Enhancement of Human Cancer Cell Motility and Invasiveness by Anaphylatoxin C5a via Aberrantly Expressed C5a Receptor (CD88)

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Abstract

Purpose: The anaphylatoxin C5a is a chemoattractant that induces leukocyte migration via C5a receptor (C5aR). There is emerging evidence that C5a is generated in the cancer microenvironment. We therefore sought C5aR expression and a direct influence of the C5a–C5aR axis on cancer cells.

Experimental Design: C5aR expression was investigated in human cancer tissues and cell lines. Effects of C5a stimulation on cancer cells were studied by cytoskeletal rearrangement, time-lapse analysis, Matrigel chamber assay, and invasion in nude mouse in a comparison of C5aR-expressing cancer cells with control cells.

Results: C5aR was aberrantly expressed in various human cancers. Several cancer cell lines also expressed C5aR. C5a triggered cytoskeletal rearrangement and enhanced cell motility three-fold and invasiveness 13-fold of C5aR-expressing cancer cells. Such enhancement by C5a was not observed in control cells. Cancer cell invasion was still enhanced in the absence of C5a concentration gradient and even after the removal of C5a stimulation, suggesting that random cell locomotion plays an important role in C5a-triggered cancer cell invasion. C5a increased the release of matrix metalloproteinases (MMP) from cancer cells by two- to 11-fold, and inhibition of MMP activity abolished the C5a-enhancing effect on cancer cell invasion. Compared with control cells, C5aR-expressing cells spread 1.8-fold more broadly at implanted nude mouse skin sites only when stimulated with C5a.

Conclusions: These results illustrate a novel activity of the C5a–C5aR axis that promotes cancer cell invasion through motility activation and MMP release. Targeting this signaling pathway may provide a useful therapeutic option for cancer treatment.

Introduction

The complement system is a biochemical cascade involved in immune responses (1). Previous reports showed that the complement system is activated on cancer cells in both an animal model (2) and in tissue specimens (3). It was initially suggested that the complement system might be involved in cancer immune surveillance by its direct cytolytic effect (3) and the sensitization of cancer cells to the immune effector cells via release of chemoattractants (4). However, cancer cells seem to evade the complement attack by expressing either soluble or membrane-associated regulators of complement, for example, CD55, which protects cancer cells from complement-dependent cytolysis (5, 6) and anticancer immune responses (7, 8). Thus, the complement system in cancer tissues does not seem to lead to cancer cell eradication.

Anaphylatoxin C5a is an N-terminal 74 amino acid fragment of the α-chain of the complement fifth component (C5), and is well known to act as a leukocyte chemoattractant and inflammatory mediator (9, 10). C5a is released by C5-convertase formed during the process of complement system activation (11), possibly triggered in response to cancer cells (3). Other C5a-producing pathways include C5 cleavage by thrombin (12), the ultimate product of the coagulation reaction. This cascade reaction can be triggered by tissue factor, which is expressed in a wide range of cell types including cancer cells (13). C5a is also generated by
serine proteases from activated phagocytes (14), which frequently accumulate in cancer tissues. These findings lead us to the idea that C5a is also likely to be generated in the cancer microenvironment.

C5a activities are mediated by its binding to the membrane-associated C5a receptor (C5aR; CD88), which was originally identified in leukocyte cell lines (15). C5aR has since been reported to be expressed in other types of cells such as vascular endothelial cells, mesangial cells, and renal proximal tubular cells. Further studies have revealed that C5aR expression is also inducible in epithelial cells by inflammatory and infection stimuli (16). About cancer cells, functional C5aR expression was shown in a human hepatoma cell line HepG2 (17), whereas normal hepatocytes lack in its expression (16). These suggest that expression of C5aR is induced in cancer cells as a consequence of malignant transformation.

C5a and chemokines are chemoattractants, and a body of evidence indicates that a network of chemokines and their receptors influences the development of primary cancers (18–22). Recently, C5a was reported to recruit myeloid-derived suppressor cells for suppressing the antitumor CD8+ T-cell response (2, 23), suggesting its indirect role in fostering cancer cells by protecting them from the antitumor CD8+ T cells. However, the direct biologic role of C5a–C5aR system in cancer cells is largely unknown. In this study, we investigated the expression of C5aR in cancer cells of various origins and analyzed its impact on cancer cell motility and invasiveness upon C5a stimulation.

