Treatment-Induced Oxidative Stress and Cellular Antioxidant Capacity Determine Response to Bortezomib in Mantle Cell Lymphoma

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Abstract

**Purpose:** Proteasome inhibition disrupts protein homeostasis and induces apoptosis. Up to 50% of patients with relapsed mantle cell lymphoma (MCL) respond to bortezomib. We used gene expression profiling to investigate the connection between proteasome inhibition, cellular response, and clinical efficacy.

**Experimental Design:** We assessed transcriptional changes in primary tumor cells from five patients during treatment with bortezomib in vivo, and in 10 MCL cell lines exposed to bortezomib in vitro, on Affymetrix microarrays. Key findings were confirmed by western blotting.

**Results:** MCL cell lines exposed to bortezomib in vitro showed upregulation of endoplasmic reticulum and oxidative stress response pathways. Gene expression changes were strongest in bortezomib-sensitive cells and these cells were also more sensitive to oxidative stress induced by H2O2. Purified tumor cells obtained at several timepoints during bortezomib treatment in 5 previously untreated patients with leukemic MCL showed strong activation of the antioxidant response controlled by NRF2. Unexpectedly, activation of this homeostatic program was significantly stronger in tumors with the best clinical response. Consistent with its proapoptotic function, we found upregulation of NOXA in circulating tumor cells of responding patients. In resistant cells, gene expression changes in response to bortezomib were limited and upregulation of NOXA was absent. Interestingly, at baseline, bortezomib-resistant cells displayed a relatively higher expression of the NRF2 gene-expression signature than sensitive cells (P < 0.001).

**Conclusion:** Bortezomib triggers an oxidative stress response in vitro and in vivo. High cellular antioxidant capacity contributes to bortezomib resistance. *Clin Cancer Res; 17(15); 5101–12. ©2011 AACR.*
of bortezomib action. However, recent studies in MCL and MM cells do not support this hypothesis (10, 11), and in some settings bortezomib may actually increase NF-kB activity (10, 12). On a more general level, proteasome inhibition disrupts protein homeostasis in both cytoplasm and the endoplasmic reticulum (ER). Bortezomib thus can elicit ER stress (13–15) that triggers a homeostatic response termed the unfolded protein response (UPR). The UPR orchestrates a complex transcriptional program to alleviate ER stress and restore protein homeostasis (16, 17). Three ER-resident regulatory switches control the UPR leading to increased expression of proteins involved in ER biogenesis and capacity, redox pathways, and protein folding. ER stress activates an ER-membrane bound–protein kinase IRE1 to splice XBP1 mRNA, to produce a key transcription factor of ER biogenesis. In addition, ATF6, an ER-anchored transcription factor, is cleaved and translocates to the nucleus. These two transcription factors regulate ER-resident proteins, chaperones, and protein transporters thereby building the capacity to deal with protein load. The third UPR switch is PERK, an ER-resident kinase that phosphorylates eIF2α leading to reduced protein synthesis while increasing the translation of select mRNAs in particular of the transcription factor ATF4 (17). Failure to restore ER homeostasis ultimately leads to cell death (18). Several effectors of UPR-mediated cell death have been identified and include caspase-4 (19), CHOP (20), and the Bcl-2 family members BIM (21), and NOXA (22).

Proteasome inhibition has also been reported to lead to oxidative stress (13, 22–24). This effect is not unique to bortezomib but rather seems to be a consequence of the accumulation of misfolded proteins that would normally be degraded through the proteasome (19, 25). The ensuing attempts at protein folding generate high levels of reactive oxygen species (ROS; ref. 19). Given that ROS scavengers protect from and depletion of glutathione increases bortezomib-induced cell death in vitro, it is apparent that ROS contribute to the cytotoxic effect of bortezomib (22, 26, 27). Oxidative stress activates transcription of genes containing the so-called antioxidant response element (ARE) (28). A key regulator of this oxidative stress response is the transcription factor NRF2, which in unstressed cells is sequestered in the cytoplasm by the adaptor protein KEAP1 (29). KEAP1 can be oxidized by ROS resulting in conformational changes that release NRF2. In addition, the UPR transducer PERK phosphorylates a threonine residue in the KEAP1 binding domain of NRF2 leading to its dissociation from KEAP1 and nuclear translocation (30).

