The clinicopathological significance of SPC18 in colorectal cancer: SPC18 participates in tumor progression

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Colorectal cancer (CRC) is one of the leading causes of cancer-related death worldwide. (1) Although the survival rate of early-stage CRC patients has increased, the long-term survival rate still remains very poor, mainly due to local relapse and distant metastases. (2,3) It would be valuable to identify new therapeutic markers and to encode standard clinicopathological staging using molecular markers to more precisely define the subset of patients at highest or lowest risk of recurrence following CRC surgery. In the search for new therapeutic or diagnostic markers, it is generally accepted that genes expressed at high levels in tumors and at very low levels in normal tissues are ideal diagnostic or therapeutic molecules. (4,5) We previously reported that Reg IV, olfactomedin 4, claudin-18 and h-prune are prognostic makers for CRC. (6-9) In the present study, we searched for the candidate genes that met these conditions in our comprehensive gene expression libraries, and focused on SEC11A, which encodes the SPC18 protein. (10,11) To the best of our knowledge, the expression and function of SPC18 have not been investigated in human cancers with the exception of GC.

SPC18 is one of the subunits of the signal peptidase complex (SPC). SPCs participate in the endoplasmic reticulum (ER)-Golgi secretory pathway and it is considered that the overexpression of the SPC18 protein can induce the secretion of growth factors, including TGF-α (12-14). TGF-α can phosphorylate the epidermal growth factor receptor (EGFR), which subsequently stimulates multiple signaling pathways involved in cell proliferation. We investigated the clinicopathological significance and biological function of SPC18 in CRC.

The conventional adenoma-carcinoma pathway and the serrated pathway are considered to be the main colorectal carcinogenesis pathways. (15,16) It was reported that the activation of Wnt/β-catenin signaling occurred via distinct mechanisms in both pathways. (17) Furthermore, there are several immunohistochemical markers that can assist in the conventional morphological diagnosis in tumors that develop via the colorectal carcinogenesis pathway, including, but not limited to p53, β-catenin, claudin-18, MLH1 and MSH2. (9,18) In the present study, we analyzed the significance of SPC18 in pre-cancerous lesions of both colorectal carcinogenesis pathways.

Materials and Methods

Tissue samples and cell lines. In a retrospective study design, 137 primary tumors were collected from patients diagnosed with CRC who underwent surgery at Hiroshima University Hospital (Hiroshima, Japan). All patients underwent curative resection. Only patients without preoperative radiotherapy or chemotherapy were enrolled in the study. The study population included 46 men and 87 women. The mean age was 63 years (range, 29–89 years). Postoperative follow-up was scheduled every 1, 2 or 3 months during the first 2 years after surgery and every 6 months thereafter, unless more frequent follow-up was deemed necessary. Chest X-rays, chest computed...
tomography scans and serum chemistry analyses were performed at every follow-up visit. Recurrence was evaluated from the records at Hiroshima University Hospital. Archival formalin-fixed, paraffin-embedded tissues were collected from patients who underwent endoscopic or surgical resection at Hiroshima University Hospital or its affiliated hospitals. The distribution of colorectal polyps was as follows: conventional adenoma low grade (CALG), n = 24 (tubular adenoma, n = 17 and villous or tubulovillous adenoma, n = 7); conventional adenoma high grade (CAHG), n = 29 (tubular adenoma, n = 26 and villous or tubulovillous adenoma, n = 3); HP (hyperplastic polyp), n = 20; TSA (traditional serrated adenoma), n = 31; sessile serrated adenoma/polyp (SSA/P), n = 18 and non-neoplastic mucosa, n = 20. Written informed consent was not obtained. Thus, for strict privacy protection, all of the identifying information associated with the samples was removed before the analysis; this procedure is in accordance with the Ethical Guidelines for Human Genome/Gene Research that were enacted by the Japanese Government.

