Overexpression of the Circadian Clock Gene Bmal1 Increases Sensitivity to Oxaliplatin in Colorectal Cancer

Zhao-lei Zeng1,2, Hui-yan Luo1,3,4, Jing Yang1,2, Wen-jing Wu1,3, Dong-liang Chen1,3, Peng Huang1,2, and Rui-hua Xu1,3

Abstract

Purpose: The circadian clock gene Bmal1 is involved in cancer cell proliferation and DNA damage sensitivity. The aim of this study was to explore the effect of Bmal1 on oxaliplatin sensitivity and to determine its clinical significance in colorectal cancer.

Experimental Design: Three colorectal cancer cell lines, HCT116, THC8307 and HT29, were used. The Bmal1-mediated control of colorectal cancer cell proliferation was tested in vitro and in vivo. MTT and colony formation assays were performed to determine the sensitivity of colorectal cancer cells to oxaliplatin. Flow cytometry was used to examine changes in the cell-cycle distribution and apoptosis rate. Proteins expressed downstream of Bmal1 upon its overexpression were determined by Western blotting. Immunohistochemistry was used to analyze Bmal1 expression in 82 archived colorectal cancer tumors from patients treated with oxaliplatin-based regimens.

Results: Bmal1 overexpression inhibited colorectal cancer cell proliferation and increased colorectal cancer sensitivity to oxaliplatin in three colorectal cancer cell lines and HCT116 cells model in vivo. Furthermore, the overall survival of patients with colorectal cancer with high Bmal1 levels in their primary tumors was significantly longer than that of patients with low Bmal1 levels (27 vs. 19 months; P = 0.043). The progression-free survival of patients with high Bmal1 expression was also significantly longer than that of patients with low Bmal1 expression (11 vs. 5 months; P = 0.015). Mechanistically, the effect of Bmal1 was associated with its ability to regulate G2-M arrest by activating the ATM pathway.

Conclusion: Bmal1 shows the potential as a novel prognostic biomarker and may represent a new therapeutic target in colorectal cancer. Clin Cancer Res; 20(4); 1042–52. ©2013 AACR.

Introduction

The circadian rhythm is a biochemical and biophysical process that has an approximately 24-hour cycle and is driven by the endogenous clock system (1). The hierarchically organized network of the circadian clocks regulate various physiologic processes in the human body, including blood pressure, hormone secretion, sleep, and immune activity (2). Deregulation of circadian rhythms can result in increased risk of cardiovascular diseases, immune system diseases, and cancer (3, 4).

The Bmal1 gene, encodes the Bmal1 protein, is a core component of the circadian clock in mammals (5). Bmal1 belongs to the bHLH-PAS structural domain transcription factor family, which controls the circadian genes Per, Cry, and Rev-Erb and maintains the normal circadian rhythm (6, 7). In addition to its function in controlling biologic rhythm, Bmal1 is closely related to aging, angiocardiopathy, immune disorders, and cancers (8–12). Recent evidence suggests that Bmal1 is correlated with proliferation and the cell cycle, indicating that Bmal1 may play an important role in tumorigenesis (11, 13–15). For instance, Bmal1 has been shown to affect the cell cycle and cell proliferation by regulating the p53/p21 signaling pathway (14, 15). Epigenetic inactivation of Bmal1 is associated with the development of B-cell lymphoma and certain types of leukemia, whereas the reintroduction of Bmal1 inhibits of cancer cell growth in vitro and in vivo (11).

Colorectal cancer is the third most common cancer diagnosed in both men and women and is the third leading cause of cancer-related deaths in the United States according to the American Cancer Society in 2013. More than 1 million new cases of colorectal cancer are clinically diagnosed each year and more than 500,000 patients die from colorectal cancer annually (16). More than 20% of
Moreover, the effect of Bmal1 appears to be mechanistically associated with its ability to regulate G2–M phase arrest by activating the ATM signaling pathway.

