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A cell-penetrating ARF peptide inhibitor of FoxM1 in mouse hepatocellular carcinoma treatment

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The forkhead box m1 (Foxm1) transcription factor is essential for initiation of carcinogen-induced liver tumors; however, whether FoxM1 constitutes a therapeutic target for liver cancer treatment remains unknown. In this study, we used diethylnitrosamine/phenobarbital treatment to induce hepatocellular carcinomas (HCCs) in either WT mice or Arf+/− Rosa26-FoxM1b Tg mice, in which forhead box M1b (FoxM1b) is overexpressed and alternative reading frame (ARF) inhibition of FoxM1 transcriptional activity is eliminated. To pharmacologically reduce FoxM1 activity in HCCs, we subjected these HCC-bearing mice to daily injections of a cell-penetrating ARF26–44 peptide inhibitor of FoxM1 function. After 4 weeks of this treatment, HCC regions displayed reduced tumor cell proliferation and angiogenesis and a significant increase in apoptosis within the HCC region but not in the adjacent normal liver tissue. ARF peptide treatment also induced apoptosis of several distinct human hepatoma cell lines, which correlated with reduced protein levels of the mitotic regulatory genes encoding polo-like kinase 1, aurora B kinase, and survivin, all of which are transcriptional targets of FoxM1 that are highly expressed in cancer cells and function to prevent apoptosis. These studies indicate that ARF peptide treatment is an effective therapeutic approach to limit proliferation and induce apoptosis of liver cancer cells in vivo.

Introduction

Human hepatocellular carcinoma (HCC) is the fifth most common cancer, yet it is among the most lethal cancers worldwide because late detection and high frequency of tumor recurrence render current HCC therapy ineffective (1). The primary etiology of human HCC involves HBV and HCV infections, which are primarily responsible for the high incidence of HCC in Africa and Asia and increasing occurrence of HCC in Europe and America (1). Persistent hepatic infection by either human HBV or HCV results in chronic hepatic inflammatory injury and activation of hepatic stellate cells, which oversecrete collagen, leading to hepatic fibrosis, cirrhosis, and subsequent development of HCC (1). Other causes of human HCC involve hepatic damage and fibrosis resulting from iron or copper deposition, alcohol, or nonalcoholic steatohepatitis (NASH, or fatty liver disease) as well as exposure to the potent hepatic carcinogen aflatoxin B1 produced by specific strains of mold (1).

Activation of the Ras/MAPK signaling pathway drives cell-cycle progression by temporal expression of cyclin regulatory subunits, which activate their corresponding cyclin-dependent kinases (CDKs) through complex formation and phosphorylate substrates critical for cell-cycle progression (2). Development of cancer is a multistep process involving gain-of-function mutations that activate the Ras/MAPK and PI3K/Akt signaling pathways that stimulate cell-cycle progression and enhance cell survival (2, 3). Cancer progression also requires inactivation of tumor suppressor genes that function to arrest cell proliferation in response to oncogenic stimuli (4). In mouse models of liver cancer, loss-of-function mutations in the p53 tumor suppressor gene or gain-of-function mutations in either the Ras/MAPK, PI3K/Akt, or TGF-β signaling pathways are known to stimulate formation of HCC tumors (5–7). A well-established mouse liver tumor induction and promotion protocol is available and consists of a single postnatal injection of the DNA-damaging diethylnitrosamine (DEN; tumor initiator) and continuous administration of the tumor promoter phenobarbital (PB) (8). Gene expression profiling studies demonstrated that mouse HCCs induced by DEN treatment express genes similar to those found in the poorer survival group of human HCCs (9), supporting the relevance of using DEN-induced mouse liver tumors as a model for the study of human liver tumors.

Expression of the alternative reading frame (ARF) tumor suppressor protein is induced in response to oncogenic stimuli and prevents abnormal cell proliferation through a p53-dependent G1 cell-cycle arrest by increasing stability of the p53 tumor suppressor through nucleolar targeting of the p53 ubiquitin ligase protein Mdm2 (10). The ARF protein also mediates p53-independent cell-cycle arrest, as the mouse ARF protein targets both the E2F1 and c-Myc transcription factors to the nucleolus, thus preventing their transcriptional activation of S-phase–promoting target genes (11–14). Loss of ARF function is a critical event for tumor promotion, as evidenced by extinguished expression of the ARF protein in a variety of tumors through DNA methylation and silencing of the ARF promoter region (4).

Nonstandard abbreviations used: ARF, alternative reading frame; CDK, cyclin-dependent kinase; CDKI, CDK inhibitor; CKO, conditional knockout; D-Arg, d-arginine; DEN, diethylnitrosamine; dsRNA, double-stranded RNA; Fox, forkhead box; HCC, hepatocellular carcinoma; HMEC-1 cell, human microvascular endothelial cell; PB, phenobarbital; PLK1, polo-like kinase 1; PKMA, p53-upregulated modifier of apoptosis; TMR, tetramethylrhodamine.

Conflict of interest: The authors have declared that no conflict of interest exists.

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The mammalian forkhead box (Fox) family of transcription factors consists of more than 50 mammalian proteins (15, 16) that share homology in the winged helix DNA-binding domain (17, 18). Expression of FoxM1 (or FoxM1b) is ubiquitous in all proliferating mammalian cells, and its expression is induced during the G1 phase of the cell cycle and continues during S-phase and mitosis (19–23). FoxM1b transcriptional activity requires activation of the RAS/MAPK pathway and binding of activated CDK-cyclin complexes to the activation domain, which mediate phosphorylation-dependent recruitment of the CREB-binding protein (CBP) transcriptional coactivator (24). Liver regeneration studies that used the albumin promoter/enhancer cre recombinase (Alb-Cre) transgene to mediate hepatocyte-specific deletion of the mouse Foxm1 LoxP/LoxP targeted allele (Foxm1fl/fl) demonstrated that Foxm1 is required for hepatocyte DNA replication and mitosis (25). Foxm1-deficient hepatocytes accumulate nuclear levels of the CDK inhibitor (CDKI) proteins p21<sup>Cip1</sup> and p27<sup>Kip1</sup> (8, 25) because FoxM1 regulates expression of S-phase kinase-associated protein 2 (Skp2) and CDK subunit 1 (Cks1) proteins (26), which are involved in targeting these CDKI proteins for degradation during the G1/S transition (27). For G2/M progression, FoxM1 regulates transcription of cyclin B1 and the Cdk1-activating Cdc25B phosphatase (25, 28), and FoxM1 is essential for transcription of the mitotic regulatory genes polo-like kinase 1 (PLK1), aurora B kinase, survivin, centromere protein A (CENPA), and CENPB (26, 29, 30).

