S-Glutathionylated Serine Proteinase Inhibitors as Plasma Biomarkers in Assessing Response to Redox-Modulating Drugs

Christina L. Grek1, Danyelle M. Townsend2, Joachim D. Uys1, Yefim Manevich1, Woodrow J. Coker III3, Christopher J. Pazoles4, and Kenneth D. Tew1

Abstract

Many cancer drugs impact cancer cell redox regulatory mechanisms and disrupt redox homeostasis. Pharmacodynamic biomarkers that measure therapeutic efficacy or toxicity could improve patient management. Using immunoblot analyses and mass spectrometry, we identified that serpins A1 and A3 were S-glutathionylated in a dose- and time-dependent manner following treatment of mice with drugs that alter reactive oxygen or nitrogen species. Tandem mass spectrometry analyses identified Cys226 of serpin A1 and Cys367 of serpin A3 as the S-glutathionylated residues. In human plasma from cancer patients, there were higher levels of unmodified serpin A1 and A3, but following treatments with redox active drugs, relative S-glutathionylation of these serpins was higher in plasma from normal individuals. There is potential for S-glutathionylated serpins A1 and A3 to act as pharmacodynamic biomarkers for evaluation of patient response to drugs that target redox pathways. Cancer Res; 72(9); 2383–93. ©2012 AACR.

Introduction

Preclinical and early clinical testing of novel anticancer drugs can be significantly enabled by the inclusion of direct or surrogate biomarkers that correlate with pharmacologic effects (1, 2). Incorporation of such biomarkers can enhance data interpretation, provide an explanation for either positive or negative correlations with efficacy or toxicity, and aid in early decision candidate selection. In complex diseases such as cancer, recent trends in drug development have moved toward targeted therapies to provide maximal therapeutic response while minimizing side effects. Failure of early stage clinical trials incurs great expense and there is merit in including biomarkers, both to estimate treatment efficacy and to identify patients with phenotypic characteristics that might predict response outcomes or toxicities.

In evaluating drug response, a single biomarker can lend itself to quantitative measurements through dose and time response studies. The metabolism of many drugs leads to production of electrophilic species that can generate reactive oxygen or nitrogen species (ROS, RNS). These can directly influence redox balance in both blood and tissue compartments. Biologic sensing of redox changes is most actively monitored through select cysteine residues in various proteins. Although there is debate as to the precise definition of what constitutes redox sensing versus redox signaling (3), there is little doubt that cysteines at various oxidation states are integral. S-glutathionylation is a posttranslational modification that occurs when a cysteine in a low pK environment forms a disulfide bond with GS−. This is reversible and the resultant S-glutathionylation cycle has the potential to selectively regulate the function of numerous enzymes, receptors, structural proteins, transcription factors, and transport proteins. Moreover, posttranslational modification may alter a variety of protein–protein interactions (4). The activities of serine protease inhibitors (serpins) are regulated by modifications of key cysteines (5, 6), in which, for example, S-glutathionylation of serpin A1 results in conformational changes that weaken its affinity for its target protease, thereby reducing its effectiveness in preventing proteolytic activity (7).

Vertebrate serpins are classified into 6 subgroups and represent approximately 2% of the total protein in human plasma (8). Although most are defined by their inhibitory activities, certain serpins have noninhibitory roles as hormone transporters (9), molecular chaperones (10), or tumor suppressors (11). Moreover, serpins can influence myeloproliferation and hematopoietic progenitor cell mobilization. Serpins A1 and A3 have redox-sensitive cysteines and are downregulated in bone marrow during mobilization of hematopoietic progenitor cells into the peripheral bloodstream (12), implicating a regulatory function for S-glutathionylation and redox homeostasis in the marrow compartment. This is consistent with the
fact that certain redox active drugs [including the glutathione disulfide mimetic NOV-002 (13) and the GSH peptidomimetic, Telintra (14)] have both preclinical and clinical myeloproliferative effects (15).

