

T-box Transcription Factor Tbx3 Contributes to Human Hepatocellular Carcinoma Cell Migration and Invasion by Repressing E-Cadherin Expression

Xianguang Feng,* Wenhuan Yao,† Zengzhen Zhang,* Fangshui Yuan,* Li Liang,*
Jingqiang Zhou,* Shuang Liu,* and Jiqing Song‡

*Department of Hepatobiliary Surgery, Shandong Provincial Third Hospital, Tianqiao District, Jinan, Shandong, P.R. China

†Institute of Toxicology and Function Inspection, Shandong Center for Disease Control and Prevention,
Lixia District, Jinan, Shandong, P.R. China

‡Department of Radiology, Shandong Provincial Hospital Affiliated to Shandong University,
Huaiyin District, Jinan, Shandong, P.R. China

Tbx3, a member of the T-box family of transcription factors, contributes directly to tumor formation, migration, and invasion. However, the role of Tbx3 in the metastasis of HCC remains unclear. In the present study, Tbx3 expression was detected in HCC tissues and cells by Western blot, and Tbx3 expression was regulated by use of siRNAs or lentivirus-mediated vectors. Here we found that Tbx3 protein expression increased in HCC tissues and cell lines. Tbx3 expression was positively associated with multiple tumor nodes, venous infiltration, and advanced TNM tumor stage. Survival analysis demonstrated that Tbx3 expression was an independent prognostic factor for HCC patients. In vitro assays further validated that Tbx3 indeed prompted HCC cell migration and invasion. In addition, Tbx3 expression was negatively related with E-cadherin expression in HCC tissues. Mechanically, Tbx3 inhibited the expression of E-cadherin, and then facilitated epithelial–mesenchymal transition (EMT) of HCC cells. Furthermore, the effect of Tbx3 knockdown on HCC cells was attenuated by E-cadherin knockdown. In conclusion, Tbx3 may be a novel prognostic factor, and it contributes to HCC cell migration, invasion, and EMT by repressing E-cadherin expression. Thus, Tbx3 may be recommended as a therapeutic target for HCC patients.

Key words: Tbx3; E-Cadherin; Metastasis; Hepatocellular carcinoma (HCC)

INTRODUCTION

Hepatocellular carcinoma (HCC) is one of the most common malignant tumors, and it is the most common cause of cancer-related mortality worldwide^{1,2}. Postoperative recurrence and metastasis have become tricky and account for poor prognosis of HCC patients³. E-Cadherin has been identified to play an important role in regulating the epithelial cell adhesion⁴. Thus, deregulation of E-cadherin results in loss of epithelial phenotype and facilitates cancer cell migration, invasion, and epithelial–mesenchymal transition (EMT)^{5,6}. It has been reported that E-cadherin expression was decreased and was associated with human HCC invasion and metastasis⁷. Mechanically, Snail, Slug, Twist, Zinc finger E-box-binding homeobox 1/2, and C-terminal-binding protein all regulate E-cadherin expression^{8,9}. However, more regulation pathways need to be elucidated.

Tbx3 is a member of the T-box transcription factor family and plays an important role in cell proliferation, invasion, and apoptosis in different cancers¹⁰. Tbx3 is a transcription repressor and has similar DNA-binding domains to Tbx2^{11–13}. Tbx3 expression is upregulated in some kinds of cancers, including gastric cancer, breast cancer, pancreatic cancer, and liver cancer^{14–17}, and Tbx3 also plays an important role in repressing the expression of p19 alternate reading frame/cyclin-dependent kinase inhibitor 2A (p19ARF) and phosphatase and tensin homolog (PTEN)^{18,19}. However, the role of Tbx3 in regulating E-cadherin expression of HCC is not still clear.

In the present study, we detected the expression of Tbx3 in HCC tumor tissues, matched normal tissues, HCC cell lines, and normal hepatic cell line using Western blot. We changed Tbx3 expression by utilizing small interfering RNAs (siRNAs) or lentivirus-mediated

vectors. Transwell assays were also carried out to examine HCC cell invasion and migration. This study will lay a foundation for the treatment of HCC patients.

MATERIALS AND METHODS

Cell Culture and Transfection

Human HCC cells (HepG2, Hep3B, HCCLM3, and MHCC97H) and immortalized liver cell line (LO2) were purchased from the Institute of Biochemistry and Cell Biology (Chinese Academy of Science, Beijing, P.R. China) and cultured according to the provided guidelines. Cells were maintained in Dulbecco's modified Eagle's medium (DMEM; Gibco, Grand Island, NY, USA), containing 10% fetal bovine serum (Gibco), 100 µg/ml penicillin, and 100 µg/ml streptomycin (Sigma-Aldrich, St. Louis, MO, USA) at 37°C in a 5% CO₂ incubator.

