NDRG2 correlated with favorable recurrence-free survival inhibits metastasis of mouse breast cancer cells via attenuation of active TGF-β production

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N-myc downstream-regulated gene 2 (NDRG2) has been studied for its inhibitory effects against growth and metastasis of many tumor cell types. In this study, we showed NDRG2 expression was correlated with favorable recurrence-free survival of patients with breast cancer and inhibited metastasis of breast cancer cells (4T1). NDRG2 expression was examined in 189 breast carcinoma tissues and paired normal breast tissues using immunohistochemistry. Histological and clinicopathological data were correlated using Pearson’s chi-square test of independence. NDRG2 expression in human breast cancer tissues was inversely associated with lymph node metastasis and pTNM stage. Furthermore, patients with breast cancer with a high level of NDRG2 expression showed favorable recurrence-free survival (P = 0.038). To study the effect of NDRG2 on metastasis in vitro, we established an NDRG2-overexpressing mouse breast cancer cell line (4T1-NDRG2) and measured the metastasis and survival of 4T1-NDRG2 tumor-bearing mice. To test whether transforming growth factor β (TGF-β)–mediated metastasis of 4T1 was inhibited by NDRG2 expression, TGF–Smad-binding element (SBE)–luciferase activity and/or measurement of active TGF-β were performed in cell or tumor tissue level. 4T1-NDRG2 cells grew gradually and showed less metastatic activity in vitro. 4T1-NDRG2 cells showed lower SBE–luciferase activity and lower level of active autocrine TGF-β than 4T1-Mock did. Correctly, our data show that NDRG2 significantly suppress tumor metastasis by attenuating active autocrine TGF-β production, and the attenuation might be typically associated with the favorable recurrence-free survival of patients clinically.

Introduction

Genetic or epigenetic changes in the genome have been studied in the context of transformation of normal cells into cancer cells. Those changes activate pro-oncogenes or inactivate tumor-suppressor genes. N-myc downstream-regulated gene 2 (NDRG2)—identified through sequence homology to N-myc downstream-regulated gene 1—is highly expressed in several tissues such as the adult brain, salivary glands, and skeletal muscle. It has been reported as a candidate tumor-suppressor gene in many types of cancer (1–4). The expression of NDRG2 is regulated by epigenetic promoter methylation in several types of human cancer (5–8).

Abbreviations: NDRG2, N-myc downstream-regulated gene 2; RR, relative risk; SBE, Smad-binding element; TGF-β, transforming growth factor β.

NDRG2 has been widely implicated in tumor cell growth of tumor cell (9), differentiation of dendritic cells (10), and apoptosis (11). NDRG2 attenuates cell proliferation through down-regulation of activator protein 1 (AP-1) activity in human colon carcinoma cells (4) and inhibited metastasis through suppression of nuclear factor kappa B activity (3). NDRG2 antagonizes transforming growth factor β (TGF-β)–mediated hepatocarcinoma cell invasion (12) as well as T-cell factor β–catenin signaling in human colon carcinoma (13).

Metastasis is the major cause of lethality among patients with cancer, including patients with breast cancer (14, 15). Unfortunately, targeted therapy against metastatic tumors has been not clinically available because the molecular mechanism underlying metastasis is not clear (16). Therefore, identifying genes that functionally inhibit metastasis and understanding their molecular mechanisms is a key in the cancer research.

In this study, we found that protein levels of NDRG2 were correlated with clinical prognosis of breast cancer. NDRG2 expression in breast cancer tissue was associated with favorable recurrence-free survival, and loss of expression resulted in increased lymph node metastasis and mortality in patients with breast cancer. To test the antimetastatic effects of NDRG2 in vitro and in vivo, we established an NDRG2-overexpressing mouse breast tumor cell line (4T1). This cell line (4T1-NDRG2) showed less ability to invade in vitro and metastasize in vivo. The transcript levels of PAI-1 and integrin β6 were down-regulated in 4T1-NDRG2 cells, and this down-regulation was associated with a reduction in the expression of bioactive autocrine TGF-β, which could induce the invasiveness of 4T1. To summarize, NDRG2 is a negative regulator of metastasis and a prognostic marker for recurrence of breast tumor.

