Hepatitis B Virus X Protein (HBx) Is Responsible for Resistance to Targeted Therapies in Hepatocellular Carcinoma: Ex Vivo Culture Evidence

Pinbo Huang, Baoxiong Zhuang, Heyun Zhang, Haiyan Yan, Zhiyu Xiao, Wenbin Li, Jianlong Zhang, Qibin Tang, Kaishun Hu, H. Phillip Koef, Jie Wang, and Dong Yin

Abstract

Purpose: Molecular targeted therapy is an important approach for advanced hepatocellular carcinoma (HCC). Hepatitis B virus–related HCC (HBV–HCC) accounts for approximately 50% of all HCC cases. Bortezomib, a proteasome inhibitor (PI), is used extensively for the treatment of hematologic malignancies, but its application in HCC, particularly in HBV–HCC, has not been fully explored.

Experimental Design: The effects of bortezomib on HCC tissues were evaluated by TUNEL assays. The growth inhibitory activity was measured using cell viability assays, and apoptosis was measured using flow cytometry. The levels of HBx, P-Raf/Raf, and P-Erk/Erk expression were measured by Western blot analysis. The ability of the MEK inhibitor PD98059 to enhance the cell killing activity of bortezomib was evaluated using ex vivo and in vivo methods.

Results: The potency of bortezomib varied among HCC samples and cell lines, and HBV/HBx expression was associated with resistance to bortezomib. Bortezomib increased the levels of P-Raf and P-Erk in HBV/HBx–positive cells but not in HBV/HBx–negative HCC cells or in breast cancer or glioblastoma multiforme cells. HBx was also upregulated after exposure to bortezomib, which was associated with the inhibition of proteasome activity. P-Erk upregulation mediated by bortezomib was effectively suppressed by the addition of the MEK inhibitor PD98059. Moreover, bortezomib and PD98059 synergistically inhibited HCC cell proliferation, as measured using both ex vivo and in vivo models.

Conclusions: Our studies demonstrate for the first time that HBx causes resistance to bortezomib in HCC, and this resistance can be antagonized by a MEK signaling inhibitor, providing a novel therapeutic approach. Clin Cancer Res; 21(19): 4420–30. ©2015 AACR.

Introduction

Hepatocellular carcinoma (HCC) is the sixth most prevalent type of tumor and the second most common cause of cancer-related death worldwide (1). Surgery is currently the best therapeutic choice, but it is limited to early-stage disease. The responses to traditional chemotherapy are quite poor for those patients with advanced-stage HCC (2). Thus, novel drugs and therapeutic strategies are urgently needed.

Human hepatitis B virus (HBV) infection is a global health problem, and HBV infection plays an important role in the pathogenesis of cirrhosis and HCC (3), with 350 million individuals chronically infected with HBV (4). HBV-related HCC (HBV–HCC) accounts for approximately 50% of all HCC cases (5). Several HBV factors, including the HBx gene, the pre-S2/S gene, and the HBV spliced protein, have been implicated in the progression and prognosis of liver cancer (6). HBx, which is encoded by the fourth open reading frame of the HBV genome, is regularly detected in the tumors of patients with HBV–HCC (7, 8), and a few studies have demonstrated that both HBx RNA and protein expression are present in human HCC cells in the absence of HBV replication (9, 10). The activation of signaling cascades Ras/Raf/MAPK by HBx is important in HBV-associated pathogenesis (11, 12). Taken together, these findings demonstrate that HBx plays a key role in the molecular pathogenesis of HBV–HCC (13).

Bortezomib (Velcade/PS-341), a proteasome inhibitor (PI), has been approved since 2003 by the U.S. Food and Drug Administration (FDA) for the treatment of refractory multiple myeloma and mantle cell lymphoma (14). As such, most clinical trials of bortezomib have focused on hematologic malignancies (15, 16). Recently, PIs were noted to have antitumor effects against diverse solid neoplasms, including HCC (17). In hematologic malignancies, bortezomib stabilized HbB, resulting in decreased NF-kB activity (18, 19). Studies of HCC indicated that bortezomib downregulated the level of phospho-Akt (P-Akt; ref. 20). Bortezomib was also shown to differentially affect the
expression of E2F1, p21, and p27 (21) and to mediate a specific dual antitumor effect via natural killer (NK) cell antitumor reactivity (22). An international, multicenter phase II trial (23) and several preclinical studies (24–26) of bortezomib in HCC patients have been reported. However, to our knowledge, no studies have focused on the relationship between bortezomib and HBV-related HCC (HBV-HCC).