Bortezomib inhibits proteasome activity in all cells but its clinical activity is limited to a few select malignancies (4, 9). Likewise, activation of the UPR and/or generation of ROS have been described in many different tumor cell lines in vitro. However, in vitro sensitivity of the respective cell lines does not predict clinical tumor response. Given the central role of the protein ubiquitination pathway in cell signaling and cellular function ranging from protein secretion and cell growth to starvation, it is possible that the cellular reaction to proteasome inhibition differs in vitro and in vivo. Thus, it remains ill-defined what mechanisms determine bortezomib-induced cytotoxicity in vivo.

We chose gene expression profiling to systematically study the effect of proteasome inhibition on the tumor biology of MCL in vitro and in patients during treatment. We hypothesized that resistant tumors would show preferential upregulation of homeostatic responses enabling them to withstand proteasome inhibition. Surprisingly, we found the opposite. In response to proteasome inhibition, sensitive tumors showed strong upregulation of NRF2 target genes, of proteasome components, and protein ubiquitination gene expression programs, whereas resistant cells showed minimal gene expression changes. Furthermore, we discovered that increased expression of NRF2 target genes at baseline correlated with decreased sensitivity to proteasome inhibition.

**Materials and Methods**

**Cell lines and patient samples**

The MCL cell lines HBL-2, Jeko-1, JVM-2, Mino, NCEB-1, REC-1, SP-53, UPN1, and Z-138 were grown in RPMI 1640 (Cellgro) supplemented with 10% FBS (HyClone), 2 mmol/L L-glutamine, 100 units/ml of penicillin G, and 100 mg/ml of streptomycin (Gibco) as previously reported (31). Granta-519 cell line was grown in Dulbecco’s modified Eagle’s medium instead of RPMI (Cellgro). Peripheral blood samples from 5 previously untreated patients with leukemia disease, who were treated on clinical studies at the NCI, were collected before (0 hours), at 6 and 24 hours after the first and at 24 hours after the second injection of bortezomib (1.5 mg/m², days 1, 4, 8, and 11). Written

**Translational Relevance**

MCL is incurable with conventional chemotherapy. Bortezomib, the first proteasome inhibitor approved for the treatment of hematologic malignancies, is active in up to 50% of patients with otherwise refractory disease. The molecular mechanism of selective antitumor activity of bortezomib and determinants of resistance to proteasome inhibition are ill-defined. Gene expression profiling has become a powerful method to dissect disease heterogeneity. We used gene expression profiling to investigate the cellular response to proteasome inhibition in vitro and in vivo. Our data indicate that induction of oxidative stress is key to bortezomib-induced apoptosis and clinical response. Moreover, we find evidence that high basal antioxidant capacity is associated with reduced responsiveness and inferior clinical outcome to bortezomib treatment. The correlation of cellular antioxidant capacity with bortezomib resistance could yield predictive markers of treatment success and identifies avenues for synergistic treatment approaches.
informed consent for all research collections was obtained. Diagnosis was confirmed by flow cytometry and all cases had a translocation t(11;14)(q13;q32). Clinical response to bortezomib treatment was determined by the decrease in absolute lymphocyte count. Peripheral blood mononuclear cells were separated by gradient centrifugation using Lymphocyte Separation Medium (MP Biomedicals) and CD19+ cells (> 99% tumor cells, < 1% normal B cells) were purified by magnetic-activated cell sorting using CD19 microbeads (Miltenyi). CD19+ cells were aliquoted and stored as pellets at −80°C.

