The Prognostic Significance and Therapeutic Potential of Hedgehog Signaling in Intrahepatic Cholangiocellular Carcinoma

Liang Tang, Ye-Xiong Tan, Bei-Ge Jiang, Yu-Fei Pan, Shuang-Xi Li, Guang-Zhen Yang, Min Wang, Qing Wang, Jian Zhang, Wei-Ping Zhou, Li-Wei Dong, and Hong-Yang Wang

Abstract

Purpose: The correlation of the hedgehog signaling pathway with the progression, prognosis, and therapeutics of intrahepatic cholangiocellular carcinoma (ICC) has not been well documented. The study aimed to investigate the expression, prognostic significance, and therapeutic value of hedgehog components in ICC.

Experimental Design: Two independent cohorts of 200 patients with ICC were enrolled. By real-time PCR and immunohistochemistry assay, hedgehog components expression was evaluated. The prognostic values of hedgehog proteins were identified and verified. Cyclopamine or siRNA-targeting Gli1 was used to block the hedgehog signaling. Cell proliferation and apoptosis were observed by CCK8, cell cycle, and annexin V staining assays. In vivo murine tumor model was used to evaluate the role of hedgehog in ICC.

Results: In ICC tissues, the Gli1 nuclear immune-intensity was associated with intrahepatic metastasis and the expression of Gli2 was associated with intrahepatic metastasis, venous invasion, and UICC Internationale Contra Cancrum (UICC) pT characteristics. In survival analysis, high Gli1 or Gli2 expressers had an unfavorable overall survival (OS) prognosis and a shorter disease-free survival (DFS) than those with low expression. In multivariate analysis, Gli1 expression was found to be an independent prognostic factor of OS, which was validated by another independent cohort. Furthermore, blocking the hedgehog signaling by cyclopamine or siRNA-targeting Gli1 resulted in apoptosis and growth inhibition in ICC cells.

Conclusions: This study shows, for the first time, activation of hedgehog pathway associated with the progression and metastasis in ICC, which may provide prognostic and therapeutic values for this tumor.

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Introduction

Intrahepatic cholangiocellular carcinoma (ICC) is a malignant neoplasm originating from epithelium of the biliary tree with high mortality (1) and a rare primary malignant liver tumor compared with hepatocellular carcinoma (HCC). Unfortunately, the vast majority of patients with cholangiocarcinoma do not have optimal situation for curative surgery when diagnosis is confirmed. Patients with resection generally have the higher recurrence rate (2, 3). The conventional chemotherapy and radiotherapy to date have proved to play limited effect in improving long-term survival and it still cannot be satisfied (4). So, the mortality from ICC is very high, with the 5-year survival rates being less than 15% to 20% in most series (5, 6). Although several molecules have been reported to be associated with prognosis and metastasis of ICC (7), more valuable biomarkers are needed to predict the clinical outcome or provide therapeutic values of patients with ICC.

Hedgehog was first identified in a Drosophila screen for genes important in early embryonic development (8). Sonic hedgehog (Shh), Indian hedgehog (Ihh), and desert hedgehog (Dhh) are 3 mammalian hedgehog genes that have been identified (9). Two transmembrane proteins function to transduce the hedgehog signal: patched (Ptc) and smoothened (Smo). Smo can transduce signals intracellularly, and this results in the nuclear localization of the transcription factor Glioma-associated oncogene homolog (Gli). Three Gli proteins, Gli1, Gli2, and Gli3 are known to be present in...
This study shows that hedgehog signaling is activated in intrahepatic cholangiocellular carcinoma (ICC) compared with normal cholangiocytes. Higher Gli1 and Gli2 protein levels in ICC tissues are significantly associated with unfavorable overall survival (OS) prognosis and shorter disease-free survival (DFS). Gli1 is an independent prognostic factor for clinical outcome in patients with ICC. Blocking the hedgehog signaling by chemical inhibitor or siRNA-targeting Gli1 resulted in apoptosis and growth detenion in cultured cells and xenograft tumors. These findings imply that the intratumoral Gli1 levels of ICC can be used to identify subgroups of patients with a favorable or poor OS prognosis and Gli1 may have a potential clinical application as a biomarker and a therapeutic target for ICC. Regulation of hedgehog signaling by agents may influence proliferation and apoptosis of ICC cells during tumor progression that provides an innovative strategy for future clinical trials.