In this study, we have identified the S-glutathionylation of plasma serpins A1 and A3 as potential quantifiable response biomarkers for assessing response to 2 different types of drugs that either directly or indirectly impact redox status. NOV-002 is a formulation of disodium glutathione disulfide (GSSG) that in combination protocols is in phase II trials for the treatment of breast cancer. NOV-002 causes a redox regulation of protein thiols that persists in plasma for approximately 4 hours and in rodents and humans stimulates proliferation of bone marrow progenitor cells (13). PABA/NO is a diazeniumdiolate that acts as a direct nitrogen monoxide (NO) donor and is in development as an anticancer drug. We show that plasma serpin S-glutathionylation correlates with drug treatment in vivo and in vitro. Furthermore, analysis of cancer patient plasma samples suggests disease-specific variation in unmodified and S-glutathionylated serpin profiles correlating with drug concentrations.

Materials and Methods

Reagents

Reduced GSH was from Sigma. NOV-002 provided by Nove
os Therapeutics, and PABA/NO from Dr. Larry Keefer (Na
tional Cancer Institute at Frederick, Frederick, MD; refs. 16, 17).

Animal and human plasma studies

Mice were treated with an intravenous bolus of 25 mg/kg NOV-002 and after 1 hour blood was collected via orbital bleed in heparin-coated tubes. Plasma was separated by centrifugation and proteins separated on SDS-PAGE and transferred for immunoblot analyses. Human blood samples were obtained with informed consent from 8 cancer-free volunteers and 47 oncology patients with various types/stages of cancer: 20 acute myeloid leukemia (AML); 10 acute lymphoblastic leukemia (ALL); 1 CML; 2 lung carcinomas; 2 urothelial carcinomas; 1 leiomyosarcoma; 1 neuroblastoma; 1 spindle cell carcinoma, 1 invasive ductal carcinoma. Eight to 10 cc of blood was collected into Vacutainer tubes containing EDTA. Plasma was separated via centrifugation and treated with NOV-002 or PABA/NO at 37°C.

Immunoblot analysis

Equal amounts of purified recombinant serpins A1/A3 or total plasma protein, as determined by Bradford assay (Bio-Rad Laboratories), were separated on nonreducing SDS-polyacrylamide gels. Proteins were transferred onto poly
vinyldene difluoride membranes (Bio-Rad Laboratories) and probed with a monoclonal anti-GSSG antibody (Virogen) to detect S-glutathionylation, or polyclonal antibodies for serpins A1 and A3 (R&D systems), glutaredoxin1 (Abcam) or GSTP (MBL). Equal loading was estimated by polyclonal rabbit albumin antibody (Abcam). Secondary antibodies were from Amersham Biosciences.

Identification of S-glutathionylated plasma proteins

Plasma S-glutathionylated protein bands were isolated from gels run simultaneously with immunoblots and trypsin digested. Peptide mass was analyzed by matrix-assisted laser desorption/ionization, time-of-flight (MALDI-TOF) mass spectrometry at the Proteomics Core Facility. Protein identification was done using software from the NCBI protein database.

Immunoprecipitation

Human plasma samples (2 mg) were treated with 50 μmol/L of NOV-002 for 60 minutes at 37°C. Biotinylated rabbit polyclonal antibodies to serpins A1 and A3 (Abcam, 5 μg) were used to pull-down respective proteins by overnight incubations at 4°C. Antibody complexes were isolated through incubation with NeutrAvidin agarose resin (Thermo Scientific) for 2 hours. Resin-bound complexes were washed 5× with immunoprecipitation buffer (20 mmol/L HEPES, 300 mmol/L NaCl, 1% Triton, 10% glycerol) and proteins eluted in nonreducing SDS-sample buffer. Immunoprecipitated proteins were separated by nonreducing SDS-PAGE and S-glutathionylation of serpins A1 and A3 evaluated by immunoblot.