**Gene expression profiling**

Total RNA of CD19-selected tumor cells was isolated using Qiagen RNA isolation kit (Invitrogen) and 1 μg was used for cRNA amplification according to manufacturer’s instructions. RNA yield and integrity of biotin-labeled cRNA were determined using the Agilent 2100 bioanalyzer (Agilent Technologies). For gene expression profiling, 20 μg of labeled RNA was fragmented and hybridized to Affymetrix Human Genome U133 A arrays (Affymetrix) for 16 hours, washed and stained on an Affymetrix fluidics station. Affymetrix GeneChip operating software (v1.4) was used to calculate signal intensity and present calls. Signal intensity values were transformed with an adaptive logarithm referred to as S10 (Symmetric Adapted transformation, base 10) available at http://abs.cit.nih.gov/MSCL/toolbox/ (MSCL Analyzer’s toolbox software, Peter J. Munson, GeneLogic Workshop of Low Level Analysis of Affymetrix GeneChip Data, 2001).

**Data analysis**

Gene set enrichment analysis (v2.0) was carried out using curated (C2) and motif (C3) gene sets from the molecular signature database (v2.5; Broad Institute). Gene sets were identified using a false discovery rate (FDR) of < 0.1 (except for analysis of curated gene sets on MCL patients where a FDR of < 0.2 was used), and a normalized enrichment score (NES) of > 1.8 or < −1.8. Gene sets were ranked by NES. The leading edge genes, i.e., the genes that contribute most to the identification of the corresponding gene set, were averaged to a score that was used as a comparative measure of expression. Ingenuity pathway analysis was carried out using the Benjamini–Hochberg method for multiple testing correction and a cutoff of FDR < 0.05 was used (Ingenuity Systems). Probesets identified were collapsed to genes by maximum expression value. Signaling pathways identified must contain at least 3 genes. Gene expression data were visualized using Cluster (v2.11) and TreeView (v1.6; Eisen laboratory). Statistical significance was assessed by Mann–Whitney nonparametric U test using Prism 4 software (v4, GraphPad Software Inc.) or Student’s t test as indicated in the figure legends.

**Protein extraction and immunoblot analysis**

Preparation of whole cell extracts was carried out as described previously (31). Briefly, pelleted cells were resuspended in lysis buffer (50 mmol/L Tris-HCl pH 7.4), 1% Triton, 0.25% sodium deoxycholate, 150 mmol/L NaCl, 1 mmol/L Na2VO4, and a cocktail of protease and phosphatase inhibitors (Complete and PhosphoSTOP, Roche Diagnostics; Phosphatase inhibitor cocktail I, Sigma) and vortexed. Cytoplasmic and nuclear protein extracts were prepared using a nuclear/lysosomal fractionation kit (BioVision) following the manufacturer’s instructions with minor modifications. The cytosol extraction buffer was supplemented with protease and phosphatase inhibitors as described above. Proteins were quantified using the Bradford method (Bradford reagent; Bio-Rad). Proteins were separated using NuPAGE Bis-Tris gels (Invitrogen) and transferred to nitrocellulose membranes (iBlot Gel Transfer Stacks; Invitrogen) using the iBlot dry blotting system (Invitrogen). Following immunodetection with indicated primary and corresponding secondary antibodies, membranes were incubated with chemiluminescence horseradish peroxidase substrate (Millipore Corporation) and images were acquired with the Fujifilm LAS-4000 image reader (Fujifilm life science) and Multi Gauge V3.0 software (Fujifilm Life Science). Immunoblots were stained using antibodies to ATF3, ATF4, and NRF2 (Santa Cruz Biotechnology), CHOP, TBP, and MAFG (Abcam), NOXA (Calbiochem), and p97 (Fitzgerald Industries International). Horseradish peroxidase linked antimouse and antirabbit secondary antibodies were purchased from Amersham Biosciences.

**PCR for detection of XBP1 splicing**

PCR analysis was carried out to detect splicing of XBP1 using the following primers: forward 5’-TTACGAGAAACCTCATGCC-3’ and reverse 5’-GGGTCCAAGTTGATCGGCTC-3’ (32). PCR products were visualized on a 2.5% agarose gel and imaged using ChemiImager 5500 (Alpha Innotech Cell Biosciences) and AlphaEase Software (v3.2.2).