For transfection, Tbx3 siRNA, E-cadherin siRNA, and nonspecific duplex oligonucleotide as a negative control were synthesized by Sangon Biotech Co., Ltd. (Shanghai, P.R. China). The siRNAs mentioned above were transfected into HCC cells by Lipofectamine 2000 according to the manufacturer's guidelines (Invitrogen, Carlsbad, CA, USA).

Migration, Invasion, and Proliferation Assay

The migration and invasion of HCC cells were evaluated using 24-well Transwell plates containing polycarbonate filter inserts with 8-µm pores (Corning Inc., Cambridge, MA, USA). For migration assays, 5×10^4 cells suspended in 200 µl of serum-free DMEM were added into the upper inserts. For invasion assays, chamber inserts were coated with Matrigel (BD Biosciences, Franklin Lakes, NJ, USA) at 1:7 dilutions. For the proliferation assay, HCC cells were seeded into 96-well plates at 5×10^3 cells per well for 24 h and detected by a Cell Proliferation ELISA, chemiluminescent BrdU (5-bromodeoxyuridine; Roche, Indianapolis, IN, USA). All experiments were carried out in triplicate.

Tissue Specimens and Follow-Up

This study was approved by Shandong Provincial Third Hospital and Shandong Provincial Hospital Affiliated to Shandong University (Shandong, P.R. China). HCC specimens and corresponding tumor-adjacent tissues were obtained from 86 adult patients who underwent surgical resection of primary HCC between 2009 and 2011. All patients provided informed consent. The diagnosis was confirmed by pathological analysis, and patients who received preoperative chemotherapy or radiotherapy or with distant metastases were excluded. Tumor differentiation level was assessed based on Edmondson–Steiner grading. TNM stage of HCC was determined according to the guide of the 6th International

Union Against Cancer/American Joint Committee on Cancer (UICC/AJCC). The follow-up data were collected until December 2016 with a median follow-up time of 35.5 months. We analyzed the recurrence and overall survival (OS) of the patients. The date between resection and tumor recurrence diagnosis was defined as the time to recurrence. The OS was calculated from the date of resection to death or last follow-up.

RNA Isolation and Quantitative Real-Time Reverse Transcriptase Polymerase Chain Reaction (qRT-PCR)

Total RNA was extracted from tumor cells using RNAiso (TaKaRa, Dalian, P.R. China). Complementary DNA synthesis was performed using a PrimeScript RT reagent kit (TaKaRa), and qRT-PCR was performed with SYBR Premix Ex Taq II (TaKaRa) using a Stratagene Mx3000P real-time PCR system (Agilent Technologies, Santa Clara, CA, USA). qPCR primers against *Homo sapiens* E-cadherin and GAPDH were obtained from Genecopoeia (Guangzhou, P.R. China).

Western Blotting

Proteins from lysed cells were separated by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). After electrophoresis, the proteins were transferred onto nitrocellulose membranes (Bio-Rad, Hercules, CA, USA). Nonspecific binding sites were blocked in 5% bovine serum albumin (BSA; Sigma-Aldrich Chemical Co., Shanghai, P.R. China) in Tris-buffered saline plus Tween 20 (TBST; Sigma-Aldrich, St. Louis, MO, USA) for 1 h at room temperature. Blots were incubated with Tbx3, E-cadherin, or GAPDH antibodies overnight at 4°C. Then the membranes were incubated with horseradish peroxidase (HRP)-conjugated sheep anti-mouse or donkey anti-rabbit secondary antibodies (1:10,000 dilution; Abcam Company, Cambridge, MA, USA) and detected using the Western Blotting Luminol Reagent (sc-2048; Santa Cruz, Santa Cruz, CA, USA).

Immunohistochemical Analysis

Immunohistochemistry was performed on paraformaldehyde-fixed paraffin sections. Tbx3 and E-cadherin antibodies (Santa Cruz) were diluted at 1:1,000. Briefly, immunohistochemistry was conducted using a highly sensitive streptavidin–biotin–peroxidase detection system. The staining intensity was scored as follows: 1, weak staining; 2, moderate staining; and 3, strong staining. The stained area was identified by determining the percentage of positively stained cells, which was scored as follows: 0, no staining; 1, 1%–10% positively stained cells; 2, 10–50% positively stained cells; or 3, >50% positively stained cells. The immunohistochemical score (IS) for each slice was scored by multiplying the staining intensity

and area scores to yield a final score ranging from 0 to 9. Samples with an IS ≥ 6 were defined as expressing high antigen levels, and samples with an IS < 6 were defined as expressing low antigen levels.

