Secreted Protein Acidic and Rich in Cysteines-like 1 Suppresses Aggressiveness and Predicts Better Survival in Colorectal Cancers

Hanguang Hu, Hang Zhang, Weiting Ge, Xiyong Liu, Peiguo Chu, Huarong Chen, Jiaping Peng, Lun Zhou, Shujing Yu, Ying Yuan, Suzhan Zhang, Lily Lai, Yun Yen, and Shu Zheng

Abstract

**Purpose:** Secreted protein acidic and rich in cysteines-like 1 (SPARCL1) is an extracellular matrix glycoprotein with malignancy-suppressing potential. The hypothesis that SPARCL1 reduces cancer invasiveness and predicts better survival in colorectal cancers (CRC) was investigated.

**Experimental Design:** Stable SPARCL1 transfectants, RKO-SPARCL1, and corresponding vector control were constructed and implanted into nude mice to generate a mouse xenograft model of liver metastasis. Also, a retrospective outcome study was conducted on the COH set (222 CRCs) and ZJU set (412 CRCs). The protein expression level of SPARCL1 was determined by immunohistochemistry. The Kaplan–Meier and Cox analyses were used for survival analysis. The association of SPARCL1 with mesenchymal–epithelial transition (MET) was examined by reverse transcription PCR (RT-PCR) and Western blot analysis.

**Results:** The ectopic expression of SPARCL1 significantly reduced the potential for anchorage-independent growth, migration, invasion and induced cell differentiation in RKO and SW620 cells. In mouse xenograft model, the expression of SPARCL1 significantly reduced the liver metastasis (P < 0.01). The patient-based studies revealed that the expression of SPARCL1 was related to better differentiation (P < 0.01), less lymph node involvement [OR, 0.67; 95% confidence interval (CI), 0.45–1.00], and less distant metastasis (OR, 0.38; 95% CI, 0.18–0.79). The Kaplan–Meier and Cox analysis showed that the expression of SPARCL1 was associated with better overall survival (log-rank: P < 0.01; HR, 0.57; 95% CI, 0.39–0.84). Transfection of SPARCL1 induced MET of colon cancer cells.

**Conclusion:** SPARCL1 functions as a tumor suppressor promoting differentiation possibly via MET, which inhibits the aggressiveness of CRCs. Clin Cancer Res; 18(19); 5438–48. ©2012 AACR.

Introduction

Colorectal cancer (CRC) is one of the leading causes of cancer mortality in the world (1). Despite improvements in early detection and treatment of CRC in the last few decades, the 5-year survival rate remains about 50% to 60% (2, 3). This high mortality is partially attributable to liver metastasis which accounts for 40% to 50% of recurrences in patients with CRCs (4). Exploring the molecular basis of liver metastasis may provide further improvements in early detection, prevention, intervention, and prognostic evaluation for patients with CRCs.

Secreted protein acidic and rich in cysteines (SPARC) family includes SPARC, SPARCL1, and SMOC-2. SPARCL1, which is also known as Hevin, SC1, or MAST9, is an extracellular matrix (ECM) glycoprotein, whose gene is located in 4q22 (5, 6). SPARCL1 was first isolated from a human high endothelial venules cDNA library and is involved in many physiologic functions, such as cell adhesion (7, 8), cell proliferation (7), central nervous system development (9), and B-lymphocyte maturation (10). SPARCL1 is widely expressed in normal tissues such as brain, heart, lung, muscle, colon, and kidney (5, 6, 11–13). In contrast, its full-length expression was strongly downregulated in several carcinomas such as metastatic prostate adenocarcinoma and non–small cell lung cancer (5, 8, 14–16). The downregulation of SPARCL1 mRNA in colorectal carcinomas was confirmed by Northern blotting (9) and oligonucleotide array (17). Previously, pilot studies showed that
Translational Relevance

Secreted protein acidic and rich in cysteines-like 1 (SPARCL1) is an extracellular matrix glycoprotein with malignancy-suppressing potential that is vital to the development of neural system. Here, our findings displayed that SPARCL1 inhibits cell proliferation, anchorage-independent growth, and invasion and induces differentiation in colon cancer cells. This study also explored the metastasis-suppressing ability of SPARCL1 in a mouse xenograft model. Meanwhile, the invasion-suppressing potential of SPARCL1 was assessed with outcome study based on two sets of patients with colorectal cancer (CRC). The findings consistently validated that high expression of SPARCL1 was negatively associated with poor differentiation and metastasis, resulting in a better survival of CRCs. Furthermore, we showed that the SPARCL1 induced differentiation by mesenchymal–epithelial transition in colon cancer cells. These findings provided evidences for SPARCL1 as a potential prognostic biomarker, indicative of tumor invasion and metastasis of CRCs.