Materials and methods

Patients and samples

The biospecimens for this study were provided by the Biobank of Chonbuk National University Hospital, a member of the National Biobank of Korea, which is supported by the Ministry of Health, Welfare and Family Affairs. A total of 189 patients were diagnosed and received their first line treatment at Chonbuk National University between January 1997 and January 2005. All samples derived from the National Biobank of Korea were obtained with informed consent under institutional review board-approved protocols. All of the 189 breast carcinoma tissues and paired normal breast tissues taken from a site distant from the tumor lesion were fixed in 10% neutralized formalin solution for 24 h and embedded in paraffin wax. The histological grade was assessed using a modified Bloom–Richardson classification, and nuclear grade was evaluated according to a modified version of Black’s nuclear grade (17, 18).

Medical records were reviewed for clinical information, including follow-up status, and histological parameters were determined from the hematoxylin and eosin–stained slides. The cutoff date for vital status analysis was December 2010.

Immunohistochemistry

Tissue specimens were cut into 4-μm-thick serial sections and mounted on charged glass slides (Superfrost Plus; Fisher Scientific). In brief, tissue sections were microwaved twice for 10 min in citrate buffer (pH 6.0) for antigen retrieval. Thereafter, the sections were treated with 3% hydrogen peroxide in methanol to quench the endogenous peroxidase activity followed by incubation with 1% BSA. The tissue sections were incubated with mouse monoclonal antibodies against NDRG2 (1:100; Abnova) overnight at 4°C in a wet chamber. Subsequently, the sections were stained using a standard EnVision-HRP kit (Dako) and developed with diaminobenzidine as a substrate. An irrelevant mouse immunoglobulin G of the same isotype as the primary antibody dilution solution served as a negative control.

Assessment of immunostaining

We evaluated the intensity of immunohistochemical staining relative to the staining intensity of adjacent ductal epithelium within the same section as...
NDRG2 attenuates active TGF-β production in breast cancer

Cell invasion assay

4T1 cell invasion was tested using a modified Boyden chamber assay. Cells were allowed to grow to subconfluency (70–80%) and were serum-starved for 24 h after detachment with trypsin/EDTA and washing with Dulbecco’s modified Eagle’s medium containing 1% fetal bovine serum, the cells (1.5 × 10⁶ cells/300 μl) were added to the upper chamber of QCM™ 24-well cell invasion assay inserts (Millipore) and incubated for 48 h and then analyzed according to the manufacturer’s instructions.

Luciferase reporter gene assays

4T1 cells were transiently transfected with SBE–firefly luciferase vector and the pNull–Renilla luciferase vector in the absence or presence of TGF-β. Sometimes, HEK293 cells were transiently cotransfected with either pDNA3.1/hygro(+)-NDRG2 or a pDNA3.1/hygro(-) as a mock control by using the Lipofectamine™ 3000 transfection reagent (Invitrogen). Stably transfected clones were selected using complete growth medium containing 0.2 mg/ml hygromycin B (Calbiochem), and NDRG2 expression was confirmed by reverse transcriptase polymerase chain reaction (RT-PCR) and western blotting.

RT-PCR

Total RNA was extracted from cells using the total RNA isolation solution (RiboExTM; GeneAll, Korea) according to the manufacturer’s instructions. Immunohistochemistry conditions for NDRG2 were optimized and evaluated by two independent pathologists. The intensity of staining was coded as follows: 0, lower than the adjacent normal-appearing ductal epithelium; 1, similar to the adjacent ductal epithelium; and 2, stronger than the adjacent ductal epithelium. The percentage of cells displaying a stronger staining intensity than the adjacent ductal epithelium was scored as 1 (0–24% tumor cells stained), 2 (25–49% tumor cells stained), 3 (50–74% tumor cells stained), and 4 (75–100% tumor cells stained). For statistical analysis, the median of this series (25%, 50%, and 75% malignant cells showing a stronger intensity than adjacent ductal epithelium) was used as a cutoff value to distinguish tumors with low (<25%) or high (≥25%) levels of NDRG2 expression.