**Cell survival assay**

5 × 10^4 cells per well were exposed to serial doubling concentrations of hydrogen peroxide (Sigma) for 24 hours in 96-well plates. Then, 0.5 mg/ml MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide) reagent (Chemicon, Temecula, CA) was added 4 hours before the reaction was terminated by the addition of 0.01 mol/L HCl, 10% SDS. Absorbance was measured at the wavelengths of 570 nm (test) and 650 nm (reference) after overnight incubation.

**Flow cytometry**

To detect cell viability by flow cytometry, MitoTracker Green FM, and MitoTracker Red CMX Ros were used (Invitrogen). Briefly, cells were incubated in media with 100 nmol/L of each probe for 30 minutes at 37°C, and
10,000 cells per tube were analyzed for data acquisition. To detect changes in mitochondrial transmembrane potential cells were stained with 20 nmol/L 3,3-dicyxylodihydroxyarnine (DiOC6[3]; Invitrogen) and the generation of reactive oxygen species was determined by staining cells with 2 μmol/L dihydroethidine (Invitrogen) as described elsewhere (22).

Results

Bortezomib induces a transcriptional response in MCL cell lines

We have previously characterized MCL cell lines with regard to bortezomib sensitivity (31). A cutoff of 10 nmol/L bortezomib was established to divide MCL cell lines into sensitive and resistant groups. Baseline proteasome activity and inhibition of the chymotrypsin-like activity by bortezomib was comparable between the two groups (31). As it is now well established that proteasome inhibition triggers a complex cellular response activating both pro- and anti-apoptotic pathways, we hypothesized that differences in the cellular stress response to proteasome inhibition could explain differential drug sensitivity. Specifically, we wished to test whether induction of a protective response could give rise to bortezomib resistance. To this end, we used gene expression profiling to characterize the stress response to bortezomib for less than 6 hours induced very little cell death even in sensitive cells and failed to induce any cell death in resistant cells up to 8 hours (Fig. 1A). We next analyzed the transcriptional response to proteasome inhibition after short (3 and 6 hours) and long drug exposure (24 hours). Only few genes showed significant changes (at least 2-fold change, FDR < 0.1) in expression at the early time points but at 24 hours widespread changes were present especially in the sensitive cell lines (Fig. 1B). Expression of 553 genes changed significantly in sensitive and of 129 genes in resistant cell lines, respectively, including 73 genes that changed in both groups. Of 480 genes that changed only in the sensitive group, 236 were increased and 244 decreased. Of 56 genes that changed only in the resistant cell lines, 42 were increased and 14 decreased. Of 73 genes that changed in both groups, 61 genes were increased and 12 decreased (Fig. 1C).

To better understand the biologic basis of this response we submitted all genes that changed significantly in response to bortezomib to Ingenuity pathway analysis. In the sensitive cell lines we identified 3 pathways induced by bortezomib, most prominently the protein ubiquitination and the NRF2-mediated oxidative stress response pathways (P < 0.0001; Fig. 1D). Twelve signaling pathways were found to be downregulated, most prominently the antigen presentation pathway (P < 0.0001). Contrary to our initial hypothesis, no distinct pathways were identified among genes that changed in the resistant cell lines. Thus, bortezomib induced a transcriptional response involving protein ubiquitination and oxidative stress response pathways that was activated only in sensitive cells.

Bortezomib induces oxidative and endoplasmic reticulum–stress response pathways in vitro

To further dissect the transcriptional response we carried out gene-set enrichment analysis on bortezomib-induced gene expression changes (Supplementary Table S1 and S2). Several gene sets controlled by specific transcription factors were strongly upregulated in sensitive but less so in resistant cell lines (Fig. 2A). Biologic functions controlled by these transcription factors involve the response to oxidative stress (NRF2, NFE2, TCF11_MAFG, and BACH2), the UPR (NRF2 and XBP1), and heat shock (HSF and HSF1). The only gene sets significantly downregulated by bortezomib relate to cell cycle and are controlled by E2F transcription factors (Supplementary Table S1).