In this study, the effects of bortezomib were investigated in HBV/HBV+–positive and HBV/HBV−–negative HCC clinical samples and cell lines. We discovered that the upregulation of HBx is one of the mechanisms that mediate bortezomib resistance in HBV-HCC. We provide evidence that combining bortezomib with the MAPK signaling inhibitor PD98059 can overcome this resistance and suggest that this combination may be a novel approach for the treatment of HBV-HCC.

### Materials and Methods

#### Reagents

Bortezomib, GW5074, and PD98059 were purchased from Selleck Chemicals. All of these reagents were dissolved in dimethyl sulfoxide (DMSO) and then added to cells in culture medium. The final DMSO concentration was 0.1% after addition to the medium.

**Ex vivo culture of clinical HCC samples**

Liver cancer tissue samples were obtained from surgical specimens of either liver segmental resections or hemihepatectomies.
The procedures were approved by the ethical committee of the Sun Yat-Sen Memorial Hospital (Guangzhou, China). The clinical characteristics of the tumors used in this study are detailed in Supplementary Table S1. Among the patients sampled, 10 exhibited HBV-related HCC, and 10 were HBV negative. An 8-mm core of tissue was dissected into 1-mm³ pieces and cultured in a static incubating system using 24-well plastic tissue culture plates containing 500 μL of Dulbecco’s Modified Eagle Medium (DMEM) with 10% fetal bovine serum (FBS) and penicillin (100 U/mL)/streptomycin (100 mg/mL) at 37°C with saturated humidity and 5% CO₂. Following a resting phase on a rotating platform (60 rpm) for 2 hours, drug exposure was initiated. After treatment, the tissues were either formalin-fixed and paraffin-embedded for immunohistochemistry or lysed with RIPA buffer for Western blot analysis (Supplementary Fig. S1A). H&E and Ki-67 staining were used to assess the viability of the ex vivo cultured tissues (Supplementary Fig. S1B and S1C).

Transferase-mediated dUTP nick end-labeling assay

The transferase-mediated dUTP nick end-labeling (TUNEL) assay was used to detect the apoptotic cells in tissues with the Cell Death Detection Kit (Roche). Chamber slides were fixed with 4% paraformaldehyde and permeabilized in 0.1% Triton X-100 and then incubated with the TUNEL reaction mixture for 1 hour at 37°C. After the slides were washed with PBS, they were incubated with peroxidase-conjugated antibody for 30 minutes at 37°C and were developed with the DAB system. The apoptosis index was calculated by counting the number of brown-stained nuclei, and the total number of cells measured by light microscopy represented at least 10 fields at ×40 magnification submitted to Figure 2.
investigator-blinded counting. The results are expressed as a percentage of the number of apoptotic cells/total cells.

**Cell lines, stable infected cell lines, and plasmids**

The human HCC cell lines HepG2 (HBV-negative), Huh7 (HBV-negative), Sk-Hep1 (HBV-negative), PLC/PRF/5, and Hep3B (derived from HBV-infected liver) were purchased from the Chinese Academy of Sciences Cell Bank of Type Culture Collection (CBTCCCAS). HepG2.2.15 (HepG2-derivative with integration of the HBV genome; refs. 27, 28) was purchased from BioHermes. All cells were obtained in 2013 directly from either CBTCCCAS or BioHermes, which guaranteed cell line authenticity through short tandem repeat profiling and comparison with known cell line DNA profiles. All cell lines were cultured in DMEM supplemented with 10% FBS (Gibco) under an atmosphere of 5% CO₂.

Three HCC cell lines (HepG2, Huh7, and Sk-Hep1) were selected to generate stable cell lines in this study. A retroviral packaging system was purchased from Clontech. Retroviral vector pMSCV-eGFP inserted with HBx-HA was generated according to the procedure described in the manufacturer's instructions. These retroviruses were used to infect HepG2, Huh7, and Sk-Hep1 cells in the presence of 10 μg/mL Polybrene (Sigma-Aldrich) followed by selection with 1 μg/mL of puromycin (Calbiochem) for 2 weeks.

An expression plasmid containing Flag-tagged ubiquitin (Ub-Flag) for use in the in vivo ubiquitination assays was constructed as previously described (29). The pcDNA3.1-HBx-HA plasmid was obtained by inserting HBx-HA into pcDNA3.1.

