α2,6-Sialylation mediates hepatocellular carcinoma growth in vitro and in vivo by targeting the Wnt/β-catenin pathway

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Abnormal sialylation due to overexpression of sialyltransferases has been associated with tumorigenesis and tumor progression. Although ST6Gal-I influences cancer persistence and progression by affecting various receptors, the underlying mechanisms and mediators remain largely obscure, especially in hepatocellular carcinoma (HCC). We found that ST6Gal-I expression was markedly upregulated in HCC tissues and cells, high levels being associated with aggressive phenotype and poor prognosis. Furthermore, we examined the roles and mechanisms of ST6Gal-I in HCC tumorigenesis and metastasis in vitro and in vivo. ST6Gal-I overexpression promoted proliferation, migration and invasion of Huh-7 cells, whereas its knockdown restricted these abilities in MHCC97-H cells. Additionally, in a mouse xenograft model, ST6Gal-I knockdown MHCC97-H cells formed significantly smaller tumors, implying that ST6Gal-I overexpression can induce HCC cell malignant transformation. Importantly, enhanced HCC tumorigenesis and metastasis by ST6Gal-I may be associated with Wnt/β-catenin signaling promotion, including β-catenin nuclear transition and upregulation of downstream molecules. Together, our results suggest a role for ST6Gal-I in promoting the growth and invasion of HCC cells through the modulation of Wnt/β-catenin signaling molecules, and that ST6Gal-I might be a promising marker for prognosis and therapy of HCC.

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and a close correlation with survival rate. We found that ST6Gal-I upregulation promoted the proliferation, migration, and invasion ability of HCC cells. Furthermore, of the pathways tested, ST6Gal-I had the largest influence on Wnt/β-catenin signaling. Therefore, ST6Gal-I might be a promising marker for prognosis and therapy of HCC.

RESULTS
ST6Gal-I expression is significantly upregulated in HCC tissues and cell lines
To explore the role of ST6Gal-I in HCC development, ST6Gal-I was stained by immunohistochemistry (IH) in representative pairs of cancerous and matched non-tumor liver sections from HCC patients (Figure 1a). Pearson’s chi-squared test identified a significant correlation between ST6Gal-I expression with patient sex, number of lesions and pathologic grade (Table 1). We found that ST6Gal-I-positive patients experienced poorer 5-year overall survival than ST6Gal-I-negative patients (Figure 1b). Moreover, ST6Gal-I positive expression was found to correlate with a short disease-free survival time (Figure 1c). The results are consistent with ST6Gal-I being a potential biomarker of carcinoma progression.25,26 In HCC and normal liver cell lines, ST6Gal-I was expressed in all tested cells as indicated by qPCR and western blot assays. The highest expression was observed in MHCC97-H cells, compared to which Huh-7 cells exhibited low expression (Figures 1d and e). ST6Gal-I expression and localization were confirmed by confocal microscopy, and the results revealed low ST6Gal-I expression in the latter, but high expression in the Golgi apparatus of the former (Figure 1f).

ST6Gal-I overexpression promotes Huh-7 cell proliferation, invasion and migration in vitro
To investigate its function in HCC, ST6Gal-I was overexpressed by transfecting Huh-7 cells with the recombinant vector pcDNA3.1/ST6Gal-I. Expression of ST6Gal-I at mRNA and protein levels was increased in these cells compared to those transfected with an empty pcDNA3.1 plasmid (mock) and parental cells (Huh-7) (Figures 2a and b). Immunofluorescence demonstrated that compared to the control treatment, overexpression of ST6Gal-I increased its presence in the Golgi apparatus of Huh-7 cells (Figure 2d). In addition, ST6Gal-I overexpression resulted in a significant increase in α2,6-sialylation on Huh-7 cell surface (Figures 2c and e). CCK-8 assay showed that at 24, 48, 72 and 96 h after transfection, ST6Gal-I significantly enhanced cell growth rate (Figure 2f). Cancer cell growth was also assessed by colony formation assay. Huh-7 cells overexpressing ST6Gal-I formed significantly more colonies than control cells (Figure 2g). Accordingly, ST6Gal-I overexpression in Huh-7 cells triggered cell cycle arrest in S phase and a reduction in the number of cells in G0/G1 (Figure 2h). Moreover, the wound closure ability of Huh-7/ST6Gal-I cells was remarkably higher than that of control cells after 0, 4, 8 and 12 h (Figure 2i). Using Transwell/Matrigel assays, we found that in vitro, the mobility and invasiveness were dramatically increased in ST6Gal-I-overexpressing cells as compared to control groups (Figures 2j and k). Taken together, these findings suggest that ST6Gal-I functions as an oncogene by promoting cancer cell proliferation.

