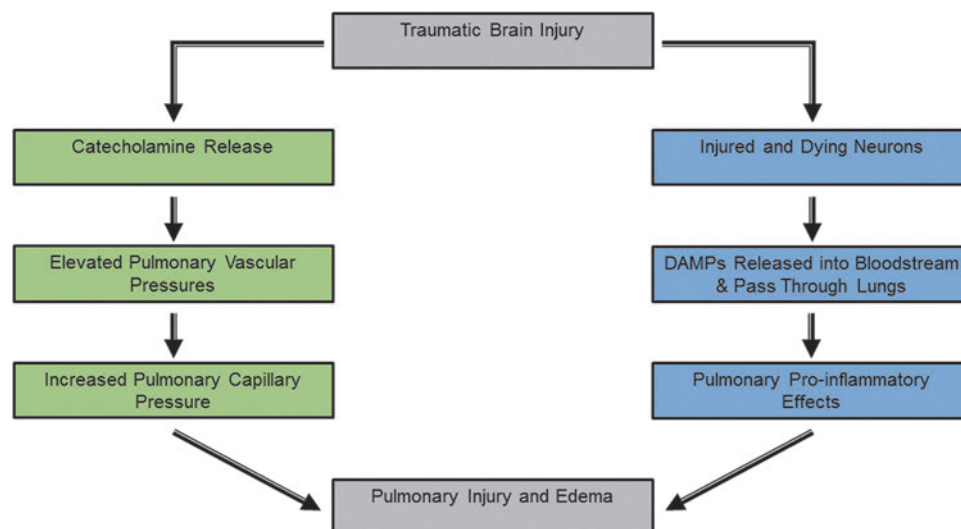


FIG. 1. Canonical and noncanonical mechanisms of traumatic brain injury induced pulmonary dysfunction. The canonical pathway (*green rectangles*) described for traumatic brain injury-induced effects in the lung depends on the release of catecholamines, which enter the bloodstream and cause elevated pulmonary capillary pressures and permeability. Fluid is able to cross capillary endothelial cells causing pulmonary edema. The noncanonical pathway (*blue rectangles*) for the effects of traumatic brain injury on pulmonary function involves the release of damage-associated molecular patterns (DAMPs) by injured or dead neurons, which then enter venous blood in the lungs *via* the pulmonary circulation and cause pulmonary injury and dysfunction. To see this illustration in color, the reader is referred to the web version of this article at www.liebertpub.com/ars

of 215 amino acids, HMGB1 contains two N-terminal DNA-binding domains, HMG box A and box B, and an acidic C-terminal domain. Interestingly, HMGB1 lacks endoplasmic reticulum localization sequences, but instead has two nuclear localization sequences (17, 46, 93, 126). When not acetylated, HMGB1 remains localized in the nucleus and is not secreted or released regardless of injury or insult (34, 64, 70). However, hyperacetylation of the molecule results in cytosolic relocation, allowing for further secretion into the cellular milieu under proper signaling stimulation (34, 70). The N-terminal DNA-binding domains, box A and box B, demonstrate nonspecific interaction with DNA and transcription factors to alter chromosomal architecture. Additional molecular properties of three cysteine residues have been implicated to be involved in extracellular HMGB1 activity, including the redox state of cysteine (C) 106, and a disulfide bond between C23 and C45 (50, 96, 97, 111) (Fig. 2).

HMGB1 is known to interact with transcription factors and chromatin, although this interaction is generally transient or unstable (116). For example, HMGB1 interacts with numerous transcriptional regulators, such as p53, HOX proteins, Rel, NFAT2, and PU.1, to facilitate expression or repression of targeted genes (2, 68, 71, 76, 140). There is also substantial evidence demonstrating that HMGB1 and histone H1, a chromatin-binding protein, compete for binding sites on chromatin, further regulating transcriptional activation (25, 59, 77). Collectively, HMGB1 can interact directly with DNA, chromatin, and transcription factors to regulate transcription and genetic recombination. HMGB1 is also able to activate cells *via* several surface receptors, including TLR2, TLR4, and RAGE (51, 57, 84).

