Regulation of HMGA1 Expression by MicroRNA-296 Affects Prostate Cancer Growth and Invasion

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Abstract

**Purpose:** High-motility group AT-hook gene 1 (HMGA1) is a non-histone nuclear binding protein that is developmentally regulated. HMGA1 is significantly overexpressed in and associated with high grade and advance stage of prostate cancer (PC). The oncogenic role of HMGA1 is at least mediated through chromosomal instability and structural aberrations. However, regulation of HMGA1 expression is not well understood. Identification of microRNA-mediated HMGA1 regulation will provide a promising therapeutic target in treating PC.

**Experimental Design:** In this study, we examined the functional relation between miR-296 and HMGA1 expression in several PC cell lines and a large PC cohort. We further examined the oncogenic property of HMGA1 regulated by miR-296.

**Results:** Here we report that miR-296, a microRNA predicted to target HMGA1, specifically represses HMGA1 expression by promoting degradation and inhibiting HMGA1 translation. Repression of HMGA1 by miR-296 is direct and sequence specific. Importantly, ectopic miR-296 expression significantly reduced PC cell proliferation and invasion, in part through the downregulation of HMGA1. Examining PC patient samples, we found an inverse correlation between HMGA1 and miR-296 expression: high levels of HMGA1 were associated with low miR-296 expression and strongly linked to more advanced tumor grade and stage.

**Conclusions:** Our results indicate that miR-296 regulates HMGA1 expression and is associated with PC growth and invasion. *Clin Cancer Res;* 17(6); 1–9. ©2010 AACR.

Introduction

High-motility group AT-hook genes, HMGA1 and HMGA2, are present at high levels in embryonic cells (1). Most differentiated normal mammalian cells express extremely low levels of HMGA1 mRNA and protein. HMGA1 is located on the short arm of human chromosome 6 (6p21), a region involved in chromosomal abnormalities associated with human neoplasms (2). Whereas expression of HMGA1 is largely undetectable in non-malignant prostate specimens (3), previous studies have shown that an increase in the level of HMGA1 expression is associated with high-grade tumors and late stage prostate cancer (PC; ref. 4). In a transgenic mouse model for PC, analysis of successive stages of PC revealed that HMGA1 protein expression was confined to the later stages of neoplastic progression and was not detected at early stages of disease or in control prostate tissues from nontransgenic mice (5). The oncogenic property of HMGA1 is mediated, at least in part, through inhibition of p53 function (6). Furthermore, in PC cell lines, high levels of HMGA1 expression is associated with enhanced proliferation and metastatic potential *in vitro* (7). In fact, overexpression of HMGA1 in PC cell lines resulted in chromosomal instability and structural aberrations (8). The findings suggest that HMGA1 is involved in the development of unbalanced chromosomal rearrangements associated with PC (8).

MicroRNAs (miRNAs) are a class of small, noncoding RNAs that regulate the expression of certain genes, including tumor suppressors and oncogenes (9), at posttranscriptional and translational levels. Both increases and decreases in the expression of select miRNA has been documented in PC (9–12). Derepression of miRNA expression is often associated with changes in the regulation of genes involved in cell proliferation and androgen independence (hormone naive vs. hormone refractory; refs. 12 and 13).
**Translational Significance**

High-motility group At-hook gene 1 (HMGA1) protein is an oncofetal protein that is significantly overexpressed in and associated with high grade and advance stage of prostate cancer. In vitro studies reveal that HMGA1 overexpression enhances PC proliferation and metastatic potential. In particular, the oncogenic role of HMGA1 is at least mediated through chromosomal instability and structural aberrations. Identification of microRNA-mediated HMGA1 regulation will provide a promising therapeutic target in treating PC.

MiRNA signatures accurately separated the carcinomas from the BPH samples and further classified the carcinomas according to their androgen dependence. Thus, miRNAs are potentially novel diagnostic and prognostic tools for PC (11). Interestingly, recent studies have shown that the expression of the HMGA family member, HMGA2, is regulated by the let-7 microRNA (14–17). However, the mechanism whereby HMGA1 expression is regulated is not well understood and the potential role of microRNAs in HMGA1 regulation has not been explored.

HMGA1 is a predicted target gene for both let-7 and miR-296 based on computer analyses. We conducted this study to characterize whether let-7 and miR-296 can specifically repress HMGA1 expression and regulate PC growth and invasion. We found that miR-296, but not let-7, significantly repressed HMGA1 expression at posttranscriptional and translational levels and reduced PC proliferation and invasion in vitro. Moreover, we found an inverse correlation between miR-296 and HMGA1 levels in advanced PC, associating changes in miR-296 expression with tumor progression via increased HMGA1 expression.