We previously used the Alb-Cre transgene to conditionally delete the mouse Foxm1<sup>fl/fl</sup> allele in hepatocytes prior to DEN/PB liver...
Results

The mouse Foxm1 transcription factor is required for hepatic tumor progression. We previously showed that conditional deletion of Foxm1 in hepatocytes prior to DEN/PB liver tumor induction is sufficient to inhibit hepatic tumor initiation (8, 31). Here, we determined that Foxm1 is required for hepatic tumor progression. In order to do so, we used the IFN-α/β-regulated Mx-Cre transgene (36) to conditionally knock out (CKO) or delete the Foxm1<sup>fl/fl</sup> targeted allele in preexisting mouse liver tumors induced by DEN/PB treatment and demonstrated that FoxM1 is required for tumor progression of hepatic cancer cells. We show that administering the WT ARF<sub>26–44</sub> peptide to mice following DEN/PB exposure is an effective treatment to diminish Foxm1 function in vivo, causing selective HCC apoptosis and reduced proliferation and angiogenesis in HCC regions. We also show that Arf<sup>+/-</sup> Rosa26-FoxM1b Tg mice, in which FoxM1b is overexpressed and ARF inhibition of FoxM1 transcriptional activity is eliminated, developed highly proliferative liver tumors following DEN/PB exposure. We showed that WT ARF<sub>26–44</sub> peptide treatment of these Arf<sup>+/−</sup> Rosa26-FoxM1b Tg mice efficiently diminished HCC proliferation and selectively induced apoptosis of the HCC region.

Table 1

WT ARF peptide treatment diminishes the number and size of hepatic adenomas and HCCs per square centimeter liver tissue

<table>
<thead>
<tr>
<th>Foxm1 mouse genotype or ARF peptide treatment (40 weeks DEN/PB)&lt;sup&gt;a&lt;/sup&gt;</th>
<th>No. mice&lt;sup&gt;b&lt;/sup&gt;</th>
<th>No. liver tumors between 0.1 and 2.0 mm&lt;sup&gt;2&lt;/sup&gt; in size&lt;sup&gt;c&lt;/sup&gt;</th>
<th>No. liver tumors greater than 2.0 mm&lt;sup&gt;2&lt;/sup&gt; in size&lt;sup&gt;d&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>dsRNA (control) Foxm1&lt;sup&gt;fl/fl&lt;/sup&gt;</td>
<td>6</td>
<td>2.8 ± 1.8</td>
<td>7.1 ± 4.0</td>
</tr>
<tr>
<td>PBS (control) Mx-Cre Foxm1&lt;sup&gt;fl/fl&lt;/sup&gt;</td>
<td>5</td>
<td>1.3 ± 0.7</td>
<td>9.2 ± 4.6</td>
</tr>
<tr>
<td>dsRNA (CKO) Mx-Cre Foxm1&lt;sup&gt;fl/fl&lt;/sup&gt; (FoxM1 inhibitor) WT ARF&lt;sub&gt;26–44&lt;/sub&gt; peptide treatment</td>
<td>6</td>
<td>2.2 ± 1.7</td>
<td>3.0 ± 1.1&lt;sup&gt;e&lt;/sup&gt;</td>
</tr>
<tr>
<td>(Control) mutant ARF&lt;sub&gt;26–44&lt;/sub&gt; peptide treatment</td>
<td>5</td>
<td>1.6 ± 0.6&lt;sup&gt;f&lt;/sup&gt;</td>
<td>3.0 ± 2.1&lt;sup&gt;f&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>4.9 ± 1.5</td>
<td>11.7 ± 2.7</td>
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</table>

<sup>a</sup>See Methods for details of conditional deletion of Foxm1<sup>fl/fl</sup> targeted allele and for induction of hepatic tumors in response to DEN/PB exposure and treatment with WT ARF<sub>26–44</sub> peptide or mutant ARF<sub>37–44</sub> peptide. <sup>b</sup>No. mice: number of male mice analyzed for liver tumors after 40 weeks of DEN/PB exposure. <sup>c</sup>No. liver tumors were counted in liver sections stained with H&E; size was determined using the Axioplan 2 microscope (Zeiss) and the AxioVision program (version 4.3; Zeiss). <sup>d</sup>No. liver tumors greater than 2.0 mm<sup>2</sup> in size were counted in liver sections stained with H&E; size was determined using the Axioplan 2 microscope (Zeiss) and the AxioVision program (version 4.3; Zeiss). <sup>e</sup>P < 0.05, <sup>f</sup> P < 0.01. We compared tumor size of WT ARF<sub>26–44</sub> peptide-treated versus mutant ARF<sub>37–44</sub> peptide-treated liver tumors. We also compared liver tumor size in dsRNA CKO Mx-Cre Foxm1<sup>fl/fl</sup> and control mice.

We used liver sections stained with H&E to determine the number of tumors per square centimeter of liver tissue (Figure 1, B–D). To calculate the area or size of liver tumors, we used micrographs of H&E-stained liver tumor sections taken with an Axioplan 2 microscope (Zeiss) and the AxioVision program (version 4.3; Zeiss). After 40 weeks of DEN/PB exposure, control mice displayed hepatic adenomas and HCCs that were larger than 2 mm<sup>2</sup> in size (Table 1). Deletion of Foxm1 in preexisting hepatic tumors in dsRNA CKO Mx-Cre Foxm1<sup>fl/fl</sup> mice caused a significant reduction in the number of liver tumors larger than 2 mm<sup>2</sup> in size compared with control liver tumors after 40 weeks of DEN/PB exposure (Table 1). We next measured tumor cell proliferation by determining the number of BrdU-positive cells in liver tumors stained with anti-BrdU antibody (Figure 1K). Taken together, these results indicate that deletion of Foxm1 in preexisting liver tumors significantly diminished proliferation and growth of hepatic cancer cells.

The cell-penetrating WT ARF<sub>26–44</sub> peptide targets the endogenous mouse FoxM1 protein to the nucleus of hepatic tumor cells. We previously synthesized a cell-penetrating ARF<sub>26–44</sub> peptide fused to 9 N-terminal D-Arg residues (32, 33), which efficiently transduced into osteosarcoma U2OS cells and inhibited FoxM1b transcriptional activity (8). Treatment of U2OS cells with 12 μM of (D-Arg)<sub>9</sub>-ARF<sub>26–44</sub> peptide (WT ARF<sub>26–44</sub>) peptide fluorescently tagged with tetracythrylphodamine (TMR) targeted nuclear GFP-FoxM1b green fluorescence colocalized with red WT ARF<sub>26–44</sub> peptide fluorescence in the nucleus (Figure 2, C and D). In contrast, GFP-FoxM1b protein remained nuclear in U2OS cells when treated with a TMR fluorescently tagged mutant ung.
The WT ARF\textsubscript{26–44} peptide targets the liver tumor FoxM1 protein to the nucleolus. (A) Experimental design diagram of ARF peptide treatment of liver tumor–bearing mice. Liver tumors were induced in mice with DEN/PB exposure, and then they were subjected to daily i.p. injections of the WT ARF\textsubscript{26–44} peptide or mutant ARF\textsubscript{37–44} peptide (Mut. ARF\textsubscript{37–44} peptide) as described in Methods. (B–F) GFP-FoxM1b protein is targeted to the nucleolus by the WT ARF\textsubscript{26–44} peptide. U2OS cells were transfected with GFP-FoxM1b expression vector and were either left untreated or incubated for 48 hours with TMR fluorescently tagged WT ARF\textsubscript{26–44} peptide (C and D) or mutant ARF\textsubscript{37–44} peptide (E and F) and then analyzed for GFP (green) or peptide (red) fluorescence. (G) TMR fluorescence labeling revealed that the WT ARF\textsubscript{26–44} peptide was localized to the hepatocyte cytoplasm and nucleolus (white arrow) as determined by laser confocal microscopy. Immunostaining of tumor sections with antibody specific to either NPM protein (black arrows) (J) or FoxM1 protein (K–M). WT ARF\textsubscript{37–44} peptide targets tumor FoxM1 to the nucleolus (black arrows), whereas FoxM1 remains nuclear after treatment with mutant ARF\textsubscript{37–44} peptide or PBS (red arrows). Magnification: ×400 (B–F and J–M); ×200 (G); and ×600 (H and I).