**Analysis of cell viability and apoptosis**

The effects of bortezomib and PD98059 on hepatoma cell viability were assessed with the Cell Counting Kit-8 (CCK-8; Dojindo Laboratories). In brief, 3,000 cells were seeded in 96-well culture plates and incubated overnight, followed by the addition of vehicle, bortezomib, PD98059, or a combination of...
bortezomib and PD98059 for 48 hours; then, they were incubated with CCK-8 reagent for 1 hour at 37°C. The staining intensity in the medium was measured at 450 nm. Cytotoxicity was expressed as a percentage of the control cells. The values were expressed as the mean ± standard deviation (SD) of three separate experiments, each performed in triplicate.

After being incubated with the drugs for 48 hours, adherent cells were collected and washed once with PBS. The cells were stained with Annexin V and propidium iodide (PI; BD Pharmingen TM), and the percentage of Annexin V–positive cells was calculated by flow cytometry.

Determination of synergistic activity
The synergistic activity of bortezomib and MEK inhibitor was determined by the method described by Chou and Talalay (30) using CalcuSyn software (Biosoft). A combination index (CI) less than 1 was defined as synergy.

Western blot analysis
Cell cytosolic protein fractions were prepared using RIPA buffer (Beyotime Biotechnology). For the Western blot analyses, antibodies against c-Raf, Phospho-c-Raf, Flag (Cell Signaling Technology), Erk, P-Erk, GAPDH, HA (Santa Cruz Biotechnology Inc.), and HBx (ab2741; Abcam) were used. Quantitative increases in protein phosphorylation were evaluated with a densitometry analysis of the ratio of phosphorylated protein/total protein of the treated cells. All Western blot analyses were repeated two to three times, and the mean increases in the drug-treated groups versus nontreated cells are shown under the gels in the figures.

HBx knockdown using short-interfering RNA
HBx RNA interference was achieved by specific small-interfering RNA (siRNA) duplexes. Sense primers targeting HBx and a negative control were purchased from GenePharma Company. The sequences of the siRNAs for HBx were as follows: si#1 GAGGCUGUAGGCAUAAAUU, si#2 GCACUUCGCUUCACCU-CUG. siRNAs were transfected with the Lipofectamine 2000 transfection reagent (Invitrogen Corporation) according to the manufacturer’s protocol. The knockdown efficiency was validated by Western blot analysis.

In vivo ubiquitination assay and cycloheximide chase assay
This procedure was performed as previously described (29). Briefly, HepG2 cells were transfected with the indicated plasmids for 24 hours and then treated with either 10 μmol/L MG132 or 150 nmol/L bortezomib for 6 hours prior to harvesting the cells. The cells were lysed in RIPA buffer with a protease inhibitor cocktail (Sigma-Aldrich) and a phosphatase inhibitor cocktail (Calbiochem). The cell lysis solution was immunoprecipitated using anti-HA agarose for 4 hours at 4°C. Polyubiquitinated HBx was detected using an anti-Flag antibody. For the cycloheximide chase assay, cells were treated with 20 μg/mL...
of 1.3 mg/m² doses, the Millennium stated that following the intravenous administration tissues were treated with bortezomib at 250 nmol/L (data from developed. Ten non-HBV
related and non-HBV
–related HCC, HCC cell lines (HepG2, Sk-Hep1 and Huh7) were
ed to overexpress HBx to evaluate the relation-
ship between HBx and bortezomib. HBx protein expression was
confirmed by Western blot analysis. Bortezomib exhibited a selective inhibition of HCC cells depending on the expression of HBx (Fig. 1C). The IC₅₀ of HepG2-HBx cells (IC₅₀ 371 nmol/L) was 2-fold greater than that of HepG2-Ctrl cells (IC₅₀ 178 nmol/L). Similar results were noted with Sk-Hep1-HBx (IC₅₀ 393 nmol/L) and Sk-Hep1-Ctrl (IC₅₀ 192 nmol/L) cells, as well as with Huh7-HBx (IC₅₀ 308 nmol/L) and Huh7-Ctrl (IC₅₀ 146 nmol/L) cells. As HBx can influence cell proliferation (Supplementary Fig. S2A and S2B), the HepG2-Ctrl and HepG2-HBx
cells were cultured in 10% FBS or 1% FBS (Supplementary Fig. S2C, top) and then treated with different concentrations of bortezomib (Supplementary Fig. S2C, bottom). The proliferation rates in 1% and 10% FBS exhibited obvious differences, whereas the ratio of inhibition of bortezomib was nearly the same, suggesting that bortezomib resistance may not be related to changes in the proliferation rate.