Next we interrogated bortezomib-induced gene expression changes relative to the activity of signaling pathways and the effects of chemical and genetic perturbations on cell biology. We again identified gene sets indicating an oxidative stress response including genes upregulated by H2O2 in breast-cancer cell lines and genes in the ARE-NRF2 pathway. We also observed downregulation of genes whose expression is known to be suppressed by oxidizing agents (Fig. 2B and Supplementary Table S2). In addition, two gene sets of the proteasome pathway were upregulated. Thus, this independent analysis using gene-set enrichment analysis confirmed the key pathways identified by Ingenuity pathway analysis. Most gene sets linked to cell proliferation were downregulated in good agreement with the reduced expression of E2F-controlled genes (Supplementary Table S2) and reflects decreased proliferation of bortezomib-treated cells in agreement with reports that it can induce cell cycle arrest (33, 34). Changes in expression of these gene sets were again more striking in sensitive than in resistant cell lines (Fig. 2B). In the oxidative stress pathway the transcription factor NRF2 regulates numerous detoxifying and antioxidant genes (35). Li and colleagues established a specific NRF2 signature in a genetic mouse model (36). To compare the NRF2 response between different cell lines we derived an expression average of the NRF2 signature genes, which increased 15-fold in response to bortezomib in sensitive but only 2-fold in resistant cell lines (P < 0.0063; Fig. 2C and D).

The transcriptional changes in MCL cell lines indicated engagement of both ER and oxidative stress pathways in response to proteasome inhibition. Consistent with UPR activation primarily in sensitive cells, we found bortezomib-induced IRE1 phosphorylation and XBP1 splicing in Jeko-1 but not in Mino cells (Fig. 3A). Activation of a second UPR pathway controlled by PERK upregulates the transcription factors ATF4, ATF3, and CHOP. In keeping with their ability to promote apoptosis, nuclear accumulation of these proteins correlated with bortezomib-induced apoptosis (Fig. 3B). Next we measured
production of reactive oxygen species (ROS) in response to bortezomib in 2 sensitive and 2 resistant cell lines. Bortezomib caused a striking increase in ROS production as measured with dihydroethidium in the sensitive cell lines. The increase in ROS was paralleled by a decrease in mitochondrial membrane potential indicating cell death. In contrast, resistant cell lines showed only minimal increase in ROS and little or no cell death (Fig. 3C). The time-dependent increase in ROS production and its correlation with bortezomib sensitivity are in agreement with the strong induction of an NRF2 signature in sensitive cell lines. Finally, to directly assess the response to oxidative stress these 4 cell lines were treated with hydrogen peroxide and viability was analyzed by MTT assay. Again, bortezomib resistant cell lines were less affected by oxidative stress than sensitive cell lines (Fig. 3D).
Bortezomib-induced transcriptional response in vivo