Archival formalin-fixed, paraffin-embedded tissues from 137 patients who had undergone the surgical excision of CRC and from 97 patients who had undergone surgical or endoscopic resection were used for the immunohistochemical analysis. The histological classifications of CRC were based on the World Health Organization system. Tumor staging was performed according to the TNM stage grouping system. Ninety-two primary colorectal polyps from the Japanese Collection of Research Bioresources Cell Bank (Osaka, Japan). All of the cell lines were maintained in RPMI 1640 (Nissui Pharmaceutical, Tokyo, Japan) containing 10% fetal bovine serum (FBS, Whittaker, Walkersville, MD, USA). Antigen retrieval was performed by omission of the primary antibody. Statistical analysis. Correlations between the clinicopathological parameters and the expression of SPC18 were analyzed using the Spearman’s correlation coefficient.

RNA interference. To knockdown endogenous SPC18, RNAi was carried out as described previously. siRNA oligonucleotides for SPC18 and a negative control were purchased from Invitrogen. Transfection was performed using Lipofectamine RNAiMAX (Invitrogen) according to the manufacturer’s protocol. Briefly, 60 pmol of siRNA and 10 μL of Lipofectamine RNAiMAX were mixed in 1 mL of RPMI medium (10 mmol/L final siRNA concentration). After 20 min of incubation, the mixture was added to the cells and these were plated on dishes for each assay. In all of the experiments, the cells were analyzed at 48 h after transfection.

Cell growth and in vitro invasion assays. A 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay was performed to examine cell growth. The cells were seeded at a density of 2000 cells per well in 96-well plates. Cell growth was monitored after 1, 2 and 4 days. Modified Boyden chamber assays were performed using Matrigel coated inserts. Cells were plated at 10 000 cells per well in RPMI 1640 medium plus 1% serum in the upper chamber of a Transwell insert (pre diameter, 8 mm; Chemicon, Temecula, CA, USA) coated with Matrigel. Medium containing 10% serum was placed in the bottom chamber. After 1 and 2 days, the cells in the upper chamber were removed by scraping, and the cells remaining on the lower surface of the insert were stained with CyQuant GR dye to assess the number of cells. We performed three different experiments and calculated the mean and standard deviation (SD) in each of the MTT assays and the Modified Boyden chamber assays.

Western blotting. Tumor cells were lysed for Western blotting as described previously. The lysates (40 μg) were solubilized in Laemmli sample buffer by boiling and then subjected to 12% SDS-polyacrylamide gel electrophoresis and then electrotransferred onto a nitrocellulose filter. The filter was incubated with the primary antibody against SPC18. The SPC18 antibody was a polyclonal antibody that had been raised in our laboratory, the specificity of which has been characterized in detail. Peroxidase-conjugated anti-mouse IgG was used in the secondary reaction. Immunocomplexes were visualized with an ECL Western Blot Detection System (Amersham Biosciences). β-actin antibody (Sigma Chemical, St. Louis, MO, USA) was also used as a loading control.

Immunohistochemistry. One or two representative tumor blocks, including the tumor center, invading front, and the tumor-associated non-neoplastic mucosa, from each patient were examined by immunohistochemistry. In cases of large, late-stage tumors, two different sections were examined to include representative areas of the tumor center as well as of the lateral and deep tumor invasive front. The immunohistochemical analysis was performed with a Dako Envision+ Mouse Peroxidase Detection System (Dako Cytomation, Carpinteria, CA, USA). Antigen retrieval was performed by microwave heating in citrate buffer (pH 6.0) for 30 min. Peroxidase activity was blocked with 3% H2O2-methanol for 10 min, and the sections were incubated with normal goat serum (Dako Cytomation) for 20 min to block nonspecific antibody binding sites. Sections were incubated with a rabbit polyclonal anti-SPC18 antibody (dilution 1:50) for 1 h at room temperature, followed by incubation with Envision+ anti-mouse peroxidase for 1 h. The sections were incubated with the DAB Substrate-Chromogen Solution (Dako Cytomation) for 10 min for the color reaction. The sections were counterstained with 0.1% hematoxylin. Negative controls were created by omission of the primary antibody.
used to evaluate the associations between clinical covariates and survival. The SPSS software program (SPSS Inc., Chicago, IL, USA) was used for all of the statistical analyses. The hazard ratio (HR) and 95% confidence interval (CI) were estimated from Cox proportional hazard models. Age was treated as a categorical variable (≥65 years vs ≤65 years). All of the variables that were found to be moderately associated (P < 0.10) with survival by a univariate analysis were included in the final multivariate Cox regression models. P-values of < 0.05 were considered to indicate statistical significance.

