Antitumor Activity of the Investigational Proteasome Inhibitor MLN9708 in Mouse Models of B-cell and Plasma Cell Malignancies

Edmund C. Lee¹, Michael Fitzgerald¹, Bret Bannerman¹, Jill Donelan¹, Kristen Bano¹, Jennifer Terkelsen¹, Daniel P. Bradley¹, Ozlem Subakan¹, Matthew D. Silva¹, Ray Liu¹, Michael Pickard¹, Zhi Li¹, Olga Tayber¹, Ping Li¹, Paul Hales¹, Mary Carsillo¹, Vishala T. Neppalli², Allison J. Berger¹, Erik Kupperman¹, Mark Manfredi¹, Joseph B. Bolen¹, Brian Van Ness³, and Siegfried Janz²

Abstract

Purpose: The clinical success of the first-in-class proteasome inhibitor bortezomib (VELCADE) has validated the proteasome as a therapeutic target for treating human cancers. MLN9708 is an investigational proteasome inhibitor that, compared with bortezomib, has improved pharmacokinetics, pharmacodynamics, and antitumor activity in preclinical studies. Here, we focused on evaluating the in vivo activity of MLN2238 (the biologically active form of MLN9708) in a variety of mouse models of hematologic malignancies, including tumor xenograft models derived from a human lymphoma cell line and primary human lymphoma tissue, and genetically engineered mouse (GEM) models of plasma cell malignancies (PCM).

Experimental Design: Both cell line–derived OCI-Ly10 and primary human lymphoma–derived PHTX22L xenograft models of diffuse large B-cell lymphoma were used to evaluate the pharmacodynamics and antitumor effects of MLN2238 and bortezomib. The iMycCa/Bcl-Xl GEM model was used to assess their effects on de novo PCM and overall survival. The newly developed DP54-Luc–disseminated model of iMycCa/Bcl-Xl was used to determine antitumor activity and effects on osteolytic bone disease.

Results: MLN2238 has an improved pharmacodynamic profile and antitumor activity compared with bortezomib in both OCI-Ly10 and PHTX22L models. Although both MLN2238 and bortezomib prolonged overall survival, reduced splenomegaly, and attenuated IgG2a levels in the iMycCa/Bcl-Xl GEM model, only MLN2238 alleviated osteolytic bone disease in the DP54-Luc model.

Conclusions: Our results clearly showed the antitumor activity of MLN2238 in a variety of mouse models of B-cell lymphoma and PCM, supporting its clinical development. MLN9708 is being evaluated in multiple phase I and I/II trials. Clin Cancer Res; 17(23); 7313–23. ©2011 AACR.

Introduction

The proteasome is a critical component of the ubiquitin–proteasome system, which is responsible for the regulation and degradation of the majority of intracellular proteins, including those involved in growth control, cell-cycle regulation, and apoptosis (1, 2). Inhibition of the proteasome leads to stabilization and accumulation of these proteasome substrates, resulting in concomitant activation of pro- and antiproliferative signals, disruption of cell-cycle regulation, and, ultimately, activation of apoptotic pathways and cell death (3, 4). As validated by the clinical success of the first-in-class small-molecule proteasome inhibitor bortezomib (VELCADE; Millennium Pharmaceuticals, Inc.), inhibition of the proteasome is an effective therapeutic approach for treating human cancer (5–7). Consequently, several small-molecule proteasome inhibitors, including the reversible inhibitor CEP-18770 and the irreversible inhibitors NPI-0052 and PR-171 (carfilzomib), are currently in different stages of clinical development for various oncology indications.

MLN9708 (Millennium Pharmaceuticals, Inc.) is an investigational small-molecule proteasome inhibitor currently being developed for a broad range of human malignancies (8, 9). MLN9708 is a citrate ester that immediately hydrolyzes to its biologically active form MLN2238 upon exposure to aqueous solutions or plasma in preclinical...
Translational Relevance

The success of bortezomib (VELCADE) for the treatment of multiple myeloma and relapsed mantle cell lymphoma validated the proteasome as an oncology target. Several small-molecule proteasome inhibitors, including CEP-18770, NPI-0052, and PR-171 (carfilzomib), are in different stages of clinical development for various oncology indications. Here, we evaluated the investigational proteasome inhibitor MLN9708 in a variety of mouse models of B-cell and plasma cell malignancies (PCM), including traditional tumor xenograft models and genetically engineered mouse models. We showed that its biologically active form MLN2238 has improved pharmacodynamics and antitumor activity compared with bortezomib in various B-cell lymphoma models and showed that only MLN2238 alleviated osteolytic bone disease in our PCM model. Our preclinical data served as the basis for the ongoing clinical development of MLN9708 in hematologic malignancies. MLN9708 is being evaluated in multiple phase I and I/II studies as monotherapy or in combination with other chemotherapeutic agents.