high SPARCL1 expression level is associated with well-differentiated status, less metastasis, and better survival in CRCs (18). Similar results were obtained by other investigators that indicated that the expression of SPARCL1 increased with greater level of differentiation and decreased in progressing from Dukes stage B to D. However, their data showed that expression of SPARCL1 led to poor survival in CRCs (19). Therefore, the prognostic value of SPARCL1 needs to be further investigated at multiple centers with colorectal cancer (CRC). The findings consistently validated that high expression of SPARCL1 was negatively associated with poor differentiation and metastasis, resulting in better survival of CRCs. Meanwhile, the pLXSN vector was also transfected in the same way as a control.

Antibodies

Mouse monoclonal antibodies against SPARCL1 were produced by HuAan Bio-Technology Co., Ltd. using synthesized peptide (aa351–364: CDGPRHSASDDYFIP) as the antigen. The efficiency of antibodies was visualized by using recombinant human SPARCL1 protein (R&D) in Western blot analysis. The mouse monoclonal antibody IgG named No.C11 was preselected for further Western blot and immunohistochemical (IHC) staining experiments. In Western blot analysis, No.C11 significantly reduced nonspecific signals in comparison with commercial antibody (Supplementary Fig. S1). Moreover, the signal of recombinant SPARCL1 protein and endogenous SPARCL1 (75 kDa and 130 kDa) could be specifically blocked by recombinant SPARCL1 full-length peptide (Supplementary Fig. S1), which indicated the specificity of antibody. The E-cadherin (#3195), N-cadherin (#4061), and Vimentin (#3390) antibodies were from Cell Signaling Technology and diluted as recommended. Anti-β-actin antibody was from Sigma and secondary antibodies were from Bio-Rad.

Quantitative reverse transcription PCR analysis and Western blot analysis

RNA and protein were extracted from subconfluent cells in the exponential phase of growth. Total RNA was extracted and purified using Rneasy kit (Qiagen). Each mRNA sample (4 μg) was reverse transcribed using the LongRange 25step RT-PCR Kit (Qiagen). An ABI One-Step Real-Time PCR System (Applied Biosystem) was used for quantitative reverse transcription PCR (qRT-PCR) analysis. The experiments were carried out in triplicate and normalized by β-actin (loading control). Primer sequences applied in qRT-PCR experiments are listed in Supplementary Table S1.

Secreted protein in cell culture supernatant was extracted using Trichloroacetic Acid-Acetone (Sigma) Precipitation. Protein in 20 mL serum-free supernatant was resuspended in 20 μL loading buffer. Cell lysate samples were extracted by M-PER Mammalian Protein Extraction Reagent (Pierce) containing the protease inhibitor cocktail (Sigma). For Western blot analysis, about 40 μg lysate samples or 20 μL secreted protein were loaded into each well and separated by SDS-PAGE then transferred to polyvinylidene fluoride.
membrane. Immunoblotting was conducted by incubation with anti-SPARC,L1 (No.C11, 1:200), E-cadherin, N-cadherin, Vimentin, and β-actin antibodies as mentioned above and then followed by incubation with corresponding alkaline phosphatase–conjugated secondary antibodies. Immunoreactive bands were visualized by enhanced-ECL or SuperSignal bands.

**In vitro cell growth assays**

The measurement of cell proliferation was based on cell counting on 24-well plates. At initiation of the study, approximately 1 × 10⁶ cells were seeded per well. At each time point, cells on 24-well plates were trypsinized and then harvested. For cell counting, trypan blue staining was used to indicate viable cells. The proliferative activity was also determined by MTS assay (CellTiter 96 Non-Radioactive Cell Proliferation Assay, Promega Corporation), which monitors the number of viable cells after 4 hours in medium containing MTS. The conversion of MTS to formazan was measured in a plate reader at 490 nm. The colony formation assay was used to reflect anchorage-independent cell growth. About 1 × 10⁴ cells were layered in 60-mm plate, the medium was replenished every 5 days, and colonies that grew beyond 50 μm in diameter after 3 weeks were scored as countable. Recombinant SPARCL1 protein (AF2728, R&D) was added into the medium at the concentration of 1 μg/μL. The mean and SD were calculated from 3 independent experiments.