Materials and Methods

Cell lines and cell culture

The HCT116 and HT29 colorectal cancer cell lines were purchased from American Type Culture Collection in 2009 and cultured in McCoy’s 5A Medium (Gibco) containing 10% FBS (HyClone). The THC8307 cell line was a gift from the Institute of Hematology (CAMS & PUMC, Tianjin, China) in 2010 and was cultured in RPMI-1640 (Gibco) containing 10% FBS. All cell lines were tested and authenticated by Beijing Microread Gene Tech. Co. Ltd. by short tandem repeat DNA testing in 2012. Cells were seeded in 6-well plates (NEST) at an initial density of 5–8 x 10⁵ cells per well. The next day, they were treated with 50% FBS for 2 hours for synchronization. After synchronization, some of the cells were harvested for RNA and protein extraction and others were reseeded in 6-well or 96-well for cell growth, colony formation, MTT, and flow cytometry analysis.

Xenografted tumor model

Male BALB/c nude mice (4–5 weeks of age, 18–20 g) were purchased from the Guangdong Province Laboratory Animal Center. All mice were synchronized with a 12-h light/dark cycle in an autonomous chronobiological animal facility (Sujing, Suzhou, China), with the lights on from 6 am (Zeitgeber time 0) to 6 pm (Zeitgeber time 12) for 3 weeks, after which they were randomly assigned to groups. All experimental procedures were approved by the Institutional Animal Care and Use Committee of Sun Yat-Sen University (Guangzhou, China). Two in vivo experiments were designed. In experiment 1, the mice were randomly divided into the HCT116_EV, HCT116_Bmal1, HCT116_EV+L-OHP, and HCT116_Bmal1+L-OHP groups (n = 6 per group), and equal amounts of HCT116_Bmal1 or control cells (2 x 10⁶) were injected subcutaneously into the flank of each mouse. In experiment 2, the mice were also randomly divided into the abovementioned 4 groups (n = 5 per group), and different amounts of HCT116_Bmal1 (3 x 10⁶) or control (2 x 10⁶) cells were injected subcutaneously into the flank of each mouse. Oxaliplatin was administered at a dose of 5 mg/kg at 10 am twice a week for 3 weeks. Treatment began on day 7, when the tumors were measurable. The tumors were examined twice weekly, length and width measurements were obtained with calipers, and the tumor volumes were calculated. On day 25, the animals were euthanized and the tumors were excised and weighed.

Patients and samples

Eighty-two patients with histopathologically and clinically diagnosed metastatic colorectal cancer were enrolled in our study from 2000 to 2007. All patients received FOLFOX (fluorouracil, leucovorin, and oxaliplatin) or XELOX (capecitabine and oxaliplatin) regimens as first-line chemotherapy at the Sun Yat-Sen University Cancer Center. Before chemotherapy, primary tumor samples were obtained during colonoscopy biopsies or palliative surgeries.
operations and embedded in paraffin. The clinical and clinicopathologic classification and stage were determined according to the American Joint Committee on Cancer (AJCC) criteria. Before using these clinical materials for research purposes, patient consent and approval from the Institutional Research Ethics Committee were obtained.

Overall survival (OS) was defined as the interval between the date that first-line chemotherapy treatment was started and the date of death or the last known follow-up. Progression-free survival (PFS) was defined as the interval between the date that first-line chemotherapy treatment was started and the date of disease progression.

The criteria for inclusion were as follows: age >18 years; histologically confirmed colorectal cancer with at least 1 measurable lesion as defined by the Response Evaluation Criteria in Solid Tumors; Eastern Cooperative Oncology Group performance status (ECOG PS) of B2, life expectancy >3 months. Other criteria also included: adequate hematologic (neutrophil count: 1,500/L, platelet count: 100,000/L), hepatic (bilirubin: 1.5 times the upper limit of normal, SGOT and SGPT: 2.5 times the upper limit of normal), and renal (creatinine clearance: 30 mL/min) functions. No previous chemotherapy for the target lesions was allowed; however, patients who had received adjuvant/neo-adjuvant chemotherapy were included if the interval after the end of chemotherapy was >12 months. Patients were excluded based on the following criteria: unresolved bowel obstruction or malabsorption syndrome; central nervous system metastases, bone metastases as the only disease site, active uncontrollable infection, other malignancies in the past 5 years, uncontrolled diabetes mellitus, a history of neurological or psychiatric disorders or congestive heart failure.

