

## Sonic hedgehog-Gli1 pathway in colorectal adenocarcinomas

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### Abstract

**AIM:** To determine the role of Sonic hedgehog (Shh) pathway in colorectal adenocarcinomas through analysis of the expression of Shh pathway-related molecules, Shh, Ptch1, hedgehog-interacting protein (Hip), Gli1, Gli3 and PDGFR $\alpha$ .

**METHODS:** Expression of Shh in 25 colorectal adenocarcinomas was detected by RT-PCR, *in situ* hybridization and immunohistochemistry. Expression of Ptch1 was observed by *in situ* hybridization and immunohistochemistry. Expression of Hip, Gli1, Gli3 and PDGFR $\alpha$  was analyzed by *in situ* hybridization.

**RESULTS:** Expression of cytokeratin AE1/AE3 was observed in the cytoplasm of colorectal crypts. Members of the Hh signaling pathway were expressed in colorectal epithelium. Shh was expressed in cytoplasm of dysplastic epithelial cells, while expression of Ptch1, Hip and Gli1 were mainly detected in the malignant crypts of adenocarcinomas. In contrast, PDGFR $\alpha$  was expressed highly in aberrant crypts and moderately in the stroma. Expression of Gli3 could not be detected in colorectal adenocarcinomas.

**CONCLUSION:** These data suggest that Shh-Ptch1-Gli1 signaling pathway may play a role in the progression of colorectal tumor.

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**Key words:** Sonic hedgehog pathway; Sonic hedgehog; Ptch1; Hedgehog-interacting protein; Gli1; Gli3; PDGFR $\alpha$ ; Colorectal adenocarcinomas

### INTRODUCTION

Hedgehog (Hh) signaling plays key roles in embryonic organ patterning, cell differentiation and cell proliferation during embryonic development. Hh signaling is essential for the development of the limb, lung, brain and foregut. Single hedgehog gene in *Drosophila* and three hedgehog genes, Sonic (Shh), Indian (Ihh) and Desert (Dhh) in vertebrates have been identified. All three Hh proteins in vertebrates appear to be processed by the same mechanism, use the same receptors and can elicit similar biological responses, but their relative potencies differ in an assay-dependent manner<sup>[1-3]</sup>. Hhs bind to receptor Patched (Ptch), a 12-transmembrane protein. Ptch acts to inhibit the 7-transmembrane protein Smoothed (Smo), rendering the pathway inactive in the absence of Hh ligand. After binding of Hh to Ptch, the repression of Smo is released and the target genes (e.g. Ptch1, Gli, PDGFR $\alpha$ , Wnts, CyclinD1 and Bmp) are activated<sup>[4,5]</sup>. The Hh signaling is negatively regulated by a hedgehog-interacting protein (Hip), which is also inducible by hedgehog and is lost in hedgehog mutant<sup>[6]</sup>.

In the mouse, both Shh and Ihh are expressed in the gut endoderm and have been shown to participate in radial axis patterning of the gut<sup>[7]</sup>. Recent studies have shown that Shh is expressed in the normal adult human gut<sup>[8]</sup>. Aberrant activation of Hh signaling pathway has been shown to cause the occurrence of basal-cell carcinoma (BCC) and medulloblastoma, and mutations of Hh pathway components have been found both in familial and sporadic cases<sup>[9-12]</sup>. More recently, small-cell lung cancer (SCLC), prostate cancer and pancreatic adenocarcinoma have been linked to Hh signaling pathway, providing a molecular mechanism for these aggressive diseases<sup>[13-15]</sup>. Dysregulation of Hh signaling pathway may also play a role in gastrointestinal (GI) tumors<sup>[16,17]</sup>. To better understand the mechanism of colorectal adenocarcinoma, a common cancer worldwide, we examined here the expression of several key molecules functioned in the Hh signaling pathway at protein and mRNA levels.