Results

Expression and distribution of SPC18 in CRC and its relationship with clinicopathological parameters. We used immunohistochemistry to investigate the expression of SPC18 in 137 human CRC samples. In the non-neoplastic colonic mucosa, the staining of SPC18 was either weak or absent in epithelial and stromal cells, whereas corresponding CRC tissue showed relatively stronger and more extensive staining (Fig. 1a). SPC18 staining was observed in the cytoplasm of tumor cells (Fig. 1b). In total, 79 (58%) of the 137 CRC cases were positive for SPC18. We found that the cancer cells that robustly expressed SPC18 were preferentially located in the deeper invasive region of the tumors (Fig. 1c). Next, we analyzed the relationship between the expression of SPC18 and various clinicopathological characteristics. SPC18-positive CRC cases showed a more advanced N classification (P = 0.0315), and tumor stage (P = 0.0240) than SPC18-negative CRC cases (Table 1). The expression of SPC18 was not associated with age, sex, M classification or budding grade.

The relationship between the expression of SPC18 in CRC and the prognosis. We performed a Kaplan–Meier analysis to investigate the association between the expression of SPC18 and the prognosis in order to further elucidate the clinical impact of SPC18 on CRC in our 137 patients. The expression of SPC18 was significantly associated with a poorer prognosis (P = 0.0055, Log-rank test, Fig. 1d). Univariate and multivariate Cox proportional hazards analyses were used to further evaluate the association between the expression of SPC18 and survival in CRC patients (n = 137, Table 2). In the univariate analysis, the expression of SPC18 (hazard ratio [HR] 2.74; 95% confidence interval [CI] 1.28–6.50; P = 0.0078), tumor stage (HR 5.08; 95% CI 2.39–12.04; P < 0.0001) and budding grade (HR 3.41; 95% CI 1.69–7.31; P = 0.0006) were found to be associated with survival. We also performed a multivariate analysis using a model that included the expression of SPC18, tumor stage and budding grade. The expression of SPC18 and tumor stage were found to be independent prognostic predictors for survival in CRC patients (HR 2.47; 95% CI 1.06–5.44; P = 0.0336).

Effect of SPC18 inhibition on the cell growth and invasive activity of CRC cells. We performed a biological study of SPC18 using CRC cell lines. Western blotting revealed that all
SPC18 activity through SEC11A transfected DLD-1 cells. Knockdown was associated with invasiveness of both DLD-1 and LoVo with SPC18 in the invasiveness of CRC cells (Fig. 2e,f). On day 2, the swell invasion assay to determine the possible role of SPC18 results were obtained (Fig. 2d). Next, we performed a transfection of siRNA. The viability of the SPC18 siRNA1 and knockdown, we performed an MTT assay at 4 days after the experiments to knockdown the endogenous SPC18. To investigate the possible anti-proliferative effects of SPC18 because the highest expression of SPC18 was detected in both of these cell lines (Fig. 2b). The expression of the SPC18 protein in DLD-1 and LoVo was strongly suppressed by treatment with siRNA 1 and 3. Thus, we used siRNA1 and 3 in the following experiments to knockdown the endogenous SPC18. To investigate the possible anti-proliferative effects of SPC18 knockdown, we performed an MTT assay at 4 days after the transfection of siRNA. The viability of the SPC18 siRNA1 and the 3-transfected DLD-1 cells was significantly in comparison to negative control siRNA-transfected DLD-1 cells (Fig. 2c). We performed the same assay in LoVo cells, and similar results were obtained (Fig. 2d). Next, we performed a transwell-invasion assay to determine the possible role of SPC18 in the invasiveness of CRC cells (Fig. 2e.f). On day 2, the invasiveness of both DLD-1 and LoVo with SPC18 knockdown was <30% that of the negative control siRNA-transfected DLD-1 cells.