**Materials and Methods**

**Cell lines**
The human bile duct cancer cell lines MEC and HuCCT1 and the human colon cancer cell lines HCT15, COLO205, and DLD1 were provided by the Cell Resource Center for Biomedical Research Institute of Development, Aging, and Cancer, Tohoku University (Sendai, Japan). Human bile duct cancer cell lines Ssp-25 and RBE were obtained from the Riken Cell Bank. Human colon cancer cell lines HCT116 and SW620 were gifts from Dr. B. Vogelstein, Johns Hopkins University (Baltimore, MD), and Dr. Kyogo Ito, Kurume University (Kurume, Japan), respectively. Cells were cultured in RPMI-1640 or Dulbecco’s modified Eagle’s medium supplemented with 10% FBS, penicillin (40 U/mL), and streptomycin (40 μg/mL) and were maintained at 37°C in 5% CO2.

**Tissue samples, immunohistochemistry, and retrospective analysis**
Cancer tissue samples were obtained by surgical resection or core needle biopsy in Kumamoto University Hospital (Kumamoto, Japan), and usage of those samples for this study was approved by the internal ethics committee. Deparaffinized 2-μm thick sections were pretreated with 0.3% H2O2 in methanol for 20 minutes, followed by Protein Block, Serum-Free (Dako Cytomation) treatment for 20 minutes. Sections were incubated with the primary antibody against C5aR (2 μg/mL; Hycult Biotechnology) at 4°C overnight, and subsequently stained using EnVision+ solution (Dako Cytomation) and 3,3’-diaminobenzidine tetrahydrochloride solution containing 0.006% H2O2, according to the manufacturer’s instructions. Nuclei were counterstained with hematoxylin. Retrospective analysis was conducted on 42 patients with intrahepatic cholangiocarcinoma who had undergone liver resection from May 2000 to November 2009. The relationship between cancer cell C5aR expression and vascular invasiveness was investigated and analyzed by Fisher exact test.

**Real time PCR**
RNA was isolated from cancer cells using the Qiagen RNAeasy Kit (Qiagen). cDNA was synthesized from extracted RNA using the RNA PCR Kit AMV (Takara), according to the manufacturer’s instructions. PCR was conducted using TaKaRa Ex Taq HS and primers (sense 5’-CGGGAGAGTGACTTTCCAC-3’ and antisense 5’-CTGACATCTGGGTTCATCA-3’ for human C5aR and sense 5’-CATCCACGAAACTACCTCACA-3’ and antisense 5’-TGCTCCATAGAGAATGTGGTG-3’ for β-actin) under the following conditions: 36 cycles for C5aR and 32 cycles for β-actin, 30 seconds at 94°C, 30 seconds at 58°C, and 30 seconds at 72°C. PCR products were resolved by electrophoresis using 1% agarose gels and were visualized by ethidium bromide staining.

**Immunoblotting**
To detect C5aR, cell lysates obtained from bile duct or colon cancer cells were analyzed by SDS-PAGE under reducing conditions using 10% polyacrylamide gels and were transferred to polyvinylidene difluoride (PVDF) membranes (Immobilon Transfer Membranes; Millipore). After blocking with 5% fat-free milk, the membranes were
incubated with anti-human C5aR rabbit immunoglobulin G (IgG, 1,000-fold dilution; Santa Cruz Biotechnology) or polyclonal anti-actin rabbit IgG (500-fold dilution; Santa Cruz Biotechnology). This was followed by incubation with horseradish peroxidase (HRP)–conjugated anti-rabbit IgG goat antibody (1,000-fold dilution; Amersham Biosciences), and bands were visualized via enhanced chemiluminescence (ECL), according to the manufacturer’s instructions.

**Establishment of C5aR stably expressing HuCCT1 cells**

Full-length human C5aR cDNA of 1,053 bp was amplified by PCR using human macrophage cDNA library and subsequently subcloned into the pENTR/D-TOPO-vector (Invitrogen). After confirming the sequence, the cDNA was inserted into pCAG-ires-puro vector using the Gateway system (Invitrogen). The purified plasmid was transfected into HuCCT1 cells using Lipofectamine 2000 (Invitrogen). After 48 hours, medium was replaced with selection medium supplemented with puromycin (1 μg/mL) to be cultured for 2 weeks. Puromycin-resistant cells were collected and were subjected to cell sorting by fluorescence-activated cell sorting (FACS) Vantage to isolate those cells highly expressing C5aR (designated HuCCT1/C5aR). HuCCT1 cells transfected with empty-pCAG-ires-puro vectors were used as the control (HuCCT1/mock).

