Redox Modification of Cysteine Residues Regulates the Cytokine Activity of High Mobility Group Box-1 (HMGB1)

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High mobility group box 1 (HMGB1) is a nuclear protein with extracellular inflammatory cytokine activity. It is released passively during cell injury and necrosis, and secreted actively by immune cells. HMGB1 contains three conserved redox-sensitive cysteine residues: C23 and C45 can form an intramolecular disulfide bond, whereas C106 is unpaired and is essential for the interaction with Toll-Like Receptor (TLR) 4. However, a comprehensive characterization of the dynamic redox states of each cysteine residue and of their impacts on innate immune responses is lacking. Using tandem mass spectrometric analysis, we now have established that the C106 thiol and the C23-C45 disulfide bond are required for HMGB1 to induce nuclear NF-κB translocation and tumor necrosis factor (TNF) production in macrophages. Both irreversible oxidation to sulphonates and complete reduction to thiols of these cysteines inhibited TNF production markedly. In a proof-of-concept murine model of hepatic necrosis induced by acetaminophen, during inflammation, the predominant form of serum HMGB1 is the active one, containing a C106 thiol group and a disulfide bond between C23 and C45, whereas the inactive form of HMGB1, containing terminally oxidized cysteines, accumulates during inflammation resolution and hepatic regeneration. These results reveal critical posttranslational redox mechanisms that control the proinflammatory activity of HMGB1 and its inactivation during pathogenesis.

INTRODUCTION

High mobility group box-1 (HMGB1), a 25 KDa nuclear protein, has been implicated as a mediator of tissue damage and inflammation during sterile injury and infection (1). It is released passively during cell injury, and is secreted actively by macrophages and other cell types activated by exposure to products of infection or injury. Extracellular HMGB1 interacts with TLRs to activate macrophages to release TNF, interleukin-1 (IL-1), IL-6 and other cytokines (2).

Neutralizing HMGB1 antibodies reverses inflammation and attenuates disease severity in animal models (3–5).

HMGB1 has three major protein domains consisting of two tandem DNA-binding domains (A and B boxes), and an acidic carboxyl terminus comprised of a string of aspartate and glutamate residues (6). Initial studies of the structural basis for the extracellular proinflammatory cytokine activity of HMGB1 revealed a critical role for residues in the B box domain (7). The first 20 amino acid

residues (position 89–108) of the B box domain represent the minimal peptide sequence that retains cytokine-inducing activity by macrophages (7). The activity of HMGB1 to stimulate macrophage cytokine production requires HMGB1 binding to TLR4, and both binding and signaling require the cysteine in position 106 (C106) within the B box domain (2).

The induction of immune responses is critically intertwined with a dynamic redox environment, and posttranslational redox modifications represent key mechanisms to regulate protein functions. Understanding the functional relationship between redox modifications of key inflammatory extracellular signaling proteins, such as HMGB1, is thus of great importance. Recently, it was suggested that oxidation of C106 modulates the activity of HMGB1 and prevents its capacity to activate dendritic cells (8). Moreover, we showed previously that the predominant forms of serum HMGB1

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contain a reduced C106 thiol during hepatic damage, and C106 sulphone during the resolution of damage, respectively (4). While the focus to date on redox remodeling has been on C106, there are two additional conserved cysteine residues present within HMGB1 (C23 and C45). The structure:function relationship between modifications on these residues to the inflammatory activity of HMGB1 is unknown. The formation of an intramolecular disulfide bond between C23 and C45 stabilizes the folded state of the full-length protein and generates a conformation change (9) that might impact upon the signaling function of HMGB1 as an inflammatory mediator (9,10). The results of our present study indicate that the inflammatory activities of HMGB1 require both reduced C106 and the formation of an intramolecular disulfide bond between C23 and C45.

MATERIALS AND METHODS

Materials

Lipopolysaccharide (LPS, *E. coli.* 0111:B4), triton X-114 and human macrophage-colony stimulating factor (M-CSF) were purchased from Sigma (St. Louis, MO, USA). Isopropyl-D-thiogalactopyranoside (IPTG) was from Pierce (Rockford, IL, USA). DNase I and 2xYT medium were obtained from Life Technologies (Grand Island, NY, USA). Hydrogen peroxide (3%) was from Fisher Scientific (Waltham, MA, USA). Dithiothreitol (DTT, 100 mmol/L) was obtained from Invitrogen (Carlsbad, CA, USA). Polyclonal rabbit anti-human HMGB1 antibodies were purchased from Abcam (Cat #ab18256, Cambridge, UK). HMGB1 enzyme-linked immunosorbent assay (ELISA) was purchased from Shino-Test Corporation (Tokyo, Japan). Infinity™ ALT (GPT) Liquid Stable Reagent was purchased from Alpha Laboratories (Eastleigh, UK). Bio-Rad Protein Assay Dye Reagent was purchased from Bio-Rad Laboratories Ltd (Hemel Hempstead, UK). For protein analysis α-cyano-4-hydroxycinnamic acid was purchased from LaserBiolabs (Antibes,

France), Trypsin from Promega (Southampton, UK) and ZipTips from Millipore (Watford, UK). All solvents were of high quality and liquid chromatography mass spectrometry grade and were the products of Fischer Scientific (Loughborough, UK). Unless otherwise stated, all other chemicals, peptide standards and materials were purchased from Sigma-Aldrich (Poole, UK). Monoclonal antibodies for NF-κB (F-6) were purchased from Insight Biotechnology Ltd (Middlesex, UK).