(D-Arg)\textsubscript{3}ARF\textsubscript{37–44} (mutant ARF\textsubscript{37–44}) peptide (Figure 2E), which lacked the amino acids 26–37 required to interact with the FoxM1b protein (8). Because Arg-rich sequences are sufficient for nucleolar targeting (38), the mutant ARF\textsubscript{37–44} peptide fluorescence also localized to the nucleolus of U2OS cells (Figure 2F). We did not observe any signal in the absence of the ARF peptide (data not shown).

Dose-response curve determined that only i.p. injection of 5 mg/kg body weight or greater of the TMR fluorescently tagged WT ARF\textsubscript{26–44} peptide was detectable in cytoplasm and nucleolus of hepatocytes and in hepatic mesenchymal cells at 24 hours after administration (Figure 2G; see Methods). After 32 weeks of DEN/PB liver tumor induction, we subjected Foxm1\textsubscript{fl/fl} mice to daily i.p. injections of 5 mg/kg body weight of the WT ARF\textsubscript{26–44} peptide or mutant ARF\textsubscript{37–44} peptide for 4 weeks and of WT ARF\textsubscript{26–44} peptide for 8 weeks (Figure 2A). After 4 weeks of treatment with TMR fluorescently tagged ARF peptides, laser confocal microscopy of paraffin-embedded mouse liver tumor sections revealed that ARF peptide fluorescence localized to the hepatocyte cytoplasm and nucleolus (Figure 2, H and I) and was uniformly distributed throughout the liver parenchyma (data not shown). The FoxM1 protein staining in WT ARF\textsubscript{26–44} peptide–treated liver tumor sections was partially localized to the nucleolus in hepatic tumor cells (Figure 2L, black arrows), which was similar to the immunostaining pattern of the nucleolar protein nucleophosmin (NPM; Figure 2G), black arrows). In contrast, mutant ARF\textsubscript{37–44} peptide– or PBS-treated liver tumor cells displayed only nuclear FoxM1 staining (compare Figure 2K and Figure 2M, red arrows). These studies demonstrate that the WT ARF\textsubscript{26–44} peptide reduces in vivo function of FoxM1 by partially targeting the endogenous FoxM1 protein to the nucleolus of hepatic tumor cells.

WT ARF\textsubscript{26–44} peptide diminishes proliferation and size of liver tumors. We next determined the number of hepatic tumor cells that incorporated BrdU in mice treated with WT ARF\textsubscript{26–44} Peptide, mutant ARF\textsubscript{37–44} peptide, or PBS. Significant reduction in BrdU incorporation was found in liver tumors that had been treated with the WT ARF\textsubscript{26–44} peptide for 4 or 8 weeks compared with mouse liver tumors treated with mutant ARF\textsubscript{37–44} peptide or PBS (Figure 3, A–K). Compared with control treatment, treatment with the WT ARF\textsubscript{26–44} peptide for 8 weeks significantly reduced tumor growth and prevented development of HCCs larger than 2 mm\textsuperscript{2} in size (Table 1). These results indicate that treatment with the WT ARF\textsubscript{26–44} peptide is an effective method with which to reduce proliferation and growth of HCCs.

We previously demonstrated that tumor resistance in Foxm1\textsuperscript{−/−} hepatic tumors was associated with persistent nuclear accumulation of the CDK1 protein p27\textsuperscript{Kip1} (8). WT ARF\textsubscript{26–44} Peptide–treated HCC cells increased nuclear levels of the p27\textsuperscript{Kip1} protein, which were similar to those found with dsRNA CKO Mx-Cre Foxm1\textsuperscript{−/−} liver tumors (Figure 4, B and E). In contrast, p27\textsuperscript{Kip1} immunostaining was predominantly cytoplasmic in mutant ARF\textsubscript{37–44} peptide– or PBS-treated mouse HCCs (Figure 4, A, C, D, and F). These studies indicate that the WT ARF\textsubscript{26–44} peptide is effective in reducing FoxM1 function in vivo and that nuclear accumulation of p27\textsuperscript{Kip1} protein was associated with reduced hepatic tumor proliferation.

WT ARF\textsubscript{26–44} peptide causes selective apoptosis of hepatic tumor cells. Analysis of H&E-stained liver tumor sections from mice treated with the WT ARF\textsubscript{26–44} peptide revealed that many of the hepatic
Figure 3
Treatment of mice with the WT ARF<sub>36–44</sub> peptide diminishes proliferation of mouse hepatic tumors. Hepatic tumors were induced in Fox<sub>mt</sub><sup>1</sup> mice with DEN/PB treatment, and then they were treated with daily i.p. injections of 5 mg/kg body weight of WT ARF<sub>36–44</sub> peptide or mutant ARF<sub>37–44</sub> peptide or PBS for 4 or 8 weeks as described in the Figure 2A legend. These ARF peptide–treated mice were given drinking water with 1 mg/ml of BrdU for 4 days before sacrifice in order to obtain long-term labeling of the liver tumors (37). Arrows indicate nuclear staining for BrdU incorporation, and arrowheads show liver tumor margins. (A–J) BrdU incorporation was detected by immunohistochemical staining of liver tumor sections with monoclonal BrdU antibody from mice treated with the indicated ARF peptides. (K) A graph of mean number of BrdU-positive cells per square millimeter liver tumor (±SD) following treatment with WT ARF<sub>36–44</sub> peptide or mutant ARF<sub>37–44</sub> peptide or PBS. We calculated the mean number (±SD) of BrdU-positive hepatocyte nuclei per square millimeter liver tumor from 3 distinct mice treated with ARF peptide as described in Methods. The asterisks indicate statistically significant changes: **P ≤ 0.01 and ***P ≤ 0.001. Magnification: ×200 (A–J).

adenomas and HCC tumor cells stained red and exhibited disruption of nuclear membrane, which is indicative of apoptosis (Figure 5, A–F). These red-staining cells were found neither in the surrounding normal liver tissue (Figure 5, A–F) nor in hepatic tumors from mice treated with either the mutant ARF<sub>37–44</sub> peptide or PBS (Figure 5, G–L). Furthermore, these apoptotic tumor cells were not apparent in deficient livers in dsoRNA CKO Mx<sup>Cre</sup> Fox<sub>mt</sub><sup>1</sup> mice (Figure 1, E–G), a finding consistent with our previous tumor studies with Alb-Cre Fox<sub>mt</sub><sup>1</sup> mice (8).