**Materials and Methods**

**Patients and tissue samples**

Formalin-fixed and paraffin-embedded ICC tissues from 200 consecutive patients and normal liver tissues from 8 patients, who underwent primary hepatectomy due to ICC or metastatic liver tumors in our Hospital from January 2002 to December 2004, were retrieved for immunohistochemistry. We divided the patients into training set (all the 108 cases of patients in 2002) and validation cohort (the 92 cases of patients underwent hepatectomy in 2003–2004). The study population consisted of patients with ICC as confirmed by pathologic analysis. Tumor differentiation was defined according to the Edmondson grading system. Tumor staging was determined according to the sixth edition of the tumor–node–metastasis (TNM) classification of the International Union Against Cancer. The selection of this specific material was conducted to include patients who underwent surgery alone without chemotherapy or radiotherapy at a time when these adjunctive therapies were not the standard of treatment. In this way, the analysis of data in this series will reflect the actual impact of the tumor biology on the clinical outcome. The patients included in this series also had available paraffin-embedded tumor tissue and the tumor cell subtype proven by immunohistochemistry. Patients were excluded from this cohort with the following exclusion criteria: uncontrolled infection; previously received any anticancer therapy; pregnancy and lactation; prior malignancy; impaired heart, lung, liver, or kidney function; and previous malignant disease. The follow-up period was defined as the interval from the date of operation to the date of death or the last follow-up. Deaths from other causes were treated as censored cases. All patients were observed until December 2010, ranged from 2 to 82 months (median, 17 months).

Fresh-frozen ICC tissues from 41 patients and normal intrahepatic bile duct epithelia from 5 patients who underwent primary hepatectomy between 2001 and 2007 were used for RNA extraction. Overall survival (OS) was defined as the interval between the dates of surgery and death. Disease-free survival (DFS) was defined as the interval between the dates of surgery and recurrence; if recurrence was not diagnosed, patients were censored on the date of death or the last follow-up. Informed consent was obtained from all patients before subsequent use of their resected tissues. The present study was conducted in accordance with the ethical standards of the Helsinki Declaration in 1975, after approval of the Ethics Committee of Human Experimentation of Second Military Medical University (Shanghai, P.R. China).

**Tissue microarray and immunohistochemistry**

Tissue microarray slides were prescreened with hematoxylin and eosin staining (Shanghai Biochip Company, Ltd.). Two cores were taken from each formalin-fixed, paraffin-embedded ICC samples and normal liver samples by using punch cores that measured 0.8 mm in greatest dimension from the center of tumor foci. The sections were heated in a primary polyclonal antibodies against Shh (sc-9024), Gli1 (sc-20687; Santa Cruz Biotechnology), and Gli2 (ab-26056; Abcam Ltd.) at 1:100 dilution. Finally, the visualization signal was developed with diaminobenzidine and the slides were counterstained in hematoxylin. Stained sections were evaluated in a blinded manner without prior knowledge of the clinical information using the German immunoreactive score, immunoreactive score (IRS). Briefly, the IRS assigns subscores for immunoreactive distribution (0–4) and intensity (0–3), then multiplies them to yield the IRS score. The percentage positivity was scored as "0" (<5%), "1" (5%–25%), "2" (25%–50%), "3" (50%–75%), or "4" (>75%).
The staining intensity was scored as "0" (no staining), "1" (weakly stained), "2" (moderately stained), or "3" (strongly stained). Cases with discrepancies in IRS score were discussed together with other pathologists until consensus was reached. Nuclear staining is considered as active form of Glis, IRS score was used to assess nuclear immune-reactivity of Glis and the patients were separated into high and low expression groups.