**In vitro cell migration and invasion assay**

Wound-healing assay was used to measure the ability of cell migration, 2 × 10⁵ viable cells were mixed thoroughly and seeded in 6-well plates. Twenty-four hours after seeding, the cell formed monolayer. A linear wound was created by scraping the cell monolayer with a 200-μl sterile pipette tip. The media were carefully changed to remove any floating cells and cultured at 5% CO₂ and 37 °C for another 24 hours. To elucidate the role of SPARC,L1 protein in wound healing, recombinant SPARC,L1 protein was added into the medium at a concentration of 500 ng/μL. Cells that spread into the scraped region were considered migrating cells. The ability of migration was represented by the migrating distance. To further validate the wound-healing assay, Boyden chamber (BD) was used with interleukin (IL)-8 as a chemotactrant at the concentration of 1 μg/μL. A Matrigel chamber (BD) was used to evaluate the invasion ability of cancer cells. Assays were conducted in 24-well plates with an 8-μm polycarbonate filter membrane coated with growth factor–reduced Matrigel diluted in 20%. Cells in serum-free medium (2.5 × 10⁴ cells per well) were added to the upper chambers. Conditioned medium with 10% FBS was placed in the lower chambers as a chemotactrant. The chambers were incubated for 24 hours at 37 °C with 5% CO₂. Migrated cells on the undersides of filter membrane were fixed in 90% (v/v) ethanol and stained with crystal violet. The migrated cells were counted using light microscopy and the experiments were carried out in triplicate.

**Construction of xenograft mouse models**

All animal experiments were carried out under an approved protocol from the Institutional Animal Care and Use Committee (IACUC) of City of Hope (COH; Duarte, CA). For subcutaneous xenograft mouse model, fifteen 6-week-old male athymic nude mice (BALB/c nude) were divided into 3 groups: RKO (group 1), RKO-pLXSN (group 2), and RKO-SPARCL1 (group 3). Five mice of each group were injected subcutaneously with 5 × 10⁶ viable tumor cells at the site of costal region. Tumor size was measured every 3 days. Tumor volume was calculated on the basis of length and width (20) and plotted against days postinjection. The mice were euthanized on day 23 postinjection or when tumor diameter became larger than 1,000 mm³. The fresh tumor specimen was divided into 2 parts. One part was fixed with 10% formalin and embedded in paraffin for histologic examination; another part was snap-frozen and stored at −80°C for mRNA and protein extraction.

For liver metastasis mouse model, 6-week-old male athymic nude mice (BALB/c nude) were grouped as mentioned above. Under sterilization, mice were anesthetized with pentobarbital sodium. A transverse incision was made in the left flank to expose the spleen. Total of 5 × 10⁶ viable tumor cells were injected into the spleen vein carefully to avoid extravasations. After 5 minutes postinjection, the spleen was excised via ligation at the hilum of the spleen. The mice were euthanized at the day 40 postoperation. Abdominal autopsy was conducted to examine liver metastatic nodules. Histologic examination was further committed by pathologists.

**Design of outcome study**

This is a retrospective population-based outcome study. The design of study is described in Supplementary Fig. S2. The protocol of human subject application was reviewed and approved by the Institutional Review Board (IRB) of City of Hope and Second Affiliated Hospital of Zhejiang University (ZJU; Hangzhou, Zhejiang, China), respectively. All eligible participants received surgical operation and were diagnosed as colon or rectal adenocarcinoma. A total of 222 CRCs during 1980 to 2004 from COH (training set) and 412 CRCs during 1999 to 2006 from ZJU (validation set) were collected separately according to the following inclusion criteria: (i) diagnosis of CRC by pathologist; (ii) informed consent obtained; and (iii) follow-up data available. The exclusion criteria included: (i) no histologic diagnosis; (ii) informed consent unobtainable; (iii) no follow-up data available; and (iv) multiple cancers. The participants in the COH set included 185 Caucasian, 5 African-American, 13 Asian, and 19 unknown ethnicity. All patients were Asian (Chinese) in the ZJU set. After surgical treatment, all patients were followed up until June 2007 for COH set and September 2010 for ZJU set. The median follow-up period is 166 months in COH set and 46 months in ZJU set. All demographic data and pathologic information were obtained by reviewing the hospital records (Supplementary Table S2). Follow-up data of COH set were obtained from cancer registry at COH. For ZJU set, it was obtained from a
follow-up work team. Variables assessed included age, gender, date of operation, tumor location (colon or rectal), differentiation, tumor node metastasis (TNM) stage, adjuvant chemotherapy, radiotherapy, date of last follow-up, and vital status at last follow-up. In ZJUI, 88 patients were treated with chemotherapy and 3 with radiotherapy. For 222 cases in COH, 90 patients obtained postsurgery chemotherapy and 44 cases received radiotherapy. The chemotherapy regimen in both center is based on 5-fluorouracil. The survival period was calculated from the date of surgical operation to the date patient was last seen. Only deaths from metastasis and local relapse of CRCs were considered as disease-related death.