In vitro S-glutathionylation assays

Purified serpin A1 or A3 (50 ng) was incubated at 37°C in 50 mmol/L potassium phosphate buffer (pH 7.2). 1 mmol/L GSH with either NOV-002 or PABA/NO. Samples were run on nonreducing SDS-PAGE gels for subsequent transfer and immunoblot analysis.

Tandem mass spectroscopy

Purified serpins A1 and A3 were treated with 100 μmol/L PABA/NO or 1 mmol/L NOV-002 for 30 minutes at 37°C, digested with Lys-C and analyzed via liquid chromatography (LC)–electrospray ionization (ESI)–tandem mass spectrome
try (MS/MS) on a linear ion trap mass spectrometer (LTQ, Thermo Finnigan) coupled to an LC Packings nano LC system. S-glutathionylated serpin A3 peptides required additional trypsin digestion (See Supplementary Data for instrument settings).

Spectroscopic analysis of serpin A1 and A3 in vitro

The effect of serpin S-glutathionylation on enzyme secondary structure was examined by circular dichroism (CD) measurements carried out on a 202 AVIT Associates CD spectrometer using a semi-micro quartz rectangular 1 × 10 × 40 mm cuvette. Serpins A1 and A3 (~2 mg/mL) were S-glutathionylated by treatment with 40 μmol/L PABA/NO and 1 mmol/L GSH for 30 minutes in 20 mmol/L PB, pH 7.4, at 37°C. Excess PABA/NO and GSH were eliminated using Biospin-6 (Bio-Rad) SEC micro-spin columns.

Purified native and S-glutathionylated serpins A1 and A3 (~95% homogeneous, 40 μmol/L in 20 mmol/L PB, pH 7.4) were maintained at 22°C using a Pelletier element. Spectra were recorded while scanning in the far-ultraviolet region (190–260 nm), with bandwidth of 1.0 nm, step size of 0.5 nm, integration time of 30 seconds. Protein tryptophanyl fluorescence was recorded on a QM-4 spectrophluorometer (PTI) using 10 × 10 × 40-mm quartz cuvette, excitation and 2.5 and 5.0 nm
emission slits. To minimize effects of protein tyrosines and phenylalanines, an excitation wavelength of 295 nm was used. Background spectra were subtracted from final emission data.

Statistical analyses
Statistical analyses were carried out using GraphPad Prism (GraphPad Software). *P* values lower than 0.05 were considered significant. Parametric data were statistically evaluated using *t*-tests and nonparametric data were evaluated using Mann–Whitney or Wilcoxon matched pairs signed rank tests, based on data distribution. Multiple comparisons were analyzed using ANOVAs with Dunnett’s Multiple Comparison tests or Kruskall–Wallis tests with Dunn’s multiple Comparison test. Corrections were applied based on program recommendation. Relative S-glutathionylation levels induced in cancer were analyzed using 2-way ANOVAs.

Results
*In vivo* treatment with NOV-002 leads to S-glutathionylation of a limited subset of plasma proteins in mice (Fig. 1A). Immunoblots from animals detected 4 prevalent S-glutathionylated proteins within 15 minutes of treatment. Excised bands were trypsin digested and peptide mass analyzed by MALDI-TOF. Protein identification (Fig. 1C, Table) used software from the NCBI protein database. Complement C3 appears as a common S-glutathionylated protein throughout the analysis, even before drug treatments. Proteins bands B and D were identified as serpin A1, whereas band C was identified as serpin A3. Murine contrapsin is homologous to human serpin A3. *Ex vivo* treatment of mouse plasma with various concentrations of NOV-002 showed similar S-glutathionylation induction. Quantification of band densities showed increasing serpin S-glutathionylation with dose exposure (Fig. 1B).

