Repression of Prostaglandin Dehydrogenase by Epidermal Growth Factor and Snail Increases Prostaglandin E2 and Promotes Cancer Progression


Abstract

Prostaglandin E2 (PGE2), a proinflammatory bioactive lipid, promotes cancer progression by modulating proliferation, apoptosis, and angiogenesis. PGE2 is a downstream product of cyclooxygenase (COX) and is biochemically inactivated by prostaglandin dehydrogenase (PGDH). In the present study, we investigated the mechanisms by which PGDH is down-regulated in cancer. We show that epidermal growth factor (EGF) represses PGDH expression in colorectal cancer cells. EGF receptor (EGFR) signaling induces Snail, which binds conserved E-box elements in the PGDH promoter to repress transcription. Induction of PGE2 catabolism through inhibition of EGFR signaling blocks cancer growth in vivo. In human colon cancers, elevated Snail expression correlates well with down-regulation of PGDH. These data indicate that PGDH may serve a tumor suppressor function in colorectal cancer and provide a possible COX-2–independent way to target PGE2 to inhibit cancer progression. (Cancer Res 2006; 66(13): 6649-56)

Introduction

The intestine represents a unique system to study carcinogenesis. Homeostasis of the intestinal epithelium is governed by a host of balanced regulatory mechanisms that are often subverted during the transformation process (1, 2). These include Wnt (3, 4), bone morphogenetic protein/transforming growth factor-β (TGF-β; refs. 5, 6), Notch (7), and Hedgehog (8) signaling pathways. Interestingly, whereas prevention of cancer in the intestine remains an important clinical goal, the only clinically tested chemopreventive agents do not directly regulate any of these pathways. Rather, aspirin and other nonsteroidal anti-inflammatory drugs (NSAIDs) are known to block production of a bioactive lipid prostaglandin E2 (PGE2) at normal doses of drugs.

Prostaglandins, including PGE2, derive from prostaglandin endoperoxide H2 synthase-1 and -2 [cyclooxygenase-1 (COX-1) and COX-2] enzymes and regulate many biological functions, including hemostasis, salt balance, female reproduction, and a host of other processes (9). COX-2 production of PGE2, the most abundant prostaglandin in gastrointestinal tumors, can promote carcinogenesis by modulating apoptosis, proliferation, and angiogenesis (10, 11). Recent studies suggest that administration of PGE2 accelerates tumor progression (12), and that PGE2 may stabilize β-catenin through axin regulation (13). Although NSAIDs confer a protective effect by blocking PGE2 synthesis, the endogenous mechanism for inactivating PGE2 through catabolism by prostaglandin dehydrogenase (PGDH) remains poorly understood.

Previously, we observed down-regulation of PGDH in a subset of colorectal carcinomas and found preliminary evidence suggesting that epidermal growth factor (EGF) regulates PGDH expression (14). In the present study, we examine the mechanism of PGDH repression by EGF and conduct meta-analysis of PGDH expression in multiple cancers, including colon, breast, liver, lung, and prostate. Our data suggest that EGF represses PGDH expression. Specifically, EGF can induce Snail to bind the PGDH promoter and repress transcription. We show that disruption of EGFR signaling induces PGDH expression and activity in vivo. Finally, analysis of clinical data sets supports the hypothesis that PGDH is repressed in multiple cancers, and that elevated Snail expression correlates with down-regulation of PGDH in colon cancers.

Materials and Methods

Cell lines and reagents. HCT-15, HCA-7, HCT-116, and HT-29 cells were in McCoy's 5A medium containing 10% fetal bovine serum, 100 units/mL penicillin, and 100 µg/mL streptomycin in a 5% CO2 atmosphere. EGF and actinomycin D were from Sigma (St. Louis, MO), and erlotinib (Tarceva) was obtained from Genentech (South San Francisco, CA).

Quantitative real-time PCR. PCR reaction contained iQ SYBR Green Supermix (Bio-Rad, Hercules, CA), 50 ng of each primer, and 5 µL of 1:1,000 diluted reverse transcriptase template in a 25-µL reaction volume. Amplification specificity was confirmed by melt-curve analysis, and expression values were normalized to β-actin. See Table 1 for oligonucleotide sequences.