Production of Recombinant and a C45A Mutant HMGB1 Protein

Wild-type rat *HMGB1* was cloned, expressed and purified as described previously (2). For generating C45A mutant HMGB1, cysteine at position 45 in the wild-type HMGB1 clone was substituted with alanine using the QuikChange, Site-Directed Mutagenesis kit according to the manufacturer's instructions (Stratagene, Skarholmen, Sweden). The primers used were forward: 5′-GAG TTC TCC AAG AAG GGC TCA GAG AGG TGG AAG ACC-3′ and reverse: 5′-GGT CTT CCA CCT CTC TGA GGC CTT CTT GGA GAA CTC-3′. The PCR product was subcloned into the pCAL-n vector, 3′ to the T7 promotor and CBP tag, expressed and purified as described previously (2). DNase I was added at 100 U/mL to the beads to remove any contaminating DNA. Degradation of DNA was verified by ethidium bromide staining of agarose gel containing HMGB1 proteins before and after DNase I treatment. The purity and integrity of purified HMGB1 proteins was verified by Coomassie Blue staining after SDS-PAGE, with purity predominantly above 90%. Point mutations of the C23 and C45 residues with a serine and C106 with a glutamic acid also were produced based on the above-described methods.

LPS Removal from HMGB1 Protein Preparations

Contaminating LPS from protein preparations was removed by Triton X-114 extraction as described previously (11). LPS

content in the protein preparations was typically less than 1 pg/μg protein.

Preparation of Reduced, Oxidized or Mercury-Exposed HMGB1

Redox-modified HMGB1. HMGB1 was exposed to either H_2O_2 (0–50 μmol/L) or DTT (0–5 mmol/L) for up to 2 h prior to the addition of the protein to cell culture or other analysis. For rHMGB1 that had been produced in the presence of DTT, an exposure to 50 μmol/L H_2O_2 for 2 h was utilized.

Mercury-modified HMGB1. HMGB1 solution was treated with 1:1 or 1:10 molar equivalents of 4-(hydroxyl-mercury) benzoic sodium salt. The reaction was stirred at room temperature for 2 h and excess mercury was subsequently removed by dialysis against PBS at 4°C overnight.

Cell Culture and Treatment

Peripheral blood mononuclear cells were isolated from the blood of normal volunteers (Long Island Blood Services, Melville, NY, USA) and differentiated into macrophages using M-CSF. Murine macrophage-like RAW 264.7 cells were obtained from American Type Culture Collection (Rockville, MD, USA). Cells were cultured in 96 well plates as described previously (2).

Cytokine Measurements

TNF released in the supernatants of macrophage cultures were measured by commercially available enzyme-linked immunosorbent assay (ELISA) kits according to instructions of the manufacturer (R&D Systems Inc., Minneapolis, MN, USA).

Western Blotting for Nuclear Expression of the NF-κB p65 Subunit

Nuclear extracts were resolved by denaturing electrophoresis on 4% to 12% Novex Bis-Tris polyacrylamide gels (Invitrogen), using a 3-(N-morpholino) propanesulfonic acid running buffer. Separated proteins were transferred to Hybond nitrocellulose membranes (GE Healthcare Life Sciences, Little Chalfont, UK), which were blocked for 15 min in

10% non-fat milk (Bio-Rad) in Tris-buffered saline (TBS, pH 7.0) containing 0.1% Tween 20. Blocked membranes were probed with mouse anti-human NF-κB p65 (1:5000) in 2% bovine serum albumin (BSA) for 1 h. After several washes, membranes were probed with rabbit anti-mouse (1:10,000) horseradish peroxidase-conjugated anti-IgG for 1 h. Western blots were visualized using enhanced chemiluminescence (PerkinElmer, Beaconsfield, UK) and Hyperfilm (GE Healthcare Life Sciences, Amersham, UK). All blots also were probed for actin (1:5000) as a loading control.

Mass Spectrometric Characterization of the Cysteine Oxidation Status of Recombinant or Circulating HMGB1

Initially, reduced cysteine residues within HMGB1, either recombinant or obtained from serum of mice treated with acetaminophen, were characterized by the thiol specific alkylation with N-ethylmalemide (NEM) for 2–5 min (50 mmol/L). The alkylation with NEM yields a mass shift of 125 amu (atomic mass unit) compared with the NEM un-exposed protein. Following the incubation, recombinant HMGB1 preparations were precipitated with ice-cold methanol (MeOH). MeOH was recovered by centrifuging at 14,000*g* at 4°C for 10 min. For serum preparations, free thiol groups within HMGB1 were first NEM capped as described above in the absence of methanol precipitation. The selective analysis of SOH containing cysteines was carried out following a 2-min incubation with 0.1 mmol/L dimedone (5,5-dimethyl-1,3-cyclohexanedione). SO_2H and SO_3H oxidative modifications were determined by the mass increase of 32 and 48 amu respectively on the particular cysteine residue. Remaining cysteine residues that were present in a disulfide bond then were reduced with 1 mmol/L DTT at 4°C for 15 min. Newly DTT reduced cysteines then were alkylated with a heavy labeled d_5NEM (NEM + 5× deuterium) which yields a mass shift of 130 amu compared with the NEM-unexposed protein and 5 amu compared

with the NEM-alkylated protein. HMGB1 was isolated by immunoprecipitation from mice sera as described previously (12). HMGB1 preparations then were separated by nonreducing SDS PAGE and protein bands corresponding to the molecular weight of HMGB1 were excised. Recovered protein was then subjected to tryptic digestion and resulting peptides were characterized by liquid chromatography–electrospray tandem mass spectrometry (LC-MS/MS) as described previously (12). The subsequent stepwise determination and amino acid sequence following individual peptide fragmentation to produce b and y ions was utilized to confirm the presence of particular redox modification on a particular amino acid.

Animal Studies

The protocols described here were undertaken in accordance with criteria outlined in a license granted under the Animals (Scientific Procedures) Act 1986 and approved by the Institution local animal ethics committee. Groups of six male CD-1 mice (25–35 g, 6–8 wks old, Charles River, UK) with free access to food and water were included in the study. Mice were injected with either acetaminophen (530 mg/kg; intraperitoneal [IP]) or 0.9% saline as a control. At 5, 15 or 24 h later, mice were euthanized and hepatotoxicity was determined by serum alanine aminotransferase (ALT) activity and by histological determination as described previously (4,12).