Cell culture and chemicals

The intrahepatic cholangiocarcinoma cell line RBE and HCCC9810 was purchased from Shanghai Cell Bank of Chinese Academy of Sciences (Shanghai, China). The cholangiocarcinoma cell lines QBC939 was purchased from Xiangya Central Experiment Laboratory (Hunan, China). All cells were cultured in RPMI-1640 media supplemented with 10% FBS and 1% antibiotic/antimycotic solution (Sigma-Aldrich) and maintained at 37°C in an atmosphere of humidified air containing 5% CO2. A specific hedgehog signal inhibitor, KAAD-cyclopamine, was purchased from Toronto Research Chemicals and its nonfunctional analog, tomatidine hydrochloride, was purchased from Sigma-Aldrich.

RNA collection, cDNA synthesis, and real-time PCR analysis

Pure normal intrahepatic cholangiocytes from human liver tissues were isolated by laser capture microdissection (LCM), as described previously (20). Total RNA was extracted from fresh-frozen tumor specimens, healthy control tissues, and cell lines in Trizol (Invitrogen). Reverse transcription of total RNA was conducted using random hexamers (Roche Diagnostics) and SuperScriptII reverse transcriptase of total RNA was conducted with 40 ng complementary DNA, 500 nmol/L forward and reverse primer, and iTaqSYBRGreen (Bio-Rad Laboratories) in a final volume of 20 μL.

Cell proliferation assay and apoptosis analysis

Cholangiocarcinoma cells (5 × 10^5 cells/well) were seeded in 96-well plates and cultured overnight at 37°C, then the cells were treated with different concentrations of KAAD-cyclopamine or tomatidine for another 48 hours or were transfected for indicated time. Cell proliferation was detected by CCK-8 assay at various time points according to the guidance of the manufacturer. Apoptosis was also assessed by using an annexin V–fluorescein isothiocyanate (FITC) apoptosis detection kit (Invitrogen, V13241) according to the manufacturer’s protocol. For clonogenic assays as described (21), different cell lines were seeded in 6-well plates (5,000 cells/well) and grown under the indicated conditions for 10 days. The number of colonies (defined as cell clusters consisting of at least 50 cells) was quantified by Analysis software.

Statistical analysis

The Pearson χ² test or Fisher exact test was used to analyze the relationship between Gli1 or Gli2 expression and the clinicopathologic features. Survival curves were calculated using the Kaplan–Meier method and compared by the log-rank test. The Cox proportional-hazard regression model was used to explore the effects of the clinicopathologic variables and Gli1 and Gli2 expression on survival. SPSS 15.0 software (SPSS Inc.) was used for all statistical analyses and a P value of less than 0.05 was considered significant.

Results

Hedgehog signaling components mRNA expression in intrahepatic cholangiocellular carcinoma specimens

RNA extracted from 41 cases of ICC specimens and 5 normal cholangiocytes tissues showed transcripts of all essential hedgehog signaling components, including genes encoding the extracellular ligands Shh and Ihh, the transmembrane protein Smo, and the known hedgehog target genes Gli1, Gli2, Gli3, and Ptc1. The hedgehog pathway competing component Hhip1 was also included. As the results shown in Fig. 1, Ihh, Shh, Ptc1, Smo, Gli1, and Gli2 mRNA expressions were markedly increased in 78% (32 of 41), 87.8% (36 of 41), 89.2% (34 of 41), 85.4% (35 of 41), 65.9% (27 of 41), and 87.8% (36 of 41), respectively. While Gli3 and Hhip1, the 2 known negative factors in hedgehog signaling, showed only 36.6% (15 of 41) and 17.9% (7 of 41) samples high expression. The hedgehog target genes, c-Myc and Bcl-2 were also detected and further confirmed activation of the signaling (Supplementary Fig. S1). For further validation of the results, we applied LCM to obtain tumor tissues from another 30 ICC samples to evaluate hedgehog components expression and found the similar expression pattern (Supplementary Fig. S2A). We detected some key genes’ copy number in fresh ICC tissues and found there few copy number changes in these genes (Supplementary Fig. S2B).