Statistical Analysis

All data were analyzed using SPSS 18.0 statistical software (version 18.0; Chicago, IL, USA). The data are presented as mean \pm SD of three independent experiments. Correlations between the expression and clinicopathological parameters were evaluated using chi-square and Fisher's exact tests. The statistical tests were two sided, and values of $p < 0.05$ were considered significant. Survival curves were generated according to the Kaplan–Meier method, and statistical analysis was performed using the log-rank test. The Cox proportional hazards regression model was used to identify independent prognostic factors. Calculations were performed using GraphPad Prism Software (La Jolla, CA, USA).

RESULTS

Expression of Tbx3 in HCC Tissues and Cell Lines

In this study, 86 pairs of HCC samples and corresponding normal samples were subjected to Western blot. As shown in Figure 1A, the expression of Tbx3 protein in HCC cancer tissues was obviously higher than that in paired nontumor tissues ($p < 0.05$). Furthermore, we detected the expression of Tbx3 protein in normal human hepatic cell line LO2 and a series of HCC cell lines HepG2, Hep3B, MHCC97H, and HCCLM3 using Western blot. Our results revealed that the expression of Tbx3 protein in HCC cell lines was markedly increased compared with that in the LO2 cells ($p < 0.05$) (Fig. 1B). Notably, the expression of Tbx3 protein in MHCC97H and HCCLM3 cell lines with high metastatic ability was obviously higher than that in HepG2 and Hep3B cell lines with low metastatic ability ($p < 0.05$) (Fig. 1B). Inversely, the expression of E-cadherin mRNA was

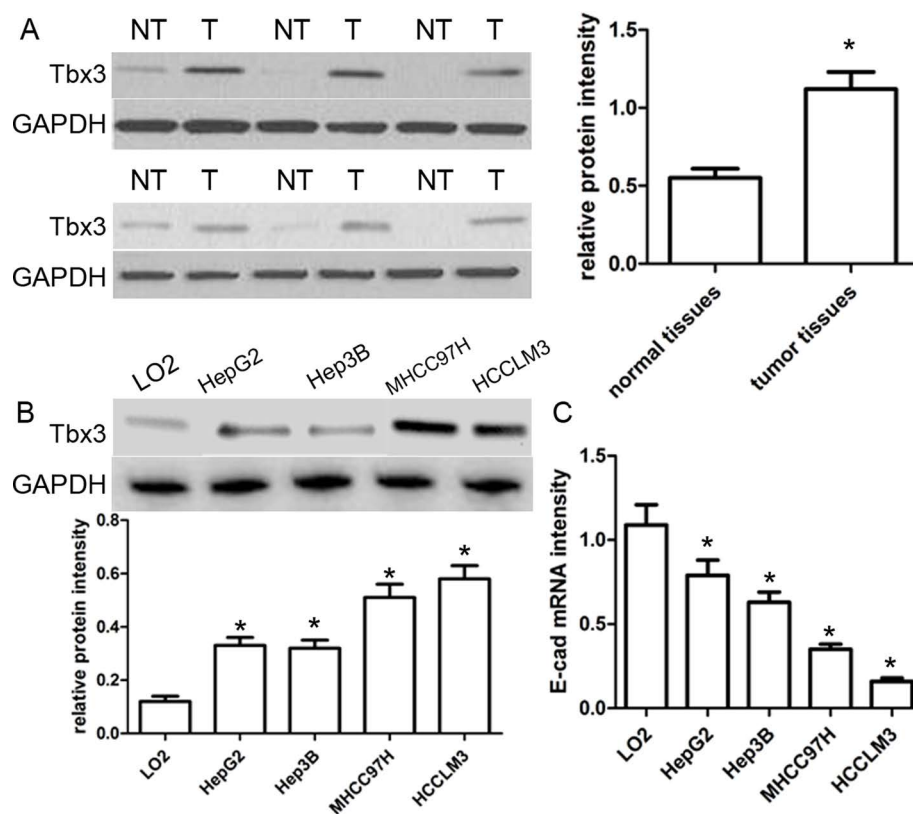


Figure 1. Tbx3 is abnormally upregulated in human hepatocellular carcinoma (HCC). (A) Representative Western blot analysis showed the expression of Tbx3 in the HCC (T) and matched nontumor tissues (NT). Quantitative analysis indicated that Tbx3 protein was significantly upregulated in HCC tissues compared with that in nontumor tissues. $n = 86$; $*p < 0.05$, by t -test. (B) Expression levels of Tbx3 protein in HCC cell lines (HepG2, Hep3B, MHCC97H, and HCCLM3) and a normal hepatic cell line (LO2). $n = 3$; $*p < 0.05$ by ANOVA. (C) The expression levels of E-cadherin mRNA in HCC cell lines and a normal hepatic cell line. $n = 3$; $*p < 0.05$, by ANOVA. GAPDH was used as a loading control.

significantly lower in HCC cell lines, especially in cell lines with high invasiveness, compared with LO2 cells ($p < 0.05$) (Fig. 1C). These findings suggest that Tbx3 is involved in the development of HCC.