Statistical Analysis

Data are presented as mean ± SEM. Differences between treatment groups were determined by Student *t* test; *P* values less than 0.05 were considered statistically significant by using the Stats Direct statistical software throughout.

RESULTS

Mass Spectrometric Characterization of Cytokine-Stimulating HMGB1

It has been demonstrated previously that HMGB1 is a redox-sensitive protein

and that the intracellular oxidation of cysteine residues can impact its inflammatory properties (8). Furthermore, the mutation of C106 to an alanine also inhibits the cytokine inducing capacity of HMGB1 significantly (8). However, the structure:function relationship of the three cysteine residues and the cytokine-inducing activity of HMGB1 were previously unknown.

Here we utilized LC-MS/MS, a tool for unambiguous analyte identification, to characterize the redox state of the HMGB1 cysteines associated with TNF release and NF-κB activation from macrophages. Tryptic digestion and mass spectrometric analysis of HMGB1 produced exclusively cysteine-containing peptides with the molecular weights of 2,070.0 (triply-charged ion 690.0^{3+}), 1,569.1 (doubly-charged ion 784.5^{2+}) and 622.6Da (doubly-charged ion 311.3^{2+}). These fragments corresponded to peptides containing C106, C23 and C45 respectively. Tandem mass spectrometric analysis (MS/MS) of these peptides revealed an NEM adduct localized to C106, indicative of a thiol side chain (–SH) on C106 (Figure 1, molecule A, A-1) and a second round of MS/MS analysis of the peptides containing C23 and C45 demonstrated exclusively a deuterated NEM (d_5NEM) adduct on each cysteine (Figure 1, molecule A, A-2, A-3), reflecting that C23 and C45 formed part of a disulfide bond. No SOH, SO_2H or SO_3H oxidative modification on any cysteine residue was identified within this form of HMGB1. These data indicate that molecule A represents the schematic redox conformation of this form of HMGB1 required for cytokine induction from cultured macrophages (Figures 2A, B).

Mass Spectrometric Characterization and Effects of Cysteine Oxidation on the Cytokine-Stimulating Capability of HMGB1

Previous studies showed that a mutation of C106 prevents its binding to TLR4/MD2 and subsequent cytokine release from activated macrophages/monocytes (2,8). The molecular form of
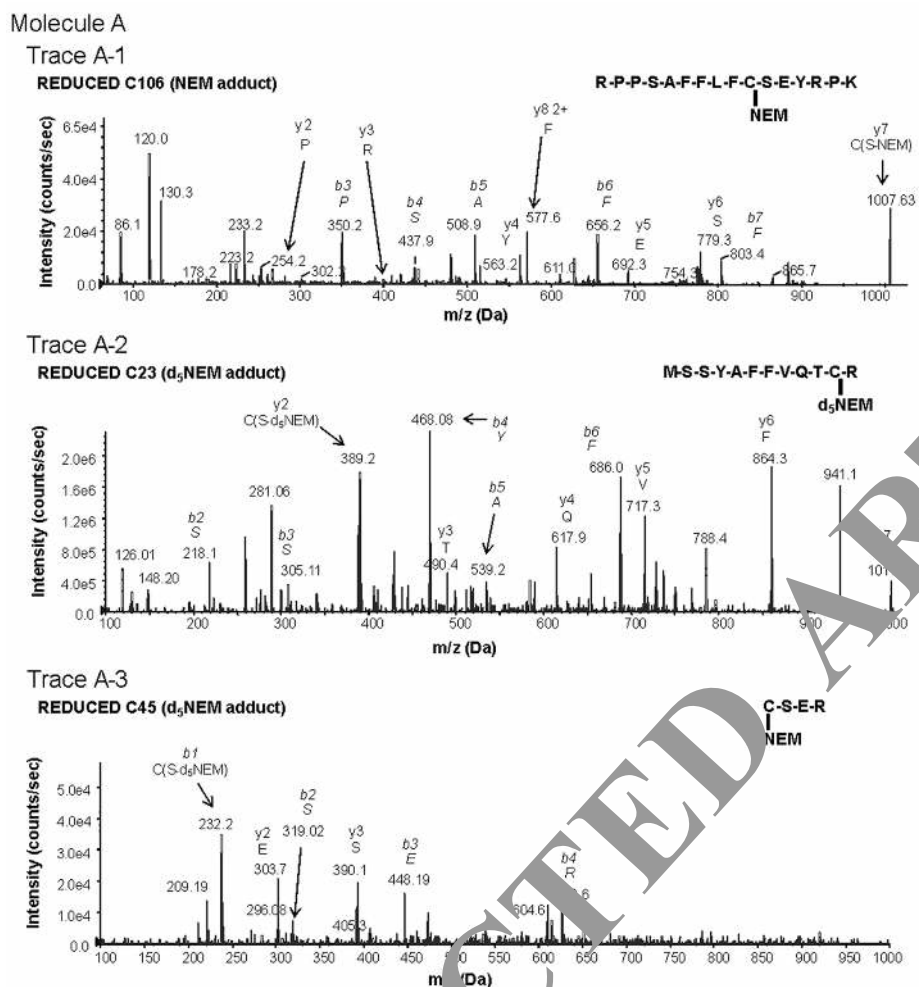
Figure 1. Characterization of redox-dependent modifications of cysteine residues in HMGB1 using mass spectrometry. Molecule A: mass spectrometric characterization of molecule A on C106 (A-1), C23 (A-2) and C45 (A-3). A-1: Peptide-containing HMGB1 amino acids 97–112 with a thiol capped NEM adduct indicating reduced C106. A-2: Peptide-containing HMGB1 amino acids 13–24 following reduction of a disulfide bond and subsequent adduction of C23 with d_5NEM. A-3: Peptide-containing HMGB1 amino acids 45–48 following DTT reduction of a disulfide bond and subsequent adduction of C45 with d_5NEM. Molecule B: mass spectrometric characterization of molecule B on C106 (B-1), C23 (B-2) and C45 (B-3). B-1: Peptide-containing HMGB1 amino acids 97–112 containing a C106 as a sulphonic acid. B-2: Peptide-containing HMGB1 amino acids 13–24 containing a C23 as a sulphonic acid. B-3: Peptide-containing HMGB1 amino acids 45–48 containing a C45 as a sulphonic acid. Molecule C: mass spectrometric characterization of molecule C on C23 (C-1) and C45 (C-2). C-1: Mass spectrometric characterization of C23. Peptide-containing HMGB1 amino acids 13–24 with a thiol-capped NEM adduct indicating reduced C23. C-2: Peptide-containing HMGB1 amino acids 45–48 with a thiol-capped NEM adduct indicating reduced C45. Peptide sequences and b and y ions are indicated on each trace as required. MS/MS traces are representative of three independent investigations.