Extracellular Forms of HMGB1

Although HMGB1 is typically associated with chromatin in normal cells, it can be quickly released into the cytoplasm following stress, injury, or disease. The extracellular form of HMGB1 is known to differ dramatically based on the oxidative environment, be it saliva, serum, or tissue parenchyma, and subsequently produces different cellular action (4). For example, the initial form of HMGB1 present upon release into the extracellular space is the all-thiol state. All-thiol HMGB1 is thought to largely act on a member of the Ig superfamily, RAGE, and produces chemoattractant actions on leukocytes (120). There are also reports that all-thiol HMGB1 can form a complex with the chemokine, CXCL12, and act through its cognate receptor, CXCR4 (101, 120).

When present in the oxidative environment, cysteines 23 and 46 present in the HMGB1 A box form a sulfide bond, effectively producing the disulfide form of HMGB1 (133). Disulfide HMGB1 can only act on the receptor, TLR4 (110), and influences the production of inflammatory cytokines (133–135). Important work using an NMR-based approach to distinguish the oxidation states and half-lives of HMGB1 in serum, saliva, and cell culture media revealed that the half-life of all-thiol HMGB1 is as short as 17–18 min in human serum and saliva, and the subsequent clearance of the disulfide HMGB1 varies between 65 and 642 min depending on the extracellular fluid (139) (Fig. 3). Disulfide HMGB1 is then further reduced following oxidation of Cys-106 in the B-domain to an inert form (139).

HMGB1 Release

Numerous cells types throughout the body can undergo passive release of loosely bound nuclear HMGB1 following tissue injury, including cells of the nervous system (41, 62, 63, 100, 114). However, 25 years after HMGB1 was discovered, Tracey and colleagues determined that HMGB1 can also be actively released from primary monocytes and it functions as a critical cytokine to mediate the immune response to infection and injury (123). Other cell types known to actively release HMGB1 include astrocytes, microglia, and neurons (37, 38, 40, 62, 86, 123). In both ways, HMGB1 orchestrates different cellular functions in consequence to environmental and homeostatic cues to act as a signal for tissue damage, injury, and/or infection.

As noted previously, extracellular HMGB1 may form a complex with other molecules to enhance proinflammatory responses, including lipopolysaccharide (LPS), IL-1, bacterial DNA, CXCL12, CD24, and viral RNA (24, 52, 103). Interestingly, in some cases, application of recombinant HMGB1 alone was shown to lack cytokine function (113). It is likely that this protein took the all-thiol form of HMGB1 as it had chemotactic qualities to recruit enterocytes and smooth muscle, endothelial, and stem cells (32, 51, 74, 81, 99, 121, 131). During active inflammation, the predominant form of HMGB1 is thought to be the disulfide bond between C23 and C45 (disulfide HMGB1); however, when inflammation begins to subside, HMGB1 is terminally oxidized at the cysteine residues, rendering it biological inactive (oxidized HMGB1) (6, 121, 135). Subsequently, an oxidizing environment following inflammation or injury may promote HMGB1 cytokine activity instead of cellular repair by monocyte recruitment (121).

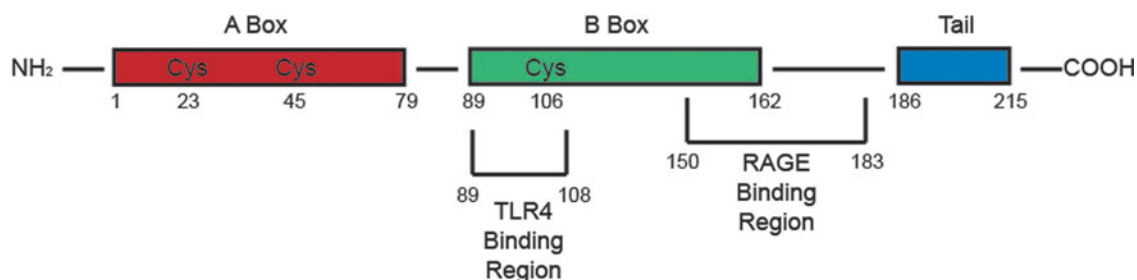


FIG. 2. HMGB1 structure. HMGB1 structure with the A and B box-binding regions as well as the acidic tail. The TLR4 and RAGE4-binding regions are also highlighted. The three cysteine residues are apparent at the 23, 45, and 106 positions. HMGB1, high-mobility group box protein 1; RAGE, receptor for advanced glycation end-products; TLR4, toll-like receptor 4. To see this illustration in color, the reader is referred to the web version of this article at www.liebertpub.com/ars

Less is known about HMGB1-mediated degradation. Extracellular HMGB1 undergoes limited proteolysis by serine proteinases that are secreted by stimulated cells. Although the degradation of HMGB1 can produce a 10-amino acid fragment that retains some functional activity in leukocytic cells (105), the kinetics of HMGB1 oxidation and the half-lives of all-thiol and disulfide HMGB1 species in serum, saliva, and cell culture medium are relatively restricted (139).