Figure 1. Chemical structure of MLN9708 and its biologically active form MLN2238. In preclinical studies, MLN9708 immediately hydrolyzes to its biologically active form MLN2238 upon exposure to aqueous solutions or plasma.

For decades, tumor xenograft models, which involve the subcutaneous inoculation of human tumor cell lines or tumor tissue fragments into immunocompromised mouse hosts, have been the mainstay of in vivo models for drug discovery in oncology. The robustness of these models allows for the rapid evaluation and prioritization of potential drug candidates into clinical trials. Although virtually all new cancer therapies developed in the modern era have gone through this paradigm, these tumor xenograft models do not fully depict the biology and heterogeneity of their human disease counterpart (10–14). In contrast, the de novo diseases found in most genetically engineered mouse (GEM) models of cancer often faithfully mimic the stepwise pathologic progression of human cancers: from the premalignant neoplastic stage that carries the initiating tumorigenic genetic mutations within their native tumor microenvironment to the fully transformed cancer stage that resembles the genetic heterogeneity of their human counterparts (15, 16). However, accurate depiction of the human disease often comes with significant logistical tradeoffs, necessitating prohibitively large study cohorts for establishing statistical significance (13). In addition, disease progression and tumor onset are often slow and lengthy in these GEM models (months to years), further impeding their broader use in most fast-paced drug discovery settings.

Here, we sought to take advantage of both the robustness of the tumor xenograft models and the fidelity of the GEM models. We focused on evaluating and directly comparing the in vivo activity of MLN2238 and bortezomib in a variety of mouse models of hematologic malignancies, including both tumor xenograft models derived from a human lymphoma cell line and primary human lymphoma tissue, to GEM models of plasma cell malignancies (PCM). The robustness of the tumor xenograft models allowed us to rapidly assess and relate the tumor pharmacodynamic profile of these molecules to their antitumor activities, whereas the fidelity of GEM models allowed us to preclinically assess their effects on tumor burden, osteolytic bone disease, and terminal outcome analogous to the human disease. We believe this comprehensive approach will lead to a more thorough understanding of the clinical potential of these molecules and, ultimately, better translational relevance to the clinic.

Materials and Methods

Animal care

Strain CB17-severe combined immunodeficient (SCID) and nonobese diabetic (NOD)-SCID mice were obtained from Charles River Laboratories. Strain C57BL/6j (B6) mice congenic for the TMyc\textsuperscript{CO} transgene (TG) were generated by backcrossing the TG from the mixed genetic background of...
the original gene-targeted strain (segregating B6 and 129/ Sv alleles) to B6 for more than 10 generations (17). This strain, designated B6.iMycC, was deposited to the JAX Strain Donation Program (The Jackson Laboratory) and further bred to TG homozygosity to facilitate the generation of double transgenic iMycC/Bcl-XL mice described later. Strain FVB/N mice heterozygous for the Bcl-XL TG were cryopreserved and expanded by the in vitro fertilization (IVF)-based JAX Speed Expansion Service (The Jackson Laboratory). A total of 90 age-matched double transgenic iMycC/Bcl-XL mice of the hybrid (B6 × FVB/N) F1 background were generated by intercrossing B6 mice homozygous for iMycC with FVB/N mice heterozygous for Bcl-XL. All mice were housed and maintained in a controlled environment and received food and water ad libitum. Mice reaching humane endpoints including severe weight loss (>15%), hind limb paralysis, splenomegaly, lymphadenopathy, or severe lethargy were euthanized. Veterinary care was provided in accordance with University of Iowa and Millenium Institutional Animal Care and Use Committees.

Compounds

For in vivo studies, bortezomib (dissolved in 0.9% saline) and MLN2238 [dissolved in 5% hydroxypropyl-β-cyclodextrin (HPβCD)] were dosed at their maximum tolerated dose (MTD) for the specified mouse strain and model, unless otherwise specified.