**Materials and Methods**

**Patient and tissue samples**

A total of 196 cases prepared in 2 customized high-density tissue microarrays (TMA) were included in this study (Table 1). TMA100 contained 100 PC cases (from the Cooperative PC Tissue Resource at New York University) and TMA96 contained 96 cases (from Northwestern University). The study was approved by our institutional review boards.

**Cell lines**

Six prostate cell lines were used for the study, including 4 PC cell lines: LnCaP, LnCaP-AI (variant of LnCaP; ref. 18), and PC3 and DU145 cells, as well as 2 benign immortalized prostate epithelial cell lines: RC165 and RC170 (19).

**MiR-296 in situ hybridization**

The hybridization system and probes, miRCURY LNA probes, miR-296, let-7c, and U6, were purchased from Exiqon and utilized following the detailed procedure for in situ hybridization provided by the manufacturer’s protocol (20). The relative expressions of the selected miRNAs were scaled 0 as negative, 1 as weak, 2 as moderate, and 3 as strong expression. The scores of the selected miRNA expression from each tissue was normalized by relative intensity of U6 expression (miRNA score/U6 score).

**MiR-296 and let-7c mimics and inhibitors**

MiR-296 and let-7c mimics and inhibitors were purchased from Dharmacon Inc. All experiments were controlled using a nonfunctional, double-stranded random 22 nt RNA (Block-it, Invitrogen).

**HMGA1 3’UTR wild type and mutant constructs**

The HMGA1 3’ untranslated region (UTR) cDNA (ID no. 4308914) was purchased from Invitrogen. The PCR products of HMGA1 3’UTR with 4 and 3 miR-296 complementary sites (CS) were cloned into Luciferase Reporter Vector psiCHECK2 (Promega) using the Xhol and NotI sites (Supplementary Table S1). The fidelity of the cDNA sequence was verified by sequencing analysis. The mutant HMGA1 3’UTR constructs were prepared and cloned into psiCHECK2 by RT-PCR with the degenerative mutant primers (summarized in Supplementary Table S1).

**qRT-PCR and real-time RT-PCR**

Detection of mature miRNAs was performed using real-time RT-PCR primers for mature miR-296 and qRT-PCR Detection Kits. Primers for HMGA1 were designed (forward 5’-ACTGGAGTCTCCTGGTTGTGT-3’, reverse 5’-AGTGCA-TATTTCCCCTCCCTC-3’). cDNA were quantified by qRT-PCR and normalized by the internal control products of U6 and β-actin.

**Western blot analysis**

The antibody against HMGA1 was kindly provided by Dr. Scott Lowe (21). Total proteins were prepared from fresh frozen tissue or cultured cell samples, separated through a 12% SDS-PAGE gel and then transferred to a PVDF membrane. Development of the immunoblot with anti-sera against HMGA1 and negative control HMGA1 blocking peptide (from Santa Cruz Biotechnology, Inc.)
was tested and a single, specific HMGA1 band at 25 kD was detected, as previously described.

**MiRNA transfection**

Before transfection, cells were placed in standard media without antibiotics for 24 hours. As per manufacturer’s protocol, transfection was performed using the Lipofectamine system with microRNA concentrations of 40–120 nM in 6-well plates. Cells receiving only the tagged random sequence double-stranded 22mer (Block-iT) were used as nonspecific references at all data points. Following transfection, cells were harvested and analyzed at the indicated times.

**Luciferase assays**

PC3 cells and DU145 cell cultures were transfected with either 400 ng of the luciferase reporter psicHECK2 control (Promega) or 400 ng psicHECK2 plus HMGA1 3’UTR constructs. Co-transfection of miR-296 and let-7 mimics and inhibitors at various doses (0, 40, 80, and 120 nM) was also performed. Luciferase activity was measured by the dual luciferase assays (Promega).

**Cellular proliferation assay**

PC3 and DU145 cell lines stably transduced with pBabe or pBabe-HMGA1 (with and without miR-296 CS) were passed in 24-well plates in triplicate. Cells were subsequently transfected with control RNA (Block-iT), miR-296 and let-7c mimics and inhibitors at a dose of 80 nM. Cellular proliferation was measured at 24, 48, 72, and 96 hours using the colorimetric WST-1 assay (Cell proliferation Reagent, Roche). HMGA1 siRNA (Dharmacon) was used at 100 nM.