Cell culture and mice

The murine 4T1 breast cancer cell line and the HEK293 cell line were maintained as a monolayer cultures in Dulbecco’s modified Eagle’s medium (Sigma) supplemented with 10% (v/v) heat-inactivated fetal bovine serum (Sigma) and 1% penicillin/streptomycin (WebGENE, Korea) in humidified chamber with 5% CO₂ humidified air at 37°C. Specific pathogen-free female BALB/c mice (8 weeks) purchased from Orient Bio Co. were used in this study. All mice were kept at 23°C ± 1°C with a 12 h-light-12 h-dark cycle. They had free access to water and diet. All procedures described were reviewed and approved by the Animal Ethical Committee of Gyeongsang National University.

Generation of NDRG2 transfectant

The NDRG2 transfectants were established as follows. 4T1 mouse breast cancer cells were seeded and transfected with either a pcDNA3.1/hygro(+)-NDRG2 or a pcDNA3.1/hygro(-) as a mock control by using the Lipofectamine™ 3000 transfection reagent (Invitrogen). Stably transfected clones were selected using complete growth medium containing 0.2 mg/ml hygromycin B (Calbiochem), and NDRG2 expression was confirmed by reverse transcriptase polymerase chain reaction (RT-PCR) and western blotting.

RT-PCR

Total RNA was extracted from cells using the total RNA isolation solution (RiboExTM; GeneAll, Korea) according to the manufacturer’s instructions. RNA was quantified using the NanoDrop spectrophotometer (Thermo Fisher Scientific Inc.), and complementary DNA was synthesized with oligo-dt primers and reverse transcriptase (Fermentas). RT-PCR was performed using the DNA Engine Dyad® Peltier Thermal cycler (Bio-Rad Laboratories). Real-time PCR was performed using SsoFastTM EvaGreen Supermix® and CFX96™ Real-time detection system (Bio-Rad Laboratories). The following primers were used for amplification: NDRG2, 5'-TACCAAGTGGGAGACCTCA-3' and 5'-AAGAGCATATTCGCCAGAAG-3'; Integrin α6, 5'-AGGCCGTGACTCATTTGG-3' and 5'-CCATCTCTCCAGACACGATG-3'; TGF-β1, 5'-TGGTGGAGCTGTAAGGAA-3' and 5'-GGTCTTGCCCATCTTCACAT-3'; TGF-β2, 5'-GCAGGATAATTGCTGCCTGTGGAGCTGAAGCAA-3' and 5'-AGGGGTGACTAAGAGCATATCTCGCCAGGA-3'; Integrin α6, 5'-TACCACGATGTGGGACTCAA-3' and 5'-AACACTGTTAGCAGTGGCTTTAG-3'; TGF-β1, 5'-TGGTGGAGCTGTAAGGAA-3' and 5'-GGTCTTGCCCATCTTCACAT-3'; TGF-β2, 5'-GCAGGATAATTGCTGCCTGTGGAGCTGAAGCAA-3' and 5'-AGGGGTGACTAAGAGCATATCTCGCCAGGA-3'; Integrin α6, 5'-TACCACGATGTGGGACTCAA-3'. Where applicable, measured levels from tissues were normalized to total protein content as determined by Bradford assay (Bio-Rad Laboratories).