Tumor xenograft models of activated B-cell diffuse large B-cell lymphoma

For the OCI-Ly10 model, freshly dissociated OCI-Ly10 diffuse large B-cell lymphoma cells of the hybrid cell type (ABC-DLBCL; 4 × 10⁶ N) suspended in IMDM/Matrigel (50:50) medium were inoculated subcutaneously into the right flank of CB17-SCID mice as previously described (18). For the PHTX22L model, lymphoma tissue surgically isolated from a 71-year-old man with ABC-DLBCL was maintained via serial passage of the tumor fragment (~20 mg) between the right dorsal flanks of 8- to 11-week-old NOD-SCID mice. Tumor burden was monitored by IVIS bioluminescence imaging (BLI) as previously described (9).

Disseminated mouse model and IVIS bioluminescence imaging

Ex vivo computed tomography (CT) was done on formalin-fixed cadavers on an eXplore scanner (GE Healthcare), 2 mice per session in a 2-mouse gantry. Parameters for acquisition were the following: in-plane resolution 46 μm², 720 views, 2 frames per view, angle of increment 1 degree, exposure time 100 milliseconds, voltage 80 kV, and current 450 μA. All renderings were analyzed with Analyze 4.0 software. For analysis of the cranium, 3-dimensional renderings of the caudal aspect were cropped to include the sagittal bones, sagittal sutures, and parietal sutures, before being saved as 2-dimensional images. Cranial suture widening was measured in sagittal suture separation areas (SSSA) and calculated by displaying the area of displacement between the sutures in a single-voxel layer, before being converted to cubic millimeters by multiplying the voxel dimensions. Cranial bone erosion was assessed by bone surface roughness analysis as described previously (21).

Splenomegal and mouse immunoglobulin levels

Spleens harvested from iMycC/Bcl-XL mice reaching humane endpoints were weighed as a measurement for splenomegaly. Terminal blood samples were collected by cardiac puncture, and mouse immunoglobulin (lg) and cytokine levels were determined by Searchlight Protein Array Analysis (Aushon Biosystems).

Cell culture and cell viability assay

Parental DP54 cells were stably transfected with pDEST12.2-mIgK-Luc, which constitutively expresses the firefly luciferase gene (Luc) under the control of a mouse immunoglobulin kappa light-chain promoter/enhancer similar to that previously described (19). Transfection was done using Nucleofector Kit V (VCA1003; Lonza). One clone was selected by limited dilution in the presence of 0.8 mg/mL G418 and was designated DP54-Luc. DP54-Luc cells were maintained in RPMI-1640 media supplemented with 25 mmol/L HEPES, 15% FBS, 1 mmol/L sodium pyruvate, 2 mmol/L l-glutamine, 50 μmol/L β-mercaptoethanol, 0.5 ng/mL interleukin (IL)-6, 0.8 mg/mL G418, and 50 units/mL each of penicillin and streptomycin at 37°C with 5% CO₂.

Cell culture and cell viability studies

Cell viability was determined by Searchlight Protein Array Analysis and cell viability studies were done according to the manufacturer’s instructions (Perkin-Elmer Life Sciences) as previously described (20).

Statistical analyses

Sample size determination and power analysis were calculated with the STT3 function from nQuery Adviser (version 7; Statistical Solutions). Simulated survival data were generated from a pseudo-random number generator under piece-wise constant hazard assumption and compared with log-rank statistics. Power was defined as the percentage of simulations in which the statistic indicates a significant outcome. For efficacy studies, survival curves and median overall survivals were generated by the Kaplan–Meier method. Hazard Ratios (HRs), 95% confidence intervals (CI), and P values were calculated on the basis of a Cox proportional hazard model, with treatment and gender as covariants (22). An HR of less than 1 indicated an advantage.
Figure 2. Proteasome inhibition and antitumor activity of bortezomib and MLN2238 in tumor xenograft models of activated B-cell diffuse large B-cell lymphoma. A, proteasome inhibition in OCI-Ly10 tumors 1, 24, and 48 hours following acute intravenous administration of bortezomib (0.8 mg/kg) or MLN2238 (8 mg/kg) in OCI-Ly10 tumor-bearing SCID mice. Vertical lines represent SEM at each time point (n = 4). B, OCI-Ly10 tumor-bearing SCID mice (n = 10) were treated with vehicle (0.9% saline subcutaneously once daily) or bortezomib (0.8 mg/kg intravenously twice weekly) for 4 consecutive weeks (i). OCI-Ly10 tumor-bearing SCID mice (n = 10) were treated with vehicle (5% HPβCD intravenously twice weekly) or MLN2238 (8 mg/kg intravenously once weekly) for 4 consecutive weeks (ii). Bars represent SEM at each time point. C, proteasome inhibition in PHTX22L tumors 1 hour following acute...
of drug treatment over untreated controls. Efficacy data were analyzed by a linear mixed-effects regression model as previously described (9). Statistical significance for the differences in mouse immunoglobulin G2a (IgG2a) levels, spleen weights, and SSSAs among treatment groups were determined by one-way ANOVA and Dunnett adjustment to account for multiple comparisons. A value of $P < 0.05$ was considered significant.