Effect of SPC18 inhibition on the phosphorylation of EGFR, AKT and ERK in CRC cells. We hypothesized that decreasing the expression of SPC18 was colocalized with CRC-related major molecules, including SECK11A, and CRC-related molecules.

Table 1. Relationship between SPC18 expression and clinicopathological characteristics in 137 patients with colorectal cancer

<table>
<thead>
<tr>
<th>SPC18 expression</th>
<th>Positive</th>
<th>Negative</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age ≤65</td>
<td>37 (56%)</td>
<td>28</td>
<td>NS</td>
</tr>
<tr>
<td>&gt;65</td>
<td>42 (58%)</td>
<td>30</td>
<td></td>
</tr>
<tr>
<td>Sex Female</td>
<td>52 (60%)</td>
<td>35</td>
<td>NS</td>
</tr>
<tr>
<td>Male</td>
<td>27 (46%)</td>
<td>23</td>
<td></td>
</tr>
<tr>
<td>T classification T1/2</td>
<td>24 (50%)</td>
<td>24</td>
<td>NS</td>
</tr>
<tr>
<td>T3/4</td>
<td>55 (62%)</td>
<td>34</td>
<td></td>
</tr>
<tr>
<td>N classification Negative</td>
<td>40 (50%)</td>
<td>40</td>
<td>0.0315</td>
</tr>
<tr>
<td>Positive</td>
<td>39 (68%)</td>
<td>18</td>
<td></td>
</tr>
<tr>
<td>M classification Negative</td>
<td>65 (55%)</td>
<td>54</td>
<td>NS</td>
</tr>
<tr>
<td>Positive</td>
<td>14 (78%)</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>Tumor stage Stage III</td>
<td>38 (49%)</td>
<td>39</td>
<td>0.0240</td>
</tr>
<tr>
<td>Stage III/IV</td>
<td>41 (68%)</td>
<td>19</td>
<td></td>
</tr>
<tr>
<td>Location Right</td>
<td>17 (65%)</td>
<td>9</td>
<td>NS</td>
</tr>
<tr>
<td>Left</td>
<td>62 (56%)</td>
<td>49</td>
<td></td>
</tr>
<tr>
<td>Budding grade Low (Grade 1)</td>
<td>46 (56%)</td>
<td>36</td>
<td>NS</td>
</tr>
<tr>
<td>High (Grade 2/3)</td>
<td>33 (60%)</td>
<td>22</td>
<td></td>
</tr>
<tr>
<td>Histologic classification Well/moderate</td>
<td>77 (59%)</td>
<td>54</td>
<td>NS</td>
</tr>
<tr>
<td>Poor/mucinous</td>
<td>2 (33%)</td>
<td>4</td>
<td></td>
</tr>
</tbody>
</table>

P-values were calculated by Fisher’s exact test. NS, not significant.

six CRC cell lines expressed SPC18 at various levels (Fig. 2a). The highest expression of SPC18 was detected in DLD-1 followed by LoVo. The other four remaining cell lines had expressed SPC18 at moderate or low levels. Next, we examined the transition of the expression of SPC18 by Western blotting using DLD-1 and LoVo cell lines that had been transfected with three SEC11A-specific siRNAs (siRNA1, 2, and 3) because the highest expression of SPC18 was detected in both of these cell lines (Fig. 2b). The expression of the SPC18 protein in DLD-1 and LoVo was strongly suppressed by treatment with siRNA 1 and 3. Thus, we used siRNA1 and 3 in the following experiments to knockdown the endogenous SPC18. To investigate the possible anti-proliferative effects of SPC18 knockdown, we performed an MTT assay at 4 days after the transfection of siRNA. The viability of the SPC18 siRNA1 and the 3-transfected DLD-1 cells was significantly in comparison to negative control siRNA-transfected DLD-1 cells (Fig. 2c). We performed the same assay in LoVo cells, and similar results were obtained (Fig. 2d). Next, we performed a transwell-invasion assay to determine the possible role of SPC18 in the invasiveness of CRC cells (Fig. 2e.f). On day 2, the invasiveness of both DLD-1 and LoVo with SPC18 knockdown was <30% that of the negative control siRNA-transfected DLD-1 cells.