## MATERIALS AND METHODS

### Materials

Twenty five tissue specimens of colorectal adenocarcinomas were obtained from Shandong Qilu Hospital, Jinan, China with approval from the local ethics research committee. Five of the 25 samples also included non-cancerous colorectal tissue as normal control. All of the samples were fixed in 4% paraformaldehyde with PBS at 4°C overnight. The samples were dehydrated in graded ethanol and stored in 70% ethanol at -20°C. The samples were embedded in paraffin and sectioned (6 µm). The sections were stained with H&E. Each sample was reviewed and confirmed by pathologists based on the clinical characteristics.

### Immunohistochemistry

Immunohistochemistry was performed according to the protocol described by Ma *et al*<sup>[16,17]</sup>. Antigen unmasking was achieved by boiling sections in 0.01 mol/L sodium citrate; pH 6.0, for 10 min. Tissues were blocked in 10% sheep serum twice and incubated for 2 h at 37°C with primary antibodies. Antibodies were applied at the following dilutions: Shh, and Ptch1 (1:100; Cat# 9024 for Shh and Cat# 6149 for Ptch1, Santa Cruz Biotechnology Inc, Santa Cruz, CA), PCNA (1:100; Santa Cruz Biotechnology, Inc., Santa Cruz, CA), cytokeratin AE1/AE3. (MAB 0049, Maixin Biotechnology, Inc., China). Negative controls were performed in all cases by omitting the first antibodies. All primary antibodies have been previously tested for immunohistochemistry<sup>[18]</sup>.

### In situ hybridization

The sense and antisense digoxigenin-labeled RNA probes were made using a DIG RNA labeling kit and following the manufacturer's instructions (Boehringer Mannheim). The *in situ* hybridization was performed as described previously<sup>[16,17]</sup>. In brief, rehydrated sections were treated with proteinase K (20 µg/mL) for 20 min and refixed in 4% paraformaldehyde with PBS for 5 min. Sections were washed with 50% formamide in 2 × SSC at 37°C for 2 h and hybridization was performed at 42°C overnight with 5 µg/mL of digoxigenin-labeled probe in the following hybridization buffer: 40% formamide, 10% dextran sulfate, 1 × Denhardt's solution, 1 mg/mL yeast RNA, 10 mmol/L Dithiothreitol, and 4 × SSC. Washes were done in 4 × SSC, 2 × SSC, 20 µg/mL RNase A, 1 × SSC, 0.1 × SSC at 37°C, 3 × 15 min, and then in buffer 1 (100 mmol/L Tris-Cl, 150 mmol/L NaCl, pH 7.5). Sections were incubated for 30 min in blocking buffer -2% goat serum, 0.1% TritonX-100 in buffer 1 and left overnight at room temperature in alkaline phosphatase-conjugated anti-digoxigenin antibody (Roche) at 1:500 dilution in blocking buffer. Washes were done in buffer 2 (100 mmol/L Tris-Cl, 100 mmol/L NaCl, 50 mmol/L MgCl<sub>2</sub>, pH 7.5) and 3 (100 mmol/L Tris-Cl, 100 mmol/L NaCl, 50 mmol/L MgCl<sub>2</sub>, pH 9.5), 2 × 10 min. Color reaction was performed in the NBT/BCIP (Roche) solution containing 10 mmol/L levamisole in the dark. Blue staining indicated strong hybridization. Sense probes were used in all hybridization as negative controls and no positive signals were observed.

### RT-PCR

RT-PCR was performed using RT-PCR system according to the manufacturer's protocol. Total RNA was isolated from paraffin-embedded tissue using an RNA isolation kit (Promega). Three micrograms of total RNA were reverse transcribed by using M-MLV reverse transcriptase (Promega) with a mixture of oligo (dT)<sub>15</sub> and random primers (Promega). One tenth of each RT reaction mixture was then subjected to PCR amplification using Taq DNA polymerase (TAKARA). The PCR primers for detecting specific transcripts were as follows: for Shh forward, 5'-ACCGAGGGCTGGGACGAAGA-3' and reverse, 5'-ATTTGGCCGCCACCGAGTT-3', respectively. Following denaturation at 94°C for 10 min, 35 PCR cycles were performed at 94°C for 60 s, at 52°C for 50 s, and at 72°C for 60 s.