Results

**MLN2238 shows antitumor activity in OCI-Ly10 subcutaneous ABC-DLBCL xenograft model**

We first evaluated and compared the *in vivo* activity of MLN2238 and bortezomib in the OCI-Ly10 subcutaneous xenograft model derived from a human cell line of ABC-DLBCL. OCI-Ly10 tumor–bearing SCID mice were administered a single intravenous dose of bortezomib at its twice-weekly MTD of 0.8 mg/kg or MLN2238 at 8 mg/kg, which is below its twice-weekly MTD of 14 mg/kg in SCID mice. Tumor pharmacodynamic responses were assessed by measuring the inhibition of β5 activity of the 20S proteasome after treatment. As shown in Fig. 2A, a single dose of bortezomib at MTD transiently inhibited the specific β5 activity of OCI-Ly10 tumor for less than 24 hours whereas a single dose of MLN2238 maintained proteasome inhibition for up to 48 hours even at the sub-MTD, consistent with the improved biodistribution of MLN2238 versus bortezomib in xenograft tumors. To assess whether the sustained proteasome inhibition seen with MLN2238 would translate into improved antitumor activity, efficacy studies were done in the OCI-Ly10 model. When dosed at MTD on a twice-weekly schedule, bortezomib showed moderate antitumor activity in the OCI-Ly10 model [treated vs. control (T/C) = 0.68, $P < 0.01$; Fig. 2B (i)]. In contrast, even when dosed at sub-MTD on a once-weekly schedule, MLN2238 showed greater antitumor activity [T/C = 0.37, $P < 0.01$; Fig. 2B (ii)].

**MLN2238 shows antitumor activity in PHTX22L primary human ABC-DLBCL xenograft model**

We then evaluated and compared the *in vivo* activity of MLN2238 and bortezomib in the PHTX22L primary human tumor xenograft model derived from lymphoma tissue surgically isolated from a 71-year-old man with ABC-DLBCL (18). Unlike traditional cell line–derived tumor xenograft models that often have deranged tumor architectures, primary human tumor xenograft models have been shown to retain the tissue-specific histology seen in their clinical counterparts and maintain the dynamic interactions between the transformed cancer cells and their native tumor microenvironment (23). This provides for a useful preclinical model to evaluate MLN2238 and bortezomib, in addition to our traditional repertoire of cell line–derived tumor xenograft models.

PHTX22L tumor–bearing NOD-SCID mice were administered a single intravenous dose of bortezomib at the MTD of 0.8 mg/kg or MLN2238 at the MTD of 14 mg/kg or sub-MTDs of 7 and 3.5 mg/kg. As shown in Fig. 2C, MLN2238 at all doses tested showed greater proteasome inhibition in PHTX22L tumors than bortezomib dosed at MTD. To test whether the greater proteasome inhibition seen with MLN2238 would translate into improved antitumor activity, efficacy studies were done in the PHTX22L model. As shown in Fig. 2D (i), bortezomib dosed at the MTD did not show antitumor activity in the PHTX22L model [T/C = 0.88, $P = 0.86$]. In contrast, MLN2238 showed potent antitumor activity at the MTD [T/C = 0.14, $P < 0.01$; Fig. 2D (ii)]. Importantly, MLN2238 also showed strong antitumor activity in the PHTX22L model even when dosed at sub-MTD levels of 5, 7, and 11 mg/kg on various dosing schedules [T/C ranges from 0.04 to 0.16, $P < 0.001$ for all; Fig. 2D (ii)].