Effect of SPC18 inhibition on the phosphorylation of EGFR, AKT and ERK in CRC cells. We hypothesized that decreasing the expression of SPC18 could contribute to tumor progression in CRC and the distribution of the expression of SPC18 in the deeper invasive region of tumors. We next investigated the relationship between the expression of SPC18 and CRC-related major molecules, including β-catenin nuclear localization, MMP7 and p53 (Fig. 4a–d). We revealed that the expression of SPC18 was colocalized with β-catenin nuclear localization (P = 0.0251) and the expression of MMP7 (P = 0.0218) at the invasive front (Table 3). These data indicated the possibility of a correlation between SPC18 and Wnt/β-catenin signaling.

The analysis of the expression of SPC18 in pre-cancerous lesions in each colorectal carcinogenesis pathway. Finally, we performed an immunohistochemical analysis of SPC18 in 122 human colorectal polyp specimens, including CALG, CAHG, TSA and SSA/P (Fig. 5a–f). Staining of strong or moderate intensity was more frequently observed in CAHG than in CALG (P = 0.0002). There was no significant difference between...
The expression of SPC18 was significantly stronger in conventional adenoma-carcinoma pathway-related tumors (CALG and CAHG) than in serrated pathway related tumors (HP, TSA and SSA/P) \((P < 0.001)\) (Fig. 5g). Our results imply that the expression of SPC18 is correlated with the progression.

**Fig. 2.** The effects of the inhibition of signal peptidase complex 18 (SPC18) on cell growth and invasive activity in colorectal cancer (CRC) cells. (a) The Western blotting of SPC18 in the cell lysates from six CRC cell lines. (b) The Western blotting of SPC18 in cell lysates from DLD-1 and LoVo transfected with SPC18 siRNA or negative control siRNA. β-Actin was included as a loading control. (c, d) The effect of SPC18 knockdown on the cell growth of DLD-1 (c) and LoVo (d). Cell growth was assessed by an MTT assay at 1, 2 and 4 days after seeding on 96-well plates. The mean (bars) and standard deviation (SD; error bars) of three independent experiments are shown. (e, f) The effect of the knockdown of SPC18 on cell invasion in DLD-1 (e) and LoVo (f) transfected with SPC18 siRNA (siRNA1 and 3) or negative control siRNA that were incubated in Boyden chambers. After 1 and 2 days, the invading cells were counted. NS, not significant.

**Fig. 3.** The effect of the downregulation of signal peptidase complex 18 (SPC18) on the epidermal growth factor receptor (EGFR) signaling pathway. (a, b) Western blotting of SPC18, EGFR, phospho-EGFR (pEGFR), Erk1/2, phospho-Erk1/2 (pErk1/2), Akt, and phospho-Akt (pAKT) in cell lysates from DLD-1 (a) and LoVo (b) transfected with SEC11A siRNA or negative control siRNA. β-Actin was included as a loading control.

tubular adenoma component and villous component. Furthermore, the expression of SPC18 was significantly stronger in conventional adenoma-carcinoma pathway-related tumors (CALG and CAHG) than in serrated pathway related tumors (HP, TSA and SSA/P) \((P < 0.001)\) (Fig. 5g). Our results imply that the expression of SPC18 is correlated with the progression.
of CRCs that take the conventional adenoma-carcinoma pathway. We also performed an immunohistochemical analysis of SPC18 in microsatellite instability-high (MSI-H) CRC, which is considered to be a serrated pathway related tumor. Notably, the expression of SPC18 was only detected in one (10%) of 10 MSI-H CRC specimens (Fig. 5h). There is a possibility that SPC18 is involved in the pathogenesis of the conventional adenoma-carcinoma pathway-related colorectal tumor rather than serrated pathway-related colorectal tumors.