For β-actin, forward: 5'-TCCTCCCTGGAGAAGAGC TA-3' reverse: 5'-TCAGGAGGAGCAATGATCTTG-3'. Following denaturation at 94°C for 10 min, 35 PCR cycles were performed at 94°C for 60 s, at 59°C for 50 s, and at 72°C for 60 s. The PCR products were analyzed by 0.7% agarose gel electrophoresis.

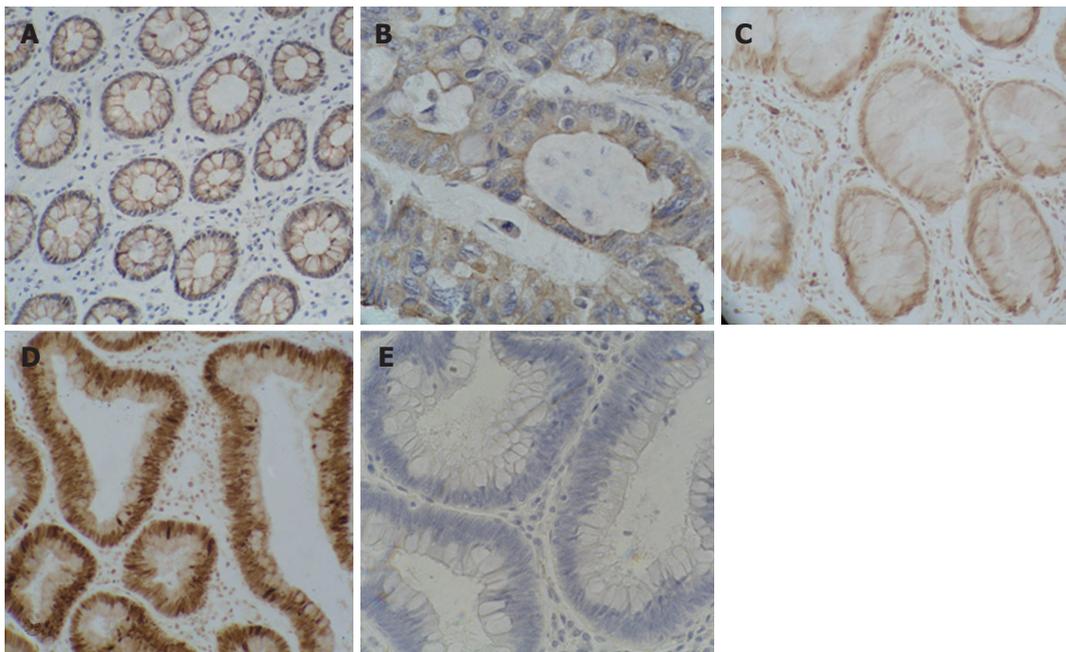
## RESULTS

### Cytokeratin AE1/AE3 expression in colorectal adenocarcinomas

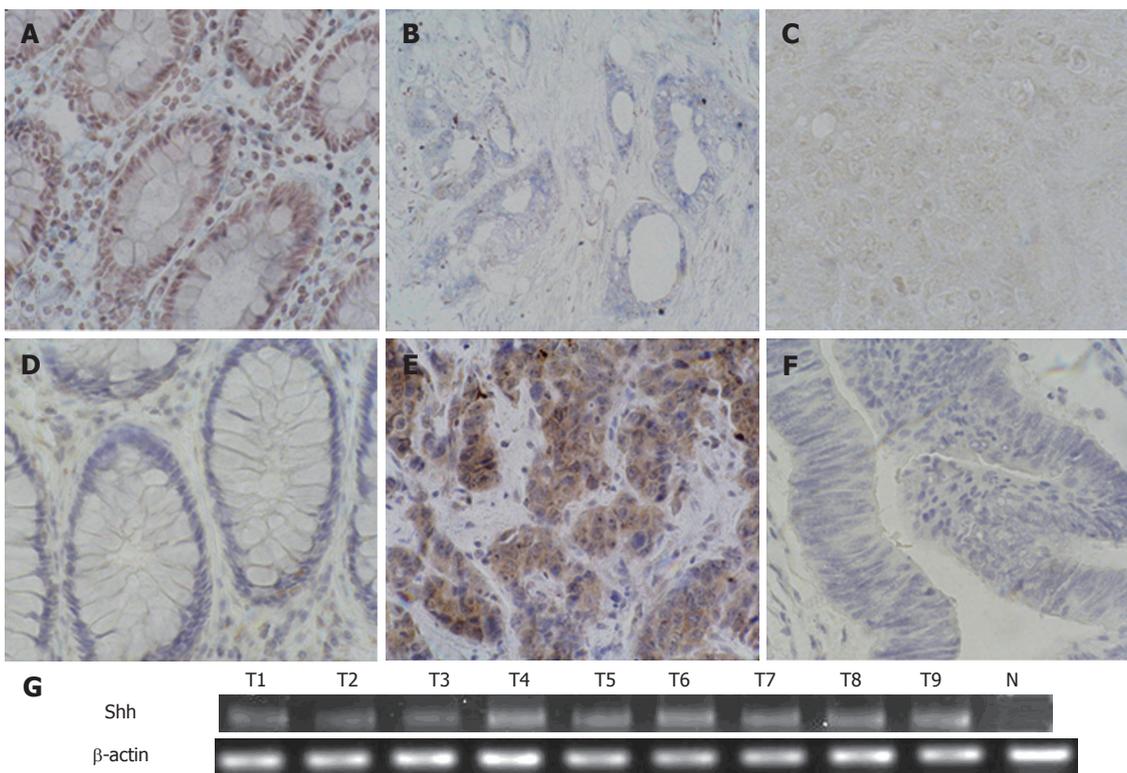
To determine whether colorectal adenocarcinomas originate from epidermis, we analyzed the expression of an epidermic molecular marker, cytokeratin AE1/AE3. Expression of cytokeratin AE1/AE3 was observed in the cytoplasm of colorectal crypts (Figure 1A and B). In addition, we examined the expression of the proliferation marker, PCNA. The results showed nuclear staining in the base of crypts in both normal (Figure 1C) and colorectal adenocarcinoma tissue (Figure 1D). However, there were a great number of stained nuclei in malignant crypts in contrast to that in normal tissue, suggesting that malignant crypts had a high level proliferation compared with normal crypts. Taken together, these data indicate that primary colorectal adenocarcinomas originate in epidermis.

### Shh expression and localization in primary colorectal adenocarcinomas

It has been shown that Shh is expressed in stomach and esophageal cancers<sup>[16,17]</sup>. To determine if Shh is expressed in colorectal adenocarcinomas, we examined the expression of Shh at mRNA and protein levels. The result of *in situ* hybridization revealed that Shh mRNA was well stained in the cytoplasm of epithelial cells throughout the section in 10 of 25 samples (Figure 2B). The sense probes gave no detectable signals (Figure 2C). This result was confirmed by immunohistochemistry and RT-PCR (Figure 2G, only in 9 of 25 samples). The pattern of staining of immunohistochemistry (13 out of 25 showed a positive reaction) was similar to that of *in situ* hybridization (Figure 2E). No staining was observed when secondary detection was performed in the absence of primary antibodies (Figure 3F). The cells except cancer cells showed a negative reaction, suggesting that the