Continued

HMGB1 that stimulated TNF release from cultured macrophages contains C106 with a thiol side chain and a disulfide bond be-tween C23 and C45 (C106-SH, C23-S-S-C45). When this form of HMGB1 was oxi-dized by exposure to H_2O_2, the product

was no longer capable of stimulating TNF release from cultured human primary macrophages and RAW 267.4 cells (see Figures 2A, B). H_2O_2 exposed lipopolysac-charide (LPS) failed to inhibit TNF-inducing activity, indicating that the effect of H_2O_2 was HMGB1 specific (Figure 2C). The functional importance of C106 in the thiol form as a reduced side chain for TNF induction was studied further by se-lective modification of thiol-containing cysteine residues. Exposure of HMGB1 to mercury (Hg), which reacts with HMGB1 to thiol side chain of cysteine residues but not other cysteine redox forms (C106-S-Hg, C23-S-S-C45, Table 1), significantly re-duced TNF release in RAW 264.7 cells as compared with Hg-unexposed HMGB1 (C106-SH, C23-S-S-C45) (Figure 2D). Fur-ther, oxidation of HMGB1 with H_2O_2 also prevented the NF-κB nuclear transloca-tion as compared with HMGB1 that had not been exposed to H_2O_2. These effects were specific, because H_2O_2 exposure failed to alter LPS-mediated NF-κB nu-clear translocation (Figure 3, lanes A, E, D and B).

When focusing analysis on cysteine modification and cysteine-containing peptides, tryptic digestion of H_2O_2-exposed HMGB1 produced only peptides with molecule weights of 1,994.8 (triply-charged ion 664.9^{3+}), 1,487.5 (doubly-charged ion 743.8^{2+}) and 541.4 Da (doubly-charged ion 270.7^{2+}). These corre-sponded to peptides containing C106, C23 and C45 respectively. MS/MS analy-sis confirmed the irreversible sulphonic acid (–SO_3H) modification on each cys-teine residue (Figure 1, molecule B, struc-ture 4-6) and the molecular structure rep-resented by molecule B (Table 1, molecule B). It is important to note that no –SOH modification on any of the cysteine residues could be detected through the use of dimedone.

Mass Spectrometric Characterization and Effects of Cysteine Reduction on the Cytokine-Stimulating Capability of HMGB1
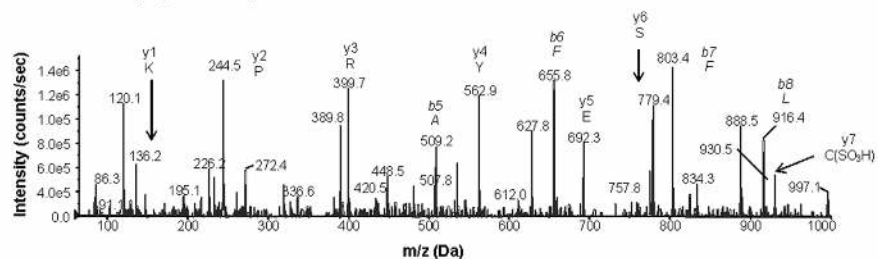
The reducing agent DTT prevents intra- and intermolecular disulfide