Extending these analyses, purified human plasma samples were similarly treated *ex vivo* with NOV-002. Anti-PSSG immunoblots showed the induction of several distinct S-glutathionylated protein bands with a profile similar to *in vitro* and *in vivo* in mouse plasma assays. Basal levels of S-glutathionylated proteins were detected in both mouse and human untreated samples, most likely the result of *ex vivo* processing. Treatment with 40 μmol/L NOV-002 caused a time-dependent increase in the relative amount (as normalized to albumin loading control) of S-glutathionylated proteins that peaked between approximately 40 to 60 minutes and gradually decreased with
additional time (Fig. 1D). This indicated a relatively rapid turnover rate involving the S-glutathionylation and deglutathionylation of proteins following drugs.

Immunoprecipitation of serpins A1 and A3 from human plasma confirmed that both these proteins are S-glutathionylated (Fig. 1E). Due to high sequence homology (~46%) between human serpins A1 and A3, a certain extent of antibody cross-reactivity may be anticipated. In particular, the immunoprecipitating serpin A3 antibody also pulled down serpin A1, as evidenced on the PSSG blot. Protein bands correspond with the approximate expected molecular weights of serpins A1 and A3 (seen on PSSG immunoblots). Detection of multiple protein bands on immunoblots probed with serpin antibodies is not uncommon. Serpins and serpin/protease complexes undergo gradual proteolysis at the serpin active site producing cleavage products, perhaps explaining the multiple protein bands seen on serpin immunoblots (18).

Purified recombinant A1 and A3 protein was treated in vivo and in vitro with agents known to induce protein S-glutathionylation (13, 19). In the presence of PABA/NO and GSH, both serpins A1 and A3 were S-glutathionylated in a time- (Fig. 2A) and concentration-dependent manner (Fig. 2B). Serpin A1 was rapidly S-glutathionylated within 1 minute and peaked at approximately 5 to 10 minutes. Following this, S-glutathionylated protein levels gradually declined. Alternatively, serpin A3 showed a more gradual increase in S-glutathionylation over a 30-minute time course, suggesting unique protein properties despite high sequence homology. Similar drug concentrations were needed to induce minimum (at ~25 µmol/L PABA/NO) and maximum (at ~75 µmol/L PABA/NO) S-glutathionylation levels of both serpins A1 and A3. However, drug-induced S-glutathionylation levels of serpin A3 became relatively saturated between 25 and 50 µmol/L PABA/NO, suggesting that serpin A3 S-glutathionylation may be more time dependent. We evaluated the effects of S-glutathionylation on serpin secondary structure. Tryptophanyl fluorescence of serpin A3 was lower than that of serpin A1 indicating a quenching in the former. Tryptophanyl fluorescence of S-glutathionylated serpin A3 had an increased intensity and a shift of emission maximum from 328 to 336 nm, interpreted as tryptophanyl exposure to a more polar environment, decrease of quenching and structural change (Fig. 2C). The CD spectrum (far UV, 190–260 nm) of S-glutathionylated serpin A1 was similar to that of native protein, consistent with a minimal increase in the α-helical content (206–220 nm) of the protein (Fig. 2D). This suggested a minor decrease in tryptophanyl fluorescence caused by S-glutathionylation, indicating a reasonably intact tertiary and quaternary structure. In contrast, the CD spectrum of S-glutathionylated serpin A3 was distinct from that of the native protein, consistent with an increase in the β-strand content of the protein and altered protein folding (Fig. 2D). These fluorescent analyses confirmed that S-glutathionylation affects the tertiary structure of serpin A3.

S-glutathionylated recombinant serpins A1 and A3 were analyzed using MS/MS to identify S-glutathionylated cysteines. Purified recombinant serpins A1 and A3 were incubated at

