Overexpression of HMGA2 Promotes Metastasis and Impacts Survival of Colorectal Cancers

Xiaochen Wang1,4, Xiyong Liu4, Angela Ying-Jian Li4, Lirong Chen2, Lily Lai5, Her Helen Lin4, Shu Zheng3, Peiguo Chu6, Suzhan Zhang1, David Kong Ann4, and Yun Yen4

Abstract

**Purpose:** This study aims to address the hypothesis that the high-mobility group A2 (HMGA2), an oncofetal protein, relates to survivability and serves as a prognostic biomarker for colorectal cancer (CRC).

**Experimental Design:** This is a retrospective multiple center study. The HMGA2 expression level was determined by performing immunohistochemistry on surgical tissue samples of 89 CRCs from a training set and 191 CRCs from a validation set. The Kaplan–Meier analysis and Cox proportional hazard model were employed to analyze the survivability.

**Results:** Multivariate logistic analysis indicated that the expression of HMGA2 significantly correlates with distant metastasis in training set (odds ratio, OR = 3.53, 95% CI: 1.37–9.70) and validation set (OR = 6.38, 95% CI: 1.47–43.95). Survival analysis revealed that the overexpression of HMGA2 is significantly associated with poor survival of CRC patients (P < 0.05). The adjusted HRs for overall survival were 2.38 (95% CI: 1.30–4.34) and 2.14 (95% CI: 1.21–3.79) in training and validation sets, respectively. Further investigation revealed that HMGA2 delays the clearance of γ-H2AX in HCT-116 and SW480 cells post-γ-irradiation, which supports our finding that CRC patients with HMAG2-positive staining in primary tumors had augmented the efficacy of adjuvant radiotherapy (HR = 0.18, 95% CI: 0.04–0.63).

**Conclusion:** Overexpression of HMGA2 is associated with metastasis and unequivocally occurred in parallel with reduced survival rates of patients with CRC. Therefore, HMGA2 may potentially serve as a biomarker for predicting aggressive CRC with poor survivability and as an indicator for better response of radiotherapy. Clin Cancer Res; 17(8); 2570–80. ©2011 AACR.

Introduction

Colorectal cancer (CRC), one of the most prevalent cancers in the world, consists of a group of histological heterogeneous diseases involving distinct tumorigenic pathways. It ranks as the 2nd leading death from cancer in the United States (1) and the 4th in China (2). Mortality from CRC is mainly due to metastatic disease detected in at least half of the cases (3). Untreated patients with liver metastases have a 5-year survival rate of a mere 2% (4). Even though numerous genes have been implicated in colon tumorigenesis, only a few of them have been validated as biomarkers for predicting metastasis and treatment response.

High-mobility group A (HMGA) gene family includes 4 chromatin-binding proteins: HMGA1a, HMGA1b, HMGA1c, and HMGA2. Each of them contains 3 "AT-hooks," the functional motif characteristic of the HMGA family (5). HMGA2 encodes a small nonhistone chromatin–associated protein that has no intrinsic transcriptional activity, but can modulate transcription by altering the chromatin architecture (6, 7). In humans, the HMGA2 gene is located at chromosome 12q14 and encodes a 109 amino acid protein. HMGA2 is expressed during embryogenesis, but is absent or present at low levels in terminally differentiated tissues. In embryonic tissues, HMGA2 reportedly plays a critical role in stimulating normal cardiogenesis (8) and mouse central and peripheral neural stem cell self-renewal (9), thereby regulating cell growth and differentiation. HMGA2 is overexpressed in many malignant neoplasms...
Translational Relevance

The high-mobility group A2 (HMGA2) protein, a nonhistone chromosomal architectural protein, regulates the expression of a cohort of genes by either enhancing or suppressing their transcription. A change in the HMGA2 mRNA or protein level correlates with the malignant phenotype. In this report, we investigated the hypothesis that the expression level of HMGA2 is related to cancer survivability and serves as a prognostic biomarker for the clinical outcome of colorectal cancer (CRC). HMGA2 overexpression led to suppression of nonhomologous end joining pathway in repairing DNA double-strand breaks. CRC patients with HMAG2-positive staining in primary tumors had augmented the efficacy of adjuvant radiotherapy. Therefore, HMGA2 is a potential predictive biomarker for CRCs’ therapeutic outcome.