**MLN2238 shows antitumor activity in the iMyc<sup>Ca</sup>/Bcl-X<sub>L</sub> GEM model of de novo PCM**

We have previously shown that intercrossing B6 mice carrying the iMyc<sup>Ca</sup>/Bcl-X<sub>L</sub> GEM model to evaluate MLN2238 and bortezomib, in addition to our traditional repertoire of cell line–derived tumor xenograft models.

Using the survival data from our earlier study (17), we simulated the hypothetical effects of different drug treatments in prolonging overall survival of iMyc<sup>Ca</sup>/Bcl-X<sub>L</sub> xenograft-bearing NOD-SCID mice. Vertical lines represent SEM of each treatment group ($n = 4$), D, PHTX22L tumor–bearing NOD-SCID mice ($n = 10$) were treated with vehicle (5% HP)/CD intravenously twice weekly), bortezomib (0.8 mg/kg intravenously twice weekly), or MLN2238 (14 mg/kg intravenously twice weekly) for 3 consecutive weeks (i), PHTX22L tumor–bearing NOD-SCID mice ($n = 10$) were treated with vehicle (5% HP)/CD intravenously twice weekly), MLN2238 (11 mg/kg intravenously once daily for 2 days followed by 5 treatment-free days) for 3 consecutive weeks (ii). Bars represent SEM at each time point. BIW, twice weekly; i.v., intravenously; QW, once weekly; QD, once daily; QDx2 once daily for 2 days.
mice in vitro. As shown in Supplementary Table S1, our power analysis showed that a sample size of 29 mice per treatment group was required to establish a statistical power of 0.80 (α = 0.05) for detecting an increase of 27 days in median overall survival. Accordingly, a total of 90 age-matched double transgenic iMyc\(^{C}_{\text{t}}\)/Bcl-X\(_L\) mice were generated and randomized to 3 treatment groups, each consisting of 30 mice. Nine-week-old iMyc\(^{C}_{\text{t}}\)/Bcl-X\(_L\) mice with established disease were left untreated or treated with bortezomib or MLN2238 at their respective MTDs for 6 consecutive weeks (n = 30 per group). B, mean spleen weights from iMyc\(^{C}_{\text{t}}\)/Bcl-X\(_L\) mice reaching humane endpoints in bortezomib-treated (n = 21) and MLN2238-treated (n = 18) arms were compared with those from untreated controls (n = 29). Vertical lines represent SEM of each treatment group. *, P < 0.05, bortezomib- or MLN2238-treated iMyc\(^{C}_{\text{t}}\)/Bcl-X\(_L\) mice versus untreated iMyc\(^{C}_{\text{t}}\)/Bcl-X\(_L\) mice. †, P < 0.05, untreated iMyc\(^{C}_{\text{t}}\)/Bcl-X\(_L\) versus 126-day-old nontransgenic (B6 × FVB/N) F1 mice (n = 9). Vertical lines represent SEM of each treatment group. ‡, P < 0.05, bortezomib- or MLN2238-treated iMyc\(^{C}_{\text{t}}\)/Bcl-X\(_L\) mice reaching humane endpoints in bortezomib-treated (n = 18) and MLN2238-treated (n = 13) arms were compared with those from untreated controls (n = 17) and 126-day-old nontransgenic (B6 × FVB/N) F1, mice. BIW, twice weekly; i.v., intravenously.

In accordance with previous reports (17, 25), de novo PCM in iMyc\(^{C}_{\text{t}}\)/Bcl-X\(_L\) mice led to the elevation in serum levels of various immunoglobulins and cytokines (Supplementary Table S2). Although comparing the average immunoglobulin and cytokine levels from mice reaching humane endpoints across different treatment groups has limitations, we showed that both bortezomib and MLN2238 treatment attenuated the IgG2a level of iMyc\(^{C}_{\text{t}}\)/Bcl-X\(_L\) mice, underscoring the in vivo activity of these proteasome inhibitors in this GEM model of de novo
Osteolytic bone disease in the iMyc<sup>CM</sup>/Bcl-X<sub>L</sub> GEM model of de novo PCM