We used a fluorescence-based TUNEL assay to determine that mouse HCC cells treated with WT ARF<sub>36–44</sub> peptide exhibited a significant, 22% increase in apoptosis (Figure 6, A, B, and E). In contrast, very few apoptotic HCC cells were found after treatment with mutant ARF<sub>37–44</sub> peptide or PBS (Figure 6, C–E). Immunostaining of liver tumor sections with proteolytically cleaved activated caspase-3 protein confirmed this selective apoptosis of mouse HCC cells treated with WT ARF<sub>36–44</sub> peptide with no proapoptotic staining in the adjacent normal liver tissue (Figure 6, F–H). These studies show that the WT ARF peptide selectively induces apoptosis of HCC cells without damaging adjacent normal hepatocytes.

DEN/PB treatment induced highly proliferative HCC<sub>m</sub> Arf<sup>−/−</sup> Rosa26–FoxM1b Tg mice that were responsive to WT ARF<sub>36–44</sub> peptide treatment. We previously showed that the ARF tumor suppressor targets the FoxM1b protein to the nucleolus and inhibits its transcriptional function (8). Furthermore, we showed that increased expression of the human FoxM1b cDNA in Rosa26–FoxM1b Tg mice (34) stimulated development and progression of prostate cancers in both TRAMP/Rosa26–FoxM1b and LADY/Rosa26–FoxM1b double-Tg mice (35). In order to develop a new genetic model of HCC that is highly dependent on the FoxM1b transcription factor, we crossed the Rosa26–FoxM1b Tg mice into the Arf<sup>−/−</sup> mouse background. After 33 weeks of DEN/PB treatment, Arf<sup>−/−</sup> Rosa26–FoxM1b Tg mice developed highly proliferative HCCs, and their HCC cells displayed a proliferation rate of 6,000 BrdU-positive cells per square millimeter tumor (Figure 7), which is approximately 30-fold greater than that observed in DEN/PB-induced HCC<sub>m</sub> WT mice (Figure 3K, 200 BrdU-positive cells per mm<sup>2</sup> tumor). The DEN/PB-treated Arf<sup>−/−</sup> Rosa26–FoxM1b Tg livers also exhibited development of necrosis and fibrosis/cirrhosis (data not shown). These HCC tumor–bearing Arf<sup>−/−</sup> Rosa26–FoxM1b Tg mice were subjected to daily treatment with either the WT ARF<sub>36–44</sub> peptide or mutant ARF<sub>37–44</sub> peptide for 4 weeks. In Arf<sup>−/−</sup> Rosa26–FoxM1b Tg mice, WT ARF<sub>36–44</sub> peptide treatment resulted in a significant, 84% reduction in BrdU labeling of HCC cells compared with treatment of these mice with either mutant ARF<sub>37–44</sub> peptide or PBS (Figure 7, A–C and J). Red-staining HCC cells with disruption of nuclear membrane indicative of apoptosis were found in H&E-stained liver tumor sections from Arf<sup>−/−</sup> Rosa26–FoxM1b Tg mice treated with the WT ARF<sub>36–44</sub> peptide but not from those treated with mutant ARF<sub>37–44</sub> peptide or PBS (Figure 7, D–F). We used a fluorescence-based TUNEL assay to determine that Arf<sup>−/−</sup> Rosa26–FoxM1b Tg HCC cells treated with WT ARF<sub>36–44</sub> peptide exhibited a 42% increase in apoptosis (Figure 7K), which was twice as high as in liver tumors from WT mice (Figure 6E). Furthermore, TUNEL-positive cells were restricted to the HCC region (white arrowheads) and were not detected in adjacent normal liver tissue (Figure 7I). In contrast, very few apoptotic HCC cells were found after treatment of Arf<sup>−/−</sup> Rosa26–FoxM1b Tg mice with mutant ARF<sub>36–44</sub> peptide or PBS (Figure 7, G, H, and K). These Arf<sup>−/−</sup> Rosa26–FoxM1b Tg liver tumor studies show that the WT ARF<sub>36–44</sub> peptide is effective in diminishing BrdU labeling of highly proliferative HCC cells and selectively induces apoptosis of HCC cells in these mice without damaging adjacent normal liver tissue.

WT ARF<sub>36–44</sub> peptide inhibits angiogenesis of the HCC region. Angiogenesis is critical to mediating HCC growth, and the endothelial
Reduced levels of the antiapoptotic survivin protein contribute to WT ARF peptide–induced HCC apoptosis. We have shown that FoxM1 regulates transcription of survivin (26), which complexes with aurora B kinase and PLK1, aurora B kinase, and survivin proteins, which function to prevent their apoptosis (45, 48, 56–62). Previous studies have demonstrated that U2OS cells transfected with siFoxM1 #2 duplex were blocked in mitotic progression and exhibited undetectable levels of FoxM1 and its downstream target mitotic regulators PLK1, aurora B kinase, and survivin (26). Consistent with these observations, diminished levels of survivin, PLK1, and aurora B kinase proteins were detected in HCC regions from WT ARF peptide–treated mice (Figure 8, G and H). Western blot analysis revealed that Foxm1+/− liver tumors displayed a 60% decrease in expression of survivin protein (Figure 8, I and J), and no apoptosis was detected in these FoxM1-deficient liver tumors (Figure 1, E–G). A more drastic, 90% decrease in survivin protein levels was found in hepatic tumors from WT ARF peptide–treated mice (Figure 8, H–J). Our hepatoma data presented below (Figure 9) support the hypothesis that WT ARF peptide treatment results in hypomorphic levels of FoxM1 activity, which reduces expression of mitotic regulators to levels that are insufficient to properly execute mitosis leading to apoptosis, whereas depleting FoxM1 levels leads to mitotic arrest.

The nucleolar nucleophosmin/B23 (NPM/B23) protein (49, 50) and the p53 negative regulator, Mdm2 protein (51), associated with the ARF tumor suppressor protein through ARF amino acid sequences 1–15 and 26–37, which partially overlapped with our WT ARF peptide sequence. Despite this partial overlap, Western blot analysis enabled us to determine that neither WT ARF peptide treatment nor Foxm1 deficiency altered expression of NPM, p53, or Mdm2 proteins in liver tumor extracts (Figure 8, J and K, and data not shown), suggesting that the ARF peptide sequence was insufficient to influence their expression levels in vivo. The proapoptotic Bel-2 family member p53-regulated modifier of apoptosis (PUMA) is a transcriptional target gene of p53 that is essential for both p53 transcriptional and cytoplasmic-dependent apoptosis (52–55). Western blot analysis showed that neither WT ARF peptide nor mutant ARF peptide treatment caused significant change in expression of PUMA in liver tumor extracts (Figure 8K), suggesting that this apoptosis of HCC cells did not involve the p53/PUMA proapoptotic pathway.