ST6Gal-I knockdown attenuates MHCC97-H cell proliferation, invasion and migration in vitro
To further verify the role of ST6Gal-I in HCC, we analyzed the effects of ST6Gal-I knockdown on the malignant phenotypes of MHCC97-H cells. ST6Gal-I mRNA and protein expression in MHCC97-H/shST6Gal-I cells was substantially lower than that in those transfected with the control construct and non-transfected MHCC97-H cells as indicated by qPCR, western blotting and immunofluorescence (Figures 3a,b and d). Lectin blotting and flow cytometry assay revealed that ST6Gal-I expression was successfully knocked down in MHCC97-H/shST6Gal-I cells (Figures 3c and e). The growth of MHCC97-H/shST6Gal-I cells was suppressed when compared to the control groups (Figure 3f). Accordingly, in an evaluation of the effects of ST6Gal-I knockdown on clonogenic capacity, colony formation was found to be reduced by shST6Gal-I knockdown (Figure 3g). Scratch assays showed that decreased ST6Gal-I expression significantly attenuated MHCC97-H cell migration (Figure 3i). The proportion of ST6Gal-I knockdown cells in S phase was smaller than that in negative control groups, and lower than the percentage arrested at G1/S (Figure 3h). Correspondingly, measurement of cell motility by Transwell/Matrigel assay revealed that suppression of ST6Gal-I restricted migration of MHCC97-H/shST6Gal-I cells (Figures 3j and k). These findings suggest that ST6Gal-I expression is positively correlated with the proliferation, migration and invasion potential of HCC cells.

Roles and expression of ST6Gal-I in liver tumorigenesis in mice
To examine the effect of ST6Gal-I on tumorigenesis in vivo, nude mice were inoculated with ST6Gal-I-knockdown or control cells. Both tumor size and growth rate were dramatically decreased in the MHCC97-H/shST6Gal-I group (Figures 4a and b). In addition, tumor weights were markedly lower in this group (Figure 4c). The average tumor volume at the injection site 4 weeks after inoculation of ST6Gal-I-knockdown cells was obviously smaller than that in the control group (Figure 4d). ST6Gal-I expression in xenograft tumor tissues was also decreased in the MHCC97-H/shST6Gal-I group (Figures 4e and f). Further, over the course of diethylnitrosamine (DENA)-induced liver tumorigenesis, ST6Gal-I expression was gradually increased, while no apparent changes were observed in the control group (Figures 4g and h). Therefore, ST6Gal-I might be involved in the tumorigenesis and development of hepatocarcinoma.