For the XELOX regimen, oxaliplatin (130 mg/m²) was diluted in 500 mL of 5% dextrose and infused intravenously over 2 hours on day 1; this treatment was followed by oral administration of capecitabine (1,000 mg/m²) twice a day over 2 hours. For the FOLFOX regiment, oxaliplatin (85 mg/m²) was given intravenously with 5-FU/LV (400 mg/m² IV, equivalent to 200 mg/m² 1-folinic acid), by infusion on day 1, followed by a bolus of 400 mg/m² 5-FU and a 46-hour continuous infusion of 2,400 mg/m² 5-FU. This therapy was repeated every 2 weeks for a minimum of 6 cycles. Oxaliplatin was administered at approximately 10 am and over a period of >2 hours. In mild allergic cases, the oxaliplatin infusion time was extended to 6 hours. Treatment was continued until 8 cycles of XELOX or 12 cycles of FOLFOX had been completed, disease progression, unacceptable toxicity, patient withdrawal, or physician’s decision. The target lesions were measured by computed tomography or magnetic resonance imaging within 1 month before study entry. Tumor assessments were repeated every 6 weeks during therapy and at the end of treatment.

**Vectors and siRNA transfection**

A Bmal1 expression construct was generated by subcloning PCR-amplified full-length human Bmal1 cDNA into the pMSCV plasmid. Recombinant retroviral vectors were generated and viral infection was performed as previously described (26). Stable cell lines expressing Bmal1 were selected over 10 days with 2 μg/mL puromycin. To verify the stable high expression of Bmal1 in these cell lines, Western blotting was performed after 30 generations of cell culture (Supplementary. Fig. 1). For Bmal1 knockdown, we used the following siRNA sequences: GAACCTCTAGGCA-CATCGT (siRNA#1) and GGGAAGCAGACAGTCAGAT (siRNA#2) (synthesized by Ribobio). Transfection of the Bmal1 siRNA was carried out using Lipofectamine 2000 (Invitrogen) according to the manufacturer’s instructions and the cells were harvested 72 hours post-transfection for Western blotting to verify and quantify the knockdown of Bmal1.

**Immunohistochemistry**

Immunohistochemistry (IHC) and the scoring of the Bmal1 staining intensity were performed as previously described (27–29). The Bmal1 antibody (1:200; Lifespan) was incubated with the colorectal cancer tissue sections at 4°C overnight. Two independent observers who were blinded to the clinical characteristics and outcomes of the patients assessed the immunohistochemical staining based on the proportion of positively stained tumor cells. The proportion of the stained cells and the extent of the staining were used as the evaluation criteria. The stained sections were evaluated at ×200 magnification, and 10 representative fields from each section were analyzed to determine the percentage of positively stained tumor cells. For each sample, the proportion of Bmal1-expressing cells varied from 0% to 100%, and the intensity of staining varied from weak to strong. The percentage of Bmal1-positive cells was scored as follows: ≤10% = 0, >10% to ≤25% = 1, >25% to ≤50% = 2, >50% to ≤75% = 3 and >75% = 4. The staining intensity was scored as follows: negative = 0, weak = 1, moderate = 2, and strong = 3. A final score was then calculated by multiplying these two scores. If the final score was ≤4, the tumor was considered to have low Bmal1 expression; whereas scores >4 indicated high Bmal1 expression.

**Western blotting**

Western blotting was performed according to standard methods, as described previously (30), using anti-Bmal1 (Lifespan), anti-ATM, anti-CHK2, anti-pCHK2Thr68, anti-p53, anti-MDM2, and anti-Wee1 antibodies (Cell Signaling Technology). An anti-α-tubulin mouse monoclonal antibody (Sigma) was used as a loading control.

**MTT assay**

Cells were seeded in 96-well plates (NEST) at an initial density of 2 × 10³ cells per well and incubated with oxaliplatin for 72 hours. Then, the cells were stained with 20 μL sterile MTT dye (5 mg/mL; Sigma) for 4 hours at 37°C followed by removal of the culture medium and the addition of 200 μL of dimethyl sulfoxide (Sigma). The absorbance was measured at 570 nm and 630 nm was used as the
reference wavelength. All experiments were conducted in triplicate.

