The HDAC Inhibitor LBH589 Enhances the Antimyeloma Effects of the IGF-1RTK Inhibitor Picropodophyllin

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Abstract

Purpose: We have previously shown the use of the insulin-like growth factor type 1 receptor tyrosine kinase (IGF-1RTK) inhibitor picropodophyllin (PPP) as an attractive strategy to combat multiple myeloma (MM) in vitro and in vivo. After a combinatorial drug screening, the histone deacetylase inhibitor LBH589 was shown to act in synergy with PPP reducing survival of MM cells. In this study, we tried to elucidate the molecular mechanisms underlying this combinatorial effect.

Experimental Design: The in vitro anti-MM effects of PPP and LBH589 alone and in combination were evaluated by studying apoptosis, cell cycle distribution, and downstream transcriptome using both human MM cell lines and cells from the murine 5T3MM model. In vivo the effect on survival of 5T33MM-inoculated mice was evaluated.

Results: In the human MM cell line RPMI8226, treatment with PPP and LBH589 in combination resulted in a five-fold increase of apoptosis, and an additive effect on the cleavage of the active forms of caspase-8 was observed as compared with the single drug treatments. Cell cycle analysis revealed an accumulation of cells in the G2-M phase and subsequent downregulation of cell cycle regulating proteins. These data were also confirmed in the 5T33MM cells in vitro. Also, the transcriptome was analyzed by Affymetrix arrays showing gene expression alterations mainly in categories of genes regulating apoptosis and cell adhesion. Combined treatment in vivo resulted in a significantly prolonged survival of 5T33MM-inoculated mice.

Conclusions: The results indicate an improved MM treatment opportunity in using a combination of PPP and LBH589. Clin Cancer Res; 18(8); 2230–9. ©2012 AACR.

Introduction

Multiple myeloma (MM) is characterized by the accumulation of monoclonal plasma cells in the bone marrow (BM), overproduction of monoclonal immunoglobulins, and bone lesions (1, 2). MM is the second most prevalent hematologic cancer that despite emerging novel therapies remains fatal. Importantly, there is a large interclonal variation between MM patients with only a few identified common chromosomal translocations to the immunoglobulin H locus (3, 4) and anomalous gene expression reflecting activated extrinsic or intrinsic signaling pathways (5). However, these genetic abnormalities have only in a few cases been proven useful as prognostic markers or therapeutic targets (4, 6). Rather, the tumor microenvironment, that is, the tumor–host interactions and soluble growth factors expressed and produced by BM stromal cells (7) are essential for MM tumor development and now constitute the focus for the development of emerging MM therapies (8). The bidirectional interactions between the MM and the BM stromal cells contribute to the survival and proliferation of the malignant cells via the activation of signaling pathways including the Ras/Raf/mitogen-activated protein kinase, the Janus-activated kinase/STAT3 and the phosphoinositide 3-kinase/Akt cascade (9).

Many MM growth factors have been identified, among which the insulin-like growth factor type 1 (IGF-1) is considered to play a major role in the tumor growth (10), supporting the survival and proliferation of both interleukin-6-dependent (11) and interleukin-6-independent MM cells (12). Besides the antiapoptotic and the
Translational Relevance

Multiple myeloma (MM) remains an incurable cancer. PPP is an insulin-like growth factor type 1 receptor tyrosine kinase (IGF-1RTK) inhibitor with promising anti-MM effects. Here, we describe the ability of histone deacetylase (HDAC) inhibitor LBH589 to potentiate the effects of PPP in human MM cell lines and murine cells from the 5T33MM model. Our results show that combinatorial treatment synergistically decreases cell survival compared with single treatment. We saw increased cell death and stronger cleavage of caspase-8 after combinatorial treatment. Cell cycle analysis revealed G2–M arrest and subsequent downregulation of cyclin B1, cyclin E, and cyclin D2. Using Affymetrix array, we observed an alteration on genes regulating apoptosis and cell adhesion. Finally, with the 5T33MM model, we saw a significantly increased survival of myeloma-inoculated mice compared with control groups. These results provide a better understanding of the molecular mechanisms underlying the anti-MM effects of PPP and LBH589 and support the rationale for the clinical evaluation of the combination in MM therapy.