Figure 1. *Continued*.
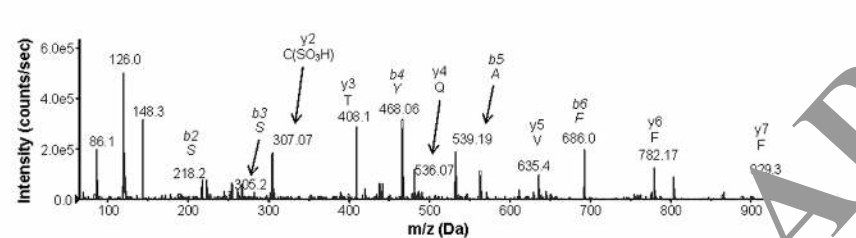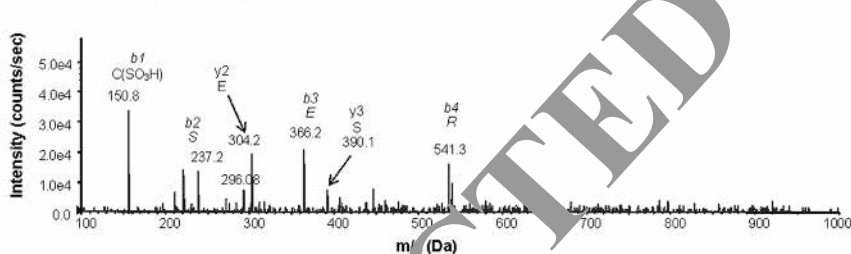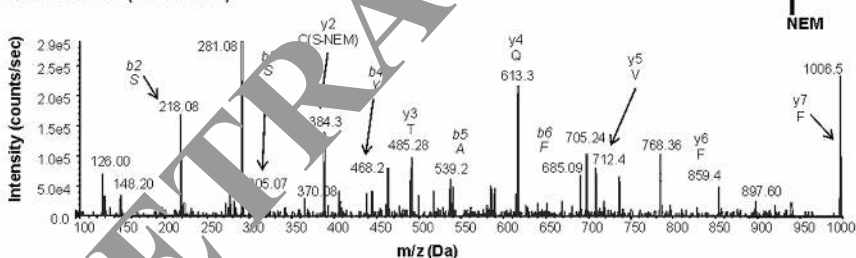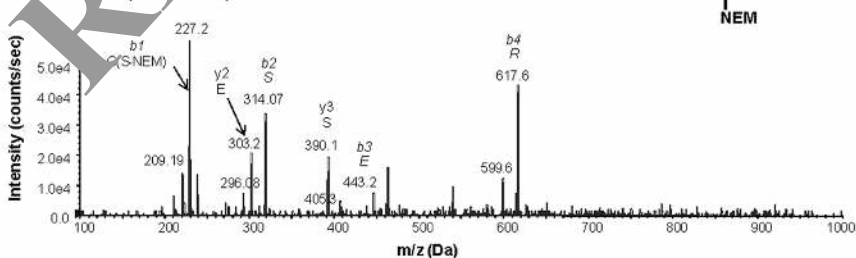
bond formation between cysteine residues, and often is added to recombinant protein preparations. On the basis of findings that oxidation of HMGB1 inhibits the TNF stimulating capacity (Figure 2), we reasoned that the addition of DTT to HMGB1 preparations would maintain the cytokine-inducing function of our recombinant HMGB1 preparations. Unexpectedly, we observed that the addition of DTT inhibited HMGB1-induced TNF release from RAW 264.7 cells significantly in a dose- and time-dependent manner (Figures 4A, B). Moreover, DTT-exposed HMGB1 failed to stimulate NF-κB translocation (Figure 3, lane C). Time course studies revealed that incubation of HMGB1 with DTT for as short as 5 min suppressed HMGB1 activity as a TNF stimulator by up to 70% (Figure 4B). Addition of DTT did not significantly alter LPS-induced TNF release (Figure 4C) or NF-κB activation in RAW 264.7 cells (Figure 3, lane D) indicating that the effects of DTT on HMGB1 are specific. Tryptic peptide from DTT-exposed HMGB1 had molecular weights corresponding to C106 (2,070.0 Da), C23 (1,564.2 Da) and C45 (617.6 Da). MS/MS analysis confirmed the presence on an NEM adduct of each cysteine residue (Figure 1, molecule A, A-1 and molecule C, C-1, C-2) indicating that, as expected, all these cysteine residues were reduced (C106-SH, C23-SH, C45-SH) as described by the schematic molecule C shown in Table 1. The findings indicate that reduced C106 alone is not sufficient for HMGB1-mediated TNF induction, and suggest that the redox state of all three cysteines contribute to the TNF-stimulating activity of HMGB1.

We next evaluated the role of the C23-C45 disulfide bond in the cytokine stimulating capacity of HMGB1. Irreversible oxidation or the reduction of the C23-C45 disulfide bond significantly prevented HMGB1-mediated cytokine induction and NF-κB nuclear translocation in cultured macrophages (Figures 2–4). The critical role of the
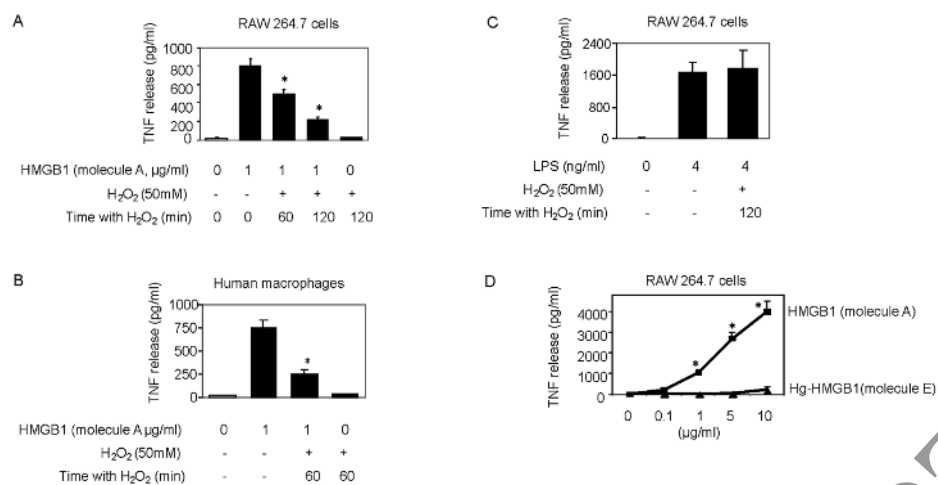
Figure 2. Effect of oxidation agents on HMGB1-induced TNF release. The time dependent inhibitory effect of H_2O_2 exposure on the TNF-stimulating activity of HMGB1 in (A) RAW 267.7 cells and (B) primary human macrophages. (C) The effect of H_2O_2 exposure on the TNF-stimulating activity of LPS in RAW 267.7 cells. Cells were cultured in 96-well plates and were stimulated with HMGB1 or LPS with or without exposure to 50 mmol/L H_2O_2 for 0–120 min. After 16 h, TNF released into the cell culture supernatant was measured by ELISA. N = 6–8. *$P < 0.05$ versus HMGB1 alone without H_2O_2 exposure. (D) The effect of mercury (Hg) on TNF release from RAW 264.7 cells induced by recombinant HMGB1 prepared in the absence of DTT. RAW 264.7 cells were cultured in 96-well plates and exposed to HMGB1 or Hg-HMGB1 over a range of concentrations (0–5 μg/mL). After 16 h, TNF released was measured. N = 3. *$P < 0.05$ versus HMGB1.