Association Between Tbx3 Expression and Clinicopathology

According to the median value of Tbx3 expression, the expression of Tbx3 was divided into a low expression group ($n=43$) and a high expression group ($n=43$). Using statistical analysis, high Tbx3 expression was obviously associated with multiple tumor nodes ($p=0.011$), venous infiltration ($p=0.018$), and advanced TNM stage ($p=0.048$). Afterward, we further determined the prognostic role of Tbx3 expression in HCC patients using Kaplan–Meier survival curves. HCC patients with high Tbx3 expression had an obviously lower 5-year OS compared with those with low Tbx3 expression ($p=0.002$) (Fig. 2). Likewise, high Tbx3 expression was significantly related to shorter recurrence-free survival (RFS) ($p=0.001$) (Fig. 2). Additionally, multivariate Cox regression analysis validated that the expression of Tbx3 was an independent prognosis factor of 5-year OS and RFS for HCC patients ($p=0.002$ and $p=0.003$). Therefore, these findings indicate that Tbx3 serves as a potential prognostic factor for HCC patients.

Tbx3 Induces HCC Cell Migration and Invasion

To determine the biological role of Tbx3 in the development of HCC, Tbx3 siRNAs were applied for loss-of-function assays in HCCLM3 cells. Western blot analysis revealed that Tbx3 siRNA obviously downregulated Tbx3 expression in HCCLM3 cells compared with control ($p < 0.05$) (Fig. 3A). Transwell migration assays revealed that knockdown of Tbx3 obviously decreased the migration and invasion abilities of HCCLM3 cells (both $p <$

0.01) (Fig. 3B). Likewise, knockdown of Tbx3 obviously repressed cell migration and invasion in MHCC97H cells, respectively (both $p < 0.01$). On the other hand, BrdU incorporation assays demonstrated that Tbx3 siRNA did not affect cell proliferation in MHCC97H and HCCLM3 cells ($p=0.102$ and $p=0.120$, respectively). Subsequently, we established Hep3B cells with Tbx3 overexpression using lentivirus-induced transfection and then determined Tbx3 expression using Western blot (Fig. 3C). We found that Tbx3 overexpression promoted Hep3B cell migration and invasion ($p < 0.01$, respectively) (Fig. 3D). Overall, our data suggest that Tbx3 indeed promotes metastasis of HCC cells.

Tbx3 Negatively Regulates E-Cadherin Expression

Next, we used immunohistochemistry to detect the expression of Tbx3 and E-cadherin in 86 cases of HCC tissues. We found that positive E-cadherin expression was observed in 70.0% (21/30) of HCC tissues concomitant with negative Tbx3 expression, while merely 35.7% (20/56) of HCC cases were accompanied by positive E-cadherin expression ($p < 0.05$) (Fig. 4A). Furthermore, Pearson's correlation analysis demonstrated that the expression of Tbx3 was inversely associated with the expression of E-cadherin in HCC tissues ($r = -0.723$, $p = 0.002$) (Fig. 4B). Afterward, we transfected Tbx3 siRNA or scrambled siRNA into HCCLM3 cells, and then detected E-cadherin expression by qRT-PCR and Western blot analysis. Our findings showed that Tbx3 depletion led to a significant increase in E-cadherin expression in the HCCLM3 cells ($p < 0.01$) (Fig. 4C and D). On the other hand, Tbx3 overexpression obviously inhibited the expression of E-cadherin in Hep3B cells ($p < 0.01$) (Fig. 4E and F). Intriguingly, Tbx3 silencing reduced the expression of vimentin and N-cadherin in HCCLM3 cells ($p < 0.01$, respectively) (Fig. 4D), whereas