(5, 10, 11), and overexpression of HMGA2 is a poor prognostic factor for lung cancer (12), oral squamous cell carcinoma (13), ovarian cancer (14), and metastatic breast cancer (15). Expression of HMGA2 has been found to be related to Dukes stages and metastasis of CRCs in a cross-section study (16). However, it is not known whether HMGA2 overexpression is associated with the survival of CRCs nor whether HMGA2 is related to response of therapies for any cancer type.

In this study, we investigated whether the HMGA2 level is associated with the survival of CRC patients. We optimized the conditions of immunohistochemistry (IHC) for HMGA2 and conducted an outcome study on a training set with 89 CRC cases collected from City of Hope National Medical Center, Duarte, CA. In addition, we validated our finding by 191 cases collected from the Second Affiliated Hospital, Zhejiang University, Hangzhou, China. We determined that a sample size of 190 patients would be needed for about 80% power with a 2-sided \( \alpha \) of 0.05.

Materials and Methods

Patients

The eligible CRCs were collected based on inclusion and exclusion criteria. Inclusion criteria: (i) CRCs with pathological diagnosis; (ii) informed consent obtained or waiver of consent; and (iii) follow-up information available. Exclusion criteria: (i) failed to get informed consent; (ii) multiple cancers; (iii) lack of histological diagnosis; and (iv) no follow-up information. A series of assessable 89 CRCs which received surgical operation in City of Hope National Medical Center from 1980 to 1985 were recruited as training set. The participants in the training set include 82 Caucasian, 2 African–American, 3 Asian, and 1 unknown. After surgical therapy, 37 cases have had adjuvant chemotherapy and 11 cases had radiotherapy. Meanwhile, 191 consecutive assessable CRC patients who received surgical treatment in the School of Medicine, Second Affiliated Hospital, Zhejiang University, between 1999 and 2004 were entered as the validation set. All CRCs in the validation set are Chinese (Asian). In the validation set, 66 of 191 cases had adjuvant chemotherapy after surgery. All patients were followed up until June 2007 and details of their demographic and survival data were updated (Table 1). All tumor node metastasis (TNM) stage data were obtained from clinical and pathological diagnosis. Primary tumor samples were obtained from surgical operation.

Study design

To avoid biases, standards and conditions of IHC for HMGA2 expression determination were optimized on the training set [multiple tissue board (MTB)] and validated on the validation set [multiple tissue array (MTA)]. Careful chart review was conducted and pathoclinical data were abstracted. Variables assessed included birth date, gender, date of diagnosis, date of operation, type of chemotherapy, date of chemotherapy, type of radiotherapy, date of radiotherapy, TNM stage, relapse/metastasis status, date of relapse/metastasis, date of last follow-up, and vital status at last follow-up. The earlier information was coded and entered into a CRC database. Double data entry and logic checks were used for error reduction.

Sample size was calculated by parameter estimates obtained from a pilot study previously conducted at City of Hope. By nQuery Advisor 6.01 software, it was determined that a sample size of 190 patients would be needed for about 80% power with a 2-sided \( \alpha \) of 0.05. All patients were periodically followed for survival; patients with curative operations were also followed for recurrence-free survival. The follow-up period was calculated from the date of surgery until the date of last contact. The time of disease-free survival was defined at the time of initial surgical therapy to tumor recurrence. Metastasis or local relapse was considered evidence of tumor recurrence. Only deaths from CRC were considered as endpoint of disease-specific survival.

Construction of MTA and MTB

In the training set, all tissue samples were reassembled as MTB. Each MTB contained 8 to 12 pieces of sections, and each piece is approximately 1 mm × 10 mm. The tumor blocks also contained both tumor and normal colorectal tissue samples as positive and negative controls for each IHC staining.

To validate the IHC results yielded from MTB, the MTA blocks were constructed by 2 mm cores taken from archival, routinely processed, and paraffin-embedded CRC specimens in the validation set. The specimens had been accessioned between 1999 and 2004 and were selected solely based on the availability of CRC in the block. Pathologic diagnosis, grade, and stage were previously determined for each case by attending pathologists from the Department of Pathology.
Both MTAs and MTBs were stored at room temperature. To determine whether the storage time affected the signal of IHC staining, we conducted a cross-tabulation between overall HMGA2 staining and year of diagnosis among the earlier samples. Both likelihood ratio ($P = 0.235$) and Pearson ($P = 0.354$) tests yielded results, indicating that the quality was not reduced due to increased storage time of samples.