Proliferative effects, IGF-1 also contributes to VEGF secretion which stimulates the angiogenic process and contributes to the homing of MM cells (13) as well as their resistance to cytotoxic treatment (14–16). All these features make IGF-1 an attractive target for therapeutic intervention in MM. Moreover, the fact that IGF-1 receptor (IGF-1R) signaling is not an absolute requirement for maintenance of normal adult cell homeostasis has encouraged the development of IGF-1R inhibitors for clinical use in MM (17, 18).

PPP, a member of the cyclolignan family, has been shown to be a potent inhibitor of the IGF-1R tyrosine kinase (IGF-1RTK) activity (19). We have previously shown strong antitumor effects of the IGF-1RTK inhibitor PPP in vitro and in vivo using the 5T33MM and 5T2MM murine models, as well as in a panel of human MM cell lines (16, 20). PPP inhibited the in vitro proliferation of MM cells and reduced the secretion of VEGF. Furthermore, PPP dramatically reduced tumor burden, angiogenesis, and bone disease in vivo and significantly increased the survival rate of 5T2MM diseased mice when used in a therapeutic setting (20, 21). However, no selective drug is likely to be sufficient for single use in a therapeutic setting. PPP constitutes no exception to this notion and despite these encouraging data, the PPP-treated mice eventually relapsed and showed signs of morbidity.

To overcome drug resistance and relapse in vivo, we studied the possibility of treating MM with PPP in drug combination. By an integrated SAIGAN Core System for high-throughput screening, a broad spectrum of substances was analyzed for synergistic effects with PPP. From this high-throughput screening, histone deacetylase (HDAC) inhibitors (HDACi) were shown to act in synergy with PPP and were therefore selected for further studies. HDACis represent a class of agents with antitumor activity against several hematologic and solid cancers as they may act to reactivate tumor suppressor genes, inhibit cell cycle progression and induce apoptosis (22).

LBH589, the cinnamic acid hydroxamate, is an HDACi acting at nanomolar concentrations and inhibiting MM growth with promising results. LBH589 has previously been shown to induce apoptosis, enhance drug cytotoxicity (23, 24), and induce cell cycle arrest of MM cells (25). Using primary MM cells from patients and 2 MM cell lines, we previously showed (26) that LBH589 may reactivate gene expression silenced by histone modifications as marked by the Polycomb repressive complex (PcG) in MM. The PcG has previously been found important for preserving self-renewal capacity in embryonic stem cells. Indeed, gene reactivation by LBH589 of selected genes was confirmed in the 5T33MM murine model. In parallel, LBH589 treatment resulted in a reduction of tumor load in vivo and increased overall survival in treated mice.

In this study, we show that the combinatorial use of PPP and LBH589 more efficiently inhibits cell proliferation by downregulating the cell cycle proteins, cyclin-dependent kinase (cdk6 and cyclin D2, in the 5T33MM cells, and cyclin E, cyclin B1, and cyclin D2 in RPMI8226 cells). Moreover, treatment with both drugs also downregulates the antiapoptotic proteins Mcl-1 and Bcl-2 and enhances the apoptotic effect in RPMI8226 cells.

The antitumor effects of PPP in combination with LBH589 in vivo were studied using the 5T33MM murine model, in a fully syngeneic BM microenvironment and showed a significant increase in overall survival as compared with the single-drug treatments.

Materials and Methods

Animals

C57BL/KaRij/Hsd mice, purchased from Harlan CPB (Horst) were used at 6 to 10 weeks of age. Animals had free access to food and water and were housed and treated following the conditions approved by the Ethical Committee for Animal Experiments, VIJB. (license no. LA1230281).

Cells

The 5T33MM cells originated spontaneously in elderly C57BL/KaRij mice and have since been propagated in vivo, by intravenous transfer of the diseased marrow in young syngeneic mice. This model closely represents the human disease with respect to clinical (i.e., selective localization in the BM, serum M component, and angiogenesis) and molecular (i.e., adhesion and chemokine profile) characteristics (27–29). When showing clear signs of morbidity, mice were sacrificed and isolation of the MM cells was carried out as previously described (30, 31). MM cells obtained from the diseased mice were 95% pure. These cells only survive for a short period in vitro.
The human MM cell lines RPMI8226 (32), Karpass707 (33), LP-1 (34), and OPM-2 (35) were maintained in RPMI1640 (Flow, Irvine, and United Kingdom) supplemented with 10% FBS (Sigma), glutamine (2 mmol/L), and antibiotics (penicillin 100 U/mL and streptomycin 50 µg/mL) at 37°C in a humidified 5% CO2 in-air atmosphere.