Statistical analysis

Statistical analysis was performed using the SPSS software package (version 14.0; SPSS Inc.). The correlation between histological index scores and other categorical clinicopathological factors was analyzed using Pearson’s chi-square test of independence. Recurrence-free survival was defined as the time from the date of surgery to the first date of recurrence of cancer or death from any cause. Overall survival was defined as the time from the date of surgery to the date of the last follow-up or death from any cause. The median follow-up period for all patients was 80.2 months (interquartile range, 61.9–92.6). Survival curve and median survival curve were estimated by the Kaplan–Meier method. Log-rank test was used to evaluate the statistical significance of differences in survival distribution. Multivariate analysis was performed using the Cox proportional hazard regression analysis. Cox proportional hazard model that included variables from the chi-square test for factors affecting survival and age variables were identified. All other data were analyzed using unpaired Student’s t-test. Results were considered statistically significant if P < 0.05

Results

Correlation between NDRG2 expression levels and clinicopathological characteristics

The immunohistochemical staining result of NDRG2 in breast cancer tissues is shown in Figure 1A–C. Although NDRG2 has been known as a candidate of tumor-suppressor, some breast tumor biologists expressed NDRG2. To analyze whether there is any correlation between NDRG2 expression level and clinical meaning, the clinical and pathological characteristics of the 189 breast cancer patients who had undergone surgical resection are summarized in Table 1. The median age at the time of resection was 47 years; the median age of patients with a low level and a high level of NDRG2 expression was 46 and 48 years, respectively. High NDRG2 expression levels were observed in 69 (36.5%) of the 189 patients. When we tested for an association between the NDRG2 expression levels and the clinicopathological parameters, we found that lymph node metastasis (P = 0.001), pTNM (tumor, node, and metastasis) stage (P = 0.011), and progesterone receptor status (P = 0.011) were significantly associated with NDRG2 expression status (Table 1). Importantly, patients with low NDRG2 expression levels showed significantly more frequent nodal metastasis and advanced tumor stage than those with high NDRG2 expression levels.
Fig. 1. Immunohistochemical expression of NDRG2 and Kaplan–Meier survival analysis as a function of NDRG2 expression status in patients with breast carcinoma. (A) NDRG2 was constitutively expressed in normal breast tissue. (B) In breast cancer tissue, NDRG2 was highly expressed on the cytosolic membrane of tumor cells. (C) In some breast cancer tissues, NDRG2 was not expressed in cancer cells; however, the adjacent normal breast tissue showed well-preserved NDRG2 expression. Magnification: 400×. (D) Cumulative recurrence-free survival differences between patients with high and low levels of NDRG2 expression. (E) Cumulative overall survival differences between patients with high and low levels of NDRG2 expression. Statistical analysis was performed using the log-rank test of the difference.

High NDRG2 expression correlates with favorable recurrence-free survival, but not with overall survival

We first carried out univariate analyses to examine whether the expression status of NDRG2 correlates with recurrence-free survival and overall survival of patients with breast cancer. In all, 38 (20.1%) of 189 patients presented recurrence during the follow-up period. At the end of the follow-up, 166 (87.8%) patients were alive and 23 had died. High NDRG2 expression levels were associated with favorable recurrence-free survival ($P = 0.038$) (Figure 1D). The mean recurrence-free survival for patients with high NDRG2 expression levels was 101.4 months (95% confidence interval [CI], 95.1–107.7), whereas the time was reduced to 94.0 months (95% CI, 86.8–101.3) for those with low levels of NDRG2. However, NDRG2 expression levels were not correlated with overall survival (Figure 1E). The mean values of the overall survival of patients with high NDRG2 levels, low NDRG2 levels, and of all of the patients was 105.2, 151.2, and 154.1 months, respectively. We carried out multivariate Cox proportional hazard analyses to assess the predictive value of NDRG2 expression status for recurrence-free survival and overall survival by adjusting for other potentially prognostic factors, including age, histological grade, pTNM stage, and hormonal status. The results confirmed a worse recurrence-free survival outcome in patients with low NDRG2 expression levels, yet the correlation did not reach statistical significance ($P = 0.071$). The relative risk (RR) of recurrence was about twice as high in patients with low NDRG2 levels (RR, 2.077; 95% CI, 0.939–4.593) than in those with high NDRG2 levels. In a multivariate Cox regression analysis, the independent prognostic factors that significantly associated with recurrence-free survival were histological grade ($P = 0.03$) (RR, 3.739; 95% CI, 1.140–12.265), progesterone receptor status ($P = 0.03$) (RR, 0.444; 95% CI, 0.212–0.930), and pTNM stage ($P < 0.001$) (RR, 4.276; 95% CI, 2.230–8.202) (Supplementary Table 1). Levels of NDRG2 were not predictive of overall survival.