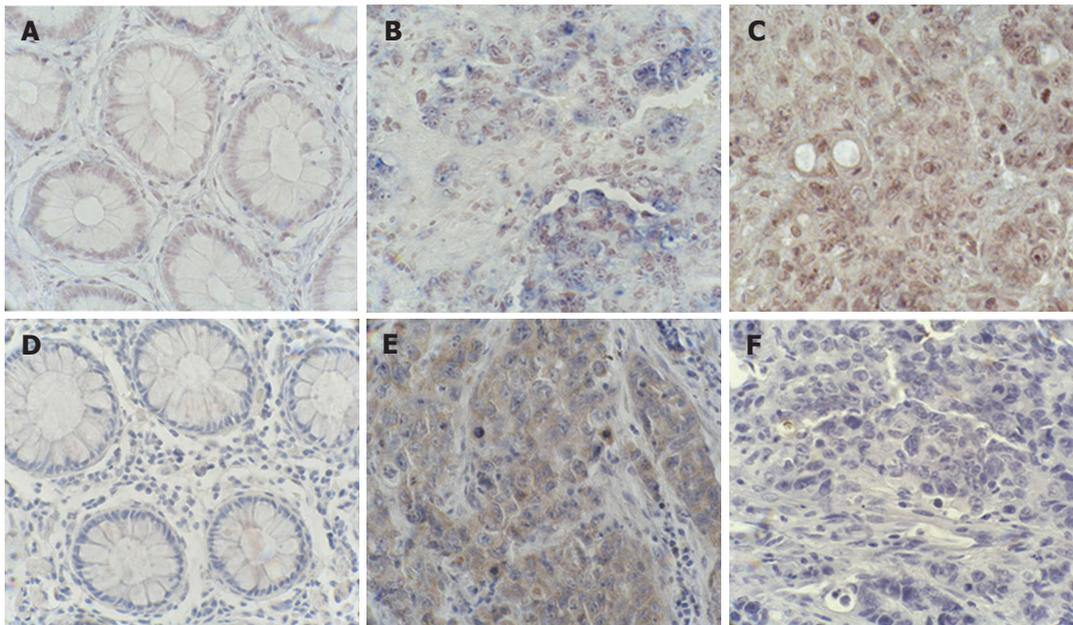
**Figure 1** Expression of cyokeratin AE1/AE3 and PCNA in primary colorectal adenocarcinomas. We performed immunohistochemistry with cyokeratin AE1/AE3 antibodies showing positive staining in cytoplasm of colorectal normal crypts (A) and malignant crypts (B) (positive in brown). While the proliferation marker PCNA stained the nuclei of the normal (C) and tumor (D) tissues (positive in brown). E is the negative control.



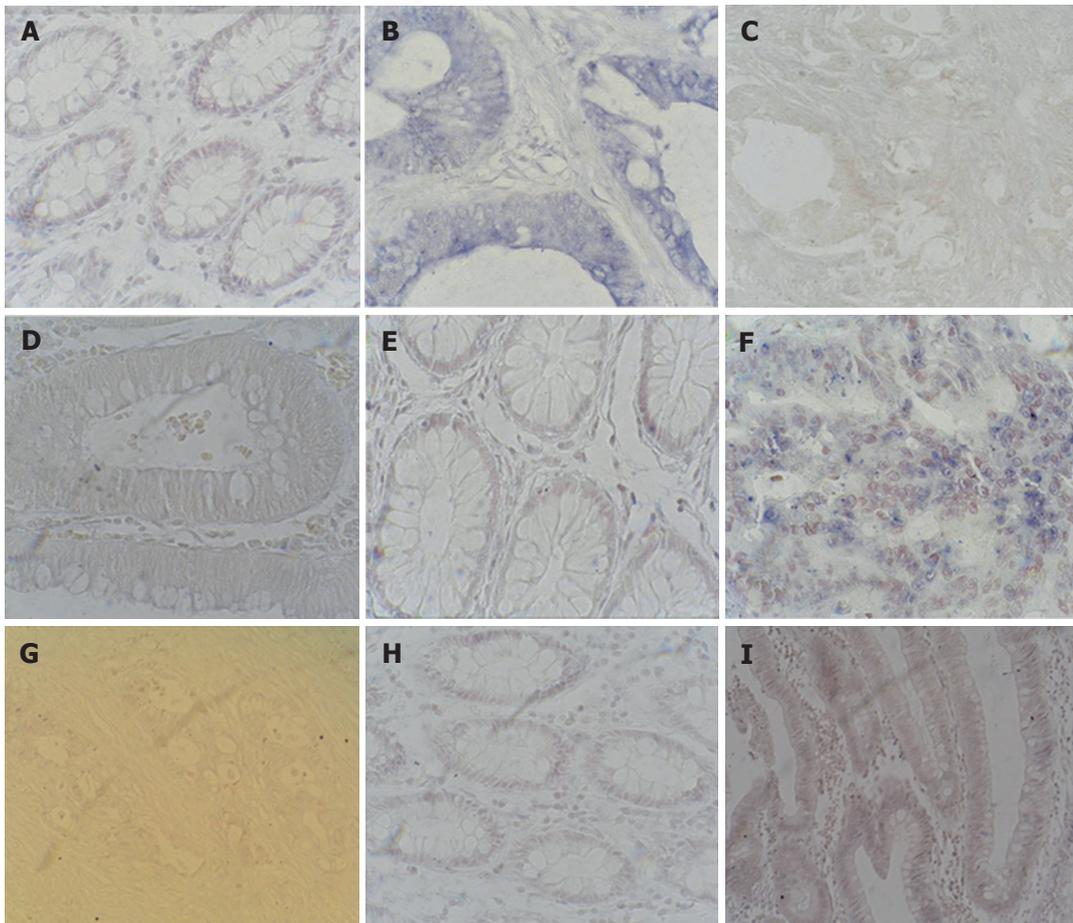
**Figure 2** Expression of Shh in primary colorectal adenocarcinomas. *In situ* hybridization was performed to detect Shh transcript in normal (A) and cancerous (B) tissues (positive in blue), and the sense probe did not reveal any positive signals (C is the sense control of B). Results of *in situ* hybridization were confirmed by immunohistochemical staining in normal (D) and tumor (E) tissues (positive in brown, F is the negative control) and by RT-PCR (G).