Reagents
For the in vitro experiments, LBH589 (Panobinostat; Novartis Pharmaceuticals Inc.) and PPP (19) were dissolved in dimethyl sulfoxide or in ethanol (final concentration <0.01%), and aliquots were stored at −20°C (LBH589) and 4°C or −20°C (PPP). For the in vivo experiments, LBH589 was dissolved in a saline solution and PPP was mixed into the food.

Screening of drugs in combination with PPP
RPMI8226 and Karpass707 cells were seeded in drug-prepared 384 well plates at a density of 10,000 cells per well. The fluorometric microculture cytotoxicity assay was used for measurement of the cytotoxic effect and is based on hydrolysis of fluorescein diacetate. An integrated SAIGAN Core System containing Orca robot, CO2 incubator, dispenser, washer, delidding station, plate hotels, barcode reader, liquid handler (Biomek 2000), and a multipurpose reader (Fluosstar Optima) enabled high-throughput readout of cell survival after drug treatment. The combinatorial study was designed as suggested in the CalcuSun manual (BioSoft). Nine concentrations were tested, and all combinations were investigated both with simultaneous and sequential addition of the drugs. The data were analyzed with the median-effect method of Chou and Talalay (36) using the Calcusyn software version 2 (BioSoft). The substances used in combination with PPP were etopside, mTOR inhibitor rapamycin, 5-fluouracil (5-FU), vincristine, the histone deacetylase inhibitor suberoylanilide hydroxamic acid (SAHA), dexamethasone, bortezomib (velcade/PS-341), 17-AAG/geldanamycin, As203, and the p38 inhibitor SB203580.

Viability assays
Purified ST33MM cells were cultured during 24 hours in RPMI1640 medium with 10% serum as described above using different concentrations of LBH589 and/or PPP. Viability was measured with CellTiter-Glo Luminescent Viability Assay (Promega) according to manufacturer's instructions, determining the number of viable cells in culture based on quantitation of ATP.

To assess the viability of the human MM cell lines, we conducted Resazurin assay using AlamarBlue (Sigma) quantifying cell proliferation and cytotoxicity in relation to the presence of metabolically active cells (37). RPMI8226, Karpass707, LP-1, and OPM-2 were incubated in round-bottomed (RPMI8226, LP-1, and OPM-2) or flat-bottomed (Karpass707) 96-well plates with different concentrations of LBH589, PPP, or in combination of both. After the indicated times, 10% AlamarBlue was added to the wells, followed by incubation for 1 to 3 hours at 37°C in a humidified 5% CO2 in-air atmosphere. Wallac Victor Multilabel Counter (Wallac) was used for analysis of the fluorescence. Mean was calculated from triplicate wells and subtracted from mean of blank wells resulting in Δfluorescence. The relative number of viable cells was expressed as percentage of untreated cells and calculated as 100 × Δfluorescence (treated cells)/Δfluorescence (untreated cells).

Analysis of cell cycle phase distribution and apoptosis
RPMI8226 cells were cultured in 6-well plates for 24 hours in the presence of reagents, LBH589, PPP, or in a combination of both. Analysis of cell cycle distribution was conducted according to Vindelöf (38), in which propidium iodide (PI)-stained nuclei were analyzed by flow cytometry (FACScan; Becton Dickinson), and modfit LT 3.1 Analysis Software (Verity Software House) was used to calculate the distribution of the cell cycle phases. Briefly, approximately 106 cells were washed in cold PBS, lysed in NP-40 buffer and treated with trypsin (0.03 mg/mL) for 10 minutes at room temperature. Trypsin inhibitor (0.5 mg/mL) and ribonuclease A (0.1 mg/mL) were added followed by 10 minutes incubation in room temperature. Finally, the cells were exposed to PI (0.42 mg/mL) for 15 minutes at 4°C. The stained nuclei were analyzed as previously described.

Apoptosis was quantified by staining with Annexin V (AV)–fluorescein isothiocyanate (FITC) and PI using TACSTM Annexin V–FITC Apoptosis Kit (R&D Systems). The samples were treated as instructed by manufacturer followed by analysis using flow cytometry (FACScan) showing apoptotic cells as AV–positive/PI-negative cells and the necrotic cells as AV–positive/PI-positive cells.