NDRG2 attenuates tumor growth in vivo and in vitro

To investigate NDRG2 function in breast cancer in vivo, we established a mouse breast cancer cell line overexpressing NDRG2 (4T1-NDRG2) (Figure 2A). The control (4T1-Mock) and 4T1-NDRG2 cells were seeded at $1.5 \times 10^5$ cells/well in 6-well plates, and cell numbers were counted with a hematocytometer at the indicated time points. After incubation for 2 days, the number of 4T1-NDRG2 cells was reduced by approximately 2.5-fold as compared with the control 4T1-Mock cells (Figure 2B). Moreover, the size of the solid tumors was smaller on back of BALB/c mice subcutaneously injected with 4T1-NDRG2 cells than on back of BALB/c mice subcutaneously injected with 4T1-Mock cells (Figure 2C). These data indicate that NDRG2 overexpression in breast cancer attenuates tumor growth in vitro and in vivo.

NDRG2 attenuates tumor invasion in vitro and inhibits tumor metastasis in vivo

To investigate whether NDRG2 affects the invasiveness and metastasis of breast cancer cells, we performed an in vitro invasion assay. 4T1-NDRG2 cells exhibited less invasiveness (40–60% inhibition)...
Fig. 2. NDRG2 attenuates tumor growth in vivo and in vitro. (A) Transcriptional and protein levels of NDRG2 in 4T1-WT, 4T1-Mock, and 4T1-NDRG2 cells were measured by RT-PCR and Western blotting, respectively. (B) Growth curves of transfected cells in vitro. Cells were plated at a low density (1.5 × 10⁵ per well) and cell numbers were counted daily for 3 days. (C) A 4T1-NDRG2 and 4T1-Mock cells (5 × 10⁴ cells) were injected subcutaneously into the dorsal region of BALB/c mice, as described in Materials and methods. Tumor dimensions were measured with a caliper on day 24 after tumor cell implantation. Tumor volumes were calculated using the following formula: (maximal length) × (perpendicular width) × (height) / 2. **P < 0.01, by t-test.

NDRG2 attenuates TGF-β-mediated tumor cell invasion through attenuation of active TGF-β production

NDRG2 was known to be a negative regulator of TGF-β-mediated Smad signaling in hepatocarcinoma (12). In line with this, we determined the expression levels of the TGF-β targets, PAI-1 and integrin β6, by using RT-PCR. 4T1-NDRG2 cells showed decreased levels of PAI-1 and integrin β6 transcripts (Supplementary Figure 1A). To confirm the inhibition of TGF-β-mediated Smad signaling by NDRG2, we transfected 4T1-Mock and 4T1-NDRG2 cells with an SBE–luciferase construct and analyzed spontaneous luciferase activity. 4T1-NDRG2 showed decreased luciferase activity (40–50% inhibition) as compared with the control (Supplementary Figure 1B). However, the levels of TGF-β1, TGF-β2, TGF-β3, and TGF-β receptor were not changed in 4T1-NDRG2 (Supplementary Figure 2A), indicating that NDRG2 might modulate TGF-β signaling without decreasing TGF-β or TGF-β receptor expression. To confirm whether NDRG2 negatively regulates TGF-β-mediated intracellular signaling, HEK293 cells were transfected with SBE–luciferase construct and pcDNA3.1/hygro(+)-NDRG2 or pcDNA3.1/hygro(+), after which they were treated with recombinant TGF-β. Unexpectedly, the luciferase activities did not differ between the Mock control and the NDRG2-overexpressing cells in the presence of TGF-β (Figure 4A), and exogenous TGF-β induced the expression of PAI-1 and integrin β6 in 4T1-NDRG2 cells (Supplementary Figure 2B). These results led us to test the amount of active TGF-β secreted from 4T1-Mock and 4T1-NDRG2 cells. The amount of active TGF-β from in vitro cell culture supernatant (Figure 4B) or tumor tissues (Figure 4C) established in vivo was calculated using ELISA, and active TGF-β was less in 4T1-NDRG2 group than in 4T1-Mock group. To test activity of TGF-β produced from both cell lines, we transiently transfected HEK293 or 4T1-NDRG2 cells with an SBE–luciferase construct and then treated them with the culture supernatant from 4T1-Mock or 4T1-NDRG2 cells. The control 4T1-Mock culture supernatant induced higher luciferase activity than 4T1-NDRG2 supernatant, which indicated that NDRG2 attenuates active TGF-β production in breast cancer