**IHC staining**

Formalin-fixed, paraffin-embedded (FFPE) cancer tissues from surgery were selected to construct multiple tissue board (MTB) for COH set and multiple tissue array (MTA) for ZJUI set (21). The condition of IHC staining for **SPARCL1** was optimized on checkerboards with different normal and tumor samples. For each IHC staining, negative and positive checkerboards were included for quality control. Standard indirect immunoperoxidase procedures were used for immunohistochemistry. Briefly, 4-μm thick sections were cut from paraffin-embedded tissue blocks, and immunostaining for each antigen was conducted using the avidin–biotin–peroxidase complex technique (MaxVision HRP). Briefly, sections were blocked with 6% horse serum. A primary monoclonal antibody (No.C11; 1:50 dilution) was used as the primary antibody. The slides resulting from the IHC reaction were evaluated individually and independently by 2 investigators in a double-blinded manner. According to the percentages of positive cells and staining intensity, the IHC result was assessed. Despite the heterogeneity of cancer cells, only cytoplasmic signal of **SPARCL1** was considered.

**Data management and statistical consideration**

MS-ACCESS was used to create a colorectal database. Double entries and logic correction were applied to reduce mistakes in the database. The JMP Statistical Discovery Software (SAS Institute) was used for data analysis. The sample size estimation was calculated using nQuery Advisor 6.01 software. It was indicated that 200 cases would be sufficient for 80% study power with a 2-sided α of 0.05. Multivariate logistic regression models were used to adjust for covariate effects on the ORs. Kaplan–Meier survival analysis and Cox hazard proportional model were used for evaluation of overall survival (OS). ANOVA was used for multiple comparisons. A P value less than 0.05 was considered as statistically significant.

**Results**

**SPARCL1 suppresses proliferation, migration, and invasion of colon cancer cells**

The mRNA level of **SPARCL1** was barely detectable in most of colorectal tumor cell lines including RKO and SW620 (Supplementary Fig. S3A). To investigate the role on malignancy, the **SPARCL1** expression plasmid (pLXSN-SPARCL1) and control vector (pLXSN) were transfected into RKO and SW620 cells. Stably expressing transfectants (RKO-SPARCL1, SW620-SPARCL1, as well as the corresponding vector controls) were isolated. Western blot analyses confirmed that the protein level of **SPARCL1** was significantly higher in the expression transfectants than in vector controls after normalizing to β-actin (Fig. 1A, top). The secretion of **SPARCL1** protein was also elevated in the culture medium of **SPARCL1**-transfected cells (Fig. 1A, bottom). In the cell proliferation study conducted using cell counting method, the growth of **SPARCL1** transfectants decreased significantly both in RKO (day 6, P = 0.03) and SW620 (day 6, P = 0.04) cells in comparison with corresponding vector control (Supplementary Fig. S3B, top). In addition, when the MTS method was used to assess cell proliferation, it showed that the growth of **SPARCL1** transfectants decreased both in RKO (day 5, P > 0.05) and SW620 (day 5, P > 0.05) cells compared with the vector control (Supplementary Fig. S3B, bottom). The ability of anchorage-independent growth also reflects the potential of cancer metastasis. Consistently, the colony formation of RKO-SPARCL1 and SW620-SPARCL1 was dropped by 34% to 62% (P < 0.01) and 19% to 48% (P = 0.03), respectively, which indicated that anchorage-dependent growth was retarded in **SPARCL1**-expressing cells (Fig. 1B). Recombinant **SPARCL1** peptide significantly reduced the colony formation by RKO cells (P < 0.01), as well as SW620 cells (P < 0.01; Supplementary Fig. S3C).

The abilities to migrate and invade were regarded as the main malignant phenotype and prerequisite of metastasis for cancer cells. In wound-healing assay, it was shown that the **SPARCL1** transfectants significantly reduced the migration ability of RKO cells (Fig. 1C, P = 0.03), as well as SW620 cells (P = 0.03). Recombinant **SPARCL1** protein also inhibits cell migration (Supplementary Fig. S3D, P = 0.03 in RKO cells and P > 0.05 in SW620 cells). The Matrigel invasion assay showed that the invasion ability of **SPARCL1** transfectants decreased significantly (Fig. 1D, P = 0.01). The invasion ability was significantly enhanced when we applied IL-8 as chemoattractant in both RKO and SW620 cells (P < 0.01), whereas it was significantly reduced by the recombinant **SPARCL1** peptide (P < 0.01; Supplementary Fig. S3E). Above findings suggested that **SPARCL1** could significantly reduce abilities of cell proliferation, anchorage-independent growth, and invasion in colon cancer cell lines.