Western blot analysis
RPMI8226 and ST33MM cells were incubated with different concentrations LBH589 and/or PPP. After different time points, cell pellets were harvested, lysed, and protein extracts were blotted as previously described (26, 39). Primary antibodies were used against CDK2, CDK4, cyclin D2, cyclin D1, Bcl-xL, Bcl-2, actin, cyclin E, IGF1-R, Mcl-1, CDK1, CDK6 (Santa Cruz Biotechnology); actin, caspase-3, caspase-8, and caspase-9 (Cell Signaling Technology); and survivin (R&D Systems). Immunodetection of actin was used as loading control.

Gene array
RPMI8226 cells were cultured in 6-well plates for 6 and 24 hours in the presence of LBH589, PPP, or in combination of both. Total RNA was extracted with TRIzol (Invitrogen) according to the manufacturer’s protocol. Expression study was conducted using whole Human Genome U133 Plus 2.0 Affymetrix oligo arrays (Affymetrix).

Survival experiment
Preliminary experiments showed that the suboptimal in vivo dose of PPP is 1.5 mg a day while that of LBH589 is 2.5 mg/kg/day (data not shown). At day 0, C57BL/KalwRij mice were inoculated with 5 × 107 ST33MM
cells purified as described above. Mice were assigned to different treatment groups receiving 1.5 mg PPP/5 g food per day per mouse \((n = 8)\), 2.5 mg/kg LBH589 \((n = 8; \text{ daily i.p. injection})\), or a combination of both \((n = 8)\). The vehicle group \((n = 8)\) received normal food and a 0.9% NaCl solution \(\text{(daily i.p. injection)}\). As control, an untreated disease-free group \((n = 8)\) was used. Each mouse was sacrificed when showing signs of morbidity (paralysis of the hind legs).

**Statistical analysis**

For the *in vitro* data, the Student t test or the 2-way ANOVA and for the *in vivo* survival analysis, the Kaplan–Meier analysis method was used. A \(P < 0.05\) was considered significant. For microarray analysis, 2-way ANOVA was used to find the differentially regulated genes and to do the Hierarchical clustering using software GeneSpring GX v11 (Agilent Technologies). We used the Chou and Talalay method (36) to calculate combination index (CI). CI > 1, = 1, or < 1 indicates antagonism, additive effect or synergy, respectively. For the calculations of the CI values, a computer software was used (ComboSyn, Inc. 599 Mill Run).

**Results**

**Screening of drugs acting in synergy with PPP**

Our previous studies have shown that treatment with PPP *in vivo* reduced tumor load and prolonged the survival of the 5TMM-diseased mice. However, eventually the myeloma tumor reappears (21). For the purpose of finding suitable partners acting in synergy or addition to the PPP, a panel of selected substances including conventional drugs used in MM high-dose chemotherapy, as well as classes of new antitumor agents recently added to the potential therapeutic armamentarium against MM were analyzed. The drugs used in the combinatorial assay were etoposide, mTOR inhibitor rapamycin, 5-FU, Vincristine, SAHA, dexamethasone, bortezomib (Velcade/PS-341), 17-AAG/geldanamycin, As2O3, and the p38 inhibitor SB203580. The survival analysis of the schedule dependency of PPP showed that of these
selected substances, the p38 inhibitor SB203580, bortezomib (Velcade/PS-341), and the histone deacetylase inhibitor (SAHA) will sensitize the cells to IGF-1RTK inhibitor PPP (data not shown). HDACis were subjected to further studies.

The effects of PPP and/or LBH589 on cell survival in mouse and human myeloma cells in vitro

For further analysis on the use of HDACi in combination with PPP, LBH589 was selected due to its potency as a novel developed hydroxamic acid–derived HDAC inhibitor at present in clinical trials for MM.