HMGB1 Receptors: RAGE and TLR4

Extracellular HMGB1 transduces cellular signals through plasma membrane receptors, including TLR2, TLR4, and RAGE (51, 57, 84). Notable binding domains present on the all-thiol HMGB1 form are amino acids 150–183 on the RAGE-binding portion (55), whereas the disulfide HMGB1-binding domains to TLR4 are amino acids 89–108 (133, 135) (Fig. 3). The disulfide bond between C23 and C45 further increases the stability of the folded full-length HMGB1 molecule (97).

Downstream signaling of HMGB1 is facilitated by a number of adaptor proteins, which converge through pathways involving mitogen-activated protein kinase (MAPK) and nuclear factor kappa B (NF κ B) and transcriptional regulator, p53 (82, 83, 89, 98) (Fig. 4). Activation of these cascades is known to result in the production and release of proinflammatory cytokines, TNF α , IL-1, IL-6, and IL-8, and several chemokines (5, 85, 87, 94, 128).

TLR4: Form and Function

Toll-like receptors, or TLRs, are membrane receptors that play a vital role in host defense by recognizing pathogen-associated molecular patterns or DAMPs with subsequent

activation of immune responses. In the 1990s, Janeway and colleagues discovered TLR4, the first identified TLR, by ligating antibodies to induced immune responses (72). Since that discovery, a total of 13 TLRs have been identified, which play a role in multiple pathways, including pathogen recognition and cellular repair and regeneration (39). Ligands for TLRs are numerous and those known to interact with TLR4 include exogenous molecules such as LPS as well as endogenous ligands (DAMPs), such as heat shock proteins, fibrinogen, peptidoglycan, and HMGB1, and others (15, 80, 138). In particular, the HMGB1-TLR4 axis has been implicated in several disease processes such as cerebral ischemia (135, 136) as well as ischemia reperfusion (IR) injury in the heart, liver, and lungs (35, 132). In particular, a translational study using clinical samples and a mouse model demonstrated that TLR4 activation by HMGB1 contributes to the development of pulmonary hypertension and that HMGB1 levels correct with pulmonary arterial pressures (13). After binding with HMGB1, TLR4 downstream inflammatory pathways are both myeloid differentiation primary response gene 88 (MyD88) independent and dependent (Fig. 5).

RAGE: Form and Function

In addition to TLR-mediated pathways of inflammation, HMGB1 is known to bind to the transmembrane receptor, RAGE. RAGE is highly conserved across the mouse, rat, and human and is constitutively expressed at high levels both on pulmonary endothelial and alveolar cells (104). It binds to several proinflammatory molecules, including S100, amyloid fibrils, and HMGB1. Upon binding, the downstream signaling pathway is MyD88 dependent, which is common to one of the TLR4 pathways (Fig. 6). RAGE exists primarily in two forms: a full-length transmembrane form as well as a soluble

Redox State	Structure	Serum Half-Life	Biological Activity
1) Reduced - All Thiol	$\begin{array}{ccccc} \text{SH} & \text{SH} & & \text{SH} & \\ & & & & \\ \text{C} & \text{---} & \text{C} & \text{-----} & \text{C} \\ 23 & 45 & & 106 & \end{array}$	17 mins ⁽¹¹⁵⁾	RAGE-Dependent Inflammatory Pathway Chemoattractant
2) Disulfide	$\begin{array}{ccccc} \text{S} & \text{---} & \text{S} & & \text{SH} \\ & & & & \\ \text{C} & \text{---} & \text{C} & \text{-----} & \text{C} \\ 23 & 45 & & 106 & \end{array}$	642 mins ⁽¹¹⁵⁾	TLR4-Dependent Disulfide bond increases stability Activates leukocytes
3) Oxidized - Sulfonated	$\begin{array}{ccccc} \text{HSO}_3 & \text{HSO}_3 & & \text{HSO}_3 & \\ & & & & \\ \text{C} & \text{---} & \text{C} & \text{-----} & \text{C} \\ 23 & 45 & & 106 & \end{array}$	Inactive	Present once inflammation is subsiding