ST6Gal-I overexpression augments Wnt signaling pathways in HCC cells
To explore the possible mechanisms underlying the effects of ST6Gal-I on the malignant behaviors of HCC cells, we analyzed the PI3K/Akt, MAPK and Wnt/β-catenin signaling pathways. The results showed that the expression of p-GSK-3β, β-catenin, Cyclin D1, c-Myc, TCF1 and TCF4 was significantly higher in ST6Gal-I-overexpressing cells than in control cells, while the expression of p-β-catenin and GSK-3β proteins was not changed (Figures 5a and b). Additionally, there were no apparent differences in the expression levels of Erk1/2, p-Erk1/2, JNK and p-JNK in ST6Gal-I-overexpressing compared to control cells (Figures 5c and d). Expression of MMP-2, MMP-7 and MMP-9 was generally higher in ST6Gal-I-overexpressing than in control cells (Figures 5e and f). Moreover, confocal immunofluorescence microscopy showed increased expression and accumulation of β-catenin in the cytoplasm, then β-catenin released into the nucleus (Figure 5g). Together, this indicates that ST6Gal-I overexpression could upregulate the Wnt signaling pathway in HCC cells.

ST6Gal-I knockdown inhibits Wnt signaling pathway in MHCC97-H cells
Next, we observed that whether the inhibited HCC cell proliferation results from the inhibition of Wnt signaling pathway. We found that the expression of p-GSK-3β, β-catenin and related downstream proteins significantly decreased as a result of reduced ST6Gal-I levels (Figures 6a and b), while there were no apparent changes in the proteins of Erk1/2 and JNK signaling pathways (Figures 6c and d). In addition, ST6Gal-I silencing also decreased the expression of CD147/MMPs (Figures 6e and f). Confocal microscopy revealed that β-catenin was diffusely distributed following ST6Gal-I knockdown, with a lower proportion...
Figure 1. ST6Gal-I is highly expressed in HCC cells and tumor tissues. (a) IHC analysis of ST6Gal-I expression in adjacent noncancerous tissues (ANT) and different grades of HCC tissues (n = 80). (b, c) HCC patients with higher expression of ST6Gal-I show worse overall (b) and disease-free survival (c). (d, e) q-PCR and western blot assays were analyzed for the expression of ST6Gal-I in HCC cell lines and normal human hepatocyte cells. *P < 0.05. (f) Immunofluorescence data verifying the location of ST6Gal-I in HCC cell lines and normal human hepatocyte cells. Original magnification was × 40.
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The effects of ST6Gal-I on the Wnt signaling pathway in mice from the above results, we have found ST6Gal-I knockdown inhibited Wnt signaling in MHCC97-H cells and the tumorigenicity in xenograft mice. Here, western blot analysis of Wnt signaling in xenograft tumor tissues showed significantly decreased expression of the Wnt signaling molecules in the ST6Gal-I knockdown group (Figures 7a and b). IHC demonstrated reduced ST6Gal-I expression in neoplastic tissue extracted from MHCC97-H/shST6Gal-I mice compared to control animals (Figure 7c). Next, we verified the expression levels of these molecules during DENA-induced liver tumorigenesis by western blotting (Figures 7d and e) and IHC (Figure 7f). Notably, these proteins were significantly increased in the experimental but not in the control groups at 10 and 24 weeks. Therefore, ST6Gal-I might be directly involved in the tumorigenesis and HCC growth via the Wnt pathway.

DISCUSSION

Cell surface glycosylation, affecting the interactions between proteins, regulates membrane protein organization. Abnormal sialylation was found in many cancers, potentially affecting tumor cell differentiation, adhesiveness and invasion. Here, we examined the expression and localization of ST6Gal-I and sialylation in liver tumor specimens because hepatocytes are known to produce these proteins in large quantities. IHC examination revealed that ST6Gal-I overexpression was higher in HCC tissues of different grades than in non-tumor liver tissues, and it was secreted into the cytoplasm. Additionally, the IHC results showed that patients with higher ST6Gal-I expression have a lower survival rate. This result is not consistent with that reported by Poon et al., which may be because their sample size was small, yielding inaccurate results, or because they probably focused on terminal patients, in which ST6Gal-I probably has been already released into the peripheral blood as well as body fluid. Thus, it remains to be explored whether the release of ST6Gal-I from the cytosol into peripheral blood corresponds to increased HCC grade. Experiments such as an enzyme-linked immunosorbent assay are needed to verify our current result, and serum ST6Gal-I levels in patients at different liver cancer stages should be tested. Monitoring of HCC progression using patient blood samples has not yet been achieved.