We first examined the effects of both drugs on cell viability using 4 human MM cell lines: RPMI8226, Karpas707, LP-1, and OPM-2. Cells were exposed to increasing concentrations of PPP and/or LBH589. After 72 hours, the relative number of viable cells was determined by the resazurin assay. All cell lines responded dose dependently to LBH589 and PPP as single drugs. The IC50 values for LBH589 in which at low nanomolar range for all cell lines (16.0 nmol/L for the RPMI8226 cells, 11.0 nmol/L for the Karpas707 cells, 7.42 nmol/L for the LP-1 cells, and 2.8 nmol/L for the OPM-2 cells. Data not shown). When treated with PPP, all the human cell lines showed similar IC50 values (0.33 μmol/L for the RPMI8226 cells, 0.30 μmol/L for the Karpas707 cells, 0.31 μmol/L for the LP-1 cells, and 0.24 μmol/L for the OPM-2. Data not shown). Simultaneous treatment of these cell lines with different concentrations of PPP and LBH589 resulted in a significant decrease in cell survival when compared with the single drugs (P < 0.05), with the only exception of the low combination in the RPMI8226 cells. When we combined both drugs at intermediate and high concentrations, synergistic effects were observed for all the cell lines (CI < 0.90). For the Karpas707 cells, synergy was also observed at low combination treatment (Fig. 1A–D). We then examined the effects of both drugs, alone and in combination, on the survival of 5T33MM murine cells. After 24-hour treatment, the IC50 values were 8.22 nmol/L for LBH589 and 1.58 μmol/L for PPP (data not shown). The survival of 5T33MM cells was significantly lower when treated with both drugs as compared with the single treatments (P < 0.05), and synergy was shown for all the combinations with CI < 0.90 (Fig. 1E).

The effects of PPP and/or LBH589 on cell cycle distribution and cell cycle proteins

Drugs effect on cell cycle proteins was analyzed by Western blotting. After 24 hours in RPMI8226, a more pronounced downregulation of cyclin E, cyclin B1, and cyclin D2 could be detected in the combinatorial design compared with single-dose treatment. Cyclin-dependent kinase 1 (cdk1) also got slightly downregulated in the combinatorial design but not in the single-drug treatment. The expression of cyclin-dependent kinase 4 (cdk4) and 6 (cdk6) remained unchanged (Fig. 2A).

Cell cycle distribution showed that exposure of RPMI8226 cells to PPP increased the fraction of cells in G2–M phase from 14% to 32% after 24 hours, with a corresponding decrease of fraction of cells in G1–G0 and S phases. Treatment with LBH589 for 24 hours increased the number of cells in G1–G0 phase from 42% to 69%, with a corresponding decrease of fraction of cells in S and G2–M phases. For the combinatorial design, the amount of cells increased in the G2–M, from 14% to 32% after 24 hours (Fig. 2C).

Western blot analysis of 5T33MM cells after 24 hours showed that the expression of most analyzed cell cycle proteins remained unchanged compared with the single treatments (data not shown). Cyclin-dependent kinase 6 (cdk6) expression was reduced by PPP while completely inhibited in the combinatorial design. An increased down-regulation of cyclin D2 could also be detected in the
The effect of PPP and/or LBH589 on apoptosis

Both drugs, individually, caused an increase in the relative number of apoptotic and late apoptotic/necrotic cells compared with the control in RPMI8226 cells, but to lesser extent as compared with the combinatorial design. After 48 hours, a five-fold increase of apoptotic and late apoptotic/necrotic cells was detected in the combinatorial design compared with the untreated \( (P < 0.001) \). A significant increase of apoptotic and late apoptotic/necrotic cells were found in the combinatorial design compared with LBH589 \( P < 0.01 \) for the 24-hour time point, \( P < 0.001 \) for the 48 and 72 hours time points and PPP \( P < 0.001 \) for all 3 time points (Fig. 3A).

A clear cleavage of caspase-9, caspase-8, and caspase-3 could first be detected after 24-hour treatment of RPMI8226 cells (Fig. 3B, D, and F). LBH589 induced stronger cleavage of the active forms (p37/35 and p17) of caspase-9 than PPP. The same could be detected in cleavage of caspase-3. Treatment with both drugs induced a stronger cleavage of the active forms (p43/41 and p18) of caspase-8 compared with the single-drug treatment. Similar results were observed in the 5T33MM cells (Fig. 3C, E, and G).