**Flow-cytometric analysis**

MEC, HuCCT1/mock, or HuCCT1/C5aR cells were treated for 30 minutes with a murine monoclonal fluorescein isothiocyanate (FITC)–conjugated anti-C5aR antibody (Serotec Ltd.), or a FITC-conjugated isotype-matched control antibody (Serotec Ltd.), followed by washing with PBS twice. C5aR antigen was quantified by FACSscan (BD Biosciences).

**Immunofluorescence analysis**

Filamentous actin (F-actin) formation was visualized as previously described (24). Cells were seeded at a low density on glass coverslips and were incubated for 24 hours. After 2 hours serum starvation, cells were stimulated with 100 nmol/L human C5a (Sigma) for the stated time periods. Cells were then fixed in 100% methanol and were stained with 1% toluidine blue. Invaded cells were counted in 5 power fields (×20). The invasion-enhancing effect was shown as the ratio of cell invasion by C5a stimulation versus PBS controls. To determine whether matrix metalloproteinases (MMP) were involved in C5a-elicted cancer cell invasion, GM6001 (5 μmol/L; Merck) was added to the cell suspension when cell invasion activity of 100 nmol/L C5a was measured. For checkerboard analysis for C5a cancer cell invasion activity, various concentrations of C5a were added to the HuCCT1/C5aR cell suspension in the upper chamber together with the lower chamber, and cell invasion was assessed as described earlier.

**Invasion assay in vitro**

To assess invasion of cancer cell lines in vitro, BioCoat Matrigel invasion chambers were used (24-well plate, 8-μm pore; BD Biosciences; ref. 25). HuCCT1-derived (3.75 × 10⁴ cells), or MEC (7.5 × 10⁴ cells) cells were suspended in serum-free RPMI-1640, then seeded into the upper chamber. RPMI-1640 supplemented with either C5a or carrier solution (PBS) was placed in the lower chamber. To block C5aR-mediated signaling, anti-human C5aR rabbit IgG (10 μg/mL) or nonspecific control IgG (10 μg/mL) was added to the cell suspension before seeding. For analyzing the effect of discontinuous stimulation with C5a, cells were cultured at 37°C in serum-free RPMI-1640 supplemented with C5a for 12 hours (HuCCT1-derived cells) or 24 hours (MEC) at indicated concentrations. Cells were then washed with serum-free RPMI-1640 and were seeded into the upper chamber. RPMI-1640 containing 10% FBS was set in the lower chamber. Chambers were incubated for 24 hours (HuCCT1-derived cells) or 36 hours (MEC) at 37°C. Cells on the upper surface of the filter were removed with a cotton wool swab, and cells that migrated to the lower surface were fixed in 100% methanol and were stained with 1% toluidine blue. Invaded cells were counted in 5 power fields (×20). The invasion-enhancing effect was shown as the ratio of cell invasion by C5a stimulation versus PBS controls. To determine whether matrix metalloproteinases (MMP) were involved in C5a-elicted cancer cell invasion, GM6001 (5 μmol/L; Merck) was added to the cell suspension when cell invasion activity of 100 nmol/L C5a was measured. For checkerboard analysis for C5a cancer cell invasion activity, various concentrations of C5a were added to the HuCCT1/C5aR cell suspension in the upper chamber together with the lower chamber, and cell invasion was assessed as described earlier.