![Figure 2. S-glutathionylation of serpins A1 and A3 is time and dose dependent and impacts protein structure. Recombinant serpin A1 and A3 were treated with 1 mmol/L GSH and 40 µmol/L of PABA/NO for 0 to 30 minutes (A) or 0 to 100 µmol/L of PABA/NO for 30 minutes (B). Immunoblot analyses were used to detect S-glutathionylation (PSSG) and total serpin. Spectroscopic analyses of secondary and tertiary (quaternary) structure of native (control; solid curves) and PABA/NO–GSH-treated (Glut; dashed curves) A1 (top curves, dark gray) and A3 (bottom curves, light gray) protein were done in vitro using tryptophanyl fluorescence (C) and circular dichroism (D). IB, immunoblot.](image-url)
37°C for 30 minutes the presence of 100 μmol/L PABA/NO and 10 mmol/L GSH. Analyses of (RLGMFNIQHCK) of serpin A1 (Fig. 3A and B) indicated that an additional approximately 305 Da at Cys256, representing GSH, in addition to the Cys alone (~103 Da) and water (~18 Da), was present only in the drug-treated serpin A1 (Fig. 3B). MS/MS analyses similarly identified Cys256 of (DEELSCYVTYK; Fig. 3C and D) treated serpin A3 to be modified by the addition of GSH, indicated by an additional approximately 305 Da (Fig. 3D). These data provided a platform to develop analytical methods for quantification of S-glutathionylated serpins in biologic fluids.

Human plasma samples from 47 cancer patients undergoing chemotherapy treatments and 8 cancer-free patients were analyzed for total and S-glutathionylated serpin A1 and A3 protein. Immunoblot densitometry showed significantly (P < 0.05) elevated amounts of each unmodified serpin in cancer patients (Fig. 4A and B). All protein bands were normalized to an albumin loading control as well as an internal standard incorporated on all gels. Levels of S-glutathionylated serpins A1 and A3 did not correlate with total serpin levels. In fact, serpin S-glutathionylation profiles were distinct between patients, suggesting that individual patients with specific disease and treatment profiles have unique serpin S-glutathionylation. However, when analyzing all cancers in a group, the overall ratio of S-glutathionylated serpin A1 (PSSGa and PSSGc) and A3 (PSSGb) to unmodified serpin A1 and A3, respectively, was significantly decreased (P < 0.05) in cancer patients (Fig. 4C). Thus, in reference to the total amount of serpin, the fraction of serpin protein subject to S-glutathionylation was lower in cancer patients. Table 1 summarizes the relative fold change in protein expression of unmodified and S-glutathionylated serpins in total cancer as compared with cancer-free, in addition to AML and ALL as individual groups. While general trends remain consistent between all cancers, discrepancies in significance may suggest disease-specific profiles. Of particular interest, levels of basal S-glutathionylated serpins were significantly lower in ALL patients as compared with AML and cancers as a group.

Ex vivo treatment of patient plasma with NOV-002 for 60 minutes at 100 μmol/L proportionally enhanced levels of S-glutathionylated A1 and A3 [Fig. 5A and B and Supplementary Fig. S1 (lighter exposures)]. Figure 5B shows the relative quantities of S-glutathionylated serpin A1 (PSSGa and PSSGc) and A3 (PSSGb) after NOV-002 treatment from samples of 47 cancer and 8 cancer-free patients, determined by densitometry measurements normalized to both albumin loading controls and an internal standard incorporated on all gels. S-glutathionylated serpin A1 (PSSGa and PSSGc) and A3 (PSSGb) levels were significantly increased (P < 0.05) in response to NOV-002. Two-way ANOVA analyses show that ex vivo treatment of plasma with 100 μmol/L NOV-002 resulted in significantly higher relative increases (P < 0.05) in serpin A1 S-glutathionylation (PSSGa/A1 and PSSGc/A1) in cancer-free plasma as compared with cancer patients (Fig. 5C). Thus, in response to treatment, serpin S-glutathionylation and disease status are interrelated and showed altered redox homeostasis in cancer patients. NOV-002 treatment also induced S-glutathionylation of albumin, as evidenced by the doublet band detected only at high drug concentrations. Critically, NOV-002 treatment did not alter serpin stability, as indicated by total serpin immunoblotting. Treatment with 40 μmol/L NOV-002 for 0 to 240 minutes did not change levels of unmodified serpin A1 or A3 (P > 0.05) (Fig. 5D). Additional analyses using treated and untreated plasma samples from cancer and cancer-free patients supported these data (Fig. 5E). Treatment with Velcade, vinblastine, Taxol, or tamoxifen did not induce changes in plasma serpin A1 or A3 S-glutathionylation (Supplementary Fig. S2A–D).