To explore the role of ST6Gal-I in HCC in detail, we modified its expression in Huh-7 and MHCC97-H cell lines in vitro, then aimed to comprehensively elucidate its function during human HCC progression. We found that overexpression of ST6Gal-I enhanced proliferation of HCC cells, increased their migration and invasion in vitro, and promoted cell cycle progression, with knockdown of this protein exerting contrary effects. Notably, ST6Gal-I dysregulation is tightly correlated with tumor metastasis. For the in vivo xenograft experiment, we employed MHCC97-H cells, which have a higher rate of tumorigenicity than Huh-7 cells, and found that ST6Gal-I knockdown via shRNA reduced tumor volume and growth, confirming the function of ST6Gal-I in promoting neoplasm progression. These findings clearly suggest that ST6Gal-I may positively regulate tumor cell attributes such as proliferation, migration and invasion.

Hepatocellular carcinogenesis is a complicated process resulting from multiple molecular events leading to the initiation, promotion and progression of tumors. Zhao et al. reported that sialylation might modulate the invasion and chemosensitivity of HCC, likely through ST6Gal-I or ST8SIA-II regulation of PI3K/Akt signaling. However, to clarify the function of ST6Gal-I in HCC and the associated mechanisms, we examined MAPK, Wnt and PI3K/Akt pathways. ERK signaling plays an important role in the regulation of proliferation, invasiveness and survival in cancers.

Our results demonstrated that ST6Gal-I upregulation/downregulation did not affect the phosphorylation levels of Erk and JNK. Furthermore, the tumor-cell-surface glycoprotein, EMMPRIN/CD147 (extracellular matrix metalloproteinase inducer) can induce the secretion of matrix metalloproteinases (MMPs) in the tumor-stroma interaction. MMPs are also considered to play major roles in cell processes such as migration, differentiation, angiogenesis and cancer metastasis. Additionally, the Wnt/β-catenin pathway is also involved in the modulation of tumor angiogenesis and metastasis by affecting the expression of MMP-2 and MMP-9. Our discovery partly corroborates the supposition that ST6Gal-I can regulate Wnt/β-catenin signaling.

Wnts are N-glycoproteins, and modification of some of them, such as Wnt3a, activates the Wnt/β-catenin canonical pathways. Binding of the Wnt ligand to the receptor Frizzled-7 promotes the nuclear translocation of cytoplasmic β-catenin, which then associates with TCF/LEF transcription factors, and Frizzled receptors are also N-glycosylated. These studies indicate that N-glycoproteins play essential roles in Wnt/β-catenin signaling. Our study revealed that ST6Gal-I upregulation led to a significant increase in cytoplasmic β-catenin and release into the nucleus. Furthermore, western blotting demonstrated that related molecules (p-GSK3β, β-catenin, cyclin D1, c-Myc and MMPs) were significantly decreased in MHCC97-H/shST6Gal-I cells, but increased in Huh-7/ST6Gal-I cells. These findings indicate that ST6Gal-I regulates the Wnt/β-catenin pathway which might be attributed to the modulation of N-glycosylation of Wnt receptors, and Wnt/β-catenin signaling appears to be involved in ST6Gal-I-induced malignant transformation of HCC cells. However, the detailed molecular mechanisms how ST6Gal-I modulates the Wnt signaling pathway are still needed to elucidate in further researches.