Table 1. Clinicalopathological characteristics of breast cancer patients and NDRG2 expression status

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TNM: tumor, node, metastasis

cells metastasized in the lungs (Figure 3B). On day 21 after primary tumor resection, we fixed the lungs with Bouin’s solution and counted the number of metastatic nodules in the lungs. The 4T1-NDRG2 group showed a significantly less number of nodules than did the control (Figure 3C). Therefore, to mimic the analysis of mortality of patients with breast cancer, local tumors were surgically removed on day 21 after the injection of cancer cells, and the mice were observed for 50 days. We found out that all experimental mice injected with Mock control 4T1 died, whereas mice injected with 4T1-NDRG2 were able to survive (Figure 3D). This observation revealed that the mortality might be associated with lung metastasis of mammalian cancer cells and supported clinicopathological data of human patients.

Fig. 2. NDRG2 attenuates tumor growth in vivo and in vitro. (A) Transcriptional and protein levels of NDRG2 in 4T1-WT, 4T1-Mock, and 4T1-NDRG2 cells were measured by RT-PCR and Western blotting, respectively. (B) Growth curves of transfected cells in vitro. Cells were plated at a low density (1.5 × 10⁵ per well), and cell numbers were counted daily for 3 days. (C) A 4T1-NDRG2 and 4T1-Mock cells (5 × 10⁴ cells) were injected subcutaneously into the dorsal region of BALB/c mice, as described in Materials and methods. Tumor dimensions were measured with a caliper on day 24 after tumor cell implantation. Tumor volumes were calculated using the following formula: (maximal length) × (perpendicular width) × (height) / 2. **P < 0.01, by t-test.
4T1-Mock produced more active TGF-β than 4T1-Mock (Figure 4D). Furthermore, the supernatant from 4T1-Mock enhanced the invasiveness of 4T1-NDRG2 cells (Figure 4F) like recombinant active TGF-β (Figure 4F). Taken together, NDRG2 did not inhibit intracellular TGF-β-mediated Smad signaling directly but rather inhibited the production of active TGF-β.

Discussion

Breast cancer originates from breast tissue, the inner lining of milk ducts, or the lobules supplying the ducts with milk. Breast cancer is one of the most common malignant tumors among women, accounting for 14% of the cancer deaths in 2008 (19). Patients with metastatic breast cancer have traditionally been considered incurable with conventional treatment, although the survival of patients with metastatic breast cancer has been slowly improving, as shown in recent studies (20–23). Actually, tumor metastasis has been considered the most important reason for breast cancer morbidity and mortality (24). Although the expression of NDRG2 messenger RNA was statistically down-regulated in breast cancer (25) and NDRG2-regulated metastasis of breast cancer cell line through the down-regulation of CD24 expression (26,27) and up-regulation of BMP-4 (28), the correlation between clinical and functional evidences on the NDRG2 expression of breast cancer has been currently unknown. In the present study, we showed that high NDRG2 expression correlated with favorable recurrence-free survival. When the relationship between the NDRG2 expression level and the clinicopathological factors potentially predictive of prognosis was examined, we found that patients with low NDRG2 expression levels showed more frequent nodal metastasis and advanced tumor stage than those with high NDRG2. To improve the outcome for patients with breast cancer, advances in the understanding of the pathophysiology of breast cancer and identification of proteins and molecular pathways that affect key metastasis and survival mechanisms are needed. Accumulating evidence suggests that NDRG2 is an important factor in tumor progression and metastasis, although its molecular mechanism is poorly understood (29–31).