### Table 1. Pathoclinical characteristics and HMGA2 distribution of eligible CRCs from COH and ZJU

<table>
<thead>
<tr>
<th></th>
<th>Training set (COH)</th>
<th>Validation set (ZJU)</th>
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<tr>
<td></td>
<td>$n = 89$</td>
<td>$n = 191$</td>
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<tr>
<td>Number of cases</td>
<td>Number of positive</td>
<td>Number of positive</td>
</tr>
<tr>
<td></td>
<td>HMGA2$^a$ (%)</td>
<td>HMGA2$^a$ (%)</td>
</tr>
<tr>
<td>Age$^b$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;40</td>
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<td>-distal$^d$</td>
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<td>11 (36.7)</td>
<td>20 (41.7)</td>
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<td>Tumor invasion$^b$</td>
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<td>32 (35.2)</td>
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<td>39</td>
<td>11</td>
</tr>
<tr>
<td></td>
<td>19 (48.7)</td>
<td>9 (81.8)</td>
</tr>
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</table>

**NOTE:** COH indicates that samples were collected from City of Hope; and ZJU means that samples were from Zhejiang University. All information about TNM stage (tumor invasion, lymph node involvement, and distant metastasis) was based on clinical and pathological diagnosis at the time of first surgical operation.

$^a$Positive HMGA2 includes weak positive and strong positive of nuclear staining score.

$^b$In training set, there is 1 unspecified age, 1 unspecified colon cancer, and 1 missing case in tumor invasion. In validation set, there are 2 unspecified colon cancer and 1 missing case in tumor invasion.

$^c$Proximal colon includes: hepatic flexure, transverse, cecum, appendix, ascending, and splenic flexure.

$^d$Distal colon includes: sigmoid and descending colon.

$^e$, $P < 0.05$, statistical significance.

Quantitative IHC assays

IHC was used to investigate the HMGA2 protein expression. The accuracy of IHC was validated by quantitative RT-PCR (qRT-PCR) on 2 parallel samples. The details of deparaffinization and IHC were described previously (17). Briefly, after deparaffinization, the endogenous peroxidase activity was blocked with 3% H$_2$O$_2$ (hydrogen peroxide). The array slides were incubated with normal...
goat serum for 20 minutes and then applied with primary antibody for 20 minutes at room temperature. After 7 minutes of H$_2$O$_2$ treatment, the array slides were incubated with horseradish peroxidase–labeled polymer conjugated with corresponding antibodies for 30 minutes. Then, 3, 3-diaminobenzidine (0.05 g of 3, 3-diaminobenzidine and 100 mL of 30% H$_2$O$_2$ in 100 mL of PBS) was applied for 5 and 10 minutes, respectively. Each slide was counterstained with hematoxylin (DAKO). PBS was used as a negative control.

The rabbit antibody against HMGA2 was purchased from Alexis BioCheck Company and applied for IHC staining (1:1,000 dilution). Preselection of HMGA2 antibody was according to Western blot (Supplementary Fig. S1), and the optimized IHC condition was based on a serial dilution. To reduce the image reader bias, an automated imaging system was employed to obtain digital images of the stained sections for subsequent quantitative analyses. In addition, each sample was evaluated by 2 independent investigators in a double-blind manner. Investigators reviewed and assessed the subcellular localization (e.g., cytoplasm versus nucleus), staining intensity (e.g., integrated optical density), and/or percentage of stained cells (e.g., total area or percentage of cells positive) for each image. Discrepancies in samples were resolved after joint review by the readers.

In generally, HMGA2 was predominantly nuclear staining in IHC. However, the HMGA2 was heterogeneously expressed between and within tumors. Some perinuclear granulation in cytoplasm was also observed. HMGA2 expression was quantified by a visual grading system on the basis of the extent of staining. Only immunoreactivity in the nucleus was evaluated. HMGA2 was negative (−): less than 5% positive nuclear staining from CRC cells; positive (+): 5% or more than 5% and less than 50% positive nuclear staining from tumor cells; or strong positive (++): more than 50% positive nuclear staining from tumor cells. The HMGA2 IHC standard of negative (−), weak positive (+), and strong positive (+++) were displayed in Figure 1A–C, respectively. HMGA2 expression was predominantly observed in the primary cancer cells, but not in the adjacent normal colorectal epithelium (Fig. 1D–F). Meanwhile, strong positive HMGA2 also could be seen in metastatic CRC to liver (Fig. 1G–I).