FIG. 3. HMGB1 redox states and associated biological activity. The three redox states of HMGB1 differ by structure, half-life, and activity. The reduced form contains a thiol group at all three cysteine residues with a serum half-life of 17 min. It is this form that is able to bind to RAGE and activate inflammatory pathways. The disulfide form contains a disulfide bond between the cysteine residues at positions 23 and 45. This bond increases its stability and half-life to 642 min. Additionally, this is the form that is TLR4 dependent. The final inactivated form is known as the oxidized form and has sulfonated cysteines at all three positions. This is the predominant form once inflammation has begun to subside.

isoform generated either by splicing or proteolytic cleavage (20, 45). An inert form of RAGE is also known to exist (Fig. 7). This soluble form is able to bind to RAGE ligands in the extracellular space before interaction with the transmembrane form, suggesting its role as a decoy receptor (20). Additionally, several studies have documented that RAGE has multiple splice variants, which have various ligands and functions (36, 53, 84, 137). Recent work has demonstrated that the different variants are distributed in different tissues with the full-length form being found most frequently in all tissues (60). However, over 15 variants were discovered, demonstrating a unique variant distribution in the body (Fig. 8).

HMGB1 and TBI

Severe TBI is a major public health problem that accounts for one-third of early mortality due to trauma in the United States. Late mortality is caused by injuries secondary to head trauma, which impact distal organ function and increase susceptibility to infections. In particular, severe brain injury often produces a pronounced impact on lung function (16, 124). The mechanisms by which TBI contributes to pulmonary dysfunction are poorly understood, but are thought to involve a catecholamine surge-associated pulmonary vascular permeability change leading to NPE (7). This injury-induced excess

of catecholamine also lends itself to hypertension, abnormal heart variability, and neurological deficits (44, 90, 112). More recent clinical studies implicate the production and release of inflammatory mediators, including HMGB1 (8, 49, 75, 122). Although organ failure scoring systems, present clinical markers, and single cytokine estimates have failed to predict the onset of organ dysfunction in the clinical setting, patterns of early circulating trauma markers such as HMGB1 may serve to guide and streamline damage control following TBI.

There is currently no absolute definition of pathophysiology associated with HMGB1 release following traumatic injury with or without TBI. Some clinical studies of mechanical trauma in the absence of head injury fail to find a correlation between HMGB1 levels in plasma and measures of morbidity (88). However, other studies, which included patients with trauma to the head, suggest that the release of HMGB1 is predictive of both mortality and neurological dysfunction in adult and pediatric patients (8, 28, 42). The presence of the increased HMGB1 levels in both plasma and cerebrospinal fluid may ultimately reflect release from damaged and dying cells in the brain.

No single animal model can adequately mimic all aspects of the human TBI. However, recent investigations using the controlled cortical impact model or fluid percussion in rodents reveal similar rapid changes in HMGB1 in blood and brain tissue (78, 125). The different isoforms of the protein may be integral to pulmonary functional changes and cellular responses by immune cells. For example, the initial all-thiol form of HMGB1 released from the brain may contribute to RAGE-dependent functional chemotaxis of innate immune