**SPARCL1 inhibits tumor growth and liver metastasis in a mouse xenograft model**

To validate the above findings, mouse xenograft models were used to determine whether **SPARCL1** impacts tumor growth and metastasis in vivo. The RKO, RKO-pLXSN, or RKO-SPARCL1 cells were implanted subcutaneously to form xenograft tumors. The tumor volume was monitored every 3 days. The average tumor volume of RKO-**SPARCL1** group was significantly reduced when compared with RKO
group or RKO-pLXSN group (Supplementary Fig. S4). Through RT-PCR, the presence of human SPARCL1 in RKO-SPARCL1 xenografts was verified but it was undetectable in RKO-pLXSN cells (Supplementary Fig. S4B). Representative gross views showed size disparity between RKO-pLXSN and RKO-SPARCL1 in subcutaneous xenograft mouse model (Supplementary Fig. S4C, left). The corresponding images for the hematoxylin and eosin (H&E) staining are also shown (Supplementary Fig. S4C, right). IHC staining confirmed that the SPARCL1 protein was expressed in the RKO-SPARCL1 xenograft group but absent in the RKO-pLXSN xenograft group (Supplementary Fig. S4D).

Because liver accounts for most of the CRC metastases, the impact of SPARCL1 on liver metastasis was assessed through intrasplenic implantation, a liver metastasis model described in Materials and Methods. Laparotomy was conducted on all the mice at 40 days after the implantation of tumor cells. It revealed that RKO-pLXSN cells formed on an average 98 metastatic nodules per liver in 5 mice analyzed as detected by dissection microscopy. In contrast, mice implanted with RKO-SPARCL1 cells formed on an average 11 nodules (Fig. 2A). It indicated that the metastatic nodules formation was significantly suppressed in SPARCL1-expressing transfectants (P < 0.01). The presence of human SPARCL1 in each implant tissue sample was determined by RT-PCR (Fig. 2B). Histologic analyses confirmed that the number of micrometastatic lesions was markedly reduced in the livers of mice injected with SPARCL1-expressing cells (Fig. 2C). These results indicated that the expression of SPARCL1 potentially inhibits liver metastasis of RKO cells in an orthotopic mouse model.

The SPARCL1 expression negatively associates with poor differentiation, lymph node involvement, and distant organ metastasis in CRCs

To address whether SPARCL1 suppresses the invasiveness of cancers, the optimized immunohistochemistry was applied to determine whether the expression level of SPARCL1 was associated with the clinical features of CRCs. All patients were enrolled at City of Hope (COH set, 222 cases) and Zhejiang University (ZJU set, 412 cases). The efficacy and specificity of SPARCL1 antibody was confirmed as described in Materials and Methods. On the basis of the expression level of SPARCL1 protein, all participants were divided into 4 subgroups: 0 (negative expression), 1 (weak positive), 2 (positive), and 3 (strong positive; Supplementary Fig. S5). Alternately, 0 and 1 were redefined as SPARCL1-low, whereas 2 and 3 were attributed to “SPARCL1-high.” In COH set, 65 of 222 CRC tissue samples were defined as SPARCL1-high expression; and in ZJU set, 182 of 412 patients were regarded as SPARCL1-high.

Through IHC staining, higher expression of SPARCL1 was detected in well-differentiated cancers (Supplementary Fig. S5).
S5). Statistical analysis revealed that the percentage of SPARCL1-high increased with differentiation of CRCs in COH set ($P = 0.06$) and with statistical significance in ZJU set ($P < 0.01$; Table 1). The statistical relevance between SPARCL1 and metastasis could not be determined in COH set ($P > 0.05$; Table 1), whereas a high level of SPARCL1 was negatively associated with lymph node involvement ($P = 0.049$) and distant organ metastasis ($P = 0.01$) in ZJU set (Table 1). Further multivariate logistic analysis revealed that high level of SPARCL1 expression was negatively related with lymph node involvement [OR, 0.67; 95% confidence interval (CI), 0.45–1.00] and distant metastasis (OR, 0.38; 95% CI, 0.18–0.79) in ZJU set (Table 2).

Above findings suggested that the SPARCL1 expression correlated with greater differentiation and negatively associated with lymph node involvement and distant metastasis, which implies that SPARCL1 may function as a tumor suppressor in CRCs.