expression of mRNA and protein was tumor specific. One normal tissue (the morphologically normal crypts close to the adenocarcinoma tissue) did not show the expression

of Shh (Figure 2A and D). Our data demonstrated that, like other GI cancers, colorectal cancers expressed Shh in epithelial cells.



**Figure 3** Expression of Ptch1 in primary colorectal adenocarcinomas. Ptch1 transcript (blue as positive) was detected by *in situ* hybridization in the normal control (A) and colorectal cancers (B). C is from the same tumor with B being derived from the Ptch1 sense probe. To confirm the *in situ* hybridization results, we performed immunohistochemistry with PTCH1 antibodies, showing positive staining of PTCH1 protein (positive in brown) in malignant crypts (E). D is the normal control and F is the negative control.



**Figure 4** Expression of Gli1, Gli3 and Hip in primary colorectal adenocarcinomas. We detected expression patterns of Gli1, Gli3 and Hip transcripts by *in situ* hybridization (positive in blue). Gli1 (A) and Hip (E) were not expressed in normal control tissue. B: Gli1 was expressed in cytoplasm of malignant crypt. The expression of Gli1 (C) and Hip (D) sense probe in tumor tissue. F: Hip was expressed in cytoplasm of tumor cells. G: Gli3 was not expressed in colorectal adenocarcinomas. H is the normal control of Gli3 and I is the sense control of Gli3.

**Expression of the Hh signaling pathway components Ptch1, Gli1 and Hip, but not Gli3 in primary colorectal adenocarcinomas**

The Hh signaling pathway can include Ptch receptor and Gli transcription factor, and it is also regulated by Hip. To determine if these genes are activated in colorectal cancer cells, the mRNAs of Ptch1, Gli1 and Hip were examined

in colorectal adenocarcinoma tissue. The positive staining of Ptch1 (Figure 3A-C), Gli1 (Figure 4A-C) and Hip (Figure 4D-F) appeared in the majority of the malignant crypts in adenocarcinomas, but not in the stroma. The results (Table 1) indicate that there was no consistency in the expression of Ptch1, Hip and Gli1. Interestingly, we did not examine the expression of Gli3 by *in situ* hybridization

Table 1 Colorectal adenocarcinoma specimens and summary of Shh, Ptc1, Smo, Gli1, Sufu, PDGFR $\alpha$  and Hip expression