HBx plays an important role in the resistance of HBV-HCC to bortezomib
On the basis of the above results, the role of HBx in mediating bortezomib resistance was investigated in HBV-HCC. HBx is known to induce a rapid cytoplasmic signaling cascade linking Ras, Raf, and MAP kinases, leading to transcription transactivation (11, 12). The protein levels of both HBx and members of the MAPK signaling pathway increased significantly in a dose- and time-dependent manner after treatment of HepG2.2.15 cells with bortezomib (Fig. 2A). The protein levels of total Raf and Erk did not change in these cells. Bortezomib also upregulated the level of HBx and MAPK activity in the PLC/ PRF/5 and Hep3B cells, which were derived from HBV-infected livers containing an integrated HBV genome (32–34; Fig. 2A and Supplementary Fig. S3A). In addition, HepG2-HBx, Sk-Hep1-HBx, and Huh7-HBx cells were cultured with various doses of bortezomib, which also resulted in the elevation of both HBx and the activated MAPK signal pathway (Fig. 2B and Supplementary Fig. S3B).

In vivid contrast, the HBV/HBV–negative HCC cells (HepG2, Huh7, and Sk-Hep1; Fig. 3A), the non-HCC cells (breast cancer cell lines: MCF7 and MDA-MB-231; GBM cell lines: U118 and U87; Fig. 3B), and the non-HBV–related HCC tissues (Fig. 3C) presented either decreased (HepG2, Huh7, Sk-Hep1, MCF7, U118, U87 cells, and non-HBV–related HCC samples) or unchanged (MDA-MB-231 cells) levels of P-Raf and P-Erk after treatment with bortezomib.

Furthermore, siRNA against HBx was used to reduce the level of HBx expression in the PLC/PRF/5 and Hep3B cells. The HBx siRNA silenced HBx, as confirmed by Western blot analysis (Fig. 3D, left and Supplementary Fig. S3C, top). The downregulation of HBx in the cells considerably antagonized the bortezomib-mediated upregulation of P-Raf and P-Erk (Fig. 3D, right and Supplementary Fig. S3C, bottom). Taken together, the data support the concept that HBx is an important contributor to the resistance of HBV-HCC to bortezomib.

Bortezomib increased the levels of HBx via inhibition of the ubiquitin–proteasome pathway, and the elevated expression of HBx activated the MAPK pathway
As HBx is rapidly degraded by the ubiquitin–proteasome pathway in HBV-infected cells (35), we hypothesized that bortezomib (a PI) would increase the intracellular levels of HBx by inhibiting proteasome activity. To test this hypothesis, an in vivo ubiquitination assay was performed. In the presence of either bortezomib or MG132 (a specific PI), HBx protein was ubiqui-
tinated (Fig. 4A). HBx was quickly degraded with a half-life of less than 1 hour, which contributed to the low intracellular levels of this protein in HBV-related HCC samples (Fig. 4B). Moreover, after treatment with MG132, the HBx protein accumulated in PLC/PRF/5 and Hep3B cells (Fig. 4C). Collectively, our results strongly suggested that bortezomib increased the levels of the HBx protein by inhibiting proteasome activity and that the elevated
levels of HBx enhanced the phosphorylation (activation) of Raf and Erk. Indeed, when HBx was transiently expressed in HepG2 cells, upregulation of P-Raf and P-Erk was observed (Fig. 4D). Furthermore, HBs-expressing cell lines (Sk-Hep1, Huh7, and HepG2) exhibited elevated levels of P-Raf and P-Erk (Fig. 4E). HepG2.2.15 served as a positive control.

PD98059 inhibited the MAPK pathway and reduced cell growth synergistically with bortezomib

To repress the activation of the MAPK pathway induced by bortezomib in HBx-positive cells, a MAPK pathway inhibitor was combined with bortezomib. The Raf-1 kinase inhibitor GW5074 was not effective in HepG2 cells, and it even slightly increased the levels of P-Raf in PLC/PRF/5 and Huh7 cells (Fig. 5A, top). The MEK inhibitor PD98059 effectively suppressed P-Erk (Fig. 5A, bottom) and suppressed the upregulation of P-Erk by bortezomib in HBV/HBx-HCC cells (Fig. 5B).