GSTP and Grx1 are involved in the forward and reverse reactions of S-glutathionylation. Relative protein levels were determined via densitometry and then normalized to an albumin loading control, as well as an internal standard incorporated into all gels. Plasma protein levels of GSTP were significantly decreased (P < 0.05) in cancer patients as compared with cancer free. Conversely, plasma Grx1 levels were significantly elevated (P < 0.05) in cancer patients (Fig. 6). These data are consistent with the interpretation that the decreased relative ratio of S-glutathionylated to unmodified serpin in cancer patient plasma may be linked with diminished GSTP levels and a relatively enhanced rate of serpin deglutathionylation, as a consequence of elevated Grx1.

Discussion

There is expanding interest in adopting a redox-modulating platform in drug discovery/development in cancer (20). In this study we used 2 drugs that alter redox homeostasis through distinct mechanisms. NOV-002 is an oxidized glutathione mimetic that modifies extra- and intracellular ratio of GSH:GSSG (13, 21). PABA/NO releases NO to raise levels of RNS and ROS (19). Increased efficacy and limited off-target toxicities could be facilitated by the identification of plausible pharmacodynamic biomarkers (preferably through noninvasive approaches) that serve as predictors of drug response. Initially using mice, we identified S-glutathionylated serpins A1 and A3 as quantifiable response biomarkers. These preclinical observations were extended to human plasma samples in which correlative associations with drug exposure and disease status were identified. Moreover, variations in the expression of unmodified and/or S-glutathionylated serpin profiles were identified and may reflect aberrant redox homeostasis in some cancers.

Because of the variable valence states of sulfur, cysteine-targeted oxidation has evolved as a critical regulator of protein function in a number of signal transduction pathways. Protein S-glutathionylation is cyclical in nature [the forward reaction is catalyzed by GST, the reverse by glutaredoxin (22)], providing the framework for reversible signaling (23). A number of protein clusters with roles in cell survival pathways are characteristically sensitive to posttranslational modification, including enzymes with catalytically important cysteines, signaling proteins, and transcription factors. Serine proteinase inhibitors are susceptible to modulation by redox conditions (7, 24, 25). MS/MS analyses identified Cys256 of serpinA1 and
Figure 3. Serpin A1 is S-glutathionylated at Cys256 and serpin A3 is S-glutathionylated at Cys263. Recombinant serpin A1 and A3 proteins were treated with 1 mmol/L GSH and 100 μmol/L PABA/NO for 30 minutes. To identify specific cysteine residues susceptible to S-glutathionylation, control unmodified serpin A1 (A) PABA/NO-treated serpin A1 (B); control unmodified serpin A3 (C) and PABA/NO-treated serpin A3 (D) were digested under nonreducing conditions and analyzed via LC–ESI–MS/MS to identify modification GSH addition. A single S-glutathionylated modification [+]305.6 was detected at Cys256 of serpin A1 (B) and Cys263 of treated serpin A3 (D). Arrows indicate modified peaks. The 2 arrows in D represent both forward and reverse analyses.
Figure 4. Unmodified serpin is elevated in certain cancers, whereas the ratio of S-glutathionylated to unmodified serpin is decreased. Human plasma samples from cancer-free patients \((n = 8); \text{represented in lanes 1,3,5 of A}) and cancer patients undergoing chemotherapy \((n = 47); \text{represented in lanes 2,4,6 of A}) were analyzed by immunoblotting for unmodified serpin A1 and A3 protein levels \((B)\) as well as relative levels of S-glutathionylated serpin compared with total unmodified serpin \((C)\). Relative quantities of unmodified serpins and S-glutathionylated serpin A1 \((\text{PSSGa} \text{and PSSGc})\), and serpin A3 \((\text{PSSGb})\) were determined by densitometry measurements normalized to both albumin loading controls and an internal standard incorporated on all gels. Data are \(\pm\) SEM. IB, immunoblot.