Discussion

In the current study, we analyzed the clinicopathological significance of SPC18 in CRC. Our immunohistochemical analyses demonstrated that 58% of CRC cases were positive for SPC18. The distribution of SPC18-positive CRC cells was more frequently detected in the deeper invasive region of the tumors. Moreover, the expression of SPC18 was associated with the N classification and tumor stage. The expression of SPC18 also served as an independent prognostic classifier of patients with CRC. The histological features of CRC differ widely from area to area within the same tumor due to tumor heterogeneity. The most useful clinicopathological features and molecular signatures, including the budding grade, can be deduced from the invasive front of the tumor, where the most transformed and presumably most aggressive cells reside. Although the expression of SPC18 was not significantly correlated with the budding grade, SPC18 tended to be observed at the invasive front. Thus, SPC18 is likely to promote tumor progression through several secretion proteins, especially at the invasive region in SPC18 positive cases. Indeed, the expression of SPC18 was correlated with β-catenin nuclear localization and the expression of MMP7.

Previous studies have shown that the increased SPC activity caused by the overexpression of SPC18 protein induced tumor progression through the secretion of TGF-α, to phosphorylate EGFR and stimulate the multiple signaling pathways involved in cellular proliferation, anti-apoptosis and other processes. The increased expression of TGF-α in colonic polyps and cancers has also been reported. Indeed, the present study showed that the knockdown of SEC11A by RNA interference inhibited cancer cell proliferation and invasiveness in CRC cell lines. Moreover, we showed that the levels of phosphorylated EGFR and its downstream molecules, including Erk and Akt, were lower in SPC18 siRNA-transfected CRC cells than in control cells. It was reported that the phosphorylation of Erk and Akt results in inhibition of apoptosis and contribute to tumor progression, including metastasis. Thus, these results suggest that SPC18 participates in malignant behavior, including the cell growth, metastasis and invasion of CRC cells via several growth factors, including at least TGF-α.

The main colorectal carcinogenesis pathways are the conventional adenoma-carcinoma pathway and the serrated pathway. The present study demonstrated a sequential increase in the expression of SPC18 through the conventional adenoma-carcinoma pathway. The conventional adenoma-carcinoma pathway is well known as a multistep carcinogenesis mechanism that is associated with the activation of Wnt/β-catenin signaling.

Table 3. Relationship between SPC18 expression and CRC related molecules at the invasive front in 137 patients with colorectal cancer

<table>
<thead>
<tr>
<th>SPC18 expression</th>
<th>Positive</th>
<th>Negative</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>β-catenin (nuclear localization)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Positive</td>
<td>58 (66%)</td>
<td>29</td>
<td>0.0251</td>
</tr>
<tr>
<td>Negative</td>
<td>21 (54%)</td>
<td>25</td>
<td></td>
</tr>
<tr>
<td>MMP7</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Positive</td>
<td>29 (72%)</td>
<td>11</td>
<td>0.0218</td>
</tr>
<tr>
<td>Negative</td>
<td>50 (52%)</td>
<td>47</td>
<td></td>
</tr>
<tr>
<td>p53 expression</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Positive</td>
<td>41 (58%)</td>
<td>29</td>
<td>NS</td>
</tr>
<tr>
<td>Negative</td>
<td>38 (56%)</td>
<td>29</td>
<td></td>
</tr>
</tbody>
</table>

P-values were calculated by Fisher’s exact test. NS, not significant.
It is also well known that the activation of Wnt/β-catenin signaling promotes tumor malignancy and induces the expression of MMP7. (32) In the present study, SPC18 expression was distributed extensively in the whole tumor and was unexceptionally observed at the invasive front. Although the relationship between SPC18 expression and T classification was not statistically significant, SPC18 might contribute to tumor progression. Moreover, β-catenin nuclear localization was also observed at the invasive front due to Wnt signaling activation. (33) Co-localization of these molecules at the invasive front suggests that β-catenin nuclear localization might activate SPC18 expression as well as Wnt pathway signaling. A detailed function analysis should be performed using methods such as siRNA-knock down or an in vivo analysis in order to further our understanding of the relationship between SPC18, β-catenin and MMP7.

In summary, we revealed that CRC with the expression of SPC18 was independently associated with a poor prognosis. SPC18 regulates the phosphorylation of EGFR and modulates downstream targets. Thus, SPC18 has potential as a therapeutic target and predictive biomarker for the survival of patients with CRC.

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**Disclosure Statement**

The authors declare no conflicts of interest in association with the present study.
References