**Colony formation assays**

Cells were plated in 6-well plates (NEST) at $5 \times 10^2$ cells per well and cultured for 10 days. The colonies were fixed with 10% formaldehyde for 5 minutes and then stained with 1% crystal violet for 30 seconds.

**Flow cytometry**

Cells were harvested and washed with cold PBS and the cell-cycle distribution and apoptosis rate were analyzed by flow cytometry. The protocol used for the cell-cycle analysis was previously described (31) and $5 \times 10^4$ cells were analyzed using a Cytomics FC 500 instrument (Beckman Coulter) equipped with CXP software. ModifIT LT 3.1 trial cell-cycle analysis software was used to determine the percentage of cells in each phase of the cell cycle.

For apoptosis analysis, after washing with cold PBS, the cells were stained with annexinV-FITC and PI (Keygen), according to the manufacturer’s instructions.

**Statistical analysis**

All statistical analyses were performed using the SPSS version 16.0 statistical software packages. Statistically significant differences between groups were determined using a 2-tailed, paired Student t test. Survival curves were plotted using the Kaplan–Meier method, and the different groups were compared using the log-rank test. A P value of <0.05 was considered to be statistically significant in all cases.

**Results**

**Bmal1 inhibits colorectal cancer cell proliferation**

To evaluate the role of Bmal1 in colorectal cancer cell proliferation, three colorectal cancer cell lines were chosen: HCT116 and THC8307, with low Bmal1 expression; and HT29, with high Bmal1 expression (Supplementary Fig. S2). We established the three cells stably expressing ectopic Bmal1, with Bmal1 expression more than twice as high as compared with control cell lines (Fig. 1A and Supplementary Fig. S3A). A siRNA specific for Bmal1 was transfected to knock down the expression of Bmal1 in HCT116, THC8307, and HT29 cells with more than 70% inhibition of Bmal1 expression (Fig. 1B and Supplementary Fig. S3B). A significant decrease in cell proliferation was observed in Bmal1-overexpressing cells compared with the vector control cells (Fig. 1C). These results were confirmed by colony formation assays, which showed a more than 45% decrease in the number of cell colonies in the Bmal1-overexpressing cells compared with control cells (Fig. 1D).

To further explore the significance of the proliferative function of Bmal1 in colorectal cancer cells, HCT116, THC8307, and HT29 cells were transiently transfected with specific siRNAs against Bmal1. Knockdown of Bmal1 significantly increased cell proliferation compared with control siRNA-transfected cells (Fig. 1C).

**Overexpression of Bmal1 increases oxaliplatin sensitivity in vitro**

To further investigate whether Bmal1 overexpression affects oxaliplatin sensitivity in vitro, unsynchronized, log-phase Bmal1-overexpressing or control HCT116 cells were injected subcutaneously into Balb/c nude mice. To exclude differences in the cell proliferation rate between these cell lines, two experiments were designed: in experiment I, equal amounts of Bmal1-overexpressing or control cells ($2 \times 10^6$) were injected subcutaneously; in experiment II, different amounts of Bmal1-overexpressing ($3 \times 10^5$) or control ($2 \times 10^5$) cells were injected. The tumors derived from the HCT116 cells overexpression Bmal1 were significantly more sensitive to oxaliplatin compared with the HCT116 vector control tumors (P<0.001). In experiment I, the oxaliplatin-mediated growth inhibition rates of the Bmal1-overexpressing tumors and the control tumors were 81.5% and 39.6%, respectively (Fig. 3A); in experiment II, the oxaliplatin-mediated growth inhibition rates of the Bmal1-overexpressing tumors and the control tumors were 73.6% and 38.2%, respectively (Fig. 3B).