No	WHO Classification	Differentiation	Age	Gender	Shh- <i>ish</i>	SHH- <i>ihc</i>	Ptc1- <i>ish</i>	PTCH1- <i>ihc</i>	Gli1- <i>ish</i>	PDGFR $\alpha$ - <i>ish</i>	Hip- <i>ish</i>
1	RAC	PD	50	M	+	+	-	+	+	+	-
2	RAC	WD	69	F	-	-	-	-	+-	-	-
3	RAC	PD	60	M	+	+	+	+	+	-	-
4	RAC	MD	69	F	+-	+	-	-	-	-	-
5	CAC	MD	50	F	-	-	-	-	-	-	-
6	RAC	WD	72	M	-	-	+-	+	+-	-	-
7	CAC	MD	60	F	-	-	-	-	-	-	-
8	RAC	MD	27	F	-	-	+-	+	-	-	-
9	RAC	MD	63	M	-	-	-	-	-	-	-
10	CAC	WD	55	M	-	-	-	-	+-	-	-
11	RAC	MD	66	F	-	+	-	-	+	-	-
12	CAC	PD	79	F	+	+	-	-	+	-	-
13	RAC	PD	54	M	-	-	-	-	-	-	-
14	RAC	WD	73	F	-	-	-	-	-	-	-
15	RAC	MD	68	F	+	+	+	+	-	-	-
16	RAC	MD	70	F	-	-	-	-	+-	+	-
17	RAC	MD	68	M	-	-	-	-	+	+	-
18	RAC	MD	67	F	-	-	-	-	-	-	-
19	CAC	PD	68	M	+	+	+	+	+	+	+
20	CAC	PD	48	F	-	+	+-	+	+-	-	-
21	RAC	PD	73	M	+	+	-	+	-	-	-
22	RAC	MD	51	M	-	-	-	-	+	-	-
23	RAC	MD	70	M	+	+	+	+	+	-	+
24	RAC	PD	37	F	+	+	+	+	-	-	+
25	RAC	PD	79	M	+	+	+	+	-	-	+

These data were derived from *in situ* hybridization (*ish*) and immunohistochemistry (*ihc*). + means positive result (ratio of positive cells to cancer cells  $\geq 25\%$ ), - means negative result (no positive cell or ratio of positive cells to cancer cells  $\leq 10\%$ ), +- means weakly positive result ( $10\% <$  ratio of positive cells to cancer cells  $< 25\%$ ); WD: Well differentiated; MD: Moderately differentiated; PD: Poorly differentiated; CAC: Colonic adenocarcinoma; RAC: Rectal adenocarcinoma.

in any tissue (Figure 4G-I). To confirm the results of *in situ* hybridization, we detected Ptc1 protein by immunohistochemistry. The results were in agreement with the *in situ* hybridization data (Figure 3D-G). These findings indicate that the Shh-Ptc-Gli1 pathway was likely involved in colorectal adenocarcinomas. However, it should be noted that upregulation of Shh expression may not be the sole cause of enhanced Ptc1 or Gli1 expression, because, in some cases, upregulation of Ptc1 or Gli1 expression was not in accordance with the expression of Shh (Table 1). This suggests that the hedgehog signaling pathway might be activated by other regulatory mechanisms in colorectal carcinoma.

#### Expression of PDGFR $\alpha$ in primary colorectal adenocarcinomas

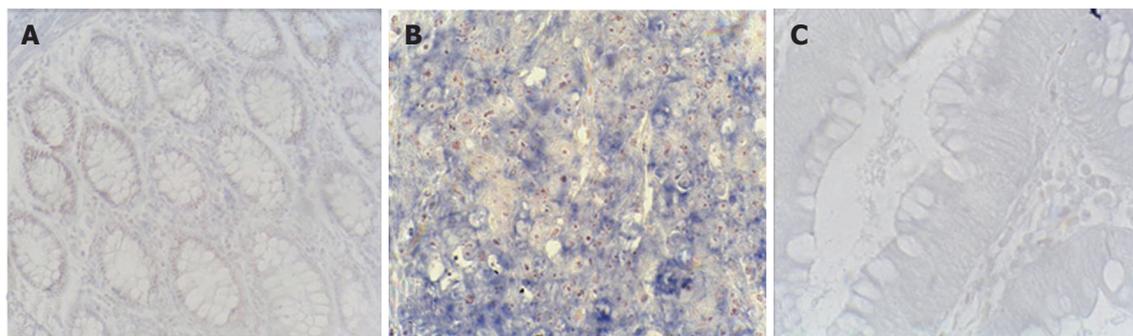
The platelet-derived growth factors (PDGFs) are a pleiotropic family of peptide growth factors that signal through cell surface tyrosine kinase receptors (PDGFR) and stimulate various cellular functions including growth, proliferation, and differentiation. In the past few years, the role of PDGF signaling has been demonstrated in cancer cell proliferation and tumor angiogenesis<sup>[19-22]</sup>. Only recently Xie *et al*<sup>[19]</sup> found that in the hedgehog-responsive cell line C3H10T1/2, Gli1 activates PDGFR $\alpha$  expression and enhances its activity. In the murine BCC cell line ASZ001 (Ptc1 null), DNA synthesis and cell proliferation can be slowed by re-expression of PTCH1 possibly through down-regulating PDGFR $\alpha$  expression, or by downstream inhibition with PDGFR $\alpha$ -neutralizing