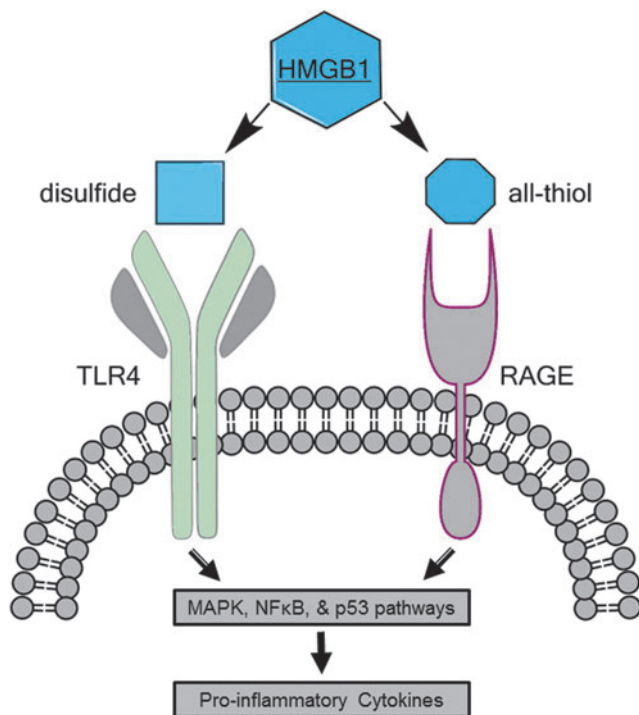


FIG. 4. The interaction between HMGB1 and RAGE/TLR4. Downstream signaling of HMGB1 *via* RAGE and TLR4 receptor activation is facilitated by a number of adaptor proteins, which converge through pathways involving MAPK, NF κ B, and the transcriptional regulator, p53. Activation of these cascades is known to result in the production and release of proinflammatory cytokines, TNF α , IL-1, IL-6, and IL-8, and several chemokines. IL, interleukin; MAPK, mitogen-activated protein kinase; NF κ B, nuclear factor kappa B. To see this illustration in color, the reader is referred to the web version of this article at www.liebertpub.com/ars

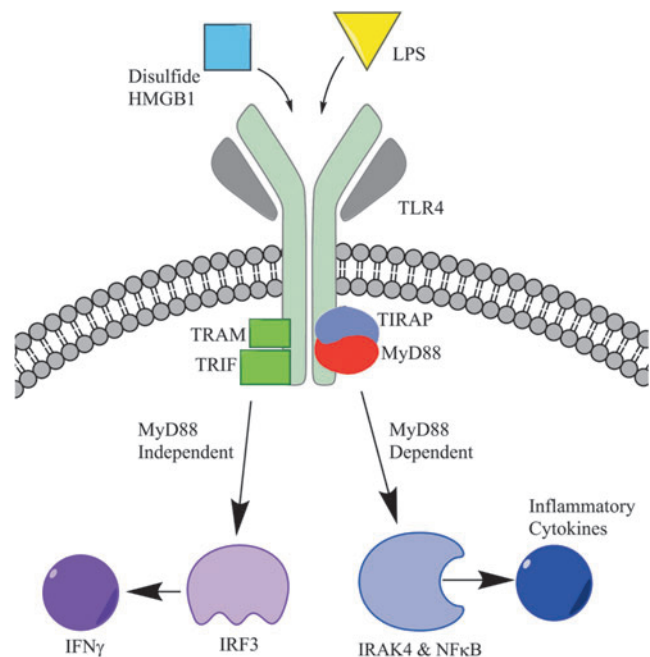


FIG. 5. HMGB1-TLR4 binding and downstream activation. TLR4 has two distinct pathway choices, varying by the involvement of the MyD88 adaptor protein. Both pathway products are key to the inflammatory process. LPS, lipopolysaccharide; MyD88, myeloid differentiation primary response gene 88. To see this illustration in color, the reader is referred to the web version of this article at www.liebertpub.com/ars

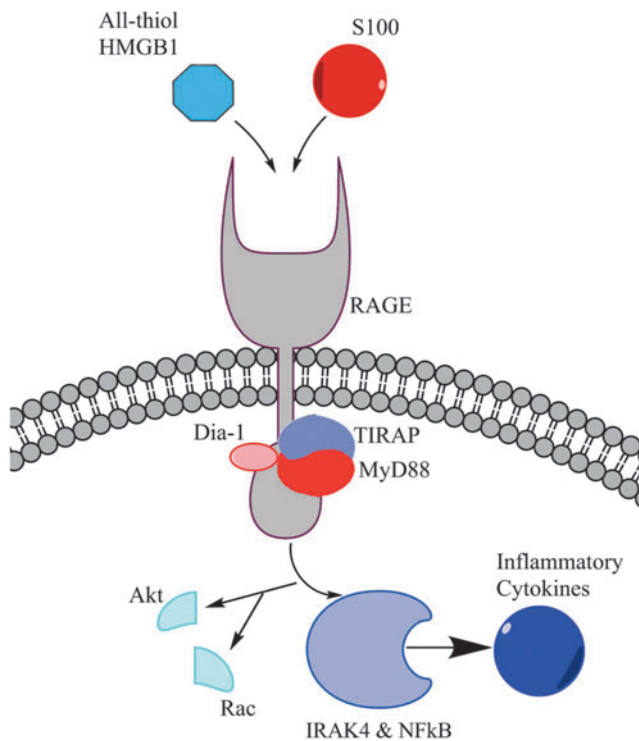


FIG. 6. HMGB1-RAGE binding and downstream activation. The signaling pathway of RAGE involves the key adaptor proteins, MyD88 and TIRAP, which it shares in common with TLR4 signaling. All-thiol HMGB1 also serves to signal an increase in chemotactic activity. To see this illustration in color, the reader is referred to the web version of this article at www.liebertpub.com/ars

system cells (119, 130). However, as the half-life of this isoform is relatively short, the disulfide form of HMGB1 may also contribute to organ dysfunction and changes in blood-brain permeability in a TLR4-dependent manner (78, 125, 139). Subsequently, HMGB1 isoforms present in injury conditions may suitably act as priming signals, which are perceived in both the nervous and immune systems (3, 38, 109, 120).