Immunohistochemical study of Shh, Gli1, and Gli2 in intrahepatic cholangiocellular carcinoma and normal liver tissues

Expression of Shh, Gli1, and Gli2 proteins was determined by immunohistochemistry staining in ICC cancer tissues and 8 cases of normal liver tissues (Supplementary Fig. S3). Shh was mainly localized in the cytoplasm of the cancer cells. Of the training cohort patients, 93.5% (101 of 108) were classified as Shh-positive. There were 87.9% (95 of 108) specimens with positive Gli1 expression, and the immunostaining was distributed in cytoplasm and nuclear in these specimens. There were 92.6% (100 of 108) specimens with positive Gli2 expression, and the positive lesion was also in the cytoplasm and nuclear. Shh, Gli1, and Gli2 were present negative or weak intensity in the bile duct of normal liver tissues and this intensity was considered as normal-like for the subsequent scoring of cancer areas. Cholangiocarcinoma-specific staining. CK-19 was also conducted on the tumor samples to confirm positive staining cells were ICC cells (Supplementary Fig. S3G and S3H).
Association of Shh, Gli1, and Gli2 expression with the clinicopathologic features

We analyzed the relationship between Shh, Gli1, Gli2 protein expression and clinical features of ICC in high and low expression groups based on the immunohistochemistry analysis. We found significant correlation between Gli1 expression and clinical features. As shown in Table 1 (training cohort), Gli1 protein level was associated with intrahepatic metastasis clinical feature ($P = 0.021$). In all, 17 (30.9%) patients without intrahepatic metastasis had high Gli1 expression compared with 28 (52.8%) of positive intrahepatic metastasis patients. The expression of Gli2 was also associated with intrahepatic metastasis ($P = 0.032$). In addition, Gli2 expression significantly correlated with venous invasion ($P = 0.032$) and Union Internationale Contre Cancrum (UICC) pT clinical characteristics ($P = 0.014$). However, Shh did not correlate with any of the clinical characteristic. The similar results were confirmed in the validation cohort (Supplementary Table S1).

Significant prognostic values of Gli1 and Gli2 expression for patients with intrahepatic cholangiocellular carcinoma

To investigate the relationship between Shh, Gli1, Gli2 expression and clinical prognosis, the ICC patients were followed up. The 1-, 3-, and 5-year OS were 65.7%, 29.6%, and 14.8% for all of the patients in this study. On the basis of the each protein intratumoral densities, the patients were divided into 2 groups: high intratumoral protein density (IRS over 6, as described in Materials and Methods) and low group (IRS 0–6). Using Kaplan–Meier analysis, we found that "high Gli1 expressers" had an unfavorable OS prognosis and a shorter DFS than those with low Gli1 expression (training set Fig. 2A and B; validation cohort Fig. 2E and F). The 1-, 3-, and 5-year OS were 68.3%, 41.3%, and 20.6% for low
Gli1 expression patients in training cohort. While the high Gli1 expressers’ 1-, 3-, and 5- OS were 48.9%, 13.3%, and 11.1%, respectively. Turning to the Gli2, patients with high reactivity of Gli2 have poor prognosis compared with those with low reactivity for either OS or DFS (training set Fig. 2C and D; validation cohort Fig. 2G and H). The 1-, 3-, and 5- OS were 67.6%, 39.7%, and 22.1% for low Gli2 expression patients in training set. While the high Gli2 expressers’ 1-, 3-, and 5- OS were 47.5%, 12.5%, and 7.5%, respectively.

Univariate analyses of clinical variables considered as potential predictors of survival are shown in Table 2 and Supplementary Table S2. By Cox regression analyses, the parameters gender, serum carcinoembryonic antigen (CEA), tumor size, intrahepatic metastasis, lymph node metastasis, venous invasion, international union against
cancer T classification (UICC pT), and UICC stage were identified as potential predictors of DFS and OS. In this model, Gli1 and Gli2 also showed correlating with DFS and OS. As Gli1 and Gli2 showed association with histopathologic variables known to affect prognosis, a multivariate analysis was conducted to assess the independence of Gli1 and Gli2 prognosis. It was shown that Gli1, together with those of tumor size, intrahepatic metastasis, and lymph node metastasis, was strongly associated with OS, but Gli1 was not significantly correlated with DFS. The results indicated that Gli2 may be not an independent prognostic factor for both DFS and OS.