disulfide bond between C23 and C45 for cytokine production and NF-κB nuclear translocation was confirmed further by oxidizing HMGB1 that had been produced in the presence of DTT. Oxidation and formation of the C23-C45 disulfide bond with mild H_2O_2 exposure restored the ability of DTT-exposed HMGB1 to induce TNF release and NK-κB nuclear translocation (Figure 5A, Figure 3, lane F). Tryptic peptides contained a mixed HMGB1 population of d_5NEM adducts (disulfide bond forming) and a sulphonic acid modification on C23 and C45 following mild oxidation (Figure 1, A-2, A-3, B-2, B-3). Mild oxidation of HMGB1 that had been exposed to DTT also resulted in the identification of a mixed HMGB1 population containing only either an NEM adduct (–SH) or a sulphonic acid modification on C106 (Figure 1, A-1, B-1). No d_5NEM adduct was identified on C106 following mild oxidation, indicating that C106 did not participate in

the formation of a disulfide bond during these experiments.

The importance of a C23-C45 disulfide bond in HMGB1-mediated cytokine production was confirmed by mutation of C45 to an alanine (A) in the full length HMGB1 protein. This point mutation prevents the formation of a disulfide bond between C23 and C45. We observed that the C45A HMGB1 mutant had significantly reduced TNF-stimulating activity in RAW 264.7 cells compared with the C45-expressing HMGB1 protein (Figure 5B). Mass spectrometric analysis revealed that C45A HMGB1 contained reduced C106 (Figure 1, A-1) and also an NEM adduct of C23 (Figure 1, C-1), indicating that C23 was present only in its reduced form (with –SH group) and that neither C106 nor C23 participated in the formation of a disulfide bond.

Together, these results showed that TNF-stimulating activity of HMGB1 occurs when C106 is in the thiol form, and
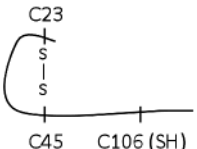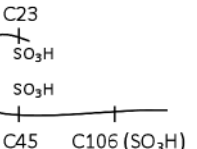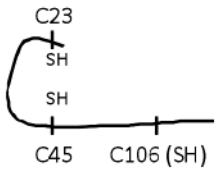
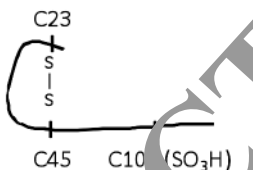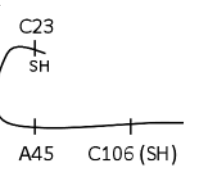C23-C45 is disulfide bonded (Table 1, molecule A).

Cysteine Redox Characterization of Circulating HMGB1 and Its Association with Hepatic Inflammation during Acetaminophen Hepatotoxicity In Vivo

We and others have demonstrated previously that hepatic inflammatory cell recruitment during acetaminophen hepatotoxicity is mediated by HMGB1 (4,13,30). Here we used this *in vivo* model to define the role of cysteine redox regulation in the inflammatory response associated with HMGB1 *in vivo*. As previously shown, HMGB1 C106 in a reduced form is associated with hepatic inflammatory cell recruitment during acetaminophen toxicity, while the sulphonic acid (SO_3H)-containing C106 did not (4). As predicted by the *in vitro* findings, we observed that the predominant form of HMGB1 in serum during the onset of hepatic inflammation contains C23 and C45 residue adducts only by d_5NEM, indicating a disulfide bond between the two cysteines (Figure 6 and Table 2). No NEM adduct (indicating a –SH group) or SOH, SO_2H or SO_3H residues were observed on either C23 or C45 of circulating HMGB1 (Table 2). As hepatic inflammation resolved, the predominant form of circulating HMGB1 pool contained C106 that is oxidized to the irreversible SO_3H (inactive) form (see Figure 6 and Table 2). Thus, the redox form of serum HMGB1 during hepatic inflammation is represented by molecule A (Figure 1, molecule A), whereas the form of HMGB1 changes to that of molecule D during the resolution of hepatic inflammation (Table 1).

DISCUSSION

Oxidative modification represents a key posttranslational alteration to regulate the functional capacity of signaling proteins. Much is known about the functional modulation of intracellular proteins such as enzymes (phosphatases and kinases) and transcriptional regula-

Table 1. Summary of redox characterized cysteine modifications with resulting inflammatory readouts and schematic molecular structure of HMGB1 (different cysteine redox states characterized by LC-MS/MS within HMGB1 and their relation to cytokine Induction and NF-κB nuclear translocation in cultured macrophages).