We then evaluated whether the expression of the apoptosis-related molecules Mcl-1, Bcl-x\(_L\), Bcl-2, Bim, and survivin were affected in the cells after treatment with the drugs. The protein levels of these molecules were analyzed by Western blotting. For the human cell line RPMI8226, a clear downregulation of the expression of the antiapoptotic protein Mcl-1, could be detected after 24-hour of treatment with PPP and in the combinatorial design (Fig. 4A). Bcl-2 was reduced when using both drugs after 24 hours in the RPMI8226 (Fig. 4A) and the 5T33MM cells (Fig. 4B). No regulation of survivin
or Bim expression could however be detected in neither RPMI8226 nor 5T33MM cells (data not shown). In the 5T33MM cells, we also observed a downregulation of BCL-xL in the combination treatment (Fig. 4B). Treatment with the drugs also induced a clear downregulation of IGF1-R in the combinatorial design in both the RPMI8226 and the 5T33MM cells (Fig. 4C and D).

Gene array data
The drug combination has more differential enhanced levels of expression, seen for several genes at 24 hours of drug combination than the single drugs alone (Supplementary Table S1). Microarray was validated with real-time PCR (data not shown). Functional analysis of the regulated genes was done using the software DAVID and several important categories were found, out of which 6.7% were apoptotic genes, 6.3% were cell adhesion, 4.5% were hematopoiesis, and 2.2% DNA packaging (Fig. 5).

Survival of 5T33MM mice using a combination of LBH589 and PPP
Using the 5TMM murine models, our groups have previously shown the antimyeloma effect of both compounds (16, 20, 26). LBH589 and PPP were able to reduce tumor load and increase the survival rate when used at optimal concentrations. Here, we examined the effect of the combinatorial treatment using suboptimal concentrations of both compounds. In vivo treatment of 5T33MM-inoculated mice with a combination of LBH589 (2.5 mg/kg/d) and PPP (1.5 mg/d) resulted in a prolonged survival when compared with the vehicle group (P < 0.0001), the LBH589-treated group (P < 0.05), and the PPP-treated group (P < 0.0001; Fig. 6).

Discussion
New treatment approaches are necessary to overcome MM disease. Not only has the expression of IGF-1R been associated with progressive disease and drug resistance (40), the use of small synthetic molecules and neutralizing antibodies targeting the IGF-1R signal have been proven useful in tumor models of MM in vitro and in vivo as shown by us and others (17, 20, 21, 41). The most salient result speaking in favor of the IGF1-1R as a candidate for novel MM therapy is the modest usage of the IGF-1 on the growth of normal nonmalignant cells. Accumulating evidence during the last decade suggests an important role for IGF-1 in migration, survival, and expansion of MM cells in the BM microenvironment and in VEGF-induced angiogenesis (7, 10). Recently, shedding some light on the control of apoptosis mediated by microenvironmental factors, we showed that IGF-1 may silence gene expression of prosapoptosis genes, that is, Bim by epigenetic mechanisms (39).
As a result of MM acquiring additional genetic lesions during its progression in vivo, compensatory pathways of survival will eventually emerge as a result of drug exposure (42). Drugs targeting the IGF-1R present no exception (40, 43) and approaches targeting the IGF-1R are therefore unlikely to be curative as a solo therapy in MM. In line with this notion, remaining MM cells after treatment with the RTK inhibitor PPP in the in vivo 5T2MM model, although initially reducing tumor load, eventually lead to relapse and mortality (20).

In this article, we report the synergistic cytotoxicity in MM cells using the selective IGF-1R inhibitor PPP in combination with the HDACi LBH589, panobinostat. LBH589 was selected from a large drug screen aiming at finding candidate drugs enhancing the effect of PPP. The drug screen in this study included conventional drugs used in MM high-dose chemotherapy, immunomodulatory analogs, the proteasome inhibitor bortezomib (Velcade/PS-341), and drugs selectively targeting parallel pathways of myeloma survival, that is, mTOR and p38 inhibitors and were also subjected to schedule dependency with PPP.

HDACi as single agents are in clinical trials for treatment of MM patients (44). However, several publications have pointed to the potential use of using HDACi in combination with conventional chemotherapeutic drugs. Recently, LBH589 was shown to have synergistic antmyeloma activity in combination with dexamethasone, bortezomib, or melphalan (23, 25).

The synergistic effect of LBH589 and PPP could be shown in the human cell lines RPMI8226, Karpas707, LP-1, and OPM-2 and also in the 5T33MM murine survival, that is, mTOR and p38 inhibitors and were also subjected to schedule dependency with PPP.

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Combination of PPP and LBH589 in Multiple Myeloma

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