Lentivirus and adenovirus-delivered Gli1 siRNA suppressed cholangiocarcinoma cells growth in vitro and in vivo

To validate the clinical significance of Gli1, we constructed the lentivirus and adenovirus-delivered siRNA (Lv-SiRNA, AdSiRNA) targeting Gli1 or Gli2. The Lv-SiRNA significantly suppressed Gli1 and Gli2 expression levels (Supplementary Fig. S4A and S4B). Furthermore, proliferation of Gli1-siRNA cells was evidently slowed down in RBE, HCCC9810, and QBC939 cells (Fig. 3A and Supplementary Fig. S4E). As shown in Fig. 3B, depleting Gli1 markedly reduced colony formation of RBE, HCCC9810, and QBC939. Stably transfected Gli1-overexpressed RBE

Figure 2. Kaplan–Meier curves for time to recurrence and OS of patients with high or low intratumoral Gli1 or Gli2 features in training cohort (A–D) and validation cohort (E–H). The different subgroups were plotted according to the cutoff value of Gli1 or Gli2 level defined as the median of the cohort.
cell was constructed and subcutaneously injected into flanks of nonobese diabetic/severe combined immunodeficient (NOD/SCID) mice. Forced expression of Gli1 enhanced tumor formation in vivo, whereas the control cell did not grow into tumor (Fig. 3C). In addition, suppressing expression of Gli1 in QBC939 cells significantly inhibited tumor growth, but interference of Gli2 did not show effects (Supplementary Fig. S4F). Furthermore, we found in Gli1-siRNA RBE cells, distinct G2–M phase arrest was observed (Fig. 3D), whereas Lv-SiRNA-targeting Gli2 did not show effects. Then, we detected the apoptosis in Lv-SiRNA-treated cells, and found inhibition of Gli1 markedly induced cell apoptosis, whereas suppression of Gli2 had no effect (Fig. 3E). In cholangiocarcinoma cells, the AdSiGli1 significantly decreased the expression of Gli1 mRNA and protein (Supplementary Fig. S4C and S4D). Knocking down Gli1 caused RBE, HCCC9810, and QBC939 cells growing slowly compared with cells with normal expression of Gli1 (Fig. 4A). AdSiGli1 also significantly inhibited colony formation of RBE and HCCC9810 cells (Fig. 4B). We tested whether blocking the Shh–Gli signaling pathway with cyclopamine, a selective Smo inhibitor, could affect the proliferation and survival of ICC cells. The results showed that cell proliferation was significantly reduced by the inhibitor (Fig. 4C) and apoptosis was induced at a late stage and at an early stage (Fig. 4D and E). We further tested the role of hedgehog

### Table 2. Univariate and multivariate Cox regression analyses Gli1, Gli2, and Shh for DFS or OS of patients in the training cohort (n = 108)