Table 1. Relative fold change in protein expression (cancer vs. cancer free) of unmodified serpins and S-glutathionylated serpins

<table>
<thead>
<tr>
<th>Protein</th>
<th>Cancer</th>
<th>AML</th>
<th>ALL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Serpin A1</td>
<td>1.96 ± 0.12a</td>
<td>2.02 ± 0.15a</td>
<td>1.99 ± 0.30a</td>
</tr>
<tr>
<td>Serpin A3</td>
<td>4.16 ± 1.07a</td>
<td>2.42 ± 0.39a</td>
<td>5.64 ± 3.30a</td>
</tr>
<tr>
<td>Glut serpin A1 ((\text{PSSGa}))</td>
<td>1.05 ± 0.11</td>
<td>1.17 ± 0.15</td>
<td>0.35 ± 0.09a</td>
</tr>
<tr>
<td>Glut serpin A3 ((\text{PSSGb}))</td>
<td>0.94 ± 0.19</td>
<td>1.00 ± 0.13</td>
<td>0.49 ± 0.08</td>
</tr>
<tr>
<td>Glut serpin A1/PSSGc ((\text{PSSGc}))</td>
<td>0.70 ± 0.11a</td>
<td>0.81 ± 0.19</td>
<td>0.37 ± 0.07a</td>
</tr>
<tr>
<td>Glut serpin A1/serpin A1 ((\text{PSSGa/serpin A1}))</td>
<td>0.56 ± 0.06a</td>
<td>0.62 ± 0.09a</td>
<td>0.19 ± 0.04a</td>
</tr>
<tr>
<td>Glut serpin A1/serpin A3 ((\text{PSSGb/serpin A3}))</td>
<td>0.43 ± 0.06a</td>
<td>0.56 ± 0.09a</td>
<td>0.22 ± 0.06a</td>
</tr>
<tr>
<td>Glut serpin A3/serpin A1 ((\text{PSSGc/serpin A1}))</td>
<td>0.37 ± 0.06a</td>
<td>0.41 ± 0.10a</td>
<td>0.19 ± 0.03a</td>
</tr>
<tr>
<td>GSTp</td>
<td>0.73 ± 0.05a</td>
<td>0.86 ± 0.07</td>
<td>0.61 ± 0.09a</td>
</tr>
<tr>
<td>Grx</td>
<td>2.18 ± 0.32a</td>
<td>2.95 ± 0.68a</td>
<td>1.60 ± 0.22</td>
</tr>
</tbody>
</table>

NOTE: SDS-PAGE and immunoblot analyses analyzed levels of unmodified and S-glutathionylated serpins A1 and A3. Relative quantities of unmodified serpins and S-glutathionylated serpin A1 \((\text{PSSGa} \text{and PSSGc})\), and serpin A3 \((\text{PSSGb})\) were determined by densitometry normalized to both albumin loading controls and internal standards incorporated on all gels. \(n = 8\), cancer free; \(n = 47\), cancer; \(n = 20\), AML; \(n = 10\), ALL. Data are fold change versus cancer-free \(\pm\) SE. 

\(^*P < 0.05\)
(Supplementary Fig. S2) the effects of Velcade (proteasome inhibitor), vinblastine and Taxol (antimicrotubule drugs), or tamoxifen (estrogen receptor antagonist). Although these drugs may produce low levels of ROS indirectly, the data suggest that there is no dose effect response on plasma serpin S-glutathionylation profiles.