**Matrigel invasion assays**

A cell suspension (5 × 10^4) in 0.5 mL of RPMI 1640 medium with 0.1% bovine serum albumin was placed on the insert of the 24-well chambers 24 hours after transfection with control, Block-iT, miR-296, and let-7c mimics and inhibitors, respectively, as described with BD Matrigel invasion chamber (22). After 24 hours, the noninvading cells on the upper surface of the membrane were removed. Invasive cells on the lower surface of the membrane were stained with Diff Quick stain and counted under a light microscope.

**Immunohistochemistry**

TMA blocks were sectioned at 4 μm. Immunohistochemical staining for HMGA1 was performed on a Ventana Nexus automated system. Immunoreactivity for HMGA1 was scored based on immunointensity (scaled 0, 1–3). For TMA100, immunoreactivity for HMGA1 in tumor tissue cores was scaled by scoring the net changes of HMGA1 (tumor minus average of normal immunointensity). For TMA96, immunoreactivity for HMGA1 was scaled by immunointensity from each case. The cases from TMA100 had well-documented pathological and clinical condition of the disease and it was used for the analysis of HMGA1 in association with clinical and biomedical factors. TMA96 was collected to represent PIN and Gleason...
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miR-296

Regression analysis was used to compare the correlation of active values. Statistical significance was analyzed by a paired t-test and \( P \)-value <0.05 was considered significant. Regression analysis was used to compare the correlation of \( \text{miR-296} \) and HMGA1 expression.

Results and Discussion

Repression of HMGA1 by \( \text{miR-296} \)

Posttranslational modification of HMGA1 protein (acetylation and phosphorylation) in PC cell lines has been shown to be one important mechanism for functional regulation of HMGA1 (23). However, other mechanisms responsible for regulation of HMGA1 expression in PC remain understudied. MiRNA-mediated gene repression is a newly identified molecular mechanism that regulates gene expression. HMGA1 mRNA contains a 1.4-kb 3’UTR. Computer analysis predicted that miRNAs \( \text{let-7} \) and \( \text{miR-296} \) can target HMGA1 (\( \text{let-7} \) contains 2 and \( \text{miR-296} \) contains 4 CSs, Fig. 1A). These 2 miRNAs were found to be frequently dysregulated in PC (10–11, 24).

We examined the expression of HMGA1 by Western blot analysis in 4 PC cell lines, androgen-dependent LNCaP, androgen-independent LNCaP-AI (expressing high levels of AR; ref. 22), PC3 (negative for AR) and DU145 (negative for AR) cells, as well as 2 benign immortalized cell lines RC165 and RC170 (19). All of the cell lines express HMGA1 protein to varying levels. In particular, PC3 and DU145 had higher levels of HMGA1 expression than other cell lines (Fig. 1B). These findings were consistent with previous report by Takaha et al. (8). The endogenous expression of \( \text{miR-296} \) was also examined (Fig. 1B), and all cell lines, excluding RC165, have relative low levels of endogenous \( \text{miR-296} \) expression.

To test whether \( \text{let-7} \) and \( \text{miR-296} \) can specifically regulate HMGA1 expression in PC cells, we transfected exogenous \( \text{let-7c} \) and \( \text{miR-296} \) mimics and inhibitors into PC3 and DU145 cells. The experiments were divided into 3 groups: negative control (Block-iT, a nonfunctional, small, double-stranded RNA), test 1 (\( \text{let-7c} \) and \( \text{miR-296} \) mimics), and test 2 (\( \text{let-7c} \) and \( \text{miR-296} \) inhibitors). Cells treated with \( \text{miR-296} \) mimic demonstrated a 5-fold reduction in HMGA1 mRNA and 2-fold reduction of HMGA1 protein (Fig. 1C). When cells were treated with \( \text{miR-296} \) inhibitor, both HMGA1 mRNA and protein either returned to original baseline expression or showed even higher levels than untreated cells. In the same experiment, no visible repression of HMGA1 by \( \text{let-7c} \) was observed (Fig. 1C). The specificity of HMGA1 repression by \( \text{miR-296} \), but not by \( \text{let-7c} \), was confirmed in PC3.