Alternative interpretations include the suggestion that macrophages exposed to catecholamine induce HMGB1 release (68). Additional evidence to support this observation can be obtained by blocking adrenergic receptors or using an agonist of α 2-adrenergic receptors, dexmedetomidine, to reduce levels of HMGB1 in blood post-TBI (26, 58).

RAGE and Lung Disease

RAGE has been implicated in several disease processes, such as cancer, diabetes, and Alzheimer's disease. Considering its high expression in the lung, it is not surprising that RAGE has also been associated with several pulmonary diseases, including lung cancer, pulmonary fibrosis, and ALI (12, 33). Multiple studies have demonstrated that several RAGE ligands, including HMGB1, are upregulated in lung cancer and are associated with metastasis and poor outcomes. The HMGB1-RAGE interaction appears to contribute to tumor invasion and metastasis and is believed to be an important target and opportunity for

antitumor therapy (69). Additionally, recent work has demonstrated that blocking of the HMGB1-RAGE pathway decreases tumor cell proliferation, invasion, and MMP activity (108).

In addition to lung cancer, RAGE has also been implicated in idiopathic pulmonary fibrosis (IPF). IPF is a progressive debilitating disease with an unclear pathogenesis and no reliable treatment. In a mouse model of pulmonary fibrosis induced by bleomycin, HMGB1 production was elevated from inflammatory cells in the airway and RAGE^{-/-} mice did not respond to HMGB1, suggesting that RAGE may contribute to bleomycin-induced pulmonary fibrosis (47). Conversely, other studies have reported that the loss of RAGE may contribute to pulmonary fibrosis. In clinical studies, patients with IPF demonstrated RAGE expression that was downregulated in lung homogenates and alveolar cells (92). Additionally, soluble RAGE (sRAGE) levels were lower in the BAL fluid of patients with IPF (11). These conflicting reports highlight that RAGE may be implicated in the pathogenesis of fibrosis, but the underlying mechanisms remain uncertain.

RAGE, IR Injury, and Lung Transplantation

Work has also been done to explore the connection between RAGE and IR injury in the setting of lung transplantation. In a murine model of pulmonary reperfusion injury, pharmacologic blockade of RAGE diminished pulmonary function measured by arterial oxygenation, capillary leakage, and histologic injury. Additionally, genetic deletion of RAGE attenuated evidence of ischemic reperfusion injury (106). Similar findings were also obtained in the setting of IR injury of the liver where RAGE blockade protected against hepatocellular death and necrosis in a murine model (141). More recently, lung injury and pulmonary dysfunction were attenuated in RAGE^{-/-} mice. Additionally, the deletion of RAGE was also able to prevent IR injury in a hyperglycemia-enhanced IR animal model (67).

The connection between RAGE and short-term outcomes after lung transplantation has also been studied. Among 20 patients who underwent lung transplantation, plasma RAGE levels were obtained 4 h after the transplant. Among these patients, higher levels of RAGE predicted long durations of mechanical ventilation and ICU stays (22). Among 317 patients undergoing lung transplantation, plasma levels of sRAGE were measured 6 and 24 h post-transplant. Patients who developed primary graft dysfunction had higher levels of sRAGE. Higher levels of sRAGE were also associated with blood transfusions and cardiopulmonary bypass (27). Both these studies demonstrate that elevated levels of sRAGE are associated with worse short-term outcomes after transplantation.