In conclusion, our data implicate that ST6Gal-I overexpression in human HCC is associated with carcinoma progression and poor clinical prognostic. In addition, ST6Gal-I may accelerate HCC

Table 1. Distribution of characteristics of patients with HCC by ST6Gal-I expression

| Patient characteristics | ST6Gal-I expression | Total | P Value |
|-------------------------|---------------------|-------|---------|
|                         | Low                 | High  |         |
| Age, years              |                     |       |         |
| >50                     | 11                  | 27    | 0.133   |
| ≥50                     | 19                  | 23    | 0.023   |
| Sex                     |                     |       |         |
| Male                    | 21                  | 45    | 0.014   |
| Female                  | 9                   | 5     |         |
| Number of lesions       |                     |       |         |
| Unifocal                | 18                  | 16    | 0.635   |
| Multifocal              | 12                  | 34    |         |
| Serum AFP (mg/l)        | >20                 | 8     | 0.015   |
|                         | ≥20                 | 22    |         |
| Extent of invasion      | T1–T2               | 13    |         |
|                         | T3–T4               | 17    |         |
| Pathologic grade        | I–II                | 14    | 0.021   |
|                         | III–IV              | 16    |         |
| Lymph node metastases   | Negative            | 28    | 0.905   |
|                         | Positive            | 2     |         |
|                         |                     | 3     |         |

Abbreviations: AFP, alpha fetoprotein; HCC, hepatocellular carcinoma. *P < 0.05 was statistically significant.
Figure 2. Overexpression of ST6Gal-I contributes to proliferation and metastasis in Huh-7 cells in vitro. (a, b, d) Analysis of ST6Gal-I expression in Huh-7 cell transfected with pcDNA3.1/ST6Gal-I by qPCR (a), western blotting (b) and immunofluorescence (d). (c, e) α2, 6-linked sialic acid expression levels determined by lectin blotting and flow cytometry. (f) ST6Gal-I overexpression enhances the viability of Huh-7 cells as indicated by CCK-8 assay. (g) Colony formation assay was used to evaluate the proliferation of Huh-7 cells after stimulating the expression of ST6Gal-I. (h) Cell cycle distribution analysis by FACS showed that the rate of S phase was higher in Huh-7/ST6Gal-I cells than in the control group. (i) Migration behaviors of Huh-7 cells with upregulated ST6Gal-I expression explored by a wound-healing assay. (j, k) Transwell assays showed that overexpression of ST6Gal-I increases the invasion and migration rates of Huh-7 cells. All quantitative data are shown as the mean ± s.d. of three independent experiments. *P < 0.05.
development through Wnt/β-catenin signaling. Our findings not only reveals the pathological roles of ST6Gal-I in HCC, but also provide a potential new marker for HCC.

MATERIALS AND METHODS

Patients and IHC
ST6Gal-I levels in hepatoma carcinoma and normal hepatic tissues were evaluated by IHC using anti-ST6Gal-I on commercial tissue arrays (Shanghai Zhuo Li Biological Technology, China) as previously described.38,39 After antigen retrieval and blocking, the slides were incubated with a rabbit anti-ST6Gal-I primary antibody (1:100; Abcam, Cambridge, UK) overnight at 4 °C. Negative control slides were processed in the same manner, without addition of the primary antibody. For detection, diaminobenzidine (DAB) (ZSGB-BIO, Beijing, China) and hematoxylin were used. Two certified pathologists blinded to the clinical data independently assessed ST6Gal-I immunostaining, scoring the results depending on the positive-staining percentages and staining intensity, as follows: (0) 0%, no staining (−); (1) 1–29%, weak positive (+); (2) 30–59%, moderate positive (++); and (3) >60%, intense staining (+++). For statistical analysis, cases were categorized as either negative (no and weak staining) or positive (moderate and intense staining). Pearson’s chi-squared test was used to assess the association between ST6Gal-I and HCC, to determine its clinical significance.

Cell culture
L02 normal liver cells and Huh-7 and MHCC97-H human HCC cells were purchased from the Cell Bank of Chinese Academy of Sciences (Shanghai, China). All cell lines were maintained in Dulbecco’s modified Eagle’s medium supplemented with 10% fetal bovine serum and 1% penicillin/streptomycin under standard culture conditions (37 °C, 5% CO2), they were tested regularly for mycoplasma contamination in the laboratory.