**Bmal1 protein expression correlates with the outcome of oxaliplatin-based first line chemotherapy in advanced colorectal cancer patients**

To further confirm the effect of Bmal1 expression on oxaliplatin activity, immunohistochemical staining for Bmal1 was performed on tumor tissues from 82 patients with advanced colorectal cancer treated with FOLFOX or XELOX regimens. According to our scoring system, high Bmal1 expression was detected in 36 of 82 (43.9%) of the colorectal carcinomas, whereas low Bmal1 expression was detected in 46 of 82 (56.1%) of the colorectal carcinomas.
Kaplan–Meier survival curves and log-rank test survival analysis revealed that the OS of patients with high tumor Bmal1 expression was significantly longer than that of patients with low Bmal1 expression (median OS: 27 vs. 19 months, respectively; \( P = 0.043 \)). Strikingly, the PFS of patients with high Bmal1 expression was also dramatically
longer than those with low Bmal1 expression (median PFS: 11 months vs. 5 months, respectively; \( P = 0.015 \); Fig. 3C).

On the basis of the above observations, we reasoned that high Bmal1 expression might correlate with good clinical response to oxaliplatin-based chemotherapy and better survival. Thus, we retrospectively analyzed the relationship between Bmal1 expression and the response to FOLFOX or XELOX chemotherapy. Thirty-one of 36 (86.1%) of the patients with high Bmal1 expression in their primary tumors benefited (CR+PR+SD) from chemotherapy, whereas only 28 of 46 (60.9%) of the patients with low Bmal1 expression benefited (Table 1). Furthermore, 31 of 59 (52.5%) patients who experienced a clinical benefit from chemotherapy expressed high Bmal1 levels, whereas only 5 of 23 (21.7%)
of the progressive disease (PD) patients expressed high Bmal1 levels ($P = 0.012$). Moreover, if only the complete response (CR) and partial response (PR) patients were assumed to have benefited from treatment, then the results remained in agreement with the above finding ($P = 0.027$). These results are consistent with our finding that Bmal1 overexpression increases oxaliplatin sensitivity in vitro and in vivo.

**Bmal1 enhances oxaliplatin induced apoptosis in colorectal cancer cells**

We further examined whether Bmal1 increase the sensitivity of colorectal cancer cells to oxaliplatin by enhancing the rate of apoptosis. An AnnexinV-PI assay was used to detect cellular apoptosis. Bmal1-overexpressing cells displayed increased cellular apoptosis and necrosis in response to oxaliplatin treatment for 48 hours (Supplementary Fig. S4). However, these phenomena were observed at only high oxaliplatin concentrations. Furthermore, the difference in the apoptosis rate between the Bmal1-overexpressing cells and the control cells was not large enough to explain the significant changes in the response to oxaliplatin treatment that were observed in vitro and in vivo. Thus, other mechanisms might be involved in this process.

![Figure 3. Bmal1 increases cellular sensitivity to oxaliplatin in vivo. A and B, the same ($2 \times 10^6$; A) or different amounts of HCT116_Bmal1 ($3 \times 10^6$) and control ($2 \times 10^6$) cells (B) were injected subcutaneously into the flanks of nude mice (left). Representative images of tumor growth (middle), and mean tumor weights (right) are shown. C, Immunohistochemical staining of Bmal1 protein expression in colorectal cancer tissues (left). The overall (middle) and progression-free survival (right) of patients with low and high Bmal1 expression are shown.](#)
higher number of cells in G2–M phase compared with platin for 6 hours and then in drug-free medium for the next formed on Bmal1-overexpressing and control cells after arrest in colorectal cancer cells

lates G2–M phase arrest in response to oxaliplatin. Therefore, we assessed the expression of ATM, the G2–M checkpoint. The ATM pathway activates DNA damage checkpoint proteins, such as CHK2 and p53, activating p53 and Wee1, which results in DNA damage-repair signaling pathway is involved in this process. Previous reports have suggested that Bmal1 affects the efficacy of DNA damage-inducing anticancer drugs and that this function is related to the circadian gating control of the cell cycle and cell proliferation (21, 34). The Bmal1/Clock heterodimer negatively controls the cell cycle and cell proliferation by repressing c-myc and p21 and activating p53 and Wee1, which results in DNA damage-induced cell-cycle arrest or apoptosis (21, 35, 36). DNA double-strand breaks recruit and activate the ATM protein, which then activates DNA damage checkpoint proteins, such as CHK2 and p53, leading to cell-cycle arrest or apoptosis (37). Some clock genes that control the ATM pathway have been reported, including per1, per2, and timeless (38–41). We also demonstrated that the ATM signaling pathway plays an important role in G2–M phase arrest in colorectal cancer cells.