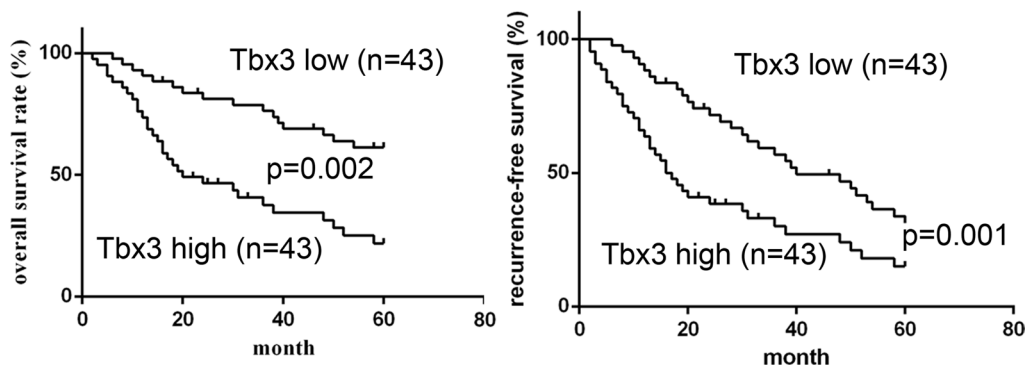


Figure 2. Prognostic value of Tbx3 for HCC patients. Kaplan–Meier overall survival (OS) and recurrence-free survival (RFS) curves of HCC patients in accordance with their expression status of Tbx3 protein. High expression of Tbx3 protein conferred a worse 5-year OS and RFS for HCC patients. The expression of Tbx3 was divided into the low-level group ($n=43$) and high-level group ($n=43$) based on the median protein level of the 86 HCC samples detected by Western blot.