Vector construction and transfection
Huh-7 cells were transfected with the recombinant pcDNA3.1/ST6Gal-I vector or a control vector.16 To inhibit ST6Gal-I expression, MHCC97-H cells were transfected with shRNA sequences targeting ST6Gal-I and a negative control vector (shNC) was constructed as described previously.16,24 These cells were transfected with a mixture of plasmids and Lipofectamine 2000 (Invitrogen, Carlsbad, CA, USA) depending on the manufacturer’s instructions. To select stably transfected cells, the culture medium was replaced with complete medium containing 800 mg/ml of G418 (Sigma-Aldrich, Darmstadt, Germany) after 48 h. Modified expression was confirmed by qPCR and western blotting.

qPCR
Total RNA was extracted using TRIzol reagent (Life Technologies, Carlsbad, CA, USA) and was employed to synthesize cDNA using a PrimeScript RT Reagent Kit (Takara, Dalian, China) and subsequently mixed with qPCR SuperMix (Takara, Otsu, Japan). Relative changes in gene expression were analyzed using the 2−ΔΔCT method. Sequences of the forward (F) and reverse (R) primers used for qPCR are shown previously.16

Western blot
Proteins were extracted from cells using lysis buffer (Beyotime, Haimen, China) containing protease inhibitors. Protein concentrations in lysates were measured with a bca kit (Beyotime). Aliquots of protein extracts were subjected to 10–15% SDS–PAGE and then transferred to polyvinylidene fluoride (PVDF) membranes (Pall Corporation, New York, NY, USA), which
Figure 3. Depletion of ST6Gal-I in MHCC97-H cell line inhibits cell growth and metastasis in vitro. (a, b, d) Analysis of ST6Gal-I expression in MHCC97-H cells transfected with shST6Gal-I by qPCR (a), western blotting (b) and immunofluorescence (d), original magnification was ×40. (c, e) Knockdown of the expression of ST6Gal-I could affect α2,6-linked sialic acid expression levels as determined by lectin blotting and flow cytometry assay. (f) Cell Counting Kit (CCK-8) assays showed that knockdown of ST6Gal-I expression leads to inhibition of cell proliferation. (g) Colony formation numbers was lower in ST6Gal-I-low expression cells (MHCC97-H/shST6Gal-I group) than in controls. (h) Flow cytometry assay showed that ST6Gal-I depletion leads to G1 arrest. (i, j) Cell migration ability as analyzed by wound healing assay in MHCC97-H cells following ST6Gal-I silencing at different time points. (j, k) Transwell assays were used to analyze the invasion and migration abilities of MHCC97-H transfected with shST6Gal-I. *P < 0.05.
were blocked for 2 h with 5% skim milk in tris buffered saline, with tween-20 (TBST). The membranes were incubated with primary antibodies of ST6Gal-I (1:600; Abcam, ab77676, Cambridge, MA, USA), PI3K (1:500, Elabscience, ENT3709, Wuhan, China), Akt (1:500, Abcam, ab8805), p-Akt (1:500, Elabscience, ENP0006), GSK-3β (1:500, Affinity Biosciences, AF5016, Cincinnati, OH, USA), phosphorylated Ser9 GSK-3β (1:500, Bioworld, BS4084), β-catenin (1:500, Elabscience, ENT0672), p-β-catenin (1:500, Elabscience, ENP0047), Erk (1:500, Elabscience, EPP12809), p-Erk (1:500, Elabscience, ENP0497), JNK (1:500, Elabscience, EPP14522), p-JNK (1:500, Elabscience, ENT0672), Cyclin D1 (1:500, Affinity Biosciences, DF6386), c-Myc (1:500, BioWorld, BS2462, Louis Park, MN, USA), TCF1 (1:200, Santa Cruz Biotechnology, Inc, Santa Cruz, CA, USA), TCF3 (1:500, BioWorld, BS2466), TCF4 (1:500, BioWorld, P15884), MMP-2 (1:200, Santa Cruz Biotechnology, SC-10736), MMP-7 (1:600, BioWorld, BS1239), MMP-9 (1:200, Santa Cruz Biotechnology, SC-10737), EMMPRIN (1:500, BioWorld) and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (1:5000; Proteintech, 10494-1-AP, Pearl Street, IL, USA) antibodies. Subsequently, the membranes were incubated with horseradish peroxidase-conjugated secondary antibody (1:10,000; ZSGB-BIO, ZB-2301). Following further washing with TBST, blots were visualized using enhanced chemiluminescence reagents (Advansta, Menlo Park, CA, USA). After exposure, protein band densitometry was conducted with the Image Lab software (Bio-Rad, Hercules, CA, USA).