In an earlier study, we reported that iMyc<sup>CM</sup>/Bcl-X<sub>L</sub> PCM can lead to bone lesions including focal osteolysis and putative pathologic fractures (17). Here, ex vivo CT imaging similarly revealed signs of osteolytic bone disease in multiple regions of our iMyc<sup>CM</sup>/Bcl-X<sub>L</sub> mice including the pelvic bone and tibiofibular complex (Fig. 4A [iv and v]). Targeted histopathologic examination of these putative bone lesions revealed extensive infiltration of the hematopoietic bone marrow with malignant CD138<sup>+</sup> plasma cells (Fig. 4B [i]). Interestingly, in-depth CT analysis of the skull revealed a previously unnoticed widening of the cranial sutures, where pronounced separations and erosions of the coronal, sagittal, and lambdoidal sutures were observed (Fig. 4A [vi]). As shown in Fig. 4B (ii), plasma tumor cell–induced osteolysis resulted in widening of the cranial sutures, extension of neoplastic cells through the calvarial bone, and infiltration of the overlying periosteum. Bone surface roughness analysis revealed that these osteolytic bone diseases often extended beyond the cranial sutures (Fig. 4C [ii]), suggesting that mouse cranial sutures may represent the locus minoris resistentiae for confining plasma cell tumor cells to the bone marrow compartment and preventing the establishment of extramedullary disease in double transgenic iMyc<sup>CM</sup>/Bcl-X<sub>L</sub> mice.

MLN2238 shows antitumor activity in the DP54-Luc–disseminated model of PCM

To seek an alternative, less time- and resource-intensive version of the iMyc<sup>CM</sup>/Bcl-X<sub>L</sub> PCM model to evaluate bortezomib and MLN2238, we developed a disseminated mouse model of PCM that recapitulates key features of the de novo disease in iMyc<sup>CM</sup>/Bcl-X<sub>L</sub> mice. DP54 is a mouse plasma cell tumor line derived from the bone marrow of a syngeneic F<sub>1</sub> (B6 × FVB/N) mouse previously inoculated with an iMyc<sup>CM</sup>/Bcl-X<sub>L</sub> tumor (24). In vitro, DP54 cells express the iMyc<sup>CM</sup> and Bcl-X<sub>L</sub> TG, various late B-cell, and early plasma cell markers including CD38, CD138, and B220, and have a gene expression profile very similar to human multiple myeloma (24). ATPLite in vitro cell viability studies showed that DP54 cells were sensitive to bortezomib and MLN2238 treatment and yielded the median lethal dose (LD<sub>50</sub>) values of 4.6 and 24.6 nmol/L, respectively, which were comparable with those observed in a variety of human cancer cells (range, 4–58 nmol/L; Supplementary Table S3).

To characterize iMyc<sup>CM</sup>/Bcl-X<sub>L</sub> tumor cells in vivo, DP54-Luc cells (which constitutively express firefly luciferase) were generated from DP54 cells and inoculated intravenously via the lateral tail vein of NOD-SCID mice. Disease progression and dissemination of DP54-Luc cells were monitored by in vitro BLI (Fig. 5A). NOD-SCID mice inoculated with DP54-Luc rapidly succumbed to PCM 25 days after inoculation, with luminescent tumor nodules PCMs after only 6 weeks of treatment (P < 0.05 for both; Fig. 3C).

Preclinical Activity of MLN9708 in Hematologic Malignancies

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Clin Cancer Res; 17(23) December 1, 2011

7319
identified by ex vivo BLI in multiple organ compartments including lymph nodes, spleen, skull, and hind limbs (Fig. 5B). Similar to the de novo PCM in iMyc<sup>Ca</sup>/Bcl-<em>X</em><sub>L</sub> mice, splenomegaly was prevalent in DP54-Luc–inoculated NOD-SCID mice. Importantly, ex vivo CT imaging [Fig. 5C (i)] and subsequent bone surface roughness analysis (Fig. 5D) revealed widening and erosion of cranial sutures similar to those observed in de novo PCM in iMyc<sup>Ca</sup>/Bcl-<em>X</em><sub>L</sub> mice [Fig. 4A (vi) and C (ii)]. Interestingly, strong ex vivo bioluminescent signals were detected from the metopic, coronal, lambdoid, and sagittal sutures [Fig. 5C (ii)], the same locations where osteolytic bone lesions were observed [Fig. 5C (i) and D], which implied a direct effect of DP54-Luc cells infiltrating the cranium. These results showed that intravenous inoculation of DP54-Luc cells resulted in a pathologic phenotype that recapitulated key features of de novo PCM in double transgenic iMyc<sup>Ca</sup>/Bcl-<em>X</em><sub>L</sub> mice.