RNA interference. A short hairpin RNA retroviral expression system, pRETOSuper (15), was employed to knock down Snail expression as previously described (16).

Immunoblotting. Cells were washed with PBS and lysed with radiolucent assay buffer. Proteins were separated on precast SDS-PAGE gels and electrotransferred onto polyvinylidene difluoride membranes. Antibodies: PGDH (200-179; 1:2,000) from Novus Biologicals; E-cadherin (H-108; 1:1,000) from Santa Cruz Biotechnology (Santa Cruz, CA); β-actin (A-5441; 1:2,500) from Sigma.

Transient transfection and reporter gene analysis. Transfection of a 2.4-kb PGDH promoter luciferase construct was carried out with LipofectAMINE (Invitrogen, Carlsbad, CA) using 100 ng of reporter plasmid and 5 ng of pRL-SV40. Firefly and Renilla luciferase activities were measured and normalized with a dual luciferase assay (Promega, Madison, WI).
Electrophoretic mobility shift assays. Electrophoretic mobility shift assay was done as previously described (17). See Table 1 for oligonucleotide sequences.

Laser capture microdissection, tissue collection, and in situ hybridization. With Vanderbilt University Institutional Review Board (IRB) approval, human colorectal tumor and matching normal mucosa specimens were obtained from surgical resections. With University of Connecticut IRB approval, hyperplastic crypts were microdissected from fresh-frozen tissue sections following isolation of human aberrant crypt foci (ACF) and matching normal mucosa with an Olympus close-focus magnifying endoscope. 35S-labeled PGDH riboprobes were used for in situ hybridization as previously described (18).

Immunohistochemistry. Paraffin sections of adult ApcMin intestine were dewaxed, rehydrated, and incubated overnight at 4°C with previously published antibodies against E-cadherin (Santa Cruz Biotechnology H-108; 1:100) and Snail (Santa Cruz Biotechnology E-18; 1:100). Negative controls received no primary antibody. The Vectastain ABC peroxidase system (Vector Laboratories, Burlingame, CA) was used for immunodetection.

In vivo PGDH functional assay. C57Bl/6 and C57Bl/6-ApcMin mice were obtained from The Jackson Laboratory (Bar Harbor, ME). Analysis of PGE2 urinary metabolites (PGE-M) following catabolism by PGDH was done by liquid chromatography tandem mass spectrometry (LC-MS/MS) of urine collected overnight following daily gavage of erlotinib (50 mg/kg) or vehicle for 1 week. All mice were housed and used in accordance with the NIH and institutional guidelines on the care and use of laboratory animals.

LC-MS/MS. The major urinary metabolite of PGE2, 11α-hydroxy-9,15-dioxo-2,3,4,5-tetranor-prostane-1,20-dioic acid (PGE-M), was measured in urine; 400 μL of urine was derivatized using methoximine HCl (16% w/v) in 1.5 mol/L sodium acetate solution. Samples were purified by extraction using a C18 SepPak, after which 12.4 ng of [2H6]-methyloxime PGE-M internal standard was added. Samples were dried under nitrogen, resuspended in 50 μL mobile phase A [95:4.9:0.1 (v/v/v) 5 mmol/L ammonium acetate/acetonitrile/acetic acid], and analyzed by LC-MS/MS.

Subcutaneous tumorigenicity assays and gas chromatography/MS. Following xenograft establishment, nude mice (n = 4) were gavaged daily with erlotinib (50 mg/kg) or vehicle for 1 week. Gene expression was

Table 1. Oligonucleotide sequences

<table>
<thead>
<tr>
<th>Gene</th>
<th>Region</th>
<th>Forward primer</th>
<th>Reverse primer</th>
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<tr>
<td>PGDH</td>
<td>E-Box 1</td>
<td>5′-TCTGTTCATCCAGTGCGATGT 5′</td>
<td>5′-ATAATGATGCCGCTTCCACT</td>
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<td>PGDH</td>
<td>E-Box 2</td>
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<td>5′-GAGGCGTACAGGATGAGCA</td>
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<td>5′-CGCTCAGGGGCCAGTGAGCAGCTGAG</td>
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analyzed by quantitative reverse transcription-PCR following isolation of RNA. Upon lipid extraction, PGE2 levels were assayed by gas chromatography-MS as previously described (19).