Oxaliplatin, a third-generation platinum analog, functions by forming both inter- and intrastrand cross-links in DNA, thus preventing DNA replication and transcription and resulting in cell death (42). Although our study was a retrospective study in which the sampling time could not be controlled, the chemotherapy timing followed the regimens described in the Materials and Methods section, making our data comparable. Thus, we found that Bmal1 overexpression increases the sensitivity of colorectal cancer to oxaliplatin-mediated G2–M phase arrest in colorectal cancer cells.

Table 1. Colorectal cancer patients with high tumor Bmal1 expression are more sensitive to oxaliplatin treatment

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<th>Oxaliplatin</th>
<th>Bmal1 expression</th>
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<td>High</td>
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<tr>
<td>Response</td>
<td>CR+PR+SD</td>
<td>31</td>
<td>28</td>
<td>59</td>
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<td>PD</td>
<td>5</td>
<td>18</td>
<td>23</td>
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<td>P = 0.012</td>
<td>Total</td>
<td>36</td>
<td>46</td>
<td>82</td>
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<td>Response</td>
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<td>PD</td>
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<td>P = 0.027</td>
<td>Total</td>
<td>25</td>
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Bmal1 regulates oxaliplatin-mediated G2–M phase arrest in colorectal cancer cells

To assess cell-cycle distribution, flow cytometry was performed on Bmal1-overexpressing and control cells after oxaliplatin treatment. The cells were incubated with oxaliplatin for 6 hours and then in drug-free medium for the next 42 hours, and the cell-cycle distribution was assessed. The Bmal1-overexpressing cells demonstrated a dramatically higher number of cells in G2–M phase compared with the control cells (Fig. 4A–C), suggesting that Bmal1 regulates G2–M phase arrest in response to oxaliplatin.

Bmal1 is involved in the G2–M checkpoint

Because Bmal1 regulates G2–M phase arrest in response to oxaliplatin, we hypothesized that Bmal1 is involved in the G2–M checkpoint. The ATM pathway activates DNA damage checkpoint proteins which result in G2–M phase arrest. Therefore, we assessed the expression of ATM, pCHK2Thr68, CHK2, p53, MDM2, and Wee1 by Western blotting in HCT116 and THC8307 cell lines. As expected, compared with the control cells, the expression levels of ATM, pCHK2Thr68, p53 and Wee1 were significantly upregulated and MDM2 was downregulated in the Bmal1-overexpressing cells after oxaliplatin treatment (Fig. 5). These results suggest that the ATM pathway plays an important role in the ability of Bmal1 to increase sensitivity to oxaliplatin.

Discussion

In the present study, we found that Bmal1 inhibits the proliferation of colorectal cancer cells, and that Bmal1 overexpression increases the sensitivity of colorectal cancer to the anticancer drug oxaliplatin in vitro and in vivo. Furthermore, we demonstrated that Bmal1 protein expression correlates with the outcome of oxaliplatin-based first-line chemotherapy in patients with advanced colorectal cancer, as patients with high tumor Bmal1 expression more frequently benefited from oxaliplatin-based chemotherapy when compared with patients with low Bmal1 expression.

In addition, we determined that the mechanism underlying the effects of Bmal1 is associated with the ability of Bmal1 to regulate G2–M phase arrest by activating the ATM signaling pathway. To the best of our knowledge, this study is the first demonstrating that Bmal1 is involved in the effect of oxaliplatin on colorectal cancer.

The current trend in chemotherapy is personalized medicine and identifying novel biomarkers and therapeutic targets is a major focus of ongoing research. Herein, we systematically explored the effect of Bmal1 on oxaliplatin sensitivity in colorectal cancer in cells, mice and clinical samples. This study is the first to explore the role of Bmal1 in chemotherapy in conjunction with clinical features and prognostic data. We found that patients with high tumor Bmal1 expression levels had better outcomes compared with those with low Bmal1 expression (median OS: 27 vs. 19 months, respectively). Impressively, the PFS of patients with high Bmal1 expression was also dramatically longer than that of patients with low Bmal1 expression (median PFS: 11 vs. 5 months, respectively). Thus, our study provides strong evidence that Bmal1 is a potential prognostic biomarker and therapeutic target for treating human colorectal cancer.