To investigate whether bortezomib plus PD98059 acted synergistically, CalcuSyn software was used to determine the type of interaction that occurred between these agents. In three cell lines, the MEK inhibitor PD98059 had little effect on cell viability when used alone (vs. control untreated cells). Compared with each alone, the combination of bortezomib and PD98059 significantly increased the efficacy of treatment (Fig. 5C: Supplementary Table S2 presents the CI observed after treatment with the two drugs and indicates their synergy). The viability of PLC/PRF/5 after treatment with bortezomib is shown in Supplementary Fig. S4. Normalized isobolograms for drug combinations applied at varying concentration ratios were also constructed for the three cell lines treated with bortezomib and PD98059 (Fig. 5D). All combination data points were plotted in the synergistic region. Overall, these data indicated that bortezomib and PD98059 interacted synergistically.

Effect of bortezomib and PD98059 on ex vivo and in vivo models

To confirm the synergistic effect of bortezomib and PD98059, their ex vivo and in vivo activities were examined. The expression of HBx and the phosphorylation of Raf and Erk were increased in all of the HBV-positive samples after treatment with bortezomib, and the addition of PD98059 decreased the levels of P-Raf (Fig. 6A and Supplementary Fig. S5A). The percentage of apoptotic cells as measured by TUNEL assays was 4.8% ± 2.56% in the control group, 19.82% ± 5.43% in the bortezomib group, 8.60% ± 3.12% in the PD98059 group, and 41.06% ± 7.56% in the bortezomib and PD98059 group (Fig. 6B). We also investigated the effect of bortezomib and PD98059 in HBV-negative HCC samples (Supplementary Fig. S5B). No obvious synergistic effects were observed between bortezomib and PD98059 compared with either drug alone.

Discussion

The overall survival rate for most advanced HCC patients is poor. Chemotherapy for HCC is limited, in part, because of drug resistance. Bortezomib is clinically effective in hematologic malignancies (14, 36). Recently, PIs exhibited antitumor effects against diverse solid neoplasms, including tumors of the breast, lung, prostate, and liver; additionally, laboratory findings have revealed that combining bortezomib with other drugs may enhance the treatment of HCC (17, 23–26). HBV infection is a major etiologic cause of HCC, with more than 60% of cases in Asia and Africa and at least 20% of HCC cases in Europe, Japan, and the United States associated with chronic infection with HBV (5). Research focused on the mechanism of resistance to bortezomib in HBV-HCC is fundamental for the efficient utilization of these drugs for HCC; in addition, these studies provide a roadmap to circumvent drug resistance to other therapeutic agents.

This study demonstrated for the first time an association between HBx and bortezomib resistance in HBV-related HCC via the upregulation of the Ras–Raf–MAPK pathway. Bortezomib combined with a MEK inhibitor (PD98059) resulted in a synergistic antitumor effect against HBV-related liver cancer as measured by using in vitro, ex vivo, and in vivo models. Ex vivo culture of primary human tissues is widely applied in many research fields, and this strategy provides a bridge between in vitro and in vivo experiments. In our article, tissue was dissected into 1-mm3 pieces; this approach has been used in cancer tissues because it maintains cell viability in both benign and malignant tissues over culture periods of at least 1 week (37, 38). To ensure adequate gas–nutrient–waste–drug exchange in all cells of the liver slices, other methods have also been applied. Ex vivo tissue slices with a thickness of 200 to 300 μm have also been used, which can maximize tissue consistency and perfusion (39).