**Microarray data analysis.** Publicly available gene expression data from 117 patients on 24,481 genes (20) was downloaded and analyzed as follows. Estrogen receptor (ER) status was determined by immunohistochemistry-validated microarray analysis, and the association between ER status and relapse-free survival was calculated using the Kaplan-Meier estimator on published outcome data. Pearson correlation coefficients were computed between ER (NM_00012) and PGDH (NM_000860), Snail (NM_00598), COX-2 (NM_000963), and E-cadherin (NM_00436). In addition, meta-analysis of gene expression in human tumor samples was conducted with Oncomine 2.0 (http://www.oncomine.org) on multiple data sets. These data are composed of two general types: two channel ratio data and single channel intensity data. All available data were included in processing and analysis, except for negative single channel intensity values. All data sets were log transformed and median centered per array.

**Statistical analyses.** Statistical significance was determined as P < 0.05 by Student’s t test. Spearman’s correlation coefficient was computed between Snail and PGDH expression in colorectal carcinoma samples. In vitro experiments were replicated in multiple cell lines, and data are expressed as mean ± SE.

**Results**

**EGF represses transcription of PGDH.** To increase understanding of the regulation of prostaglandin levels, we examined pathways complementary to COX-2 by which PGE2 may accumulate and contribute to colorectal carcinogenesis. PGDH (encoded by HPGD) catalyzes the rate-limiting step of prostaglandin catabolism, and genetic deletion of Pgdh leads to increased tissue levels of PGE2 (21). To investigate the mechanism for EGF down-regulation of PGDH, we examined several colorectal carcinoma lines, including HCT-15, HCA-7, HT-29, and HCT-116.

We observe that EGF represses PGDH protein by 24 hours and up to 72 hours following treatment (Fig. 1A). A similar reduction was observed with E-cadherin expression (Fig. 1A). EGF stimulation reduces PGDH transcript levels in a dose-dependent manner.
As EGF causes a similar decrease in steady-state protein and RNA levels, we examined transcriptional activation and stability to determine the specific level of regulation. PGDH promoter activity is decreased by EGF treatment and induced by erlotinib (Tarceva), a small-molecule kinase inhibitor specific for EGFR (Fig. 1C). However, pretreatment with erlotinib blocks EGF repression of PGDH-luciferase activity (Fig. 1C). In contrast, PGDH transcript stability following actinomycin D treatment is not altered by stimulation or inhibition of EGFR activity (Fig. 1D). These data suggest that EGF signaling represses transcription of PGDH.

EGF requires snail to repress PGDH. Lu et al. report that EGF-dependent repression of E-cadherin requires induction of a transcriptional repressor, Snail (encoded by Snai1; ref. 16). Snail and related family members mediate repression of E-cadherin through zinc-finger binding of conserved E-box elements (CANNTG) in the proximal promoter. Inspection of the PGDH promoter revealed a similar arrangement of consensus E-box elements (Fig. 2F); thus, we examined the ability of Snail to modulate PGDH expression.

EGF treatment of colon cancer cell lines induces Snail in a Ras and extracellular signal-regulated kinase–dependent manner (Fig. 2A and B). In contrast, we did not observe induction of Slug by EGF (data not shown). Addition of wild-type Snail expression construct, even 6 ng, represses PGDH transcription in a similar manner to stimulation with EGF (Fig. 2C and D). Repression of E-cadherin promoter activity is also observed with EGF and wild-type Snail (Fig. 2C). However, zinc-finger mutant Snail does not effectively repress transcription of PGDH or E-cadherin (Fig. 2C).