The HMGB1-RAGE Axis and ALI

Several recent studies have demonstrated a connection between HMGB1, RAGE, and ALI and ARDS. HMGB1 has been identified as a marker of ALI in both human and animal studies (1, 117). Aside from the brain injury, elevated HMGB1 levels have been associated with diseases such as sepsis, hemorrhagic shock, and rheumatologic disorders (66, 79). Additionally, both experimental and clinical studies have implicated HMGB1 in ALI (129). Analysis of plasma and lung epithelial lining fluid of patients with ALI secondary to sepsis demonstrated increased levels of HMGB1. HMGB1

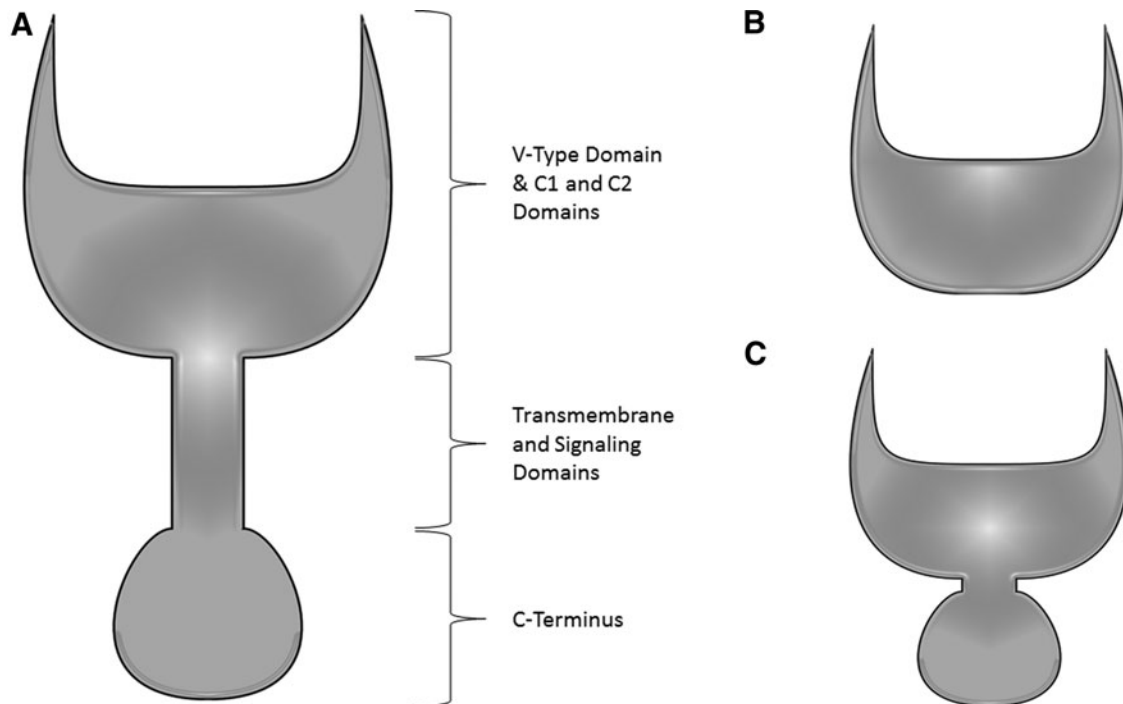


FIG. 7. Forms of RAGE. The RAGE receptor can be found in several forms throughout the organism due to splicing variations. **(A)** Full-length RAGE is the most prominent isoform of the receptor. **(B)** A soluble form of the receptor exists without the transmembrane domain, signaling domain, or C-Terminus. **(C)** Inert RAGE receptors can be found with modifications to the signaling domain, preventing signal transduction down the pathway.

was also elevated in plasma and lung fluid from LPS-induced ALI in a mouse model (117). In this scenario, it is believed that HMGB1 is released from normal airways and leaks into the bloodstream after destruction of the alveolar capillary barrier (127).

Additionally, clinical studies in patients with ALI have demonstrated a correlation with plasma sRAGE levels and worse outcomes as defined by severity of lung injury, ventilator-free days, and mortality (23). One study demonstrated sRAGE to be a marker of alveolar cell injury in a