Figure 3. Continued.

were blocked for 2 h with 5% skim milk in tris buffered saline, with tween-20 (TBST). The membranes were incubated with primary antibodies of ST6Gal-I (1:600; Abcam, b77676) and rabbit anti-β-catenin (1:100, Elabscience, ENT0672). A fluorescein-labeled secondary antibody (1:100, Proteintech, SA00006-4) was subsequently incubated with the cells for 1 h at 37 °C. Golgi apparatus were identified using a rabbit anti-GM130 antibody (1:50; BD Biosciences, Franklin Lakes, NJ, USA), and 4,6-diamidino-2-phenylindole was used to stain nuclei for 10 min. Fluorescence was observed using a confocal laser-scanning microscope (BD Biosciences).

Immunofluorescence and confocal microscopy

Cells were plated on slips for 24 h, then these cells were fixed with 4% paraformaldehyde for 30 min, and incubated overnight with rabbit anti-ST6Gal-I (1:100; Abcam, b77676) and rabbit anti-β-catenin (1:100, Elabscience, ENT0672). A fluorescein-labeled secondary antibody (1:100, Proteintech, SA00006-4) was subsequently incubated with the cells for 1 h at 37 °C. Golgi apparatus were identified using a rabbit anti-GM130 antibody (1:50; BD Biosciences, Franklin Lakes, NJ, USA), and 4,6-diamidino-2-phenylindole was used to stain nuclei for 10 min. Fluorescence was observed using a confocal laser-scanning microscope (BD Biosciences).

Soft-agar colony formation assay

0.75% low gelling temperature agarose (Sigma-Aldrich) in complete medium served as the bottom layer, and approximately 4 × 10^4 Huh-7 or 8 × 10^4 MHCC97-H cells suspended in 0.3% agarose in the same medium constituted the top layer in 6-cm dishes. After 4 weeks of incubation, the number of colonies with ≥50 cells in each dish was counted using cellSens software Olympus, Tokyo, Japan).

Flow cytometry

After washing thrice with phosphate-buffered saline (PBS), cells were collected in a tube, and fixed in 70% cold ethanol overnight. Then, they were blocked with 2% bovine serum albumin for 30 min, and incubated overnight with rabbit anti-ST6Gal-I (1:100; Abcam, b77676) and rabbit anti-β-catenin (1:100, Elabscience, ENT0672). A fluorescein-labeled secondary antibody (1:100, Proteintech, SA00006-4) was subsequently incubated with the cells for 1 h at 37 °C. Golgi apparatus were identified using a rabbit anti-GM130 antibody (1:50; BD Biosciences, Franklin Lakes, NJ, USA), and 4,6-diamidino-2-phenylindole was used to stain nuclei for 10 min. Fluorescence was observed using a confocal laser-scanning microscope (BD Biosciences).