WT ARF peptide–induced apoptosis of human hepatoma HepG2 cells correlates with diminished expression of survivin, PLK1, and aurora B kinase. We used the TUNEL assay to determine that human hepatoma HepG2 cells (Figure 9, A–E), PLC/PRF/5 cells that express mutant p53 protein, and p53-deficient Hep3B cells exhibited 50% apoptosis after 24 hours of treatment with 25 μM of WT ARF peptide (Figure 9E), whereas only low levels of apoptosis were detected in these cells following treatment with mutant ARF or PBS (Figure 9E). Diminished levels of p53 protein through p53 siRNA silencing of HepG2 cells did not influence apoptosis in response to WT ARF peptide treatment (Figure 9F). In addition, p53 protein levels were unaltered in HepG2 cells after 24 hours of treatment with WT ARF peptide (Figure 9E), or mutant ARF peptide (Figure 9F). Furthermore, protein expression of the p53 downstream proapoptotic target PUMA was unchanged in HepG2 cells in response to increasing concentrations of the WT ARF peptide (Figure 9E). These results suggest that WT ARF peptide–induced apoptosis was independent of the p53/PUMA proapoptotic pathway (52–55). Moreover, HepG2 cells in which FoxM1 levels were depleted by electroporation of FoxM1 no. 2 siRNA duplexes were resistant to apoptosis in response to WT ARF peptide treatment (Figure 9F), suggesting that induction of apoptosis by the WT ARF peptide was dependent on FoxM1 levels.

Tumor cells are known to express high levels of the mitotic regulators PLK1, aurora B kinase, and survivin proteins, which function to prevent their apoptosis (45, 48, 56–62). Previous studies demonstrated that U2OS cells transfected with siFoxM1 #2 duplex were blocked in mitotic progression and exhibited undetectable levels of FoxM1 and its downstream target mitotic regulators PLK1, aurora B kinase, and survivin (26). Consistent with these observations, diminish...
studies, FoxM1-depleted HepG2 cells exhibited undetectable protein levels of survivin, PLK1, and aurora B kinase (Figure 9G). We electroporated HepG2 cells with siFoxM1 #2 or control p27Kip1 siRNA (siP27) and grew the cells in culture for 2 days to allow for siRNA silencing, and then 2 x 10^4 HepG2 cells were plated in triplicate, and viable HepG2 cells were counted at 2, 3, 4, or 5 days following electroporation. These cell-growth studies showed that FoxM1-deficient HepG2 cells were unable to grow in culture and gradually detached from the plate with time in culture (Figure 9H). In contrast, HepG2 cells treated with WT ARF26–44 peptide exhibited a less severe reduction in levels of survivin (50%), PLK1 (80%), and aurora B kinase (80%) proteins compared with controls (Figure 9I). We also determined a growth curve of HepG2 cells at 1, 2, or 3 days following treatment with WT ARF26–44 peptide, mutant ARF27–44 peptide, or PBS. Although the WT ARF26–44 peptide–treated HepG2 cells displayed 50% apoptosis (Figure 9E), they were able to sustain proliferation of mouse liver cancer models (64). In contrast, mice treated with the cell-penetrating mutant ARF27–44 peptide, which is missing ARF sequences required for interaction with the FoxM1 inhibitor of FoxM1 function. After 33 weeks of DEN/PB treatment, Arf−/− Rosa26-FoxM1b Tg mice exhibited a significant amount of FoxM1 protein and eliminated ARF tumor suppressor inhibition of the FoxM1b protein. After 33 weeks of DEN/PB treatment, Arf−/− Rosa26-FoxM1b Tg mice exhibited highly proliferative HCC cells that displayed approximately 30-fold more BrdU incorporation than that found in WT mice in which liver tumors were induced by DEN/PB exposure. After 4 weeks of treatment with the WT ARF26–44 peptide, the Arf−/− Rosa26-FoxM1b Tg mice exhibited a significant reduction in BrdU incorporation, and apoptosis was induced in twice the number of HCC cells. The results suggest that these highly proliferative hepatic tumors with increased levels of FoxM1b protein are more susceptible to WT ARF26–44 peptide–induced apoptosis and display diminished proliferation of HCC cells.

Increased expression of antiapoptotic survivin protein in human HCC and stage II colorectal carcinomas correlates with reduced apoptosis, poor patient outcome, and tumor recurrence follow-

Discussion

Patients with HCCs have poor prognoses because late detection and high frequency of tumor recurrence render current HCC therapy ineffective (1). One of the potentially curative approaches in HCC therapy is based on interfering with HCC progression by blocking cell division and selectively inducing tumor cell apoptosis. In this study, we demonstrated that FoxM1 is required for proliferation of mouse liver cancer cells during tumor progression. To pharmacologically reduce in vivo activity of FoxM1 in HCC, mice were subjected to daily injections with a cell-penetrating ARF26–44 peptide inhibitor of FoxM1 function. After 4 weeks of ARF peptide treatment, FoxM1 protein was partially localized to the nucleus of HCC cells, and these hepatic tumor cells displayed reduced proliferation and angiogenesis with selective induction of HCC apoptosis (Figure 9K). Reduced tumor cell proliferation in Foxm1-deficient and WT ARF26–44 peptide–treated tumors was associated with nuclear accumulation of the CDK1 protein p27Kip1, which is known to negatively regulate proliferation of HCC cells in mouse liver cancer models (64). In contrast, mice treated with the cell-penetrating mutant ARF27–44 peptide, which is missing ARF sequences required for interaction with the FoxM1 inhibitor of FoxM1 function. After 33 weeks of DEN/PB treatment, Arf−/− Rosa26-FoxM1b Tg mice, which ubiquitously expressed the human FoxM1b cDNA transgene (34), into the Arf−/− mouse background. Use of the Arf−/− Rosa26-FoxM1b Tg mice allowed us to overexpress the FoxM1b protein and eliminated ARF tumor suppressor inhibition of the FoxM1b protein. After 33 weeks of DEN/PB treatment, Arf−/− Rosa26-FoxM1b Tg mice exhibited highly proliferative HCC cells that displayed approximately 30-fold more BrdU incorporation than that found in WT mice in which liver tumors were induced by DEN/PB exposure. After 4 weeks of treatment with the WT ARF26–44 peptide, the Arf−/− Rosa26-FoxM1b Tg mice exhibited a significant reduction in BrdU incorporation, and apoptosis was induced in twice the number of HCC cells. The results suggest that these highly proliferative hepatic tumors with increased levels of FoxM1b protein are more susceptible to WT ARF26–44 peptide–induced apoptosis and display diminished proliferation of HCC cells.