Molecule (representative spectra)	Schematic molecular overview	Cytokine inducing capacity and NF-κB nuclear translocation
A (Trace A-1, A-2, A-3)	C23 S—S C45 C106 (SH)	Yes
B (Trace B-1, B-2, B-3)	C23 SO₃H SO₃H C45 C106 (SO₃H)	No
C (Trace A-1,C-1, C-2)	C23 SH SH C45 C106 (SH)	No
D (Trace B-1, A-2, A-3)	C23 S—S C45 C106 (SO₃H)	No
E (Trace A-2, A-3)	C23 S C106 (Hg)	No
F (Trace A-1, C-1)	C23 SH A45 C106 (SH)	No

RAW 264.7 cells

A B C D E F

NF-kB p65

β-actin

Figure 3. Redox dependent effect on HMGB1-induced NF-κB activation in macrophages. Western analysis of the nuclear localization of the NF-κB p65 subunit following the stimulation of cultured macrophages for 1 h with 5 μg/mL of HMGB1 or 4 ng/mL of LPS. HMGB1 was exposed to either H₂O₂ (50 mmol/L, 120 min) or DTT (5 mmol/L, 120 min) prior to the assay. For HMGB1 preparations that had included DTT, HMGB1 was then oxidized with 50 μmol/L H₂O₂. β actin expression was also measured and used as a loading control. All HMGB1 preparations were characterized by LC-MS/MS prior to cell treatment with respect to cysteine redox status as described in Figure 1. Data shown are representative of three independent experiments. A, control (PBS); B, HMGB1 (molecule B + H₂O₂); C, HMGB1 (molecule C + DTT); D, LPS; E, HMGB1 (molecule A); F, HMGB1 (molecule C + H₂O₂).

the pattern of cysteine redox modifications regulating the cytokine-inducing capacity of HMGB1. By integrating the results obtained by mass spectrometric characterization of redox modifications of HMGB1 with cytokine production, we conclude that to induce cytokine release, HMGB1 must simultaneously have C106 in its reduced thiol form and C23 and C45 engaged in a disulfide bridge. Terminal oxidation of the cysteines to sulfonic acids inactivates HMGB1.

The most common covalent linkages between protein side chains are disulfide bonds, and disulfide-thiol interconversions alter protein properties through changes in chemical reactivity and conformation. These redox-dependent changes will thereby regulate many critical functions of signaling proteins including HMGB1 (18,19). C23 and C45 readily form a disulfide bond (20) which increases the stability of the folded full

tors through the chemo-selective oxidation of cysteine residues (15). Cysteine redox perturbation also is thought to alter the extracellular functionality of intercellular signaling proteins (16). During tissue inflammation and repair, the changing redox environment following cell death can have important consequences on the bioactivity of key inflammatory signaling proteins (17).

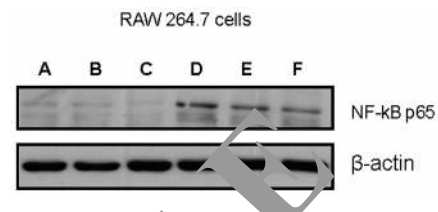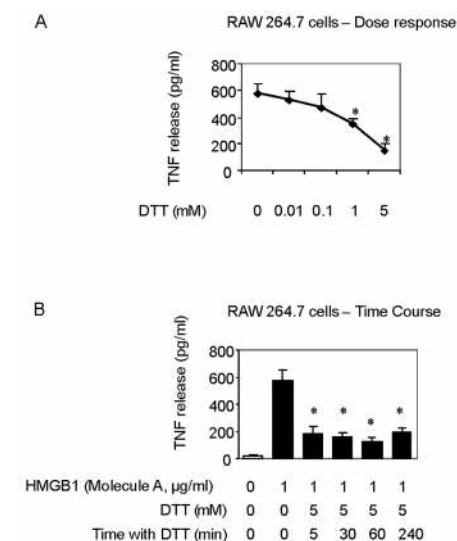The aim of the current investigation was to provide a chemical definition of

Figure 4. Effect of reducing agents on HMGB1-induced cytokine release. The (A) dose dependent and (B) time dependent effect of DTT on the TNF-stimulating activity of HMGB1 in RAW 264.7 cells. (C) The effect of DTT on the TNF-stimulating activity of LPS in RAW 264.7 cells. HMGB1 or LPS was incubated with the reducing agent DTT at (A) various concentrations as shown or with 5 mmol/L DTT at the times indicated at room temperature. Fresh DTT pretreated HMGB1 or LPS was then added to RAW 264.7 cells. After 16 h, TNF released into the cell culture supernatant was measured by ELISA. N = 3. *P < 0.05 versus HMGB1 alone without DTT pretreatment.

Figure 5. The requirement for a disulfide bond between C23-C45 for the cytokine-stimulating activity of HMGB1. (A) Effects of mild H_2O_2 exposure (50 μmol/L, 120 min) on the TNF stimulating activity of HMGB1 prepared with DTT. (B) Effects of an A45 mutation of HMGB1 on TNF release from RAW 264.7 cells induced by A45 HMGB1 compared with HMGB1 prepared in the absence of DTT. RAW 264.7 cells were incubated with HMGB1 over a range of concentrations (0 to 10 μg/mL). After 16 h, TNF released into the cell culture supernatant was measured by ELISA. N = 3. *P < 0.05 versus HMGB1. All HMGB1 preparations were characterized by LC-MS/MS prior to cell treatment with respect to cysteine redox status.

length HMGB1 molecule; NMR analysis confirms that this linkage alters the conformation of the A domain within the HMGB1 protein (9,18). C23 and C45 mutations prevent HMGB1 from binding to the intracellular target protein Beclin 1, stopping HMGB1 from initiating cellular autophagy processes (21). Mild oxidation of completely reduced HMGB1, which is unable to induce cytokine formation, partially restored the C23-C45 disulfide bond and the cytokine-inducing capacity. These findings provide a proof of concept for the critical role of the C23-S-S-C45 linkage. Future studies will be needed to determine whether and how the cleavage of this bond signals to the contact of HMGB1 with TLR4 and whether inactive HMGB1 forms compete with active HMGB1 for receptor binding.

The concept that cysteine oxidation represents an important biological switch to control the bioactivity of HMGB1 was further supported by our proof of concept *in vivo* experiments. It is well established that an increase in

ROS production is beneficial both for the development and for a successful outcome of inflammation. Our results support that the oxidation of HMGB1 acts as a physiological mechanism to control the proinflammatory function of HMGB1 *in vivo*, where the extracellular environment is largely oxidative during inflammatory processes. We noted at the early stages of acetaminophen-mediated hepatotoxicity, when HMGB1 was released by necrotic hepatocytes and when subsequent hepatic inflammatory cell infiltration took place, that the C106 in the systemic HMGB1 was reduced (C106-SH), while during restoration of damage, C106 was predominantly and irreversibly oxidized (C106-SO₃H). The oxidation restricted the proinflammatory activity of HMGB1 in a temporal and spatial manner and prevented excessive hepatic damage.