We wished to assess whether a stress response similar to what we have defined in our model in vitro is also involved in the antitumor activity of bortezomib in MCL patients. We were able to study 5 patients with leukemic MCL during their first cycle of bortezomib single-agent therapy (1.5 mg/m², days 1, 4, 8, and 11). Patients MCL1-4 continued treatment with 6 cycles of combination chemotherapy starting on day 21. Patient MCL5 could not continue treatment due to intercurrent illness. Patients MCL1, MCL3, and MCL4 had blastoid and MCL2 and MCL5 classic morphology (full patient characteristics in Supplementary Table S5). Two patients, MCL1 and MCL3 achieved a rapid and near complete reduction of circulating tumor cells in response to one cycle of single-agent bortezomib, whereas MCL2 showed no response at all (Fig. 4A). The other two patients had an intermediate response with a delayed onset in MCL4, and a moderate treatment effect in MCL5. Tumor cells obtained pretreatment and on days 2 and 5, corresponding to 24 and 96 hours after the first bortezomib injection, respectively, were analyzed by gene expression profiling. First, we identified 2004 probe sets representing 1606 genes that showed at least a 2-fold change on days 2 or 5 compared with pretreatment in at least 1 of the 5 patients. Unsupervised hierarchical clustering grouped samples in good accordance with the therapeutic effect of bortezomib (Fig. 4B).
For subsequent analyses we considered the two groups of samples identified by hierarchical clustering separately. Between both groups a total of 246 genes showed at least a 2-fold change, 240 of these were unique to MCL1 and MCL3, 5 were only identified in the MCL2, MCL4, MCL5 group, and 1 gene was found in both (Fig. 4B). By Ingenuity pathway analysis, genes upregulated by bortezomib indicated activation of protein ubiquitination and NRF2-mediated oxidative stress response pathways \((P < 0.001; \text{Fig. 4C})\). Thus, in accordance with observations in cell lines, induction of a strong transcriptional response correlated with the antitumor effect of bortezomib and the accumulation of the BH3-only protein NOXA in circulating tumor cells of patients MCL1 and MCL3 (Fig. 4D).

Figure 3. Bortezomib induces endoplasmic reticulum and oxidative stress responses in sensitive but not resistant MCL cell lines. A, Jeko-1 and Mino cells were treated with 10 nmol/L bortezomib (B) or 2 μmol/L thapsigargin (T) as positive control. Activation of IRE1 by phosphorylation (p-IRE1) was assessed by immunoblot and splicing of XBP1 mRNA by RT-PCR. PCR products of unspliced (XBP1u) and spliced (XBP1s) are indicated. A higher migrating band represents a hybrid amplicon \((47)\). Cell viability determined by flow cytometry using mitotracker probes is shown. B, induction of ER stress-related transcription factors ATF3, ATF4, and CHOP was analyzed in nuclear protein extracts by immunoblotting. TATA box binding protein (TBP) and p97 were used as loading controls in the immunoblots. C, the generation of ROS was measured using dihydroethidium \((\text{DHE}^+; \text{gray bars})\) and loss of mitochondrial membrane potential \((\Delta \psi_m; \text{black bars})\) indicative of cell death was determined using 3,3-dihexyloxacarbocyanine iodide \((\text{DiOC6}[3])\) by flow cytometry. D, cell viability by MTT assay after 24 hours exposure to increasing concentrations of hydrogen peroxide \((\text{H}_2\text{O}_2)\). Mean and standard deviation of a representative experiment using triplicates is shown.

Upregulation of proteasome and oxidative stress pathways in vivo correlates with clinical response

We used gene-set enrichment analysis to further dissect the gene expression changes in primary tumor samples during bortezomib therapy in vivo. The top 3 gene sets induced by bortezomib comprised the oxidative stress-related genes controlled by transcription factors TCF11, MAFG, NRF2, and NFE2 that we have previously identified to be upregulated in sensitive MCL cell lines (Fig. 5A and Supplementary Table S3). Likewise, we found overrepresentation of functional gene sets indicating engagement of oxidative stress and proteasome pathways (Fig. 5A and Supplementary Table S4). Next we analyzed changes in expression of proteasome subunits. Most subunits were strongly induced in MCL1 and MCL3, whereas
PSMB8-10 subunits encoding components of the immunoproteasome were slightly decreased (Fig. 5B). A similar change in the expression of proteasome subunits was also seen in cell lines, but differences between sensitive and resistant cells were less striking (data not shown). In accordance with gene expression changes, bortezomib induced protein expression of the β5 subunit (PSMB5) only in circulating tumor cells of these 2 patients (Fig. 5B). In contrast to the cell lines, XBP1 and ATF6 gene sets were not significantly enriched in primary tumor samples. Consistently, we did not detect XBP1 splicing in primary tumors (data not shown).