Figure 1. IHC staining of HMGA2. A, B, and C, upper, the standard of IHC staining with negative (−), weak positive (+), and strong positive (+++) is shown. D, middle, the HMGA2 staining in colon tumor and adjacent normal colon tissues with low magnification (100×). E and F, normal and cancer section with high magnification (200×), respectively. G, lower, HMGA2 expression in metastatic colon cancer to liver (100×). H and I, normal liver and metastatic colon cancer, respectively. The magnification is indicated in each panel.
Cell culture, HMGA2 transduction, γ-irradiation, and Western blot analysis

HCT-116 and SW480 CRC cell lines were cultured in Leibovitz’s L15 medium (Gibco) supplemented with 10% FBS (HyClone). Lentiviral vectors pRRLSin.hCMV-HMGA2 pA8.7, and pVSV-G were constructed and used for lentiviral production in HEK 293T (human embryonic kidney 293T) cells as previously described (18). HCT116 and SW480 cells were transduced with lentiviruses encoding HMGA2 or vector alone. The transduced cells were irradiated (3 Gy/minute, room temperature) by a 137Cs source (mark II, gamma irradiator). Cells were then harvested by Laemmlı sample buffer at respective time points postirradiation followed by Western analysis. The antibodies used in this study were as follow: anti-HMGA2 (Biocheck), anti-actin (Chemicon), anti-γ-H2AX (Upstate), and anti-H2AX (Santa Cruz Biotechnology).

Statistical analysis

Data were analyzed by the JMP Statistical Discovery Software version 8.0 (SAS Institute, Cary, NC). The missing cases were labeled with missing code to avoid counting in statistical analysis. Group comparisons for continuous data were done with t test for independent means or 1-way ANOVA. For categorical data, chi-square analysis, Fisher’s exact test or binomial test of proportions was used. Multivariate logistic regression models were used to adjust for covariate effects on the odds ratio (OR). The Kaplan–Meier expression in primary CRC inversely correlated with the median survival time in the training and validation sets. The "strong positive" HMGA2 (++) exhibited a significantly reduced survivability (P < 0.05). The recurrence analysis (Fig 2C and D) confirmed that the strong positive HMGA2 status significantly increased the risk for recurrence in both training and validation sets.

To avoid confounder effects, the multivariate COX analysis was conducted on both training and validation sets (Fig 2E and F, and Supplementary Table S2). In the training set, factors including TNM stage, tumor location, gender, and age were applied to adjust the HR. To reduce the variance yield from insufficient sample size of the analysis, HMGA2 (+) and HMGA2 (+++) were merged together as HMGA2 positive in COX proportional analysis. As illustrated in Figure 2E and F, HMGA2 and TNM stages were significantly associated with poor OS of CRC for both training and validation sets with HRs for HMGA2 of 2.38 (95% CI: 1.30–4.34) and 2.14 (95% CI: 1.21–3.79), respectively. The HR of TNM stage also exhibited a comparable value in both sets, supporting the accuracy of our study. The tumor location significantly affected the prognosis in the training set, but it was not a significant contributing factor for the validation set (Supplementary Table S2). The unexpected variance may be caused by small sample size of rectal cancer (only 7 cases) in the training set (Table 1). The gender and age did not correlate significantly with CRC survival in both sets. Overall, our analyses revealed that HMGA2 was significantly associated with the poor survival of CRC patients.