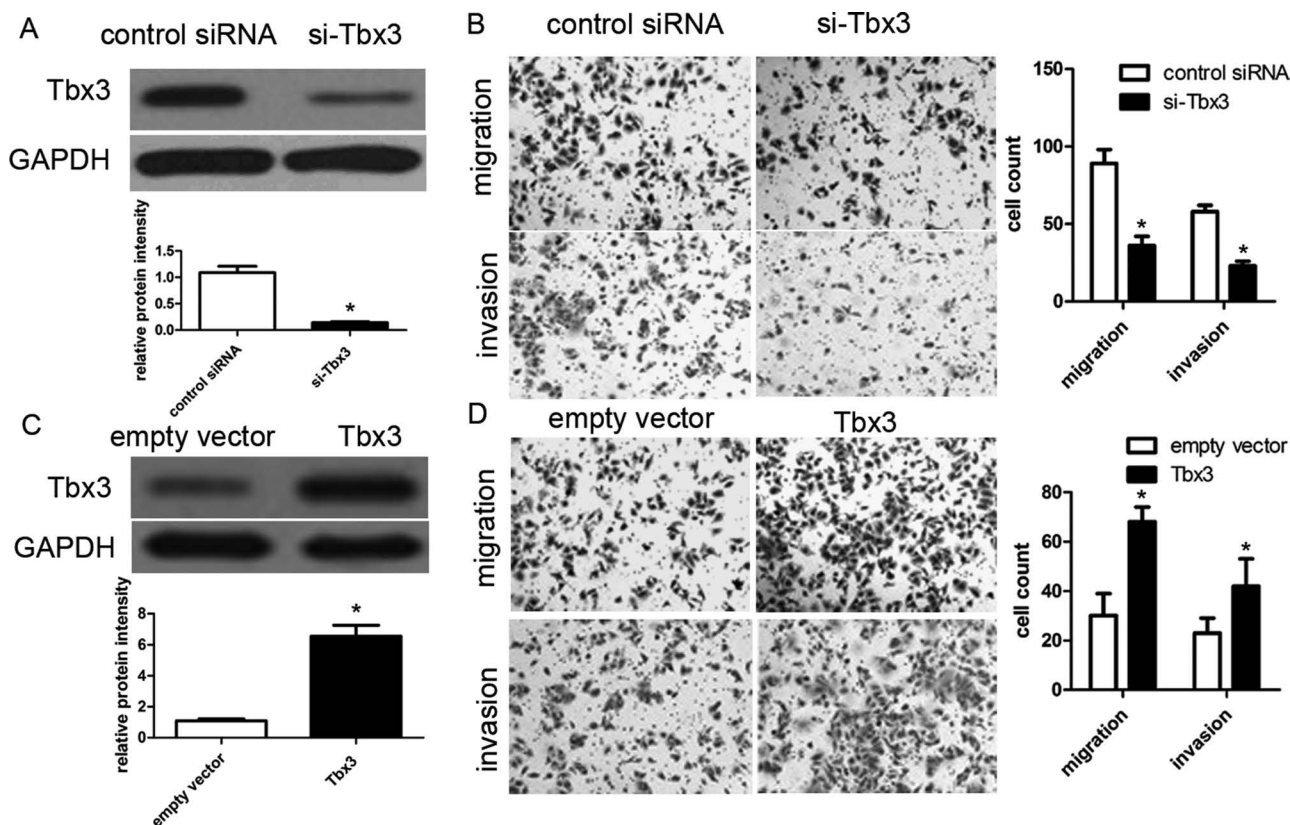


Figure 3. Tbx3 increases migrated and invading HCC cells. (A) HCCLM3 cells with Tbx3 small interfering RNA (siRNA) and scrambled siRNA transfection, respectively, were subjected to immunoblotting for Tbx3. $n=6$; $*p<0.05$ by t -test. (B) Transwell migration assays showed that Tbx3 knockdown inhibited cell migration in HCCLM3 cells. Transwell invasion assays demonstrated that HCCLM3 cell invasion was inhibited by Tbx3 knockdown. $n=3$; $*p<0.05$, by t -test. (C) Hep3B cells that were infected with Tbx3 or empty vector (EV) lentiviruses were detected by Western blot. $n=6$; $*p<0.05$ by t -test. (D) Tbx3 overexpression increased the number of migrated and invading cells as measured by Transwell assays in Hep3B cells. $n=3$; $*p<0.05$, by t -test.

Tbx3 overexpression promoted the expressions of vimentin and N-cadherin in Hep3B cells ($p<0.05$, respectively) (Fig. 4F), suggesting that Tbx3 expression regulates EMT in HCC cells.

Tbx3 Induces HCC Cell Migration and Invasion by Repressing E-Cadherin

To further identify whether E-cadherin is involved in Tbx3-induced HCC cell migration and invasion, HCCLM3 cells with downregulated Tbx3 were cotransfected with scrambled siRNA or E-cadherin siRNA. E-cadherin depletion was validated by Western blotting (Fig. 5A). Transwell assays suggested that E-cadherin depletion partially abrogated Tbx3 knockdown-induced inhibition of cell migration and invasion of HCCLM3 cells, leading to an obvious increase in migrated and invading cell numbers ($p<0.01$, respectively) (Fig. 5B). These findings indicate that Tbx3 induces HCC cell migration and invasion by repressing E-cadherin.

DISCUSSION

Previous reports have demonstrated that Tbx3 overexpression in human melanoma represses E-cadherin expression and enhances melanoma invasiveness²⁰. However, the expression of Tbx3 in HCC tissues and cells is still unclear. In the present study, we first analyzed the expression of Tbx3 protein in HCC tissues and paired nontumor tissues. We observed that Tbx3 expression in cancer tissues was obviously upregulated compared with that in normal tissues. Likewise, increased Tbx3 expression was found in HCC cell lines, especially in HCCLM3 and MHCC97H cells with malignant metastatic ability. By contrast, E-cadherin mRNA exhibited an opposite expression pattern in HCC cell lines. Correlation analysis suggested that high Tbx3 expression was positively associated with poor clinical characterizations of HCC, involving multiple tumor nodes, venous infiltration, and advanced TNM tumor stage. These findings indicate that