<table>
<thead>
<tr>
<th>Variables</th>
<th>DFS</th>
<th>P value</th>
<th>OS</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gli 1 (high vs. low)</td>
<td>1.614</td>
<td>0.002</td>
<td>1.680</td>
<td>0.005</td>
</tr>
<tr>
<td>Gli 2 (high vs. low)</td>
<td>1.660</td>
<td>0.002</td>
<td>1.978</td>
<td>0.002</td>
</tr>
<tr>
<td>Shh (high vs. low)</td>
<td>0.686</td>
<td>0.071</td>
<td>0.683</td>
<td>0.067</td>
</tr>
<tr>
<td>Age (&gt;60 vs. ≤60 y)</td>
<td>1.280</td>
<td>0.278</td>
<td>1.211</td>
<td>0.398</td>
</tr>
<tr>
<td>Gender (male vs. female)</td>
<td>0.624</td>
<td>0.048</td>
<td>0.620</td>
<td>0.046</td>
</tr>
<tr>
<td>Hepatitis B virus (negative vs. positive)</td>
<td>1.399</td>
<td>0.120</td>
<td>1.254</td>
<td>0.293</td>
</tr>
<tr>
<td>Serum CEA (&gt;37 vs. ≤37 U/mL)</td>
<td>1.494</td>
<td>0.057</td>
<td>1.478</td>
<td>0.061</td>
</tr>
<tr>
<td>Serum AFp (&gt;20 vs. ≤20 ng/mL)</td>
<td>2.276</td>
<td>0.016</td>
<td>4.259</td>
<td>0.000</td>
</tr>
<tr>
<td>Larger tumor size (&gt;5 vs. ≤5 cm)</td>
<td>2.461</td>
<td>0.000</td>
<td>2.461</td>
<td>0.000</td>
</tr>
<tr>
<td>Intrahepatic metastasis (negative vs. positive)</td>
<td>2.393</td>
<td>0.000</td>
<td>2.507</td>
<td>0.000</td>
</tr>
<tr>
<td>Lymph node metastasis (negative vs. positive)</td>
<td>2.467</td>
<td>0.000</td>
<td>3.385</td>
<td>0.000</td>
</tr>
<tr>
<td>Venous invasion (negative vs. positive)</td>
<td>1.550</td>
<td>0.043</td>
<td>1.541</td>
<td>0.043</td>
</tr>
<tr>
<td>Perineural invasion (negative vs. positive)</td>
<td>1.317</td>
<td>0.360</td>
<td>1.287</td>
<td>0.401</td>
</tr>
<tr>
<td>Histologic grading (well vs. moderate/poorly)</td>
<td>0.920</td>
<td>0.887</td>
<td>0.917</td>
<td>0.883</td>
</tr>
<tr>
<td>UICC pT (1+2 vs. 3+4)</td>
<td>2.813</td>
<td>0.000</td>
<td>3.080</td>
<td>0.000</td>
</tr>
<tr>
<td>UICC stage (I+II vs. III+IV)</td>
<td>2.898</td>
<td>0.000</td>
<td>3.268</td>
<td>0.000</td>
</tr>
<tr>
<td>Resection status (R0 vs. R1/R2)</td>
<td>1.399</td>
<td>0.265</td>
<td>1.596</td>
<td>0.120</td>
</tr>
</tbody>
</table>

NOTE: Univariate analysis, Cox proportional hazards regression; multivariate analysis, Cox proportional hazards regression; variables were adopted in multivariate analysis for their prognostic significance by univariate analysis. Abbreviation: CI, confidence interval.

*For Gli1, Gli2, and Shh median values were used as the cutoff point for definition of subgroups (low expression and high expression groups).
pathway activity in vivo by treating established subcutaneous xenograft tumors in nude mice with daily subcutaneous injections of cyclopamine or dimethyl sulfoxide (DMSO). After treatment with cyclopamine, the tumor growth was inhibited obviously (Supplementary Fig. S4G).

Discussion

ICC is an uncommon malignant disease with inadequate therapeutic methods, studies of the underlying molecular mechanism will provide potential therapeutic target. Recent years, the prognostic value of hedgehog components in some tumor types was reported (22–26). In the present study, we clearly show that many genes of hedgehog signaling upregulated in clinical ICC samples. The expression patterns of hedgehog pathway genes may be associated with bile duct epithelium tumorigenesis. A significant association was found between Gli1 and intrahepatic metastasis feature. Meanwhile, Gli2 staining associated with intrahepatic metastasis, venous invasion, and UICC T-factor classification. Compared with Gli2, Gli1 was an independent prognostic predictor for OS.