Figure 2. Luciferase activity analysis for \( \text{miR-296} \) mediated HMGA1 repression. A, luciferase activity (x-axis) was shown in PC3 cells transfected with LCF vector only (channel 1), LCF plus HMGA1 3’UTR construct (with 3 CSs) and cotransfected with \( \text{miR-296} \) mimic (channels 2–5) and inhibitor (channels 6–8). Y-axis represented the concentration of microRNAs in pmol. Reduction of luciferase activity in channel 2 could be contributed by endogenous \( \text{miR-296} \) and other microRNAs that had CSs in HMGA1 3’UTR. B, sketch diagram illustrated the wild type and 3 mutant constructs of HMGA1 3’UTR for luciferase assay. C, the relative expression levels of luciferase (y-axis) in 4 constructs (from left to right: wild type, mutants 1–3) treated with different doses of \( \text{miR-296} \) mimic. Small t-bars were standard error.
The specificity of sequence-dependent miRNA repression for HMGAs was further examined using a PC3 cell line we previously developed that stably overexpressed HMGA2 in the context of endogenous HMGA1 (25). The cell line was transfected with either let-7c or miR-296 mimics, respectively. The transcript levels of HMGA2 were determined by RT-PCR. A reduction of HMGA2 in mRNA level was present in let-7c but not in miR-296 (Fig. 1D). Therefore, findings suggest that miR-296, but not let-7c, controls HMGA1 expression, though they do not represent miRNA regulation at protein levels.

To characterize whether miR-296 repression of HMGA1 was through 3'UTR regulation, 1 control (luciferase construct without HMGA1 3'UTR) and 2 test constructs (HMGA1 3'UTR containing 4 and 3 miR-296 CSs immediately downstream of luciferase) were cotransfected with miR-296, respectively. MiR-296 showed a significant reduction of luciferase activity, with either longer (4 miR-296 CSs) or shorter (3 miR-296 CSs) HMGA1 3'UTR (Fig. 2A). The reduction of luciferase activity by miR-296 could be rescued by cotransfection of miR-296 inhibitor (Fig. 2A). To further test whether miR-296 repression of HMGA1 expression was sequence specific, we prepared 3 constructs with single nucleotide mutations in the “seed” sequence of miR-296 (Fig. 2B, Supplementary Table S1). In comparison to wild-type HMGA1 3'UTR, introduction of the site-specific mutation in “seed” sequence of miR-296 resulted in loss of luciferase interference (Fig. 2C). The findings indicated that repression of HMGA1 by miR-296 was sequence specific. As overexpression of HMGA1 is a major molecular change in PC, as well as other tumors, miR-296 may prove to play an important role in cancer through its regulation of HMGA1 expression.
Repression of HMGA1 expression by miR-296 inhibits in vitro cell growth and invasion

HMGA1 is overexpressed in many solid epithelial and mesenchymal neoplasms (26–27). Overexpression of HMGA1 in PC cell lines has been found to be associated with highly aggressive growth and a relatively high degree of metastatic potential (7). To characterize whether repression of HMGA1 by miR-296 influences PC cell growth and invasion, we conducted cell proliferation and migration analyses.

We selected PC3 and DU145 cell lines for the study. Cells treated with miR-296 had significantly decreased cell proliferation rates (P < 0.05) in comparison to baseline or Block-iT controls at day 2. However, when cells were treated with miR-296 inhibitor, cell proliferation rates returned to levels similar to Block-iT control, or even slightly higher than baseline in PC3 cells (Fig. 3A and B). The results from this experiment indicate that miR-296 functions as an antiproliferation factor, through repression of HMGA1 and other predicted target genes in PC cells.

Given that miR-296 may have many potential targets in PC cells, the antiproliferative effect of miR-296 may not to be limited to repression of HMGA1. Therefore, we argued that the downregulation of HMGA1 by siRNAs should recapitulate miR-296 effects on cell proliferation. Indeed, the growth rate of the DU145 cell line were measured and significant reduction of cell proliferation by HMGA1 siRNA was noted by day 3 and the difference was further widened over the next 3 days between control and siRNA treatment (Fig. 3C). The mitogenic effect of HMGA1 was further validated in the PC3 cell line (Fig. 3D). This finding indicated that HMGA1 is one important mitogenic factor in the regulation of PC cell growth in vitro.

HMGA1 showed moderate expression in immortalized benign prostate epithelial cell lines RC165 and RC170 (Fig. 1B). To examine whether HMGA1 expression has a role in controlling proliferation in these cell types, we introduced HMGA1 siRNA and miR-296 inhibitor and performed proliferation analysis. We found that repression of HMGA1 in RC165 and RC170 could significantly reduce cell proliferation (Supplementary Figure S1) as we saw in PC cell lines (Fig. 3).