Increased expression of antiapoptotic survivin protein in human HCC and stage II colorectal carcinomas correlates with reduced apoptosis, poor patient outcome, and tumor recurrence follow-

**Figure 5**

H&E-stained liver tumors from mice treated with WT ARF26–44 peptide. Hepatic tumors were induced in Foxm1+/− mice with DEN/PB treatment, and then they were treated with daily i.p. injections of 5 mg/kg body weight of WT ARF26–44 Peptide or mutant ARF27–44 peptide for 4 or 8 weeks (see Figure 2A legend). Arrows indicate red-staining cells undergoing apoptosis, and arrowheads show liver tumor margins. (A–F) H&E-stained liver tumor sections from WT ARF26–44 peptide–treated mice revealed that many of the hepatic adenomas and HCC tumor cells stained red and were rounded up, which is indicative of apoptosis. E and F are higher-magnification images of C and D. No red-staining apoptotic cells were found in either the surrounding, normal liver tissue or in liver tumors from dsRNA CKO Mx-Cre Foxm1−/− mice (see Figure 1, E–G). (G–L) No red-staining tumor cells were found in H&E-stained liver tumor sections from mice treated with either PBS or mutant ARF27–44 peptide. Magnification, x200 (A–D and G–L); x400 (E and F).
ing treatment (46–48). Proliferating tumor cells are known to constitutively express high levels of the mitotic regulators PLK1, aurora B kinase, and survivin proteins, while normal cells only express these proteins in the G2 phase and mitosis. Experiments that reduced expression of these mitotic regulators with siRNA transfection or reduced their activity with specific kinase inhibitors caused increased apoptosis and diminished growth of cancer cells (45, 48, 56–62). We found that HCC regions and HepG2 cells expressed high levels of PLK1, aurora B kinase, and survivin, all of which are FoxM1 transcriptional target genes (26). Previous studies demonstrated that Foxm1–/– mouse embryonic fibroblasts or FoxM1-depleted U2OS cells were blocked in mitotic progression, failed to undergo apoptosis, and were associated with undetectable levels of PLK1, aurora B kinase, and survivin (26). Interestingly, we showed that WT ARF26–44 peptide treatment induced significant apoptosis in human hepatoma HepG2 cells, PLC/PRF/5 cells that express mutant p53 protein, and p53-deficient Hep3B cells. We also showed that siRNA silencing of FoxM1 levels in HepG2 cells reduced apoptosis in response to WT ARF26–44 peptide treatment, suggesting that ARF-dependent apoptosis of this hepatoma cell line required FoxM1 expression. Furthermore, we showed that FoxM1-depleted HepG2 cells failed to grow in culture and displayed undetectable levels of the mitotic regulators PLK1, aurora B kinase, and survivin proteins (Figure 9). In contrast, treatment of HepG2 cells with the WT ARF26–44 peptide resulted in less drastic reductions in expression of survivin, PLK1, and aurora B kinase protein and allowed growth of HepG2 cells in culture but resulted in a significant induction of apoptosis (Figure 9). Consistent with these findings, published studies demonstrated that hypomorphic levels of FoxM1 protein (40% of WT FoxM1 levels) in breast cancer cell lines transfected with a different Foxm1 siRNA duplex reduced expression of mitotic regulators to levels that are insufficient to properly execute mitosis, leading to mitotic catastrophe and apoptosis (63). Taken together, our results suggest that WT ARF26–44 peptide treatment of cancer cells results in partial inhibition of Foxm1 activity, leading to mitotic catastrophe and apoptosis caused by reducing expression of the mitotic regulators PLK1, aurora B kinase, and survivin proteins to levels that are insufficient for proper mitotic progression.

Angiogenesis of HCC cells is a critical event that serves to increase blood supply to the growing tumor, and CD34 protein is expressed on new sinusoid-like endothelial cells of HCC capillaries (39–41). Mice treated with our WT ARF26–44 peptide failed to develop new CD34-positive endothelial cells in HCC capillaries (Figure 8C), whereas HCC angiogenesis was not affected in dsRNA CKO Mx-Cre Foxm1–/– mice. One explanation for the difference between these mice is that the WT ARF26–44 peptide may also be inducing apoptosis of CD34-positive endothelial cells in HCC capillaries, thus preventing angiogenesis of HCC regions required for tumor growth and expansion (Figure 9K). This is supported by the fact that WT ARF26–44 peptide treatment induces apoptosis of HMEC-1 cells in vitro (Figure 8E). Although the WT ARF26–44 peptide induces apoptosis of HepG2 cells in vitro, we cannot rule out the possibility that this WT ARF peptide is also inducing apoptosis of HCC cells by preventing tumor angiogenesis, thus limiting blood supply required for efficient growth of HCCs.

The WT ARF26–44 peptide sequences required to inhibit Foxm1 function do not completely overlap with ARF coding regions essential to inactivating other cell-cycle regulators. For example, both amino acid regions 1–14 and 26–37 of the ARF protein are required for association and nucleolar targeting of the p53-negative regulator Mdm2 protein (65) and the NPM/B23 protein (49, 50). Consistent with the specificity of our WT ARF peptide treatment of mice, we found no changes in liver tumor expression of Mdm2, p53, or NPM/B23 proteins in vivo, and apoptosis was independent of increased expression of PUMA, a p53 target gene required for mediating apoptosis (52–55). The ARF tumor suppressor protein also mediates nucleolar targeting of both the proliferation-specific E2F1 and c-Myc transcription factors (11–14). However, there is no overlap with our WT ARF26–44 peptide sequence or the ARF sequences 1–14 and 26–37 of the ARF protein are required for association with the E2F1 (ARF sequences 6–10 and 21–25) protein (66) and c-Myc (ARF sequences 1–14) protein (12).
Cotransfection assays in U2OS cells demonstrated that expression constructs containing ARF 26–37 sequences were unable to effectively inhibit FoxM1b transcripational activity, suggesting that inhibition of FoxM1 function requires the entire ARF26–44 peptide sequence (data not shown). Furthermore, in the in vitro experiments with FoxM1-deficient HepG2 cells showed a clear relationship between FoxM1 and WT ARF26–44 peptide-mediated apoptosis. Moreover, a recent study has shown that translation initiation produces an ARF protein product initiating at methionine amino acid residue 45 and that this N-terminal–truncated ARF protein is localized to the mitochondria and induces caspase-independent cell death (67). Because these ARF26–44 peptide sequences are not contained within this N-terminal–truncated ARF polypeptide, the WT ARF26–44 peptide utilizes a mechanism that is distinct from the caspase-independent function of this N-terminal–truncated ARF peptide. Based on these studies, the WT ARF26–44 peptide will specifically reduce Foxm1 function in vivo to limit growth of HCC and produce an ARF protein product initiating at methionine amino acid residue 45 and that this N-terminal–truncated ARF protein contains within this N-terminal–truncated ARF polypeptide, the WT ARF26–44 peptide utilizes a mechanism that is distinct from the caspase-independent function of this N-terminal–truncated ARF peptide. Based on these studies, the WT ARF26–44 peptide will specifically reduce Foxm1 function in vivo to limit growth of HCC and induce HCC apoptosis without diminishing the function of other known inhibitory targets of the ARF tumor suppressor protein.