We next employed RNA interference to complement gain-of-function studies of Snail-dependent repression of PGDH. Using HT-29 cells, which express elevated levels of Snail relative to HCT-15 cells, we reasoned that knock down of Snail would induce PGDH transcription. Introduction of short hairpin RNA targeted to Snail disrupts EGF repression of PGDH transcription (Fig. 2E). In gel shift experiments, Snail specifically binds conserved E-box elements in the PGDH promoter (Fig. 2F). Shifts were observed with E-boxes 1 and 3 and could be competed away with 50-fold excess of unlabeled oligonucleotide (Fig. 2F). Taken together, we...
find that Snail can mediate EGF-dependent repression of PGDH transcription.

Modulation of EGFR regulates PGDH expression and activity in vivo. Apc\textsuperscript{Min} mice harbor a nonsense APC mutation and spontaneously develop preinvasive adenomas that recapitulate many aspects of the human syndrome, familial adenomatous polyposis coli. Previous reports suggest that EGFR activity is elevated in Apc\textsuperscript{Min} adenoma tissue (22), and introduction of hypomorphic Egfr reduces Apc\textsuperscript{Min} tumor burden by 10-fold (22, 23). Moreover, progression of these tumors requires PGDE\textsuperscript{2} (24, 25). To examine EGF regulation of Pgdh in vivo, we evaluated expression patterns of Snail, E-cadherin, and Pgdh in Apc\textsuperscript{Min} mouse intestine. In normal mucosa, Snail localizes to the proliferative crypt compartment, whereas Pgdh and E-cadherin are restricted to well-differentiated villi (Fig. 3A and B). Interestingly, examination of adenomas revealed high expression of Snail, whereas Pgdh is almost completely absent (Fig. 3A). Based on our findings that erlotinib, a small-molecule EGFR inhibitor, can induce PGDH in vitro, we hypothesized that disruption of EGFR would restore prostaglandin catabolism in vivo. Following establishment of PGDE\textsuperscript{2}-dependent HCA-7 xenografts, nude mice (n = 4) were gavaged daily with erlotinib (50 mg/kg) or vehicle for 1 week. Erlotinib treatment nearly eliminated tumor growth (data not shown). In addition, disruption of EGFR signaling induces both Snail and E-cadherin while reducing Snail and COX-2 (Fig. 3C). As expected, restoration of PGDH reduces intratumoral PGDE\textsuperscript{2} levels (Fig. 3D).

To further examine PGDH repression by EGF in vivo, we assessed whole-body prostaglandin catabolism following disruption of EGFR signaling in Apc\textsuperscript{Min} mice. We used LC-MS/MS to assay PGDH catabolic products in urine and hypothesized that EGFR blockade would induce PGDH activity. Accordingly, PGDE\textsuperscript{2} M levels increased 6-fold in Apc\textsuperscript{Min} urine following daily gavage with erlotinib (50 mg/kg) for 1 week (Fig. 3E). These data suggest that EGFR can regulate PGDH expression and activity in vivo.

PGDH expression is repressed in multiple human cancers. Published reports suggest down-regulation of PGDH in a subset of colorectal carcinomas (14, 26). To more thoroughly evaluate the role of PGDH in human tumorigenesis, we conducted meta-analysis to test our hypothesis that PGDH is repressed in multiple cancer data sets generated by outside investigators. Examination of microarray expression data from eight published reports indicates that PGDH expression is reduced in multiple human cancers relative to matched normal mucosa (n = 1,114; Fig. 4A; data not shown). Moreover, PGDH is further diminished upon cancer progression (Fig. 4A). Specifically, PGDH decreases from normal (n = 222) to primary tumors (n = 571; P = 0.0098) and is further reduced from well-differentiated (n = 99) to poorly differentiated (n = 34) primary tumors (P = 0.0221). Finally, PGDH expression is further reduced from primary tumors (n = 107) to metastatic tumors (n = 29; P = 0.0177; Fig. 4A). To corroborate these findings, we analyzed a well-annotated set of 117 breast cancers with detailed data on metastatic outcomes (20). Following confirmation that ER status strongly predicts...
metastasis-free survival at 5 years (Fig. 4C), we compared Snail, PGDH, COX-2, and E-cadherin to ER expression. PGDH paired with E-cadherin and ER in unsupervised hierarchical clustering analysis (Fig. 4B; Table 2). Moreover, PGDH was repressed and Snail expression elevated during cancer progression (Fig. 4D).