Immunoblots of S-glutathionylated serpins revealed proteins of various molecular weights. Different segments of the A1 molecule may possess unique biologic properties that may or may not be linked to protease inhibitor activity. Low molecular weight fragments of serpin A1, generated by complexing with neutrophil elastase or by macrophage metalloelastase attack, possess chemotactant properties (28). In this context, serpin S-glutathionylation may have a mechanistic connection with the in vivo myeloproliferative activity of NOV-002 (13). The redox-sensitive serpin, bomapin, is directly involved in the responsiveness of myeloid progenitor cells to their microenvironment (29). Posttranslational regulation of serpins in the peripheral circulation may indicate a role in the control of proteolytic pathways. Whatever the functional association, as the plasma half-life of S-glutathionylated proteins is approximately 4 hours (19), our mouse studies provided evidence that these posttranslationally modified proteins could be viable as pharmacodynamic biomarkers in a clinical setting.

There is precedent for using posttranslationally modified proteins as biomarkers. In initial trials of the CML therapeutic imatinib levels of phosphorylated CRKL correlated directly with BCR-ABL inhibition and proved useful in determining appropriate dosing strategies (30, 31). In addition, success of small-molecule inhibitors of epidermal growth factor receptor tyrosine kinase (EGFR) is contingent on the levels of activated EGFR (32). In this context, the ex vivo treatment with NOV-002 induces serpin A1 and A3 S-glutathionylation and results in greater relative increases in serpin A1 glutathionylation in cancer-free human plasma. Cancer (samples 2–8) and cancer-free (sample 1) human plasma samples were treated with 100 µmol/L NOV-002 for 60 minutes (A). S-glutathionylation (PSSG), serpin A1, serpin A3, and albumin levels (loading control) were evaluated by immunoblot. Levels of S-glutathionylated serpin A1 (PSSGa and PSSGc) and serpin A3 (PSSGb) after NOV-002 treatment (both cancer and cancer free) were determined by densitometry normalized to both albumin loading controls and an internal standard on all gels (B). Relative S-glutathionylation levels in reference to total unmodified serpin levels induced in response to NOV-002 treatment in cancer patient plasma as compared with those induced in cancer-free plasma were analyzed using 2-way ANOVAs (C). To confirm that S-glutathionylation of serpins does not alter serpin A1 and A3 protein stability, plasma was treated with 40 µmol/L NOV-002 for 0 to 240 minutes (D). The relative quantity of serpins A1 and A3 in treated and untreated samples (both cancer and cancer free) after 100 µmol/L NOV-002 treatment for 1 hour was normalized to both albumin loading controls and an internal standard on all gels (E). Data are mean for 8 cancer-free and 47 cancer samples ± SEM. IB, immunoblot.
tumors, suggesting the usefulness of patient serum in asse-
in cancer. High levels of oxidative stress markers in results consistent with a disrupted redox homeostasis asso-
Serpins was decreased. Furthermore, ex vivo respond preferentially to redox-targeted therapeutics.
stream redox-mediated signaling events, including NF-
involved in normal hematopoiesis, imbalances of ROS uence down-
metastatic adenocarcinomas (34–36) and with poor response in MM (37). Although the functional importance of serpins A1 and A3 in cancer is not yet clearly defined, serpin A1 has inhibitory activity against cytotoxic T lymphocytes and natural killer cells (38), suggesting that the tumor-promoting effect of serpin A1 could be related to a decreased immune response against malignant cells. Serpin A1 overexpression may also be a useful biomarker in insu-
leukemias, in which the cancer is of bone marrow origin, further defining a role of serpin A1 and A3 -glutathionylation in myeloproliferation may be valuable with regard to development of tailored treatment strategies. Chronic oxidative stress, characterized by excessive cellular ROS levels, occurs in several hematopoietic malignancies including ALL, MDS, CML, and AML (40–42). While ROS is involved in normal hematopoiesis, imbalances of ROS results in redox dysregulation and may influence down-
variables (e.g., statistical analysis, bioinformatics, computational analysis): C.L. Grek, D.M. Townsend, J.D. Uys, Y. Manevich, W. Coker III, and K.D. Tew

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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Analysis and interpretation of data (e.g., statistical analysis, bioinformatics, computational analysis): C.L. Grek, D.M. Townsend, J.D. Uys, Y. Manevich, and C. Pazoles
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Study supervision: K.D. Tew

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