Strong induction of NRF2 target gene expression in MCL1 and MCL3 but not in the other patients indicated a correlation between oxidative stress and clinical activity of bortezomib (Fig. 5C). Consistently, NRF2 protein increased in circulating tumor cells of patients with excellent clinical response, but not in the other patients (Fig. 5D). Finally, we aimed to identify genes differentially expressed between sensitive and resistant tumors at baseline. Twenty-six genes were more highly expressed in MCL1 and MCL3 compared with 75 genes whose expression was higher in MCL2, MCL4, and MCL5 (Fig. 6A). Among the 75 genes more highly expressed in resistant tumors, NRF2-controlled antioxidant genes and genes of the ubiquitin proteasome pathway were significantly overrepresented (FDR < 0.01 by Ingenuity pathway analysis). Comparison of individual samples by Student’s t-test confirmed
overexpression of the NRF2 signature average and of proteasome subunits in tumors with inferior clinical response (Fig. 6B and C).

Discussion

Bortezomib inhibits the proteasome, a universal pathway essential for all cells. To improve therapeutic strategies it is crucial to understand the underlying mechanisms for its selective cytotoxicity against tumor cells. Here we used gene expression profiling to characterize the stress response of MCL cells during bortezomib treatment in vitro and in vivo. We discovered a prominent transcriptional response indicating activation of the UPR and oxidative stress pathways. Unexpectedly, genes encoding detoxifying and antioxidant molecules were strongly upregulated in sensitive but not in resistant cells. Contrary to our expectation we could not detect a reactive homeostatic response in resistant cells that might enable these cells to tolerate proteasome inhibition. However, we discovered that high baseline expression of NRF2 target genes in untreated cells correlated with drug resistance in vitro and in vivo. Thus, our data implicate high cellular antioxidant capacity as a mechanism of bortezomib resistance. In contrast, acute upregulation of the antioxidant response in sensitive cells was not sufficient to restore homeostasis. The strong reactive upregulation of NRF2 target genes then appears as a correlate of an overwhelming cytotoxic insult. However, we cannot rule out that under certain circumstances NRF2 itself may contribute to the induction of apoptosis. ATF4 that can activate antioxidant genes as well as proapoptotic mechanisms serve as an example of such a dual role (15, 37).

The BH3-only protein NOXA is induced in response to bortezomib in many cell types in vitro. Here, we show for the first time NOXA upregulation in primary tumor cells in MCL patients undergoing treatment with bortezomib. In keeping with its function as a terminal effector of bortezomib cytotoxicity (22, 31), NOXA was upregulated only in...
cells that also showed a stress response by gene expression profiling. While originally described as a p53 target gene, p53 is not necessary for NOXA induction in response to proteasome inhibition (22). Recently, Wang and colleagues showed an alternative pathway of NOXA activation involving epigenetic modification of the promoter combined with transcriptional activation by ATF3 and ATF4 dimerization (15). As predicted by these studies, we found ATF3 and ATF4 upregulation in sensitive but not in resistant cells. Whereas ATF3 mRNA increased as part of the bortezomib-induced transcriptional response, ATF4 mRNA showed increased protein levels of ATF4 in bortezomib-treated cells lines. In contrast, in vivo we observed primarily an NRF2 gene-expression response and no activation of the IRE1/XBP1 arm of the UPR. Thus, while bortezomib induces both UPR and oxidative stress responses in vitro, our results suggest that in vivo oxidative stress may dominate, at least in some settings. Given that UPR and oxidative stress response are modulated by several cellular factors including biosynthetic load, amino acid starvation, and redox homeostasis (38), all of which can differ significantly between in vitro and in vivo environments, such differences are certainly plausible. It is also notable that proteasome inhibition with bortezomib consistently induces NOXA but not BIM (22, 31), whereas the apoptotic response of the UPR in response to classic pharmacologic or pathophysiologic ER stressors has been associated with BIM upregulation (21). Taken together, these data indicate that bortezomib-induced cytotoxicity differs in several aspects from classic UPR-associated mechanisms.