Few studies have assessed the effect of Bmal1 on anticancer drugs. An earlier report demonstrated that the transactivation status of the Clock/Bmal1 complex correlates with the response to cyclophosphamide in mice (32). Another report showed that BMAL1-deficient fibroblasts have reduced sensitivity to the DNA damage-inducing anticancer drugs, etoposide and daunorubicin (8). Our previous study also demonstrated that Bmal1 plays a role involved in the effect of cisplatin in mice (33). In the present study, we found that Bmal1 overexpression induces G2–M phase arrest in HCT116 and THC8307 cell lines after oxaliplatin treatment, indicating that the DNA damage-repair signaling pathway is involved in this process. Previous reports have suggested that Bmal1 affects the efficacy of DNA damage-inducing anticancer drugs and that this function is related to the circadian gating control of the cell cycle and cell proliferation (21, 34). The Bmal1/Clock heterodimer negatively controls the cell cycle and cell proliferation by repressing c-myc and p21 and activating p53 and Wee1, which results in DNA damage-induced cell-cycle arrest or apoptosis (21, 35, 36). DNA double-strand breaks recruit and activate the ATM protein, which then activates DNA damage checkpoint proteins, such as CHK2 and p53, leading to cell-cycle arrest or apoptosis (37). Some clock genes that control the ATM pathway have been reported, including per1, per2, and timeless (38–41). We also demonstrated that the ATM signaling pathway plays an important role in G2–M phase arrest in colorectal cancer cells.

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oxaliplatin, which is consistent with previous observations indicating that circadian timing can significantly modify drug efficiency and tolerability in tumor models and patients with cancer (22, 43). In future studies, shRNA should be used to test the effects of Bmal1 knockdown on tumor growth and drug sensitivity in animals because such
experiments will further demonstrate the role of Bmal1 in oxaliplatin sensitivity in the context of circadian timing.

Some translational studies have explored the relationship between Bmal1 and the clinical features of patients with colorectal cancer. Previous reports have suggested that Bmal1 expression in colorectal cancer tissues is lower than that in matched healthy mucosa (44). In addition, the expression of Bmal1 and Per1 also correlates with liver metastasis and colorectal cancer outcomes (45). Our data support the hypothesis that Bmal1 has the potential to be a novel prognostic biomarker and a new therapeutic target in colorectal cancer. Future studies should focus on collecting blood samples at a specific time of the day to avoid complications due to the influence of circadian rhythms.

Our experiments suggest that Bmal1 inhibits the proliferation of colorectal cancer cells in vitro and in vivo. Our findings are consistent with those of multiple studies demonstrating the role of Bmal1 in the suppression of cell proliferation, indicating that Bmal1 is a potential tumor suppressor gene (13–15). In contrast to our findings, another recent study (46) reported that Bmal1 promotes proliferation in malignant pleural mesothelioma. On the basis of this difference, we suspect that Bmal1 might play different roles in different tumor types, which further highlights the complicated mechanisms involved in tumorigenesis.

In conclusion, our results suggest that Bmal1 plays an important role in determining the sensitivity of human colorectal cancer to oxaliplatin. A complete understanding of the precise role of Bmal1 in advanced colorectal cancer may allow for the use of Bmal1 as a prognostic biomarker for patient response to oxaliplatin-based chemotherapy and aid in the development of novel therapeutic strategies.

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

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Conception and design: Z.-l. Zeng, P. Huang, R.-H. Xu
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): J. Yang, W.-j. Wu, D.-l. Chen
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): Z.-l. Zeng, H.-y. Luo, W.-j. Wu, P. Huang
Writing, review, and/or revision of the manuscript: Z.-l. Zeng, H.-y. Luo, R.-H. Xu
Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): J. Yang

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References


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