Higher SPARCL1 expression is related to better prognosis in CRCs

A retrospective outcome study was conducted on COH set (with 222 CRCs) as well as ZJU set (with 412 CRCs). In Kaplan–Meier analysis, higher expression of SPARCL1 was associated with better survival in COH set (Fig. 3A, log-rank: $P = 0.05$; univariate COX analysis: $P = 0.045$). In ZJU set, OS was improved significantly in patients with CRCs with higher SPARCL1 expression (Fig. 3B, log-rank: $P < 0.01$). Multivariate Cox analysis was conducted to eliminate the confounder effects and further validate whether SPARCL1 was associated with lower relative risk of death from CRCs. The multivariate Cox proportional hazard analysis showed that high expression of SPARCL1 represented the better survival of CRC (HR, 0.33; 95% CI, 0.33–1.13) in COH set (Fig. 3C); this finding was also confirmed in ZJU set (HR, 0.53; 95% CI, 0.31–0.89; Fig. 3D). The pattern of HRs of other cofactors including metastasis, lymph node involvement, tumor invasion, differentiation, tumor location, gender, and age are very similar, confirming the reliability of this study. To exclude the effect of chemotherapy, a multivariate Cox analysis was conducted on patients without adjuvant chemotherapy or radiotherapy. It indicated that after adjusting for age, gender, location, differentiation, and TNM stage, HR of OS is 0.47 (95% CI, 0.19–1.06) for COH set and 0.61 (95% CI, 0.38–0.98) for ZJU set. These findings suggest that higher SPARCL1 expression in primary tumor leads to better survivability of patients with CRCs.

The stratification analysis was further used to eliminate the confounders and explore whether SPARCL1 impacts prognosis differently in patients with CRCs with different TNM stages or tumor locations. For the colon cancer subgroup, the multivariate Cox analyses revealed that SPARCL1 was related to better OS (HR, 0.63; 95% CI, 0.33–1.13) in COH set (Supplementary Fig. S6A, left). The similar result could be seen in ZJU set (HR, 0.53; 95% CI, 0.31–0.89; Supplementary Fig. S6A right). However, SPARCL1 seems not to impact the OS of patients with rectal cancer in either COH set or ZJU set (Supplementary Table S3).

Further analysis of CRCs at different TNM stages indicated that SPARCL1 predicts better survival for both stage I–II CRCs (without metastasis) and stage III–IV CRCs (with metastasis). For stage I–II CRCs, Kaplan–Meier analysis indicated that SPARCL1 is associated with better survival in COH set (log-rank: $P = 0.06$; Supplementary Fig. S6B, left). It was consistent with results yielded from ZJU set (log-rank: $P = 0.023$; Supplementary Fig. S6B, right).
Meanwhile, SPARCL1 predicting better survival was also seen in patients with CRCs with stage III–IV (Supplementary Fig. S6C). Multivariate analysis also displayed similar results (Supplementary Table S3). It was indicated the SPARCL1 independently prognoses better survival of CRCs with early or later stages.

The above findings showed that SPARCL1 may serve as a potential prognostic biomarker and prognosticate better survival for patients with CRCs, especially for colon cancers.

**SPARCL1 relates to the differentiation of CRCs via mesenchymal–epithelial transition**

To explore the mechanism of SPARCL1 in malignancy suppression, the SPARCL1 and differentiation of CRCs were investigated. The IHC staining showed that SPARCL1 expression in colon cancer section eventually decreased in comparison with adjacent normal colon section (Fig. 4A, i–iii). Meanwhile, SPARCL1 steadily increased with poor, moderate, and well differentiation of CRCs (Fig. 4A, iv–vi). The lumen-like formation indicated the ability to differentiate. An in vitro study showed that upregulation of SPARCL1 by gene transfection could obviously enhance the lumen-like formation in Matrigel in RKO and SW620 cells (Fig. 4B). Correspondingly, recombinant SPARCL1 peptide also could promote the lumen-like formation (Fig. 4B). The E-cadherin, N-cadherin, and Vimentin were regarded as the mesenchymal–epithelial transition (MET)-related genes. It was indicated that the mRNA expression level of E-cadherin

### Table 1. Pathoclinical characteristics and SPARCL1 distribution of eligible CRCs from COH and ZJU

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<sup>a</sup>SPARCL1-high includes positive and strong positive of cytoplasm staining score.

<sup>b</sup>In ZJU set, there are 2 cases without data.

<sup>c</sup>Proximal colon includes cecum, appendix, ascending colon, hepatic flexure, transverse, and splenic flexure.