antibodies<sup>[19]</sup>. To test whether Shh signaling pathway in colorectal carcinomas is activated through expression of PDGFR $\alpha$ , we analyzed mRNA of PDGFR $\alpha$  using *in situ* hybridization. PDGFR $\alpha$  was detected strongly in aberrant crypts and moderately in stroma of colorectal cancers (Figure 5B) that expressed Gli1. Thus, it may imply that Shh-Gli1 pathway in colorectal cancers is activated through increased expression of PDGFR $\alpha$ .

## DISCUSSION

Hh signaling drives cell proliferation, promotes cell survival, and directs cell differentiation in the developing embryo. Abortive regulation of the pathway during development has been associated with significant human birth defects, including holoprosencephaly, basal cell nevus syndrome, and polydactyly<sup>[9,10,23-25]</sup>. Recent studies have shown that aberrant signaling of this pathway is involved in a variety of human cancers, such as basal cell carcinomas, medulloblastomas and small-cell lung cancer<sup>[9-12,15]</sup>.

Onisu *et al*<sup>[18]</sup> have studied the expression of Shh, Patch1 and Smo in colonic neoplasia by immunohistochemistry. In the current study, we showed that overexpression of Shh at both mRNA and protein levels were similar in colonic adenocarcinoma and rectal adenocarcinoma tissue. To the best of our knowledge, this is the first report on the expression of Gli3, and Hip in colorectal cancer tissue. Since overexpression of Shh, Ptc1, Hip, Gli1 and PDGFR $\alpha$  occurred in colorectal



**Figure 5** Expression of PDGFR $\alpha$  in primary colorectal adenocarcinomas. **A:** We analyzed expression pattern of PDGFR $\alpha$  transcript by *in situ* hybridization (blueas positive); **B:** Expression of PDGFR $\alpha$  in normal control was high in aberrant crypts and moderate in the stroma; **C:** The expression of PDGFR sense probe in tumor tissue.

cancers, whereas no positive signal of Gli3 was observed at mRNA or protein levels, it may imply that the Shh-Gli1 pathway is activated in colorectal cancers. This supports the view that activation of the hedgehog pathway may play a role in the development of colorectal carcinoma.

We showed in this study that upregulation of Ptch1 or Gli1 expression, in some cases, was not consistent with the expression pattern of Shh (Table 1). This suggests that upregulation of Shh expression may not be the sole cause of activated Ptch1 or Gli1 expression, and that the hedgehog signaling pathway might be activated by other regulatory mechanisms in colorectal carcinoma. Furthermore, we unexpectedly found that the negative regulator, Hip, was expressed in several samples. This may support a model in which Hip, like Ptch1, modulates the responses to Hh signaling via a negative regulatory feedback loop.

The link between the hedgehog pathway, PDGFR $\alpha$  and human cancer was first revealed in Gorlin's syndrome, a disease with a high risk of basal cell carcinoma<sup>[9,10,19,26]</sup>. Those previous studies have shown that PDGFR $\alpha$  can be regulated by Gli1 and that PDGFR $\alpha$  mediates Gli1-induced Ras/Erk activation<sup>[9,10,19,26]</sup>. In our studies, we also detected the expression of PDGFR $\alpha$  in colorectal adenocarcinomas which expressed Gli1. Therefore, upregulation of PDGFR $\alpha$  appears to be one of the mechanisms by which Sonic hedgehog-Gli1 signaling induces colorectal cancers.

Taken together, our findings suggest that activation of the Shh-Gli1 pathway may be involved in colorectal cancer progression.

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