HMGA2 impacts the survival of CRC patients with Stages III and IV

To confirm our finding, we analyzed the OS and PFS in different stages. As shown in Table 2, HMGA2 significantly impacts the survival of CRC patients with stages III and IV.
HMGA2 as a Biomarker of Poor Prognosis in Colorectal Cancer

Figure 2. Positive HMGA2 impacts OS and recurrence of CRCs. The Kaplan–Meier analysis for OS is shown in upper panel, and the recurrence analysis is illustrated in middle panel, and the multivariate COX proportional hazard analysis is displayed in lower panel. The data from training set and validation set are shown on left and right columns, respectively. A, Kaplan–Meier analysis for OS of CRCs from training set with different HMGA2 levels. B, Kaplan–Meier analysis for OS of CRCs from validation set with different HMGA2 levels. C, recurrence analysis for CRCs from training set. D, recurrence analysis for CRCs from validation set. E, multivariate COX analysis for OS of CRCs from training set. F, multivariate COX analysis for OS of CRC from validation set. The detail results of (E) and (F) were displayed in Supplementary Table S2.
Impacted the survival of patients with CRC at stages III and IV, but not stages I and II in the training set. Although the tendency in the stages I and II could be detected, it was not statistically significant (P > 0.05). By contrast, the HMGA2 expression was associated with worse OS and PFS for stages III and IV CRC with a statistical significance (P < 0.05). The HRs of positive HMGA2 for OS and PFS were 2.52 (95% CI: 1.37–4.58) and 2.95 (95% CI: 1.57–5.50), respectively. This finding was confirmed with the validation set. Stratification analysis on validation set revealed that the adjusted HRs of HMGA2 for OS and PFS were 1.91 (95% CI: 0.98–3.66) and 2.05 (95% CI: 1.05–3.95), respectively. An additional Kaplan–Meier analysis revealed that the expression level of HMGA2 is inversely correlated with the median OS of rectal cancer in the validation set (Fig. 3D). On the basis of the earlier finding, we conclude that the HMGA2 overexpression represents an important molecular change specific for stages III and IV CRC, significantly impacting the survival of patients with cancers located in colon or rectum.

**Expression of HMGA2 delays the clearance of γ-H2AX post γ-irradiation in HCT-116 and SW480 cells, suggesting a mechanism for the HMGA2-augmented sensitivity to radiotherapy in CRC patients**

Previous studies have shown that HMGA2 overexpression led to suppression of nonhomologous end joining (NHEJ) pathway in repairing double-strand breaks (DSB) of DNA (19, 20). On the basis of our previous findings, the persistence of γ-H2AX could serve as an indirect indicator for DNA damage response and the failure to repair DSBs. To investigate whether HMGA2 expression in colon cancer cells can lead to DNA damage accumulation, the clearance rates of γ-H2AX in HCT116 and SW480 cells with distinct HMGA2 contexts were assessed at various time points post γ-ray exposure. HCT116 and SW480 cells were transduced with vector- or HMGA2-harboring lentiviruses to generate vector control or HMGA2-expressing cells (Fig. 4A). Overexpression of HMGA2 rendered enhanced and prolonged phosphorylation of H2AX postirradiation compared with vector control in both HCT116 [Fig. 4B (right)] and SW480

<table>
<thead>
<tr>
<th>Tumor location</th>
<th>Cancer</th>
<th>Number of cases</th>
<th>HR of OS (95% CI)</th>
<th>HR of PFS (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colon</td>
<td>stage I</td>
<td>81</td>
<td>1.44</td>
<td>1.33</td>
</tr>
<tr>
<td></td>
<td>stage II</td>
<td>81</td>
<td>(0.81–2.50)</td>
<td>(0.76–2.24)</td>
</tr>
<tr>
<td>Rectum</td>
<td>stage I</td>
<td>7</td>
<td>N/A</td>
<td>3.19</td>
</tr>
<tr>
<td></td>
<td>stage II</td>
<td>7</td>
<td>N/A</td>
<td>(1.46–7.14)</td>
</tr>
</tbody>
</table>

**Table 2. Stratification and multivariate analysis for HMGA2 and survival of CRCs**

NOTE: Multivariate COX proportional hazard analysis was conducted to evaluate HR of HMGA2 positive versus negative. The HRs were adjusted by sex and age at diagnosis. The TNM stage was based on tumor invasion, lympho node involvement, and distance organ metastasis. The stage IV CRCs were excluded in PFS analysis. HRs of RRM2 and RRM2B were based on high expression versus low expression. N/A means not available.