To the best of our knowledge, there was no report on the correlation of the hedgehog signaling pathway with the progression and prognosis of ICC. In other type of tumors, most researches focused on Gli1, but not Gli2 for prognosis study. It is reported that Gli1 was an indicator for a poor prognosis in patients with colon cancer (25) and with head and neck squamous cell carcinoma (26). Zhu and colleagues found that patients with esophageal squamous cell carcinoma with high Gli1 expression have the shorter survival time (22). Gli1 expression is an independent prognostic marker of ovarian cancers (27). Turning to Gli2, although no report about prognostic correlation of Gli2 and tumors, there were some functional studies of the protein in tumor cells growth and tumorigenicity (28–30). Among the Gli members, Gli1 possesses only an activator domain, whereas Gli2 contains both activator and repressor domains, and Gli3 mostly functions as a repressor (31). Therefore, it is very possible that Gli proteins would not be expected to share a completely common set of genes as their downstream targets. Some of the genes identified as Gli1 targets in one cancer type were not changed in their expression in other cancer types, suggesting that Gli1 can have a preference for different targets in different cancer types (32, 33). Indeed, Gli1 itself is a transcriptional target of the hedgehog pathway, Gli1 expression serves as a reliable indicator of activated hedgehog signaling, and

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elevated Gli1 expression was linked with cancer development and progression (14).

Our results show that cyclopamine could affect the proliferation and growth of ICC cells. A recent report stated that cyclopamine and 5E1 treatments effectively inhibited cell proliferation, migration, and invasion of extrahepatic cholangiocarcinoma cells by downregulating Gli1 and Gli2, which provided further evidences to confirm the important role of hedgehog-Gli1 in cholangiocarcinoma (34). Given that some tumor cells were not sensitive or had no response to cyclopamine (35), we used siRNA-targeting Gli1. The fact that inhibition of hedgehog signaling leads to a dramatic decrease in ICC cells growth in vitro and in vivo by a massive induction of apoptosis indicates an important role of a

Figure 4. Adenovirus-delivered Gli1 siRNA and cyclopamine suppressed cholangiocarcinoma cells growth. A, AdSi-Gli1 suppressed cholangiocarcinoma cells proliferation in vitro. B, clonogenic assay of RBE and HCCC cell lines after Gli1 knockdown with adenovirus-delivered siRNA. C, cyclopamine treatment effects on proliferation of cholangiocarcinoma cells. RBE and HCCC9810 were treated with KAAD-cyclopamine or the inactive analog tomatidine with 0 to 20 μmol/L for 48 hours and the cell proliferation was detected by CCK-8 assay. D and E, cyclopamine treatment effects on proliferation of cholangiocarcinoma cells. Cells were treated for 24 and 48 hours with 10 μmol/L cyclopamine or tomatidine followed by apoptosis assay using FITC-conjugated annexin V and propidium iodide (PI).
targeted hedgehog signaling blockade for future therapeutic interventions in this tumor. In addition, some studies revealed that hedgehog signaling in development was typically mediated through paracrine effects. Yauch and colleagues reported that hedgehog–Gli activation was required in the tissue mesenchyme surrounding pancreatic cancer cells to support tumor growth by paracrine effects (35). Fingas and colleagues reported an interesting work, which revealed that myofibroblast-derived platelet-derived growth factor (PDGF) promoting survival of cholangiocarcinoma cells (36). Therefore, the role of hedgehog paracrine signaling may be required for the progression of ICC, which needs to be further investigated.

Taken together, our study showed that overexpressed Gli1 and Gli2 were correlated with progression and metastasis in ICC. Gli1 is considered to be an independent prognostic factor for OS in patients with ICC. Elucidating hedgehog pathway in cancer cells and careful classification of patients may help for development of novel therapeutic strategies.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

References

10. Authors' Contributions
Conception and design: Y.-X. Tan, L.-W. Dong
Development of methodology: Y.-X. Tan, Q. Wang
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): L. Tang, B.-G. Jiang, M. Wang
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): L. Tang, Y.-X. Tan, S.-X. Li, G.-Z. Yang, Q. Wang, J. Zhang, W.-P. Zhou
Writing, review, and/or revision of the manuscript: Y.-X. Tan, L.-W. Dong
Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): Y.-X. Tan, Y.-F. Pan, G.-Z. Yang
Study supervision: Y.-X. Tan, H.-Y. Wang

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