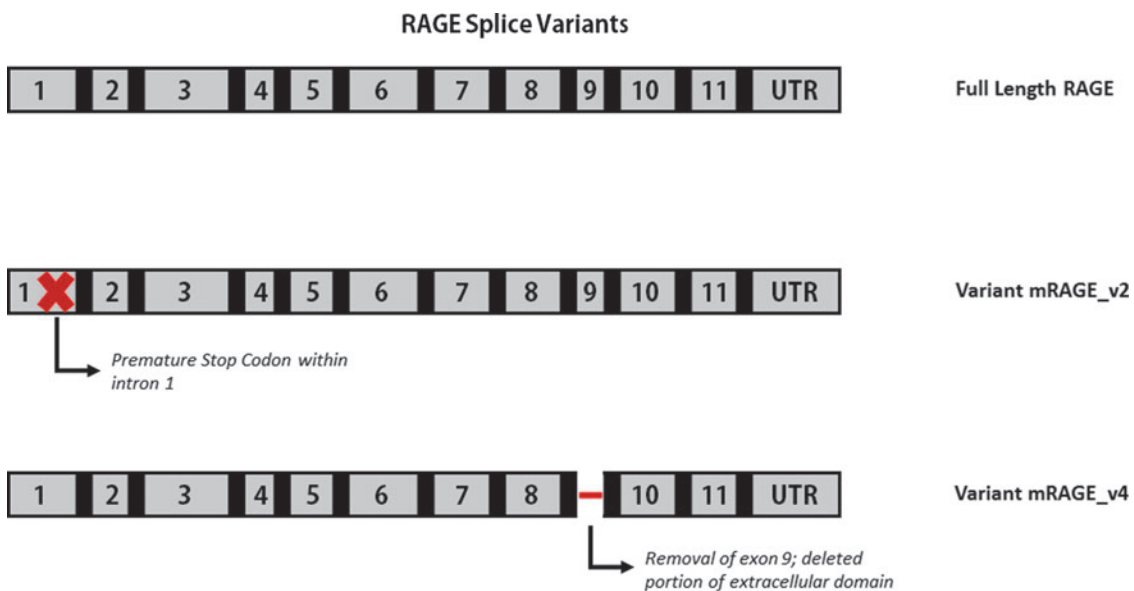


FIG. 8. Splice variants of RAGE. Although full-length RAGE is the most common form isolated in various tissues, multiple variants exist. mRAGE_v1 and mRAGE_v3 have an inclusion of intron 9 causing a shift in the reading frame hypothesis to be a source of soluble RAGE. mRAGE_v2 has a premature stop codon and is most prevalent in the brain. Exon 9 is deleted in mRAGE_v4, which does not affect the reading frame or remove either the transmembrane or cytoplasmic domains. This form is most prominent in the lung (60). To see this illustration in color, the reader is referred to the web version of this article at www.liebertpub.com/ars

rat model. In both experimental and human studies, higher sRAGE concentrations were found in the alveolar space compared with controls (115). Furthermore, RAGE levels in the alveolar fluid were measured after human lungs declined for transplant were perfused, ventilated, and rewarmed. RAGE was found to be inversely correlated with alveolar fluid clearance, suggesting that RAGE can be used as a marker for alveolar cell injury in donor lungs and possibly ALI (19).

Conclusions

This review has sought to describe evidence for the role of HMGB1-RAGE and the HMGB1-TLR4 axis associated with pulmonary dysfunction and central nervous system injury. Better understanding of the manner in which the redox isoforms of HMGB1 influence organ systems following trauma or disease may directly lead to the development of new therapeutic strategies, applying to not only patients with TBI but also the patients who demonstrate subsequent pulmonary complications as a result, as well as the recipients of transplanted lungs. Moreover, the pathogenesis manifested by release of HMGB1 throughout a number of organ systems suggests that therapeutic blockade of the protein will lead to novel directions in transplantation research. Further investigation of the mechanisms behind HMGB1 release, as well as its subsequent signaling pathways, is necessary to advancing understanding of the inflammatory process given that it is no longer restricted or solely related to the immune system. The study of HMGB1 and its receptors provides an exciting direction for the improvement of clinical outcomes of a significant portion of the patient population in a novel manner, all the while allowing for a direct translational connection from the bench to the bedside.

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Abbreviations Used

ALI = acute lung injury
 ARDS = acute respiratory distress syndrome
 DAMP = damage-associated molecular pattern
 HMGB1 = high-mobility group box protein 1
 ICU = intensive care unit
 IL = interleukin
 IPF = idiopathic pulmonary fibrosis
 IR = ischemia reperfusion
 LPS = lipopolysaccharide
 MAPK = mitogen-activated protein kinase
 MyD88 = myeloid differentiation primary response gene 88
 NF κ B = nuclear factor kappa B
 NNOD = non-neurologic organ dysfunction
 NPE = neurogenic pulmonary edema
 RAGE = receptor for advanced glycation end-products
 SBP1 = sulfoglucuronyl carbohydrate-binding protein-1
 sRAGE = soluble RAGE
 TBI = traumatic brain injury
 TLR4 = toll-like receptor 4
 TNF = tumor necrosis factor