After i.p. injection, the absorbed WT ARF26–44 peptide enters the portal circulation and then flows to the hepatic sinusoid capillaries, which are lined with fenestrated endothelial cells that allow efficient delivery of the ARF peptide to the underlying hepatocytes and hepatic mesenchymal cells (68). However, WT ARF26–44 peptide treatment of mice did not cause side effects because it could not transverse the endothelial cell barrier of blood vessels to intestinal, colonic, pulmonary, pancreatic, or kidney epithelial cells (data not shown). Likewise, ARF peptide fluorescence also remained in the vessel endothelial cells of bone marrow, spleen, and thymus yet was undetectable in the hematopoietic cells of these organs, which correlated with normal distribution of white and red blood cells in mice treated with this WT ARF26–44 peptide (data not shown). Administration of WT ARF26–44 peptide by i.p. injection is therefore a selective method for hepatic delivery of this ARF peptide in vivo to limit liver tumor progression and selectively induce apoptosis of HCC cells.

Methods

Mx-Cre-mediated deletion of the Foxm1<sup>fl/fl</sup> allele in mouse liver tumors induced by DEN/PB exposure. Generation of C57BL/6 mice containing Foxm1<sup>fl/fl</sup> was described previously (25), and they were bred into the C57BL/6 mouse background for 8 generations. The type 1 IFN–inducible Mx-Cre Tg C57BL/6 mice (C57BL/6-TgN Mx-Cre mice) were purchased from The Jackson Laboratory. The Mx-Cre Tg C57BL/6 mice were bred with Foxm1<sup>fl/+</sup> C57BL/6 mice, and the offspring were screened for Mx-Cre Foxm1<sup>fl/+</sup> mice. These mice were then backcrossed with Foxm1<sup>fl/+</sup>C57BL/6 mice to generate Mx-Cre Foxm1<sup>fl/+</sup>C57BL/6 mice. Mx-Cre Foxm1<sup>fl/+</sup>C57BL/6 mice were bred with Foxm1<sup>–/–</sup>C57BL/6 mice to generate a sufficient number of mice for the liver tumor experiments. Charles J. Sherr (St. Jude Children’s Research Hospital, Memphis, Tennessee, USA) provided the Arf<sup>–/–</sup>C57BL/6 mice (69). The Arf<sup>–/–</sup>C57BL/6 mice were backcrossed with the Rosa26-FoxM1b FVB/N Tg mice, which ubiquitously express the human FoxM1b cDNA (34), to generate Arf<sup>–/–</sup>Rosa26-FoxM1b Tg mice.

At 14 days after birth, each mouse in the litter received a single, i.p. injection of the tumor initiator DEN (5 mg/g body weight; catalog N0756; Sigma-Aldrich) to induce liver tumors (8). Two weeks later, male mice were given water containing 0.025% PB tumor promoter for the duration of the experiment (8). At 30 weeks of DEN/PB exposure (which leads to HCC formation), we subjected Mx-Cre Foxm1<sup>fl/+</sup> mice to 3 consecutive i.p. injec-

Figure 7

WT ARF<sub>26–44</sub> peptide treatment reduces proliferation and increases apoptosis of HCCs, which were induced in Arf<sup>–/–</sup>Rosa26-FoxM1b Tg mice by DEN/PB. Highly proliferative HCC tumors were induced in Arf<sup>–/–</sup>Rosa26-FoxM1b Tg mice following 33 weeks DEN/PB treatment. The Arf<sup>–/–</sup>Rosa26-FoxM1b Tg mice received daily i.p. injections of the WT ARF<sub>26–44</sub> peptide (inhibitor of FoxM1 function) or mutant ARF<sub>26–44</sub> peptide or PBS for 4 weeks. (A–C) Liver tumor sections were subjected to immunohistochemical staining with BrdU monoclonal antibody to determine HCC proliferation. Liver tumor sections were histologically stained with H&E (D and E) to identify red apoptotic cells or stained for apoptosis using the TUNEL assay (G–I). Black arrowheads indicate the boundaries of the HCC tumor, and white arrowheads (I) indicate the boundary of the HCC region. (J) We counted the BrdU-positive cells in HCCs and used this information to calculate the number of BrdU-positive cells per square millimeter liver tumor tissue (±SD). (K) We counted the TUNEL-positive cells in HCCs and used this information to calculate the percent HCC apoptosis (±SD). P values calculated by Student’s t-test: ***P ≤ 0.001. Magnification: ×200 (A–F); ×100 (G–I).
WT ARF<sub>26–44</sub> peptide reduces angiogenesis and survivin expression in mouse HCC. The CD34 protein is a marker for newly formed sinusoid-like capillaries in HCC regions (39–41), whereas survivin is critical in preventing apoptosis of tumor cells (45–48). Antibodies specific to either CD34 or survivin were used to immunostain HCC tumor sections from mice treated with mutant ARF<sub>37–44</sub> peptide, WT ARF<sub>26–44</sub> peptide, or PBS from dsRNA CKO Mx-Cre Foxm<sub>1<sup>fl/fl</sup></sub> mice. (A–D) Mice treated with WT ARF<sub>26–44</sub> peptide display no CD34-positive endothelial cells in HCC capillaries, whereas CD34 staining (indicated by arrows) was abundant in endothelial cells of control mouse HCCs. (E) WT ARF<sub>26–44</sub> peptide induces apoptosis of HMEC-1 cells. HMEC-1 cells were treated for 48 hours with 100 μM of WT ARF<sub>26–44</sub> peptide or mutant ARF<sub>37–44</sub> peptide or with PBS and then assayed for apoptosis as described in Methods. Shown graphically is the percent apoptosis of HMEC-1 cells in response to ARF peptide treatment. (F–I) Reduced survivin expression in WT ARF<sub>26–44</sub> peptide–treated and Foxm<sub>1<sup>fl/fl</sup></sub> liver tumors. Arrows indicate nuclear staining for survivin protein. (J) Western blot analysis reveals significant decrease in survivin protein expression in WT ARF<sub>26–44</sub> peptide–treated mouse tumors. (K) No decrease in expression of NPM protein or p53-regulated proapoptotic PUMA protein is found in WT ARF<sub>26–44</sub> peptide–treated mouse tumors. A slight increase in hepatic tumor levels of PUMA was found in mice treated with dsRNA. Magnification, ×400.
DAPI-positive hepatocyte nuclei per 1,000 cells or ×200 field by counting the number of positive hepatocyte nuclei using 5 different ×200 fields of liver tumor sections from male mice at the indicated times of DEN/PB exposure. We used 5 liver tumor sections from 3 mice to calculate the mean number of BrdU-positive cells (±SD) per square millimeter liver tumor. To calculate the area or size of liver tumors, we used micrographs of H&E-stained liver tumor sections taken by an Axioplan 2 microscope (Zeiss) and the AxioVision program (version 4.3; Zeiss).