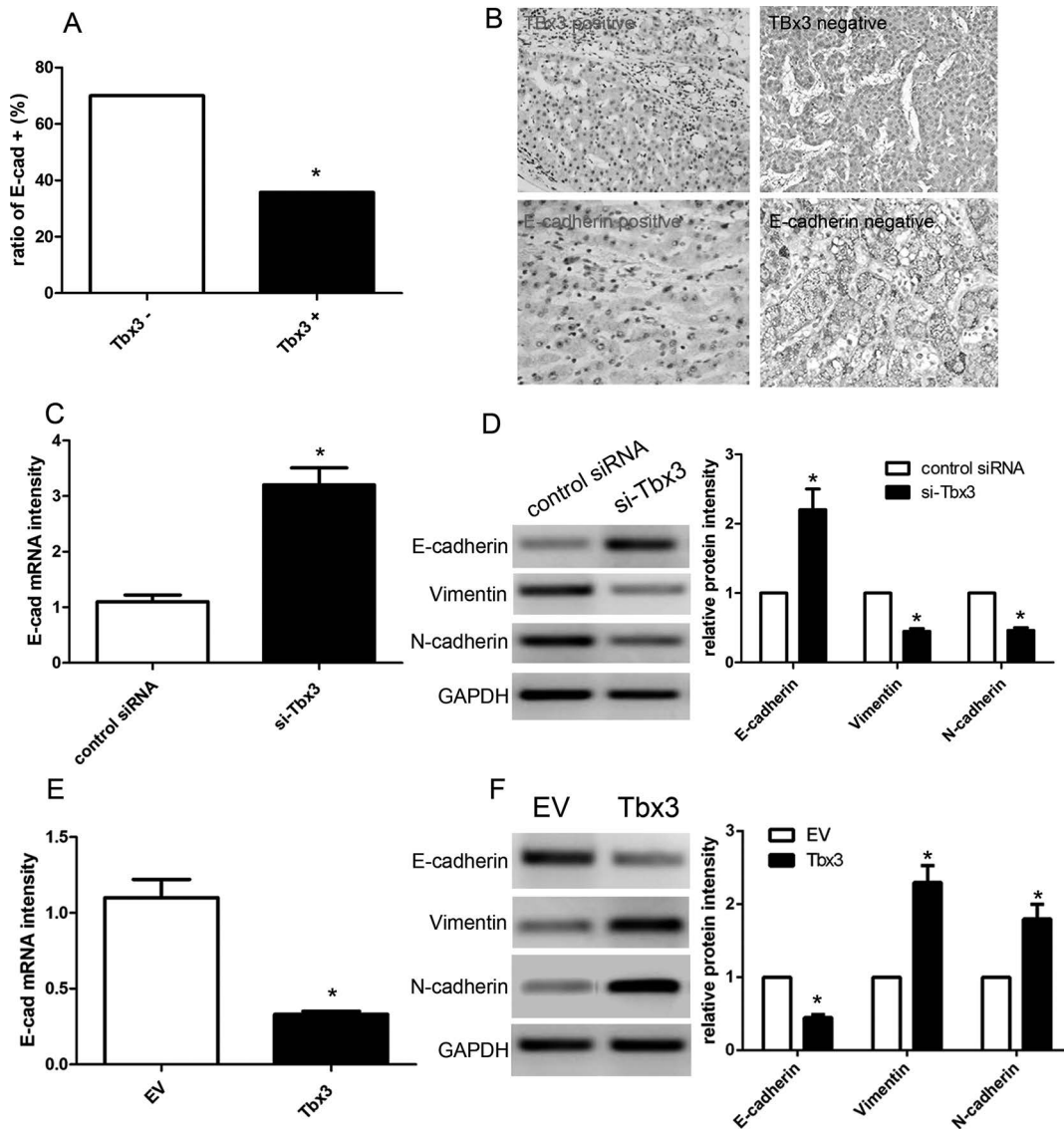


Figure 4. Tbx3 is inversely correlated with E-cadherin in HCC. (A) The positive expression of E-cadherin in Tbx3-positive HCC specimens was significantly lower than that in Tbx3-negative cases. $*p < 0.05$, by Pearson chi-square test. (B) Representative immunohistochemical staining showed weak staining of E-cadherin (III) in Tbx3-positive-expressing tumor (I) and strong staining of E-cadherin (IV) in Tbx3-negative-expressing tumor (II). (C) Quantitative real-time reverse transcriptase polymerase chain reaction (qRT-PCR) analysis of E-cadherin mRNA expression in HCCLM3 cells with Tbx3 siRNA or scrambled siRNA transfection. $n = 3$; $*p < 0.05$, by *t*-test. (D) Tbx3 knockdown increased the level of E-cadherin protein and reduced the expression of vimentin and N-cadherin in HCCLM3 cells. $n = 6$; $*p < 0.05$, by *t*-test. (E) qRT-PCR analysis of E-cadherin mRNA expression in Hep3B cells with Tbx3 or empty vector (EV) lentiviruses infection. $n = 3$; $*p < 0.05$, by *t*-test. (F) Tbx3 overexpression decreased the expression of E-cadherin protein and upregulated the expression of vimentin and N-cadherin in Hep3B cells. $n = 6$; $*p < 0.05$, by *t*-test.

Tbx3 might act as an oncogene and contributes to cancer metastasis in HCC development.

It should be noted that high expression of Tbx3 indicated a significantly shorter 5-year OS and RFS in HCC patients. Additionally, Cox regression analysis revealed that Tbx3 serves as an independent prognostic predictor for HCC patients. Emerging evidence indicated that Tbx3 expression might be implicated into malignant progression of some kinds of cancers, such as breast cancer,

bladder cancer, melanoma, and liver cancer^{21–24}. Based on our studies, Tbx3 depletion significantly decreased the migration and invasion abilities of HCC cells. On the other hand, Tbx3 overexpression obviously facilitated HCC cell migration and invasion. As reported, cancer metastasis acts as the most common predictor of prognosis-related factors. Recent studies also indicated that Tbx3 may be a downstream target of PLC ϵ to induce cell invasion and metastasis of bladder cancer via binding to