**Invasion assay in vivo**

HuCCT1/mock and HuCCT1/C5aR were incubated in serum-free medium in the presence or absence of C5a (10⁻⁷ mol/L) at 37°C for 12 hours. This was followed by labeling with CellTracker Orange CMTMR (20 μmol/L) or Cell-Tracker Green BODIFY (25 μmol/L; Molecular Probes) for HuCCT1/C5aR and HuCCT1/mock, respectively, at 37°C for 45 minutes. After washing with serum-free medium, HuCCT1/mock cells and HuCCT1/C5aR cells were equally mixed to create a concentration of 3 × 10⁷ cells/mL each. The cell mixture (50 μL) was injected intradermally into 7-week-old BALB/c A/Jc1-nu/nu mice (CLEA Japan). After 1, 2, or 3 days, the nude mice were sacrificed by cervical dislocation, and the cell injection sites including surrounding tissues were excised to prepare frozen sections in liquid nitrogen. Labeled cells in 4-μm thick sections were observed with a fluorescence microscope (BIOREVO; KEYENCE). To quantify the distribution of HuCCT1-derived cells, regions
of fluorescent dots of labeled cells were encircled (Fig. 5A) then the area of each region was measured using an imaging processor (VH-Analyzer, KEYENCE). The ratio of the distribution area of HuCCT1/C5aR versus HuCCT1/mock was calculated. Some endogenous green fluorescence background was observed in mice skin, therefore these spots were avoided and cancer cells were specifically encircled, which was confirmed by observation of the adjacent section hematoxylin and eosin (H&E)-stained. This experiment was carried out according to the criteria of animal experiments of the Kumamoto University Animal Experiment Committee.

Measurement of MMP concentration in culture supernatant of cells

MMP concentration in supernatant of cancer cells stimulated with or without C5a was measured using the Quantibody Human MMP Array 1 Kit (RayBiotech). Culture supernatant was taken from MEC (1 × 10^6 cells) or HuCCT1/C5aR (5 × 10^5 cells) grown in a 6-well plate for 24 hours in the presence or absence of C5a (100 nmol/L). The supernatant was diluted at 1:3 with PBS and then MMP concentrations were determined according to the manufacturer’s instructions.

Statistics

Statistical analyses were conducted using the unpaired Student t test. Values are expressed as means ± SD and experiments were carried out in triplicate, unless otherwise stated.

Results

Aberrant expression of C5aR in human cancer cells

We first investigated C5aR expression in human cancer specimens from 225 patients by immunohistochemistry. C5aR expression was observed in cancer cells from all the organs examined and in all the 3 cancer cell types, squamous cell carcinoma, adenocarcinoma, and transitional cell carcinoma (Fig. 1A and Supplementary Fig. S1A). Generally, C5aR was robustly expressed in a significant proportion of cancer samples. On the other hand, null or only faint reaction of C5aR immunohistochemistry was observed in their normal counterparts (Fig. 1A and Supplementary Fig. S1B) except kidney tubular epithelial cells (Supplementary Fig. S1B), which is in line with the previous report (16). Percentage of C5aR-positivity in cancer cases varied among organs. In colon, bile duct, kidney, and prostate carcinomas, more than 50% of cases examined were C5aR-positive (Fig. 1B). In bile duct-derived cancer in the liver, C5aR was positive in 26 patients. Among them, vascular invasion was found in 18 patients, whereas vascular invasion was seen in only 4 cases of 16 C5aR-negative patients. This result indicates a significant relationship between cancer cell C5aR expression and vascular invasiveness (P = 0.010 by Fisher exact test). Because vascular invasion of bile duct cancer is closely linked to metastasis and prognosis (26), C5aR expression may correlate with those clinical endpoints. Next, we examined a panel of cancer cell lines for C5aR expression. Real-time PCR (RT-PCR) revealed that several human cancer cell lines originated from bile ducts (MEC and RBE) and colon (HCT15, COLO205, and HCT116) expressed C5aR mRNA (Fig. 2A). Out of these cell lines, those except RBE also expressed C5aR protein (Fig. 2B). The localization of C5aR on the cell-surface was shown by flow cytometry (Fig. 2C). These results suggest that aberrant C5aR expression observed in human cancer specimens is actually conserved in some human cancer cell lines. It is intriguing that only MEC cells express C5aR at the protein level among the bile duct-derived cancer cell lines (Fig. 2B), whereas bile duct carcinomas showed the highest positive ratio of C5aR expression (Fig. 1B).
Analysis (Fig. 2C), which was comparable with that in MEC HuCCT1/C5aR cells. The cell surface expression of C5aR in cells but not HuCCT1/mock cells expressed C5aR (Fig. 2A and B). The cell surface expression of C5aR in cancer cells under C5a stimuli, we chose C5aR-negative C5aR-expressing cancer cells by C5a stimulus. To analyze the biologic effects of C5aR expression in cancer cell lines including HuCCT1/C5aR, we chose C5aR-negative C5aR-expressing cancer cell lines shown by RT-PCR. B. Expression of C5aR protein in bile duct and colon cancer cell lines, shown by immunoblotting using an anti-C5aR antibody. β-actin mRNA and protein were used as controls. C. Expression of C5aR on the cell membrane in MEC and HuCCT1/C5aR, shown by flow cytometry using FITC-conjugated anti-C5aR antibody (gray line) or control antibody (black line).