The 4T1 tumor cell line was derived from a spontaneously arising BALB/c mammary tumor and has been extensively used in a well-characterized metastatic model (32,33). We established NDRG2-expressing 4T1 cells (4T1-NDRG2) to investigate the mechanisms of breast cancer metastasis inhibition by NDRG2. 4T1-NDRG2 cells exhibited a low proliferative phenotype, similar to NDRG2-expressing colon cancer cell lines, and retarded tumor growth in vivo. In human colon cancer cell lines, NDRG2 decreased c-Jun phosphorylation at Ser63, thereby inhibiting the function of AP-1 as a transcription factor. The down-regulation of cyclin D1, which is a target gene induced by AP-1, has also been reported and might be a cause of NDRG2-mediated retardation of proliferation. In addition, NDRG2 overexpression inhibited the metastasis of 4T1 cells from the established local site into the lungs. Such NDRG2 overexpression was correlated with the clinicopathological data from human patients with breast cancer. TGF-β signaling has been believed to play an important role in metastatic spread of breast cancer cells (34,35). Actually, many aggressive or advanced tumors are resistant to the growth inhibitory activity of TGF-β, which is an important negative regulator that prevents cell proliferation in early lesions. On the other hand, TGF-β can activate metastatic pathways (34,36). In human hepatocarcinoma cells, NDRG2 overexpression suppresses TGF-β signaling, inducing PAI-1, and integrin α3 and inhibits metastasis of SK-Hep-1 cells (12). In this study, we also found decreased PAI-1 expression levels in NDRG2-overexpressing 4T1 cells. We tested whether NDRG2 inhibited TGF-β-mediated Smad signaling by using an SBE–luciferase system and found low
NDRG2 attenuates active TGF-β production in breast cancer

SBE–luciferase activity in 4T1-NDRG2 cells. Unlike in human hepatocarcinoma cells, the lower SBE–luciferase activity might be not attributed to NDRG2-mediated inhibition of TGF-β signaling. Indeed, NDRG2 was not able to inhibit luciferase activity in TGF-β–treated HEK293 cells cotransfected with an NDRG2 expression construct and the SBE–luciferase vector. In addition, to investigate whether NDRG2 inhibits production of functional TGF-β, culture supernatants from 4T1-Mock or 4T1-NDRG2 cells were used to treat SBE luciferase-transfected HEK293 cells. 4T1-Mock, but not 4T1-NDRG2, culture supernatants induced luciferase activity in SBE luciferase-transfected HEK293 cells, and the amount of active TGF-β was higher in 4T1-Mock than in 4T1-NDRG2 in vitro and in vivo. Exogenous recombinant TGF-β as well as supernatant from 4T1-Mock cell enhanced the invasiveness of 4T1-NDRG2, confirming that NDRG2 did not inhibit TGF-β signaling and inhibited active TGF-β production. Taken together, we concluded that NDRG2 might inhibit the metastasis of breast cancer cells by reducing the production of active TGF-β. We also found that the transcript levels of integrin β6 were reduced in 4T1-NDRG2 cells. Integrin β6 controls the switch between latent and active TGF-β by forming heterodimers with integrin αv, which when bound to the latency-associated peptides 1 and 3, lead to the activation of the latent precursor form of TGF-β1 and TGF-β3 (37,38). In several tumor cell lines, integrin β6 has been reported to function as a positive regulator for tumor progression, proliferation, invasion, and epithelial-to-mesenchymal transition (39–41). Finally, we suggested that NDRG2 improved the recurrence-free survival of patients with breast cancer via inhibition of metastasis following attenuation of active TGF-β production.

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