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Transwell migration and invasion assay

Following the manufacturer’s instructions, serum-free Dulbecco’s modified Eagle’s medium was placed in the upper chambers of a Transwell plate (pore size: 8.0 μm; diameter: 6.5 mm; Corning, NY, USA), and 600 μl complete medium Dulbecco’s modified Eagle’s medium was added to the lower chambers as a chemoattractant. In each well, 8 × 10^5 Huh-7 or 4 × 10^5 MHCC97-H cells seeded in the upper chamber and incubated for 32 h. Migrated cells were fixed in 4% paraformaldehyde and stained with 0.1%
crystal violet for 30 min, and counted in five non-overlapping fields and photographed. The invasion assay was carried out as above, except that the upper chambers of 24-well Transwell systems were coated with 40 \( \mu \)l Matrigel (diluted 1:8). After 30 min for Matrigel solidification, 1.6 \( \times 10^5 \) Huh-7 or 8 \( \times 10^4 \) MHCC97-H cells were seeded in each upper chamber and cultured for 48 h.

**Xenograft model**

All in vivo experiments were approved by and carried out according to the guidelines and regulations of the Dalian Medical University Sciences Center Animal Care and Use Committee. In addition, use of animals in the present study was consistent with Association for Assessment and Accreditation of Laboratory Animal Care International guidelines. Athymic nude mice aged 4–6 weeks were obtained from the Animal Experiment Center of Dalian Medical University, China, for analysis of tumorigenicity. They were randomly divided into three treatment groups, each of which included 10 animals: an MHCC97-H group, a negative control group and an MHCC97-H/shST6Gal-I group. Approximately 2 \( \times 10^7 \) cells in 100 \( \mu \)l of PBS were injected subcutaneously into the right dorsal flank of each mouse. Tumor diameters were measured with a vernier caliper every 3 days after 1 week, and tumor volumes being calculated using the following formula: 1/2 (length \( \times \) width\(^2\)). All mice were killed 30 days later, then tumor weights and volumes were determined. To ascertain the significance of results, the group size was chosen as to ensure that >5 animals remained in each group after 1 month when applying exclusion criteria or if death occurred during the experiment. No statistical method was used to estimate sample size.

**DENA- and CCl4-induced liver tumorigenesis**

C57BL/6J mice 6–8 weeks of age weighing 15.8 \( \pm \) 1.5 g (average \( \pm \) s.d.) were purchased from Dalian Medical University and housed in a temperature-
controlled, air-conditioned, specific pathogen-free facility, and received food and water ad libitum, taking into consideration the guidelines and regulations of the Dalian Medical University Sciences Center Animal Care and Use Committee. The mice were divided into DENA-treated and control groups, those in the former being injected with 1 mg/kg DENA in sterile 15 ml/kg PBS for 3 weeks, and those in the latter being injected with sterile PBS alone. Then, mice in the DENA group received intraperitone injections of 0.2 ml/kg sterile CCl4 diluted in sterile olive oil, twice per week for an additional 21 weeks, while control animals were injected intraperitoneally with PBS. Mice were killed at 0, 2, 4, 8, 9, 10, 16, 18, 20, 22 and 24 weeks after initial treatment to analyze liver neoplasm development. Histopathological examinations to identify liver tumors were performed as described previously. Allocation of the animals and assessment of the outcome were done without blinding.

Statistical analysis
Data were analyzed with SPSS 16.0 (SPSS Inc., Chicago, IL, USA), and every experiment was done three times and the results were shown as the mean ± s.e. Student’s t-test was used to compare two independent groups of data. Differences were considered significant at P-values < 0.05.

CONFLICT OF INTEREST
The authors declare no conflict of interest.

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Figure 7. Altered expression of ST6Gal-I affects liver tumorigenesis via the Wnt/β-catenin signaling pathway in mice. (a, c) Western blotting and IHC were used to detect the expression levels of GSK-3β, p-GSK-3β, β-catenin, p-β-catenin, Cyclin D1 and c-Myc proteins in tumor tissues. (d, f) Western blotting and IHC analyses revealed differential expression of these proteins in liver tumorigenesis. (b, e) Relative protein intensities as determined by Image Lab. *P < 0.05.
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