Figure 2. Expression of C5aR on cancer cell lines including HuCCT1/C5aR and HuCCT1/mock. A, expression of C5aR mRNA in several cancer cell lines shown by RT-PCR. B, expression of C5aR protein in bile duct and colon cancer cell lines, shown by immunoblotting using an anti-C5aR antibody. β-actin mRNA and protein were used as controls. C, expression of C5aR on the cell membrane in MEC and HuCCT1/C5aR, shown by flow cytometry using FITC-conjugated anti-C5aR antibody (gray line) or control antibody (black line).

paradoxical to the result of immunohistochemistry at a glance (Fig. 1A and B), implying that C5aR expression was lost during the process of cell line establishment from primary culture of human cancer cells, as those cells can prioritize expression of other essential proteins for clonal development in the context of 2-dimensional culture in vitro, which is usually in the absence of C5a.

Cytoskeletal rearrangement and enhanced motility of C5aR-expressing cancer cells by C5a stimulus

To analyze the biologic effects of C5aR expression in cancer cells under C5a stimuli, we chose C5aR-negative HuCCT1 cells derived from bile duct carcinomas of the highest C5aR expression ratio (Fig. 1B). HuCCT1/C5aR cells but not HuCCT1/mock cells expressed C5aR (Fig. 2A and B). The cell surface expression of C5aR in HuCCT1/C5aR cells was confirmed by flow-cytometric analysis (Fig. 2C), which was comparable with that in MEC cells (Fig. 2C). Because the chemoattractant C5a causes cytoskeletal rearrangement and stimulates migration of leukocytes (27, 28), we hypothesized that cancer cells may exploit this mechanism to gain the ability of migration and invasion by activation of aberrantly expressed C5aR on their cell surface. To test this, the effect of C5aR activation on actin rearrangement was analyzed by F-actin immunofluorescence labeling. The majority of cells at the outer edges of HuCCT1/C5aR cell clusters clearly showed strong filopodia formation 30 minutes after C5a treatment (Fig. 3A), which was followed by development of membrane ruffling and dissolution of stress fibers (Fig. 3A). Three hours after the treatment, such ruffles disappeared and formation of stress fibers became evident again (Fig. 3A). Some cells at the periphery of the cluster even changed their morphology to spindle-like shape and protruded from the cluster to the vacant area (Fig. 3A). On the other hand, HuCCT1/mock cells did not show any remarkable changes in both cell morphology and actin cytoskeleton at any time points after C5a stimulation (Fig. 3A). The time-lapse video analysis of HuCCT1/C5aR cell movement showed that C5a activated motility of the cells (Fig. 3B and Supplementary Fig. S2 video). Tracing of cell movement revealed that C5a enhanced motility of HuCCT1/C5aR cells in a dose-dependent manner, increasing motility 3-fold at 100 nmol/L (Fig. 3C), whereas motility of HuCCT1/mock cells was not significantly affected by C5a (Fig. 3B and C). This experiment confirmed that C5a enhances motility of cancer cells in a C5aR-dependent fashion.