<sup>d</sup>Distal colon includes descending colon and sigmoid.

<sup>e</sup>In COH set, there are 10 cases without differentiation data.

<sup>f</sup>According to the NCCN Clinical Practice Guidelines in Oncology Colon Cancer (V.3.2011) and Rectal Cancer (V.1.2011). In COH set, there are 8 cases without tumor invasion data; and in ZJU set, there are 3 cases without data.

<sup>g</sup>Statistical significance, P < 0.05.
was significantly upregulated on RKO-SPARCL1 and SW620-SPARCL1 transfectants, and N-cadherin and Vimentin were significantly downregulated (Fig. 4C). The Western blot analysis further confirmed that increase of E-cadherin and decrease of N-cadherin could be seen in SPARCL1-expressing RKO and SW620 transfectants (Fig. 4D). Meanwhile, qRT-PCR analysis also showed that the differentiation-related genes GPNMB, NDRG1, and IGF1R were significantly upregulated on RKO-SPARCL1 transfectants (Supplementary Fig. S3F). Above findings suggest that SPARCL1 induces differentiation through MET in colon cancer cells.

Discussion

In this study, we showed that SPARCL1 suppresses the proliferation, migration, invasion, and anchorage-independent growth of colon cancer cells (Fig. 1). The expression of SPARCL1 also induces the differentiation of colon cancer cells (Fig. 4). The results are consistent with previously conducted in vitro studies (8, 22). Here, we further report the in vivo findings obtained using xenograft animal models. In the subcutaneous xenograft mouse model, the expression of SPARCL1 retarded tumor growth, which points to its anti-proliferation potential (Supplementary Fig. S4). We used an intrasplenic injection mouse model mimicking liver metastasis of CRC at the later stages. This was based on the anatomy assumption that colon cancer cells migrate mostly through vena portae hepatic (23). The liver metastasis animal model indicated that SPARCL1 significantly reduces the liver metastasis by RKO cells (Fig. 2). These in vitro and in vivo studies validate that the expression of SPARCL1 has potential malignancy-suppressing ability in colon cancer cells.

In the outcome study, expression of SPARCL1 was significantly related to better survival of CRCs in 2 sets of patients with different socioeconomic backgrounds. The SPARCL1 expression was associated with well differentiation in patients from COH set (P = 0.06) and ZJU set (P < 0.01), which was consistent with the in vitro studies. SPARCL1 reduced the relative risk of lymph node involvement (OR, 0.66; 95% CI, 0.45–0.99) and distant organ metastasis (OR, 0.38; 95% CI, 0.17–0.79) in ZJU set. Besides the CRCs, downregulation of SPARCL1 was also reported for prostate and pancreatic cancers (22). Kaplan-Meier and Cox proportional hazard analyses revealed that SPARCL1 functions as a protective factor. It prognosticates better survival of patients with CRCs both in COH set (HR, 0.33; 95% CI, 0.33–1.05) and ZJU set (HR, 0.57; 95% CI, 0.38–0.84). The protective effect of SPARCL1 could be observed in the ZJU set (Fig. 3B, Supplementary Fig. S6B and S6C, right). Whether SPARCL1 plays protective role in rectal cancers awaits further confirmation. A Swedish research team reported that SPARCL1 was positively associated with well differentiation, which is consistent with our findings (19). However, their patient-based data indicated that SPARCL1 prognosticates poor survival in CRCs (19). The opposing results by 2 research teams may be due to different antibodies that were used for immunohistochemistry. We tested the commercial antibody (R&D) and found many nonspecific signals on Western blot analysis (Supplementary Fig. S1). Therefore, we developed a new antibody (No.C11) and showed that the nonspecific signals of No.C11 were barely seen on Western blot analysis (Supplementary Fig. S1). Meanwhile, the intensity of specific signal detected by our antibody correlates with the SPARCL1 mRNA level (Fig. 1A). The signal was blocked by SPARCL1 peptide (Supplementary Fig. S1), indicating the reliability of our IHC staining technique.