*Statistics significant on COX analysis, P < 0.05.
Fig. 4B (left) cells, suggesting that expression of HMGA2 rendered cells an inability to repair DNA timely. The aforementioned finding implied that HMGA2 levels might be affecting the outcome of radiotherapy in CRC patients. To address this hypothesis, a multivariate analysis was conducted and stratified by HMGA2 negative and positive (Fig. 4C and D, Supplementary Table S3). Those potential confounders, such as chemotherapy, TNM stage, tumor location, pathological grade, age, and gender that potentially relate to outcome of therapy were incorporated into multivariate analysis model. The results indicated that the radiotherapy did not affect the survival in HMGA2 negative CRCs (HR = 1.14, 95% CI: 0.38–2.83), but significantly reduced the relative risk from death in HMGA2-positive CRCs (HR = 0.18, 95% CI: 0.04–0.63). This finding suggests that HMGA2 might serve as a biomarker for predicting the response to radiotherapy in CRC patients.

Discussion

In this report, we examined the expression level of HMGA2 in CRCs to assess its potential role as a prognostic or predictive marker. Our findings revealed that the positive expression of HMGA2 was significantly associated with the distant metastasis in both training and validation sets (p < 0.05). The adjusted ORs of HMGA2 for the risk of distant metastasis were 3.53 (95% CI: 1.37–9.70) and 6.38...
(95% CI: 1.47–43.95) on training and validation sets, respectively. Previous studies, which showed that the HMGA2 mRNA expression was significantly escalated in invasive breast cancer cell lines (21, 22) and metastatic CRCs (16), further support our conclusion on the basis of clinical specimens. We also found that the positive expression of HMGA2 was an independent indicator of poor prognosis. The multivariate COX proportional hazard analysis revealed that the HRs of HMGA2 for OS were 2.38 (95% CI: 1.30–4.34) and 2.14 (95% CI: 1.21–3.79) on training and validation sets, respectively. Further analysis revealed that the HMGA2 overexpression impacts the survival of CRC patients with stages III and IV more significantly than those of stages I and II. The HRs of HMGA2 for OS of stages III and IV were 2.95 (95% CI: 1.57–5.50) and 2.05 (95% CI: 1.05–3.95) for the training set and the validation set, respectively. Our results are concordant with the previous studies, which indicated that a poor prognosis is associated with high-level expression of HMGA2 in lung cancer (12), gastric cancer (23), oral cancer (13), ovarian cancer (14), and metastatic breast cancer (15). Therefore, our findings suggest that the positive expression of HMGA2 is associated with the distant metastasis of CRCs and a reduced patient survival, especially for those with advanced

Figure 4. Expression of HMGA2 delayed clearance of γ-H2AX post γ-ray exposure and augmented the response to radiotherapy in CRC patients. A, expression of HMGA2 in vector- or HMGA2-transduced CHT-116 and SW480 CRC cells. B, Western blot analysis of γ-H2AX elimination in HCT-116/vector and HCT-116/HMGA2 cells (left) and SW480/vector and SW480/HMGA2 cells (right). Cells were either nonirradiated or irradiated with 3-Gy γ-rays; protein lysates were prepared at different time points after γ-ray exposure as indicated. The multivariate COX analysis for OS was stratified by HMGA2-negative (C) and HMGA2-positive (D) CRCs. Detail results of (C) and (D) were displayed in Supplementary Table S3.
stage CRC. To our knowledge, this is the first demonstration of HMGA2 overexpression as a biomarker for advanced CRC with poor prognosis.

Although the results from previous studies have suggested HMGA2 functions as an oncogene that is overexpressed in a variety of human cancers, it is not yet well understood how HMGA2 promotes cancer invasion and metastasis in these cancers. As for HMGA2, translocations often affect the third intron leading to the expression of fusion transcripts containing 3 adenine–thymine (AT) hooks and ectopic sequences of different origin (24). Also, a mutation in the breast cancer susceptibility gene BRCA1 has been shown to derepress HMGA2 in breast cancer cells (25). Transgenic mice expressing a truncated form of the HMGA2 protein comprising the first 3 binding domains exhibit a giant phenotype with high incidence of lipomas. These results indicate that primarily truncation and/or aberrant expression of HMGA2 rather than its fusion to other genes is responsible for neoplastic transformation (26, 27). The overexpression of HMGA2 occurs in various benign and malignant tumors. Disruption of the HMGA2 gene by rearrangements affecting the chromosome region 12q13–15 and the attendant overexpression of the HMGA2 protein results in several benign mesenchymal tumors such as lipoma and uterine leiomyoma (28–30). Several independent studies have identified the HMGA2 transcript as a target for the let-7 family of microRNAs (31, 32). Notably, a study investigating breast cancer initiating cells suggested that silencing of HMGA2 enhances differentiation but not self-renewal (33). In addition, HMGA2 interacts with pRB (retinoblastoma gene product) and enhances the E2F1 activity by displacing histone deacetylase 1 (HDAC1; ref. 34). Based on the results obtained by uterine leiomyomas, a balance between HMGA2 and the p19ARF-TP53-CDKN1A has been proposed to determine the tumor size (35). All these data support our notion that the degree of HMGA2 overexpression is one of the key elements determining the aggressiveness of CRC, affecting the survival of CRC patients.