To evaluate whether miR-296 downregulation/repression of HMGA1 plays a role in aggressive cancer behavior, we examined the invasion capability of PC cells in the presence or absence of exogenous miR-296. In cells transfected with miR-296, the number of cells that successfully invaded through an extra-cellular membrane was quantified after 48 hours. In the cell plates treated with miR-296, there were more than 3.2-fold reductions of tumor cells traversing the Matrigel membrane in comparison to the control and siRNA treatment (Fig. 4). This indicates that miR-296–mediated repression of HMGA1 has a significant impact on tumor cell invasion (P < 0.05).
In addition to miR-296, HMGA1 may also be regulated by other mechanisms. Of note, HMGA1 is highly expressed in PC3 and DU145 (AR negative) compared with LNCaP (AR positive) cells (Fig. 1B), and there may be an inverse relationship between AR and HMGA1. It is of great interest to determine whether AR regulates the expression of HMGA1 in future.

Inverse relation of HMGA1 and miR-296 expression in human PC

Previous studies have shown that HMGA1 is overexpressed in PC (4–5, 7–8, 28). To determine whether overexpression of HMGA1 is a common molecular alteration related to PC, we examined HMGA1 expression in a total of 196 cases by immunohistochemistry in TMAs from 2 independent sources (TMA100 and TMA96, Table 1). The relative expression level of HMGA1 was scored by 2 pathologists (J.M. and J.J.W.). We used benign prostate with or without high-grade prostatic intraepithelial neoplasia (HGPIN) tissue as internal controls.

In TMA100, we noted that benign prostate acinar epithelial cells had low levels of immunoreactivity for HMGA1. We normalized relative HMGA1 expression by obtaining the net change of HMGA1 in PC (tumor epithelium-normal epithelium; see Materials and Methods). A total of 71% (71 of 100) of PC had a net gain of immunoreactivity for HMGA1. Next, we compared the immunoreactivity of HMGA1 with patients’ age, race, preoperative PSA, tumor volume, grade, and stage. The average levels of HMGA1 immunoreactivity had a trend of positive correlation with tumor Gleason score, tumor volume, and stage (Fig. 5A). Specifically, HMGA1 expression was able to segregate between low volume (<5%) and large volume (>25%) disease and with stage pT2 and pT3b, respectively (P < 0.05, Fig. 5A).

To compare whether HMGA1 expression was correlated to miR-296 expression, we examined HMGA1 and miR-296 expression in TMA96, in which, equal numbers of cases from HGPIN, low-grade PC (Gleason grade 3), and high-grade PC (Gleason grades 4 and 5) were included. In serial sections of TMA96, the levels of HMGA1 and miR-296 were determined by immunohistochemistry and microRNA in situ hybridization (Fig. 6). The preservation of RNA in each tissue core was normalized by the expression level of U6 (Fig. 6). Levels of HMGA1 in TMA96 were scored as indicated above for TMA100.

To characterize the inverse correlation of HMGA1 and miR-296 expression, we compared the relative expression levels of these 2 molecules in serial section of same tissue cores. As illustrated in Figure 5B, a moderate inverse correlation (R = −0.39) of HMGA1 and miR-296 was observed. The level of miR-296 expression was significantly higher in tumors with lower immunoreactivity for HMGA1 than in tumors with higher HMGA1 (P < 0.01, Fig. 5B).

In TMA96, the average immunoreactivity for HMGA1 was 1.4 ± 0.10 in HGPIN, 2.14 ± 0.11 in Gleason grade 3, and 2.45 ± 0.11 in Gleason grades 4–5 (P < 0.05, Fig. 5C).
In contrast, the scores of miR-296 intensity were 2.71 ± 0.16 in HGPIN, 2.15 ± 0.31 in Gleason grade 3, and 1.79 ± 0.19 in Gleason grades 4–5 (P < 0.05, Fig. 5C). We further analyzed the distribution of different expression levels of HMGA1 and miR-296 based on the numbers of cases (in percentage) scored as negative, weak (1+), moderate (2+), and strong (3+). About 52% of cases with Gleason grades 4–5 had high (3+) levels of HMGA1 immunoreactivity, whereas 63% of cases with HGPIN had low levels of HMGA1 immunoreactivity (score 1+ or less). By contrast, nearly 47% cases with HGPIN had high levels of miR-296 expression (score 3+), whereas the majority (79%) of cases with Gleason grades 4–5 showed low level of miR-296 expression (score 1+ or less). These findings indicate that higher levels of HMGA1 and lower levels of miR-296 are characteristic of high-grade PC.

In summary, this study identifies miR-296 as a specific regulator of the oncogene HMGA1 in PC cell lines. The pair HMGA1:miR-296 can serve as a new molecular marker to study both HMGA1 regulation in tumorigenesis and the potential developmental function of miR-296 as a regulator for HMGA1 expression. Because miR-296 may regulate a large number of target genes, it is of great interest to further study its role in modulating tumor growth in relation to other target genes.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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