The unpaired cysteine C106 theoretically can form a disulfide bridge with another C106 residue on a second HMGB1 molecule. Such HMGB1 dimers
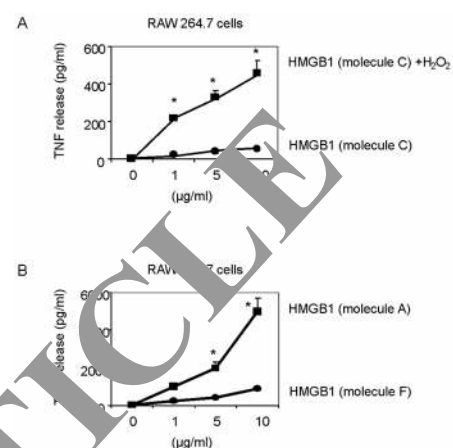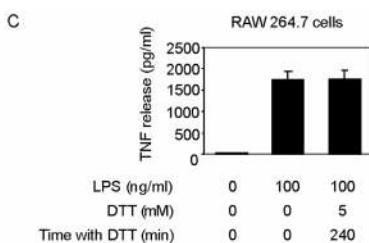
have been observed in some preparations of recombinant HMGB1, but show no cytokine-stimulating activity (EV and MEB, unpublished observations). The formation of HMGB1 dimers *in vivo* is unlikely, since unpaired thiols in other proteins and metabolites would compete for disulphide bonding to C106; in fact, we did not detect HMGB1 homodimers in serum. We rather suggest that C106 is required and conserved in evolution to allow HMGB1 inactivation when its cytokine-stimulating activity is no longer required.

Acetylation of key lysine residues within the nuclear localization sequence of HMGB1 is thought to act as a key regulatory mechanism to promote the active release of HMGB1 from macrophages and monocytes, and acetylated HMGB1
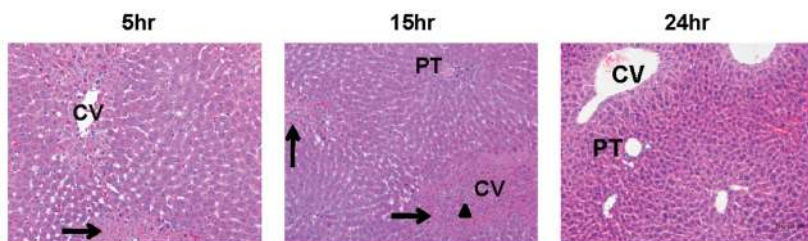
Figure 6. Mass spectrometric characterization of circulating HMGB1 and its association with hepatic inflammatory cell recruitment during acetaminophen hepatotoxicity. Histological characterization of hepatic changes induced by acetaminophen (530 mg/kg) over 5, 15 and 24 h in mice. Necrotic hepatocytes are indicated with an arrow and infiltrating inflammatory cells are highlighted with an arrow head. Data shown are representative of six animals per treatment group.

has been observed *in vivo* (22). Acetylation of nearby lysine residues might change the electrostatic potential and affect the pK_a of cysteine thiol groups; however, as previously noted (9), no lysine amino group is present within 8 Å from the thiol groups in the three-dimensional structure of the HMGB1, and therefore an impact on the regulation of the proinflammatory function of HMGB1 is unlikely.

Since the original description of HMGB1 activity in stimulating macrophage cytokine release (23), investigations have revealed that HMGB1 can act in synergy with other inflammatory mediators to promote cytokine stimulation (24). Therefore, there has been an ongoing debate concerning whether HMGB1 *per se*, uncomplexed to partner molecules, is capable of inducing cytokine production to promote inflammation. The results of the current study help to resolve this major issue: HMGB1 with reduced C106 and a disulfide bond between C23 and C45 has cytokine-stimulating activity, whereas the commercially available HMGB1 preparations, being supplemented with DTT and fully reduced, are unable to stimulate TNF production. However, the same commercial preparations promote cell migration, suggesting that the chemotactic activities of HMGB1 are associated with a different, yet to be decoded, pattern of cysteine redox modifications.

CONCLUSION

In summary, the results provided here reveal a novel mechanism to regulate the activities of a key signaling protein, HMGB1, and suggest that HMGB1 might be a key target of redox modifications during inflammation and its resolution.

DISCLOSURE

The authors declare that they have no competing interests as defined by *Molecular Medicine*, or other interests that might be perceived to influence the results and discussion reported in this paper.

Table 2. Overview of hepatic histological changes (extent of hepatic damage determined by serum ALT activity) induced by acetaminophen over time in mice and corresponding serum HMGB1 redox status.

Time post-APAP treatment[a]	0 h	5 h	15 h	24 h
Histological finding	No abnormalities detected necrosis with mild inflammatory cell infiltration	Centrilobular hepatocyte necrosis with moderate inflammatory cell infiltration (including neutrophil rolling)	Centrilobular hepatocyte detected	No abnormalities detected
Serum ALT (U/L)[b]	31 ± 10	2641 ± 1,024[c]	3,015 ± 801[c]	3,811 ± 1,514[c]
Serum HMGB1 cysteine redox status identified	Molecule A	Molecule A + D	Molecule A + D	Molecule D

[a]The corresponding LC-MS/MS characterized redox status of each cysteine within circulating HMGB1 also is given for each time point.
[b]Data are presented as mean ± SEM with six animals per group.
[c]*P* < 0.01 versus 0 h.

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