We then evaluated and compared the in vivo activity of MLN2238 and bortezomib in this disseminated model of PCM. DP54-Luc tumor–bearing NOD-SCID mice were treated with vehicle (5% HPBCD intravenously twice weekly), bortezomib (0.7 mg/kg intravenously twice weekly), or MLN2238 (11 mg/kg intravenously twice weekly) for 17 consecutive days. Tumor burden was measured by in vivo BLI [Fig. 6A (ii–iv)] and osteolytic bone disease as characterized by cranial suture widening was measured in SSSA [Fig. 6B (ii–iv)]. Both bortezomib and MLN2238 reduced tumor burden [T/C = 0.48 and 0.22, respectively; <i>P</i> < 0.01 for both; Fig. 6A (i)], whereas...
only MLN2238 alleviated osteolytic bone disease by the end of the study [average SSSA = 0.85 vs. 1.16 mm² in vehicle controls; P < 0.05; Fig. 6B (i)]. This suggested that MLN2238 may have the potential to confer additional advantages over those seen with bortezomib in PCM including multiple myeloma. Together, our data showed the improved antitumor activity of MLN2238 compared with bortezomib in a variety of mouse models of B-cell lymphoma and PCM.

Discussion

**Antitumor activity of MLN2238 across multiple DLBCL subtypes**

DLBCL is a non–Hodgkin lymphoma that has been classified into multiple subtypes on the basis of distinct gene expression profiles (26). The GCB subtype likely originates from germinal center B cells, whereas the more aggressive ABC subtype likely arises from postgerminal center activated B cells that are blocked from undergoing plasmacytic differentiation. A recent multicenter study with relapsed/refractory DLBCL patients (n = 49) suggested that bortezomib in combination with doxorubicin-based chemotherapy may preferentially improve the clinical outcome of patients with the ABC subtype (27). Here, we showed the improved pharmacodynamics and antitumor activity of MLN2238 compared with bortezomib in 2 mouse models of ABC-DLBCL: the OCI-Ly10 and PHTX22L models. In addition, we have recently shown that MLN2238 has improved antitumor activity in the OCI-Ly7 model of the GCB subtype (GCB-DLBCL) and the WSU-DLCL-2 model that was distinct from either the ABC or GCB subtypes (non-ABC/non-GCB-DLBCL; ref. 9). Together, our results suggest that MLN2238 has the potential to show broad activity across multiple DLBCL subtypes, extending beyond those seen with bortezomib.

**Manifestation of osteolytic bone disease in the cranium**

We describe for the first time the design and implementation of a preclinical study using the iMyc<sub>C<sub>o</sub></sub>/Bcl-X<sub>L</sub> GEM model of de novo PCM. By combining conventional breeding strategies with existing IVF-based colony expansion technologies, we generated a total of 90 age-matched double transgenic iMyc<sub>C<sub>o</sub></sub>/Bcl-X<sub>L</sub> mice for an efficacy study of MLN2238 and bortezomib. Like most GEM models, our original characterization of iMyc<sup>C<sub>o</sub>/Bcl-X<sub>L</sub> mice was based on a small cohort with mixed genetic background (segregating B6 and 129/SvJ alleles; ref. 17). The unprecedentedly large number of mice we have herein generated not only afforded us the ability to confirm and validate our original findings with respect to tumor penetrance, latency, and origin of the Myc- and Bcl-X<sub>L</sub>-driven de novo malignancy but also allowed us to validate the occurrence of osteolytic bone disease and, most importantly, discover the manifestation of cranial osteolytic lesions that were previously unnoticed. It will be of great importance for future studies to determine whether these cranial suture separations and erosions are idiosyncrasies particular to the myeloma-like bone disease in iMyc<sub>C<sub>o</sub>/Bcl-X<sub>L</sub> mice, or pathologies common to metastatic bone diseases in other GEM models of human cancer. Nevertheless, our experience highlighted...
another important practical lesson for implementing GEM models: new tumor phenotypes may emerge and may even be susceptible to changes as mouse lines are crossed and backcrossed into different common nonsegregating backgrounds (28–31), thus requiring in-depth validation before use in preclinical studies (13).