The above evidence showed the malignancy-suppressing ability of SPARCL1. Nevertheless, its function still remains largely unknown. In the previous studies, SPARCL1 was

### Table 2. Logistic analysis for SPARCL1 and TNM stages of CRCs

<table>
<thead>
<tr>
<th></th>
<th>COH set (N = 222)</th>
<th>ZJU set (N = 412)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No. of cases</td>
<td>OR (95% CI)</td>
</tr>
<tr>
<td>Tumor invasionb</td>
<td></td>
<td></td>
</tr>
<tr>
<td>T0–T2</td>
<td>23</td>
<td>Reference</td>
</tr>
<tr>
<td>T3 and T4</td>
<td>191</td>
<td>0.81 (0.28–2.06)</td>
</tr>
<tr>
<td>Lymph node involvement</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Negative</td>
<td>167</td>
<td>Reference</td>
</tr>
<tr>
<td>Positive</td>
<td>55</td>
<td>0.72 (0.38–1.40)</td>
</tr>
<tr>
<td>Distant metastasis</td>
<td></td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>180</td>
<td>Reference</td>
</tr>
<tr>
<td>Yes</td>
<td>42</td>
<td>1.04 (0.51–2.26)</td>
</tr>
</tbody>
</table>

NOTE: Logistic analysis was conducted to evaluate OR of SPARCL1 (high vs. low).

aAdjusted by gender and age.
bAccording to the NCCN Clinical Practice Guidelines in Oncology Colon Cancer (V.3.2011) and Rectal Cancer (V.3.2011). In COH set, there are 8 cases without tumor invasion data; and in ZJU set, there are 3 cases without data.
cStatistical significance, P < 0.05.
regarded as an astrocyte marker (24) and was proved to be essential in regulating cell–matrix interaction in the development of the brain (25). Increase in SPARC1 was reported during the differentiation of embryonic stem cells into astrocytes (26). Our in vitro experiment showed that SPARC1 induced the ability of luminal-like structure formation in Matrigel (Fig. 4B). It implied that the induction of differentiation could partly explain the malignancy suppression by SPARC1. The correlation and differentiation of SPARC1 was also confirmed in a population-based study (Table 1).

SPARC1 may function as a tumor suppressor by inducing differentiation. Our data indicated that SPARC1 expression was increased with well differentiation in CRCs. Colon cancer cells transfected with SPARC1 or cultured with SPARC1 peptide showed morphology diversity from the parental cell lines, which exhibited a luminal-like growth pattern. The E-cadherin was considered as epithelial marker; the N-cadherin and Vimentin were mesenchymal markers in epithelial–mesenchymal transition (EMT; refs. 27, 28). Our findings also suggested that SPARC1 induced differentiation probably by MET. Both qRT-PCR and Western blot analysis showed increase of E-cadherin and decrease of N-cadherin and Vimentin in RKO-SPARC1 and SW620-SPARC1 transfectants (Fig. 4C and D). On other hands, previous studies showed that GPNMB, NDRG1, and IGF1R were cell differentiation markers (29–31). GPNMB (Glycoprotein NMB, Osteoactivin) was reported to be an essential protein during the differentiation of osteoblast (32). N-Myc downstream–regulated gene 1 (NDRG1), also named differentiation-related gene-1, is involved in the development of central nervous system (33). NDRG1 was reported as a differentiation marker of breast cancer (34) and prognosticates better survival in CRCs (35). The IGF1R was considered as another differentiation-related gene in lung adenocarcinoma (29). Here, the results indicated that...
the transcripts of GPNMB, NDRG1, and IGF1R were significantly increased in SPARCL1 transfectants (Supplementary Fig. S3F). On the basis of these studies, we inferred that loss of SPARCL1 in colon epithelial might lead to deficiency of differentiation and achievement of carcinogenesis by reducing MET. Therefore, induction of differentiation may, at least, be one of the pathways through which SPARCL1 suppresses malignancy in CRCs. SPARCL1 might be a potential differentiation marker for CRCs. Nevertheless, the detail mechanism of SPARCL1 during MET process needs to be further investigated.

Overall, the above findings revealed that SPARCL1 is a potential tumor suppressor gene mediating cell differentiation, inhibiting proliferation ability, and reducing cell invasion and metastasis potential. Thus, it relates to better prognosis in patients with CRCs.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors’ Contributions


Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): H. Hu, H. Zhang, W. Ge, S. Loera, P. Chu, H. Chen, J. Peng, L. Zhou, S. Yu, L. Lai

Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): H. Hu, H. Zhang, W. Ge, X. Liu, P. Chu, S. Yu, S. Zheng

Writing, review, and/or revision of the manuscript: H. Hu, H. Zhang, X. Liu, L. Lai, Y. Yen, S. Zheng

Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): H. Hu, H. Zhang, J. Peng, L. Zhou, S. Yu, Y. Yen


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References


Secreted Protein Acidic and Rich in Cysteines-like 1 Suppresses Aggressiveness and Predicts Better Survival in Colorectal Cancers

Hanguang Hu, Hang Zhang, Weiting Ge, et al.