Enhanced invasiveness of C5aR-expressing cancer cells by C5a stimulus in vitro

Experiments using Matrigel chambers revealed that C5a stimulated invasion of HuCCT1/C5aR cells through the matrix layer in a C5a concentration-dependent manner and enhanced approximately 13-fold over carrier control (PBS) at 100 nmol/L (Fig. 4A). The enhancing effect of C5a on invasion of HuCCT1/mock cells was not seen (Fig. 4A). Intriguingly, cancer cells pretreated with C5a also showed enhanced invasiveness even in the absence of a C5a concentration gradient (Fig. 4C). This result indicates that stimulation with C5a during pretreatment is sufficient for enhancing invasion of C5aR-expressing cancer cells in vitro, and suggests that neither concentration gradient nor continuous exposure to C5a is required for activating invasion of C5aR-expressing cancer cells. Similarly, C5a enhanced invasion of MEC cells that endogenously express C5aR (Fig. 2C), in a C5aR-dependent manner, as this enhancement was abrogated by a C5aR antagonist (Supplementary Fig. S3) and by the neutralizing antibody against C5aR, but not by nonspecific IgG (Fig. 4B and D). Dose-dependent effect of C5a on invasion was also the case observed in MEC cells (Fig. 4B and D). To determine whether C5a-elicted cancer cell migration is dependent on the C5a concentration gradient, we conducted the checkerboard analysis. In addition to C5a concentration-dependent invasion in the absence of C5a in the upper chamber, HuCCT1/C5aR cell invasion by 100 nmol/L C5a in the lower chamber was
inhibited by C5a in the upper chamber in a dose-dependent manner (Fig. 4E). Moreover, invasion by 10 nmol/L C5a in the lower chamber was completely inhibited by 100 nmol/L C5a in the upper chamber (Fig. 4E). These results suggest that C5a-induced cancer cell invasion is explained partly by chemotaxis, particularly in the presence of 100 nmol/L C5a. However, when C5a concentration in the upper chamber was equal to that in the lower chamber, C5a was still able to induce HuCCT1/C5aR invasion to the significant extent. The invasion by 10 nmol/L C5a in the lower chamber was not affected by addition of 10 nmol/L C5a in the upper chamber (Fig. 4E). Furthermore, when 100 nmol/L C5a was added to the cell suspension in the upper chamber, it triggered significant cancer cell migration even in the absence of C5a in the lower chamber (Fig. 4E). These results suggest that enhanced random cell locomotion plays a vital role in the C5a-elicited cancer cell invasion.

C5a elicits MMP secretion from C5aR-expressing cancer cells

Degradation of extracellular matrix (ECM) by MMPs is an essential process for cancer cell invasion (29). The interaction of the chemokine CXCL12 and its receptor CXCR4 has been shown to increase MMP expression and invasion of
prostate cancer cells (30). While C5a induces MMP-9 release from human neutrophils (31), such C5a-elicited MMP release from cancer cells has not been reported. Interestingly, C5a-enhanced invasion of C5aR-expressing cancer cells in the transwell chambers was significantly hindered by an MMP inhibitor GM6001 (32; Fig. 4A and B), indicating that enzymatic activity of MMPs plays a crucial role in the C5a-enhanced invasion of C5aR-expressing cancer cells. Hence, we explored the possibility of C5a provoking MMP secretion from C5aR-expressing cancer cells. MMP expression array analysis showed that C5a significantly increased release of MMP-1, 3, 9, 10, and 13 from MEC cells, and MMP-8 and 10 from HuCCT1/C5aR cells (Table 1). These MMPs are known to be associated with both cancer invasion and patient prognosis (33, 34). Together with inhibition of C5a-enhanced invasion by GM6001 (Fig. 4A and B), increased secretion of MMPs by C5a (Table 1) indicates that MMPs contribute to the C5a-enhanced invasion of C5aR expressing cancer cells. Among specific MMP inhibitors, an MMP-8 inhibitor exhibited the most significant effect to impede the MEC cell invasion enhanced by C5 (Supplementary Fig. S3). Intriguingly, about a 3.2-fold increase in MEC cell invasion induced by C5a at 10 nmol/L (Fig. 4B) seemed to correlate with a 3.7-fold increase in MMP-8 (Table 1). These results suggest that MMP-8 is the most responsible MMP for C5a-elicited MEC cell invasion.

Enhanced invasiveness of C5aR-expressing cancer cells by C5a in vivo
To evaluate the effect of C5a stimulation on the invasiveness of C5aR-expressing cancer cells in vivo, HuCCT1/mock and HuCCT1/C5aR cells were pretreated with C5a, labeled with green or orange fluorescent dyes, respectively, then mixed to be injected into nude mice skin. This assay system enables direct comparison of spreading in situ between 2 different sublines. This assay revealed that C5a-treated HuCCT1/C5aR cells spread more broadly than C5a-treated...
HuCCT1/mock cells in nude mice skin tissue (Fig. 5A). The most evident induction of the spreading of HuCCT1/C5aR by C5a was observed at day 2, which was a 1.8-fold increase over HuCCT1/mock (Fig. 5B). In contrast, there was no difference in spreading between those 2 sublines of HuCCT1 when they were not treated with C5a (Fig. 5A and B). This result suggests that C5a enhances invasion of C5aR-expressing cancer cells in vivo as well as in vitro, and again stimulation with C5a before injection is sufficient for C5aR-expressing cancer cells to show such enhanced invasiveness.