We found a prominent antioxidant response in response to bortezomib both in vitro and in vivo. Oxidative stress is closely linked with ER stress. On one hand, ROS induce protein modifications that may lead to disruption of protein homeostasis and increased demands on protein degradation, on the other hand protein folding is one of the major sources of intracellular ROS (19, 25). ER and oxidative stress also overlap in the activation of NRF2; ROS directly inactivate KEAP1, which binds and sequesters NRF2 in the cytoplasm, while PERK-mediated phosphorylation of NRF2 inhibits KEAP1 binding (37). Inhibition of KEAP1 binding stabilizes NRF2 and allows its translocation to the nucleus, where it regulates genes involved in detoxification, redox homeostasis, and proteome maintenance. NRF2 thereby promotes cellular homeostasis in the face of oxidative and ER stress. In vitro, bortezomib increased ROS levels significantly in sensitive cells, but only minimally in resistant cells. We were unable to show a bortezomib-dependent increase in ROS in primary tumor cells because fresh cells were not prospectively analyzed for ROS and the freeze–thaw process in dimethyl sulfoxide (DMSO) interfered with the analysis. However, we detected increased NRF2 protein expression in tumor cells isolated directly from patients.

In cancer biology NRF2 has many at times even contradictory functions (39, 40). NRF2 can protect cells from the carcinogenic effects of ROS. Natural compounds that increase NRF2 are therefore being studied as cancer-preventing agents. On the other hand, high NRF2 expression is associated with more aggressive tumors, higher proliferation rate, and even resistance to chemotherapy. Here, we describe that high baseline activity of NRF2 in MCL cell lines as well as in primary tumors cell is associated with more aggressive tumors, higher proliferation rate, and even resistance to chemotherapy. In support of a protective role of NRF2 against bortezomib-induced cytotoxicity a genome wide RNAi screen in colon cancer identified knockdown of NRF2 as a synthetic lethal hit (41). NRF2 expression has also been linked with in vitro sensitivity to other...
NRF2 and Bortezomib Response in MCL

chemotherapeutic agents in solid-tumor cell lines (42, 43). Whether treatment resistance is due to the overall enhanced ability of cells to deal with toxic insults or one distinct NRF2 target gene is undefined. While NRF2 upregulates proteasome subunits (44), we have previously shown that proteasome capacity and the degree of inhibition of the chymotrypsin-like activity by bortezomib does not differ between sensitive and resistant cells (31). The basis for increased NRF2 activity in a subset of MCL is unclear but could reflect differences in cellular differentiation. We recently reported that partial plasma cell differentiation of MCL cells is associated with bortezomib resistance (45). Given that increased expression of genes involved in protein folding and redox homeostasis are critical elements of plasma cell differentiation (19, 25, 46), this could confer an increased ability to cope with oxidative stress and account for reduced sensitivity to bortezomib.

This study is limited to the analysis of patients with leukemic disease supported by analysis of cell-line models. Our findings thus await confirmation in nodal disease, and in a larger group of patients. Nevertheless, we have made several novel observations that direct further studies. The correlation of increased cellular antioxidant capacity with bortezomib resistance could yield predictive markers of treatment success and identifies avenues for synergistic treatment approaches. The relative contribution of NRF2 to bortezomib resistance, a possible proapoptotic role, and treatment success and identifies avenues for synergistic treatment approaches. The relative contribution of NRF2 to bortezomib resistance, a possible proapoptotic role, and the mechanism of its upregulation in a subset of MCL require further study.

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

Authors’ Contributions
M. A. Weniger, E. G. Rizzatti, P. Perez-Calán, and A. Wiestner designed the study, analyzed data, and wrote the article. Q. Wang and Y. Ye provided reagents, conducted molecular and cellular assays, and carried out data analysis. D. Liu and P. J. Munson evaluated gene expression data and carried out statistical analyses. N. Raghavachari carried out gene-expression profiling. W. H. Wilson initiated and supervised the clinical study. T. White, M. Twerdo, A. Wiestner, K. Dunleavy, and W. H. Wilson evaluated patients and collected clinical data. A. Wiestner coordinated and supervised laboratory studies.

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