HBV plays a crucial role in HCC development. The key viral protein HBx is a multifunctional regulator that modulates
Figure 6.
Effect of bortezomib and PD98059 on ex vivo and in vivo models. A, tumor samples (HBV+ #15, 16, 17, 18, 19, 20) were treated with vehicle, bortezomib (BZ), and PD98059 (PD) either alone or combined at the indicated concentrations for 48 hours and then analyzed by Western blot analysis (n = 3). B, left, representative photomicrographs of TUNEL assays of HBV-related HCC samples after treatment with vehicle (○), bortezomib (●), or PD98059 (□) alone or combined (▲) for 48 hours. Scale bars, 100 μm. Right, quantitative analysis of apoptotic cells. The data are presented as the apoptosis rate ± SD (n = 6 per experimental group). One-way ANOVA with Bonferroni post hoc correction is shown; ***, P < 0.001; **, P < 0.01. C, PLC/PRF/5 HCC cells (1 × 10⁶) were injected into the right flank of BALB/c athymic nude mice. The mice were treated with intraperitoneal injections of vehicle, bortezomib (0.5 mg/kg, twice weekly), PD98059 (10 mg/kg/d) or bortezomib and PD98059 (n = 5 per experimental group). The photographs show mice bearing subcutaneous tumors from each group (top) or the dissected tumors (bottom). D, the tumor volumes were measured and recorded every 3 days, and tumor growth curves were created for each group. The values are the means ± SD. ***, P < 0.001; **, P < 0.01; *, P < 0.05 using the Student t test. E, Western blot analysis of HBx, P-Raf/Raf, and P-Erk/Erk in PLC/PRF/5 tumors. F, schematic representation of bortezomib resistance in HBV-HCC and the rationale for the combined therapy with a MEK inhibitor (PD98059, etc.).
transcription, signal transduction, cell-cycle progression, apoptosis, protein degradation, and genetic stability through interactions with host factors (40, 41). We noted that HBV caused resistance to bortezomib at clinically achievable concentrations in our in vitro model, and this phenomenon was reconfirmed using HepG2 and HepG2.2.15 cells in vitro. Furthermore, HCC cell lines stably transfected with HBx (HepG2-HBx, Huh7-HBx, and Sk-Hep1-HBx) exhibited similar resistance to bortezomib. HBx activates several pathways, including the RAS–Raf–MAPK pathway (11, 40, 42), the JAK–STAT pathway (43), and the Wnt/β-catenin pathway (44). The MAPK pathway is activated directly by HBx, as the protein also enhances both cell proliferation and survival. We showed that bortezomib enhanced both the level of HBx and the phosphorylation of Raf and Erk in HepG2(2.15, PLC/PRF/5 and Hep3B cells (each) exhibiting integration of the HBV genome) and in HBx-expressing cell lines (genetically modified). In contrast, this cellular pathway was not stimulated by bortezomib either in HBV-negative cell lines (HepG2, Huh7, and Sk-Hep1) or in PLC/PRF/5 and Hep3B cells after silencing their HBx protein (HBx-siRNA). Taken together, these results strongly suggest that HBx plays a crucial role in the resistance to bortezomib in HBV-HCC.

The effect of proteasome inhibition on several protein kinase pathways is variable depending on the tissue type and pathology. The RAS–RAF–MAPK pathway can respond to a wide variety of stress stimuli (45). Proteasome inhibition can increase the phosphorylation of Erk in kidney cancer cells (46) and decrease its levels in human mast cells (47), glioma cells (48), NIH 3T3 murine fibroblasts and HT-1080 human fibrosarcoma cells (49). We examined the activity of the Ras–Raf–MAPK pathway after bortezomib treatment in HBV-negative HCC and non-HCC (breast cancer and GBM) cell lines. The phosphorylation levels of Raf and Erk either decreased or did not change. These findings support the concept that the upregulation of the MAPK pathway by bortezomib was a consequence of the upregulation of HBx. When a MEK inhibitor (PD98059) was added to bortezomib, the activation of Erk was effectively inhibited. We observed a similar phenomenon when studying the HBV-HCC ex vivo samples. In contrast, the Raf1 kinase inhibitor (GW5074) did not inhibit the phosphorylation of Raf and even slightly enhanced the phosphorylation of this protein in the HCC cell lines.

Bortezomib is the first clinically approved PI. We demonstrated for the first time that a MEK inhibitor (PD98059) and bortezomib synergistically inhibited cell growth in HBV/HBx-related HCC.

Several other drugs that are either approved or in clinical trials target Raf, MEK, and/or Erk. For example, sorafenib, an inhibitor of Raf kinase and P-Erk in HCC (50), may have a similar effect to that of PD98059 against HBV-HCC when combined with bortezomib. In summary, our data demonstrate that HBx is involved in the drug resistance of bortezomib by upregulating the Ras/Raf/MAPK pathway in HBV-related HCC. Furthermore, the MEK inhibitor PD98059 can block this resistance. Bortezomib combined with a MEK inhibitor results in a synergistic antitumor effect against HBV-related liver cancer. Our study lays the foundation for a novel clinical trial in HBV-related HCC.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors’ Contributions

Conception and design: P. Huang, H.P. Koeffler, D. Yin

Development of methodology: P. Huang, B. Zhuang, H. Zhang, H. Yan, K. Hu, D. Yin

Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): P. Huang, B. Zhuang, H. Zhang, J. Wang

Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): P. Huang, B. Zhuang, H. Zhang, D. Yin

Writing, review, and/or revision of the manuscript: P. Huang, H.P. Koeffler, J. Wang, D. Yin

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