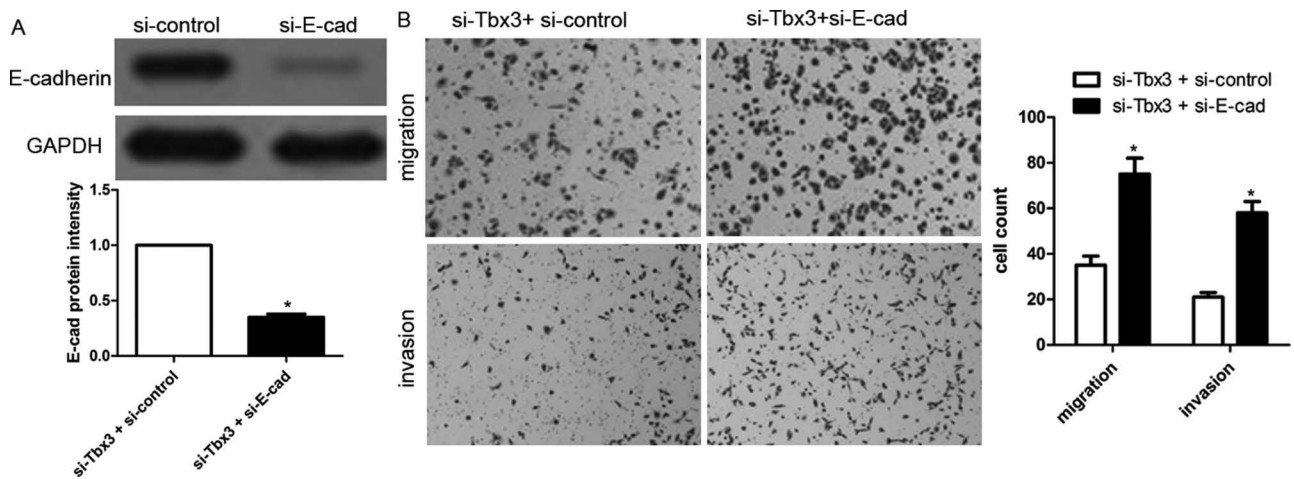


Figure 5. E-Cadherin knockdown abolishes antimetastatic effect of Tbx3 knockdown. (A) E-cadherin siRNA was transfected into HCCLM3 cells with Tbx3 downregulation and confirmed by Western blot. $n=6$; * $p<0.05$, by t -test. (B) E-cadherin knockdown increased cell migration and invasion in HCCLM3 cells with Tbx3 downregulation. $n=3$; * $p<0.05$, by t -test.

the E-cadherin promoter²². Likewise, B-RAF can regulate the expression of Tbx3 and promotes the EMT progression in the B-RAF mutant melanoma model²³. EMT enhances the capacities of antiapoptosis and chemoradiotherapy resistance^{24,25}, and we assumed that silencing of Tbx3 might enhance the sensitivity of HCC patients to adriamycin and probably abrogate apoptosis resistance of HCC cells.

In recent decades, decreased E-cadherin expression was thought to be an important biomarker of EMT, which played an important role in malignant HCC progression²⁶. We explored the effect of alterations in Tbx3 levels on the expression of E-cadherin. In HCC tissues, the expression of E-cadherin in positive Tbx3 tissues was usually lower compared with that in negative Tbx3 tissues. Statistically, an inverse association between Tbx3 and E-cadherin expression in HCC tissues was validated. In vitro assays revealed that Tbx3 depletion obviously enhanced the expression of E-cadherin mRNA and protein in HCCLM3 cells, whereas Tbx3 overexpression decreased the expression of E-cadherin. In addition, Tbx3 promoted the expression of vimentin and N-cadherin in HCC cells. These findings suggest that Tbx3 might be a new modulator of EMT in HCC development. Furthermore, E-cadherin depletion attenuated the Tbx3 knockdown-mediated repression of HCC cell migration and invasion. A couple of transcriptional repressors are reported to control the expression of E-cadherin, involving Snail, Slug²⁷, Twist²⁸, and ZEB/ δ EF1²⁹. Thus, these results indicate that Tbx3 might facilitate the migration, metastasis, and EMT of HCC cells by repressing E-cadherin expression.

In conclusion, our study demonstrated that high Tbx3 expression is inversely associated with E-cadherin expression in HCC tissues and portends poor prognosis of

HCC patients. In addition, Tbx3 expression induces HCC cell migration and invasion and inversely modulates the expression of E-cadherin. Overall, Tbx3 may play an important role in HCC metastasis and may serve as a novel prognostic indicator and therapeutic target for HCC patients.

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