It has been suggested that the aberrant expression of many genes correlates with the prognosis of CRC, but only a few of them have been validated and are used to predict the treatment response (36). For instance, high-frequency microsatellite instability (MSI-H) is associated with good survival but poor therapeutic response for stage II CRC patients who received adjuvant chemotherapy (36, 37). Oncotype DX kit has been developed to predict the survival and treatment response for stages II and III CRCs. Ki-67, a proliferative marker, is associated with a better response to 5-fluorouracil (5-FU)-based adjuvant chemotherapy for stage III CRCs (38). The mutant KRAS/BRAF is implicated for resistance to EGFR inhibiting drugs for late stage CRC (36). Our study shows that HMGA2 is relevant to metastasis and impacts the survival in advanced stage CRC. Moreover, all these findings had been validated with participants from different racial background. There are many outcome-related factors for CRCs with different racial background, such as risk factors, genomic variations, medical care, and social economic classes (39). Therefore, the fact that identical results were yielded from 2 sets with different racial backgrounds further validates that HMGA2 is potentially an independent useful prognostic factor for predicting metastasis and survival for CRC patients.

The expression of HMGA2 was shown to increase the cytotoxic effect of DNA DSBs induced by certain topoisomerase type II inhibitors, irradiation, and the chemotherapeutic agent cisplatin but not the genotoxic agent hydroxyurea, MMS, and low pH (19, 20). Our data showed that overexpression of HMGA2 delayed the clearance of γ-H2AX after 3-Gy γ-ray irradiation on HCT-116 and SW480 cells (Fig. 4B). HMGA2 disrupts the DSBs repair by altering the binding affinity between Ku and DNA ends, and delaying the release of DNA-PKcs (DNA-dependent protein kinase catalytic subunit) from DSBs (20). Therefore, the inhibition of NHEJ by HMGA2 facilitated the accumulation of chromosomal aberrations, which suggested that HMGA2 is an oncogenic molecule promoting malignancy (Supplementary Fig. S2). Under a therapeutic dose of γ-irradiation, disruption of DSBs repair by HMGA2 dramatically increased the cytotoxic effect of γ-rays and augmented the efficacy of adjuvant radiotherapy in CRCs (Supplementary Fig. S2). Studies using human samples also revealed that HMGA2 is associated with the CRC response to radiotherapy (Fig. 4C and D, Supplementary Table S3). Radiotherapy significantly reduced the relative risk death in HMGA2-positive CRCs (HR = 0.18, 95% CI: 0.04–0.64), but not in HMGA2-negative CRCs. However, this finding could not be validated, as radiotherapy was not applicable for CRCs from the validation set, representing a limitation with this study. Nonetheless, all these biomarkers including HMGA2 are useful in selecting treatment strategy such as radiotherapy against CRC and deserve further validation.

In summary, our finding that HMGA2 overexpression is an informative biomarker, which is associated with poor prognosis of patients with advanced CRC, has potential implications for CRC survival prediction, choice of treatment regimens, and future development of treatment strategies.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Acknowledgments

We thank M. Lee for digital image capturing and F. IIn and M. Kong for editing.

Grant Support

This work was supported in part by NIH research grants R01DE10742 and DE14185 (to D.K. An) and CA12767 (to Y. Yen).

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Received September 22, 2010; revised January 6, 2011; accepted January 10, 2011; published OnlineFirst January 20, 2011.
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