**PGDH inversely correlates with Snail in colorectal cancers.** Finally, we examined the expression pattern of PGDH in normal intestine and matched dysplasia ranging from ACF (early hyperplastic lesions) to high-grade colorectal carcinomas. PGDH seemed to be reduced in both microdissected ACF and colorectal carcinomas, suggesting that PGDH may play a role in prevention of tumor progression (Fig. 5A). We quantified PGDH and Snail transcript levels in 15 pairs of colorectal carcinomas and matched normal mucosa. PGDH is significantly reduced in carcinoma tissue and inversely correlates with Snail expression, which increases 7-fold on average (Fig. 5B). Notably, pairwise comparison shows that expression of PGDH and Snail seem to be mutually exclusive ($r_s = -0.57, P = 0.0005$; Fig. 5C).

**Discussion**

Induction of COX-2 and repression of PGDH provide complementary pathways to increase PGE2 levels. By inactivating endogenous PGE2, PGDH provides an important, natural way to reduce this procarcinogenic lipid mediator. These data support a novel pathway that increases PGE2 in vivo: activation of EGFR, known to be involved in colorectal cancer, represses PGDH through Snail.

<table>
<thead>
<tr>
<th>Gene</th>
<th>N/T ratio (log 2)</th>
<th>ER correlation coefficient</th>
<th>P</th>
<th>Significance</th>
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<tr>
<td>COX-2</td>
<td>0.31</td>
<td>-0.46</td>
<td>&lt;0.0001</td>
<td>*</td>
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<tr>
<td>Snail</td>
<td>-0.07</td>
<td>-0.07</td>
<td>0.443</td>
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<tr>
<td>ER</td>
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<tr>
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<td>0.020</td>
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<td>1.02</td>
<td>+0.24</td>
<td>0.009</td>
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</table>

Abbreviation: NS, not significant.

* $P < 0.001$.

† $P < 0.05$.

‡ $P < 0.01$.

Figure 5. PGDH negatively correlates with Snail in colorectal cancers. A, localization of PGDH expression by in situ analysis of hyperplastic ACF and high-grade colorectal carcinoma. Bar, 100 μm. B, summary of quantitative real-time PCR analysis for PGDH and Snail expression in 15 pairs of human colorectal carcinomas and matched normal tissue. C, independent comparison of PGDH versus Snail for 15 normal and 15 tumor samples. The Spearman coefficient was calculated to determine statistical correlation ($r_s = -0.57, P = 0.0005$).
We originally identified COX-2 as an EGF/TGF-α target gene in intestinal epithelial cells, with robust enhancement of prostaglandin production following EGF activation (27). Other reports from our group indicate COX-2-derived PGE2 can transactivate the EGFR (28). We now show that EGFR can repress PGDH, allowing intestinal epithelial cells, with robust enhancement of prostaglandin-dependent production of prostaglandins (33, 34). Moreover, poorer prognosis for carcinomas bearing increased COX-2–patients with colorectal cancer (32), and previous studies indicate current findings present important clinical implications. Expression of EGFR is known to be associated with poor survival in patients with colorectal cancer (32), and previous studies indicate proper prognostic for carcinomas bearing increased COX-2–dependent production of prostaglandins (33, 34). Moreover, simultaneous blockade of prostaglandin and EGFR signaling ablates tumor formation in ApcMin mice (35).

Although EGF and PGE2 have been targeted individually in human patients, dose-liming toxicity and selection for resistant clones indicate that administration of these agents in combination may achieve improved clinical outcomes. Moreover, understanding the mechanistic basis of PGDH repression could lead to improved approaches to chemoprevention of cancer. Because PGDH does not degrade anti-thrombotic PGI2, these data raise the possibility of selectively targeting PGE2 through PGDH and avoiding some of the cardiovascular side effects attendant with COX-2 inhibition. Thus, EGFR inhibitors may serve a role in cancer treatment or prevention by restoring PGDH expression. Measurement of PGE2 urinary metabolites provides a possible noninvasive and cost-effective method of monitoring therapeutic response (36).

Acknowledgments

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References


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