**Table 1. C5a-stimulated MMP release from C5aR-expressing cancer cells**

<table>
<thead>
<tr>
<th>MMP</th>
<th>MEC C5a (-)</th>
<th>C5a (+)</th>
<th>Ratio</th>
<th>HuCCT1/C5aR C5a (-)</th>
<th>C5a (+)</th>
<th>Ratio</th>
</tr>
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<tbody>
<tr>
<td>1</td>
<td>149,332.6 ± 17,039</td>
<td>291,140.4 ± 5,360.4</td>
<td>1.95</td>
<td>88,906.6 ± 27,436.8</td>
<td>129,408 ± 3,485</td>
<td>1.46</td>
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<tr>
<td>2</td>
<td>32.5 ± 11.3</td>
<td>116.9 ± 67.8</td>
<td>3.59</td>
<td>1,220.4 ± 184.3</td>
<td>870.7 ± 73</td>
<td>0.71</td>
</tr>
<tr>
<td>3</td>
<td>26.8 ± 12.0</td>
<td>134.7 ± 42.1</td>
<td>5.03</td>
<td>971.6 ± 224.6</td>
<td>927.5 ± 162.9</td>
<td>0.95</td>
</tr>
<tr>
<td>4</td>
<td>20.1 ± 23.6</td>
<td>74.9 ± 29.9</td>
<td>3.72</td>
<td>335.6 ± 77.7</td>
<td>1,128.3 ± 120.9</td>
<td>3.36</td>
</tr>
<tr>
<td>5</td>
<td>&lt; 0.1</td>
<td>12.3 ± 3.6</td>
<td>—</td>
<td>6,105.1 ± 2,011.3</td>
<td>6,213.4 ± 4,357.7</td>
<td>1.02</td>
</tr>
<tr>
<td>10</td>
<td>857.6 ± 740.5</td>
<td>9,301.4 ± 641.8</td>
<td>10.84</td>
<td>57,641.4 ± 5,197.5</td>
<td>111,666.4 ± 7,911.1</td>
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<td>13</td>
<td>359.2 ± 118.7</td>
<td>1,367.3 ± 309.3</td>
<td>3.80</td>
<td>1,411.9 ± 154.6</td>
<td>1,642.8 ± 287</td>
<td>1.16</td>
</tr>
</tbody>
</table>

aMMP concentrations (pg/mL) in culture supernatants of cancer cells cultured for 24 hours in the presence (+) or absence (−) of C5a (100 nmol/L).

bRatio of C5a (+) vs. C5a (−) in mean values.

cBelow the detection limit.

*, P < 0.01 (n = 4).

Discussion

C5-derived fragments were reported to enhance cancer cell locomotion, however, these were not identified as C5a when such reports were made. Rather, they seemed not to be C5a because of its molecular weight and lack of chemotactic activity for leukocytes (35, 36). When these studies were conducted, the C5aR molecule had not been identified, and neither recombinant C5a nor C5aR-specific antibodies were available to prove the activity of C5a to enhance cancer cell migration. In the present study, we have shown several lines of evidence indicating a crucial role of C5a–C5aR interaction in cancer cell invasion: (i) C5aR expression was observed in cancer cells from patients’ tissues and in various human cancer cell lines (Figs. 1 and 2), (ii) recombinant C5a enhanced cancer cell motility (Fig. 3) and invasion both in vitro (Fig. 4) and in vivo (Fig. 5), and (iii) enhanced cancer cell invasiveness elicited by the C5a–C5aR axis was dependent on the increased release of MMPs (Fig. 4 and Table 1), proteases that are indispensable for cancer cell invasion toward surrounding tissues (29). C5aR expression is essential for cancer cells of epithelial origin to enhance motility and invasiveness by C5a, given that C5aR expression is required for any remarkable changes in cell morphology (Fig. 3A) and enhanced invasiveness (Fig. 4A and C) in HuCCT1 cells after C5a stimulation (Fig. 5A and B). In addition, a C5aR antagonist (Supplementary Fig. S3) and by a neutralizing antibody against C5aR (Fig. 4B and D) abrogated C5a enhanced invasion of MEC cells. These data are consistent with the phenomenon that C5a...
enhances cancer cell invasion via C5aR, and to our knowledge, this is the first report that shows the biologic role of the C5a–C5aR axis in human cancer cell invasion. C5aR being expressed in cancerous cells but not normal epithelial cells except kidney proximal tubular epithelial cells in human tissue specimens (Fig. 1A and Supplementary Fig. S1A) may indicate C5aR expression to be a consequence of malignant transformation. A similar example is CXCR4: the receptor of CXCL12 that is a potent chemokine such as C5a and is produced in the cancer microenvironment (20). This receptor is commonly found in cancer cells and its expression is induced by factors such as hypoxia, VEGF, and estrogen in the cancer microenvironment. CXCR4 expression is also activated by mutations in genes that alter levels of hypoxia-inducible factors, and gene fusion events. Interleukin (IL)-6–induced C5aR expression in rat hepatocytes (37) suggests that C5aR can be expressed in response to specific cytokines that are rich in the cancer microenvironment (20, 38). However, IL-6 and IFN-γ did not induce C5aR expression in HuCCT1 cells (unpublished data). This may suggest that C5aR expression is dependent on genetic events characteristic in individual cancers. Such differences might reflect variation in C5aR-positivity in different primary organs (Fig. 1B).