Western blot analysis. For Western blot analysis, 75 μg of total protein extracts prepared from liver were separated on SDS-PAGE and transferred to a PVDF membrane (Bio-Rad) as described previously (25). The following commercially available antibodies and dilutions were used for Western blotting: mouse anti–Plk-1 (F-8, 1:500; Santa Cruz Biotechnology Inc.), mouse anti-p53 (FL-393, 1:500; Santa Cruz Biotechnology Inc.), mouse anti-MDM2 (SMP14, 1:500; Santa Cruz Biotechnology Inc.), mouse anti–aurora B kinase (AC-15, 1:5,000; Sigma-Aldrich), mouse anti–aurora B kinase/AIM-1 (1:1,000; BD Biosciences), rabbit anti-survivin (1:2,000; Novus Biologicals), mouse anti-PUMA (1:1,000; Cell Signaling Technology), and mouse anti-NPM/B23 (1:15,000; Zymed). The primary antibody signals were amplified by HRP-conjugated secondary antibodies (Bio-Rad) and detected with Enhanced Chemiluminescence Plus (ECL Plus; Amersham Biosciences). Western blot analysis was performed with liver extracts from 2–4 mice per indicated time point following DEN/PB treatment, and signal intensities were normalized to β-actin signals. Quantitation of expression levels was determined with tiff files from scanned films using the BioMax 1D software program (Kodak).

Treatment of doxycycline-inducible U2OS C3 cells with WT ARF26–44 peptide or mutant ARF37–44 peptide. We previously reported on the generation and growth of an osteosarcoma U2OS clone C3 cell line (U2OS C3 cells) that allowed doxycycline-inducible (Dox-inducible) expression of the GFP-FoxM1b fusion protein (24). For induced expression of the GFP-FoxM1b fusion protein, 75 μg of total protein extracts prepared from liver were separated on SDS-PAGE and transferred to a PVDF membrane (Bio-Rad) as described previously (25). The following commercially available antibodies and dilutions were used for Western blotting: mouse anti–Plk-1 (F-8, 1:500; Santa Cruz Biotechnology Inc.), mouse anti-p53 (FL-393, 1:500; Santa Cruz Biotechnology Inc.), mouse anti-MDM2 (SMP14, 1:500; Santa Cruz Biotechnology Inc.), mouse anti–aurora B kinase (AC-15, 1:5,000; Sigma-Aldrich), mouse anti–aurora B kinase/AIM-1 (1:1,000; BD Biosciences), rabbit anti-survivin (1:2,000; Novus Biologicals), mouse anti-PUMA (1:1,000; Cell Signaling Technology), and mouse anti-NPM/B23 (1:15,000; Zymed). The primary antibody signals were amplified by HRP-conjugated secondary antibodies (Bio-Rad) and detected with Enhanced Chemiluminescence Plus (ECL Plus; Amersham Biosciences). Western blot analysis was performed with liver extracts from 2–4 mice per indicated time point following DEN/PB treatment, and signal intensities were normalized to β-actin signals. Quantitation of expression levels was determined with tiff files from scanned films using the BioMax 1D software program (Kodak).

Figure 9
WT ARF26–44 peptide–induced apoptosis of human hepatoma cell lines. Human hepatoma HepG2 (A–E), PLC/PRF/5 (expressing p53 mutant protein), or Hep3B (p53-deficient) cells were treated for 24 hours with 25 μM of WT ARF26–44 or mutant ARF37–44 peptide; they were then analyzed for apoptosis by TUNEL assay, and percent apoptosis (±SD) was calculated (E; ***P ≤ 0.001). Merged DAPI and TUNEL staining (A and C) images show TUNEL-positive nuclei of HepG2 cells (white arrows, B and D). (F) Graphic representation of WT ARF26–44 peptide–treated HepG2 cells showing that apoptosis is induced in p53-depleted cells but not in FoxM1-deficient cells. Western blot analysis is presented below the graph, showing effective downregulation of p53 protein levels following p53 siRNA electroporation and that treatment with WT ARF26–44 (WT) or mutant ARF37–44 peptide (M) does not alter p53 protein levels. (G and I) At 48 hours after electroporation with siFoxM1 no. 2 or p27 siRNA duplexes (G), or treatment with WT or mutant ARF peptide (I), HepG2 cells were analyzed for protein expression of survivin, PLK1, and aurora B kinase by Western blot analysis. We also determined a growth curve of HepG2 cells at the indicated days following siRNA transfection (H) or at the indicated days after ARF peptide treatment (J) as described in Methods. (K) Model summarizing findings in this article with WT ARF26–44 peptide. Magnification, ×400.
protein, we added 1 μg/ml of Dox (Sigma-Aldrich). In order to determine the FoxM1b localization in U2OS C3 cells, they were treated with 12 μM of the TMR fluorescently tagged WT ARF53–44 or mutant ARF57–44 peptide for 24 hours. U2OS C3 cells were fixed with 10% buffered formalin (Fisher Scientific) for 20 minutes at room temperature and rinsed with PBS, and cover glasses were mounted with VECTASHIELD Mounting Medium with DAPI (catalog H-1200; Vector Laboratories). Immunofluorescence was detected using an Axioscan 2 microscope.

Treatment of human hepatoma cell lines with WT ARF53–44 or mutant ARF57–44 peptide and siRNA transfection. HepG2 cells were plated on 100-mm plates in Ham’s F-12 medium supplemented with 10% FCS, 100 IU/ml penicillin, 100 μg/ml streptomycin, 2 mM l-glutamine, and 0.5 μ Humulin (insulin; Lilly). HepG2 cells were treated with 12 μM, 25 μM, or 50 μM of WT ARF53–44 peptide or mutant ARF57–44 peptide for 24 hours and used to prepare whole-cell protein extracts using the NP40 lysis buffer as described previously (26), and Western blot analysis to examine expression of PUMA, survivin, PLK1, and caspases 3 and 7, was performed. HepG2 cells were transfected with one of the siRNA duplexes (Dharmacon Research) and examined for apoptosis as described above.

The transfection of human cells with FoxM1 or p27Kip1 siRNA duplexes (Dharmacon Research) was conducted by electroporation using a HiPerFect transfection reagent (Qiagen, Inc.). HepG2 cells were electroporated with 100 nM of FoxM1 or p27Kip1 siRNA duplexes (26) using the Nucleofector II apparatus (Amaxa Biosystems) and eletroporation buffers recommended by the manufacturer for HepG2 cells. HepG2 cells were replated for 2 days to allow siRNA silencing of FoxM1 or p27Kip1 levels, and then 2 × 10^5 HepG2 cells were plated in triplicate, and viable HepG2 cells were counted at 2, 3, 4, or 5 days following electroporation.

Mock-electroporated cells were used as controls. We also plated 2 × 10^5 HepG2 cells in triplicate, and viable HepG2 cells were counted at 1, 2, or 3 days following treatment with 50 μM of WT ARF53–44 peptide or mutant ARF57–44 peptide. After 2 days in culture, media was replaced with 50 μM of WT ARF53–44 peptide or mutant ARF57–44 peptide. PBS-treated cells were used as controls.

**Statistics.** We used the Microsoft Excel program to calculate SD and statistically significant differences between samples using the 2-tailed Student’s t test. The asterisks in each graph indicate statistically significant changes with P values calculated by Student’s t-test: *P < 0.05, **P < 0.01, and ***P < 0.001. P values less than 0.05 were considered statistically significant.

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While the revised manuscript was in preparation, Robert H. Costa died in his fight against pancreatic cancer. The authors dedicate this work to his memory.