**Future use of the iMyc<sup>Co</sup>/Bcl-X<sub>L</sub> model**

This is the first study to show the preclinical utility and translational relevance of the iMyc<sup>Co</sup>/Bcl-X<sub>L</sub> GEM model of PCM. We showed that MLN2238 prolonged overall survival, reduced splenomegaly, and attenuated IgG2a levels of iMyc<sup>Co</sup>/Bcl-X<sub>L</sub> mice after only 6 weeks of treatment. Nevertheless, comparing the average immunoglobulin and cytokine levels from mice reaching humane endpoints across different treatment groups has its limitations. Linden and colleagues showed that similar to human multiple myeloma where elevation of serum immunoglobulin often precedes the manifestation of malignant diseases, the single Bcl-X<sub>L</sub> TG alone can lead to immunoglobulin elevations in the absence of PCM (25). Given the stochastic nature of tumor development and heterogeneity of immunoglobulin elevations in the iMyc<sup>Co</sup>/Bcl-X<sub>L</sub> model (Supplementary Table S2), it is not surprising that the current cross-sectional manner of comparing the average immunoglobulin levels across different treatment groups at the end of the study did not, with the exception of IgG2a, capture changes that are inherently idiosyncratic. Future studies that longitudinally follow the serum immunoglobulin and cytokine levels of individual iMyc<sup>Co</sup>/Bcl-X<sub>L</sub> mice over the clinical course of PCM (both pre- and post–drug treatment) will help provide a better understanding of drug-related changes in immunoglobulin and cytokine levels. In addition, the relationship between the observed increases in IL-6, IL-1b, and macrophage inflammatory protein (MIP-1α) levels and the induction of osteolytic bone disease in iMyc<sup>Co</sup>/Bcl-X<sub>L</sub> mice compared with nontransgenic controls is also the subject of ongoing investigations (S. Janz, personal communication).

Although our study using the iMyc<sup>Co</sup>/Bcl-X<sub>L</sub> model of de novo PCM yielded important terminal outcome data, this approach can nevertheless be prohibitively time consuming and logistically challenging, especially for screening potential therapeutics in today’s fast-paced drug discovery settings. We have thus developed the DP54-Luc–disseminated model of PCM, which is less time- and resource-intensive than the iMyc<sup>Co</sup>/Bcl-X<sub>L</sub> PCM model but yet still mimics key features of the de novo mouse disease. Our data showed that both MLN2238 and bortezomib have potent antitumor activity whereas only MLN2238 alleviated osteolytic bone disease as indicated by reduced widening of cranial sutures. Encouraged by these results and acknowledging that a single plasma cell tumor line (e.g., DP54-Luc) would not sufficiently recapitulate the genetic heterogeneity among a diverse PCM population, we have generated more than 20 additional plasma cell tumor lines from the large number of primary iMyc<sup>Co</sup>/Bcl-X<sub>L</sub> tumors harvested in the current study. Our preliminary data have shown that these newly derived plasma cell tumor lines exhibit diversity in their sensitivities (all in the nanomolar range) toward bortezomib in vitro (B. Van Ness, personal communication). In addition, we have also isolated several bortezomib-resistant plasma cell tumor lines through in vitro dose escalation. These plasma cell tumor lines, when fully characterized, will be used to identify the specific genetic aberrations responsible for bortezomib resistance and may provide invaluable in vitro and in vivo tools for future drug screening and pharmacogenetic investigations. In particular, the activity of MLN9708 in these different plasma cell tumor lines is currently being investigated.

**MLN9708 in hematologic malignancies**

In summary, we showed the antitumor activity of MLN2238 in a variety of mouse models of B-cell lymphoma and PCM, including tumor xenograft models derived from both a human cell line and primary human tumor tissue, and GEM models that recapitulated key features of the human diseases. Our data provide comprehensive evidence to support the clinical development of MLN9708 in hematologic malignancies including lymphoma and multiple myeloma. MLN9708 is currently being evaluated in multiple phase 1 and 1/II clinical studies, whereas the irreversible proteasome inhibitors NPI-0052 and PR-171 are at their different stages of clinical development. It will be of great interest to see how these compounds, with their different proteasome dissociation kinetics, may ultimately differentiate themselves in the clinic.

**Disclosure of Potential Conflicts of Interest**

All authors except E.C. Lee, V.T. Neppalli, B. Van Ness, and S. Janz are current employees of Millennium Pharmaceuticals, Inc. E.C. Lee is a former employee of Millennium Pharmaceuticals, Inc. B. Van Ness is a consultant/advisory board member of International Myeloma Foundation.

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References

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