Leaky cancer vasculature facilitates the supply of the complement system components from the bloodstream to cancer tissues (39), in which as shown in an animal cancer model (2), C5a is generated through activation of the complement system in response to cancer cells (3), although they are protected from complement attack by complement regulators (6). Indeed, C5a is detectable in human plasma incubated with MEC or HuCCT1 cells in vitro (Supplementary Fig. S4). Besides this pathway, C5a is possibly generated directly from C5 through thrombin-dependent cleavage (12), following the coagulation reaction initiated by tissue factor that can be expressed on cells in cancer tissues including cancer cells, fibroblasts and activated leukocytes (13). C5a can also be generated from C5 by a serine protease from activated phagocytes (14) recruited to the cancer tissue. In addition, compared with tightly adhering noncancerous epithelial cells, the loose cell-to-cell contact of cancer cells allows the generated C5a to access the cancer cell membrane, enabling it to bind to C5aR. Thus, C5a produced in the cancer microenvironment can be predicted to activate C5aR-positive cancer cells to promote migration from the primary site.

C5a induced dynamic sequential reorganization of actin cytoskeleton in C5aR-expressing cancer cells, namely, filopodia formation, membrane ruffling then formation of stress fibers (Fig. 4A). These processes have been reported to be provoked by activation of Cdc42, Rac1, and RhoA, respectively (40). Such sequential activation of these small G proteins, which is a robust driving force for cell movement, has been documented previously (41). In fact, C5a induces activation of Cdc42 and Rac1 in neutrophils, leading to actin reorganization of the cell (42).

We are currently studying if the C5a–C5aR axis can activate upstream signaling pathways of those small G proteins in cancer cells.

Together with motility stimulation in the C5a-containing culture medium (Fig. 3), increased invasiveness of C5a-treated C5aR-positive cancer cells in the matrix gel (Fig. 4) and in nude mouse skin (Fig. 5) in the absence of a C5a concentration gradient suggest that C5a enhances cancer cell random locomotion instead of inducing chemotaxis, which is supported by the checkerboard analysis (Fig. 4E). If C5a were only chemotactic for cancer cells, stimulated cells would be expected to assemble in the primary cancer site where C5a is released and enriched; thus, C5a would hinder cancer cell spread. In contrast, enhanced random cell locomotion would be more relevant for promoting cancer cell invasion and spreading, namely, the phenomenon that cells leave away from the source of the stimulant. Accordingly, such C5a activity is presumed to favor cancer cell dissemination from the primary site (Fig. 5).

This study implies that the C5a–C5aR axis could be a target for anticancer therapy. For instance, depleting C5 with anti-C5 antibodies would suppress C5a generation in cancer tissues. Therefore, this suggests that C5aR may also become a possible and feasible target for molecular-based medicine by generating specific antagonists. Such agents may provide useful therapeutic options for cancer treatment in the future.

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

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Enhancement of Human Cancer Cell Motility and Invasiveness by Anaphylatoxin C5a via Aberrantly Expressed C5a Receptor (CD88)

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