COP35, a cholangiocarcinoma-binding oligo-peptide, interacts with the clathrin heavy chain accompanied by GRP78

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ABSTRACT

Cholangiocarcinoma (CCA) is a common carcinoma of the liver, and the majority of patients with CCA have a poor prognosis due to the lack of effective non-surgical therapies in addition to its rapid progression and inoperability at the time of diagnosis. The development of novel non-surgical therapeutics that efficiently target CCA could significantly improve the prognosis for patients presenting with CCA. Here, we describe the iterative production and characterization of a novel peptide, designated COP35 (CCA-binding oligo-peptide #35), which binds selectively to human CCA, identified by bacteriophage biopanning using the intrahepatic cholangiocarcinoma cell line RBE and the normal cholangiocyte cell line MMNK-1. COP35 was found to augment the growth inhibitory effects of 5-FU against RBE cells. Utilizing pull-down assay and liquid chromatography, we identify the clathrin heavy chain (CHC) accompanied by GRP78/BiP as a COP35 binding partner. In summary, we identify COP35 as a possible candidate for peptide-targeted therapies for CCA.
INTRODUCTION

Cholangiocarcinoma (CCA) is a highly malignant tumor that arises from the ductal epithelium of the biliary tree and is a common secondary carcinoma of the liver [1]. The incidence and mortality rates of CCA are increasing worldwide [2]. Although tumors originating from the common hepatic or bile duct are readily identifiable owing to obstructive jaundice, tumors originating from the small bile duct do not cause significant biliary obstruction until the tumor itself or metastatic lesions cause obstruction of the common hepatic or bile duct [3]. In terms of treatment, complete surgical resection remains the only effective means to cure patients with CCA owing to the difficulty of early diagnosis and the rapid progression of the disease. The main obstacles to complete resection for CCA are the multiplicity of the lesions, that is, multicentric occurrence, intra-hepatic extension, and distant metastasis. Therefore, establishment of a methodology that could efficiently target CCA could dramatically improve the efficacy of treatments for CCA. Most patients with unresectable disease at clinical presentation have a poor prognosis (5-year survival rates are 0-40% even in resected cases) [2, 4]. Furthermore, CCA responds poorly to chemotherapy, and radiation therapy and conventional treatments are not adequate for the vast majority of patients with CCA. Moreover, conventional chemotherapy and radiation therapy have shown no efficacy in extending median survival rates, and although photodynamic therapy combined with stenting has been reported to be effective as a palliative treatment, it is not curative. Thus, the development of novel chemopreventive and adjuvant therapeutic strategies based on
exploring select molecular targets could impact significantly upon clinical outcomes.

Several groups’ studies have identified potential candidate molecular targeting agents to achieve tumor tropism. The ligands that have been evaluated include antibodies, single-chain fragment variables, and growth factors [5-7]. More recently, peptide-presenting bacteriophage libraries that enable the selection of peptides that bind to selected cell types or ligands have been utilized [8]. The biopanning technique has been shown to be a powerful tool for identifying specific ligands on target organs and tumors since it enables forced evolution of very high-affinity targeting peptides through rounds of selection of living libraries of peptides presented on the surface of the bacteriophage particle [9-12]. This technique has classically been used to iteratively produce peptides binding purified cell-surface markers [13, 14], cultured cell lines [15, 16], or tumor-bearing animals [17-19]. We utilized a peptide-presenting bacteriophage library based on a combinatorial library of random peptide 12-mers fused to a minor coat protein pIII of the M13-bacteriophage containing approximately $2.7 \times 10^9$ different sequences, and different peptides selective for the target cells were identified with successive rounds of biopanning. We identified a new oligo-peptide (designated COP35) that specifically bound to CCA cells and its target molecules. We characterized the effects of the selected peptide on tumor inhibition in combination with anticancer agents and elucidated a potential binding partner for COP35.

**MATERIALS AND METHODS**
Patient materials

Frozen and paraffin-embedded sections of human liver and biliary duct tissue with or without tumors were obtained from Shinshu University Hospital. The analysis of patient materials was approved by the Human Research Ethical Committee of Shinshu University, School of Medicine. Written informed consent for resection was obtained from the patients.

Cell lines

The human cholangiocyte cell line MMNK-1 was provided by the Department of Surgery of Okayama University School of Medicine (Okayama, Japan) and was maintained as described previously [20, 21]. The human intrahepatic cholangiocarcinoma (ICC) cell line RBE, human ICC cell line HuH-28, human ICC cell line IHGGK, human hepatocellular carcinoma cell line Hep3B, and human extrahepatic bile duct carcinoma (ECC) cell line TFK-1 were supplied by the Cell Resource Center for the Biomedical Research Institute of Development, Aging, and Cancer of Tohoku University (Sendai, Japan). HuH-28 cells were maintained in Minimum Essential Medium (Invitrogen, Grand Island, NY) containing 10% fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin at 37°C in 5% CO₂. All other cell lines were maintained in Dulbecco’s modified Eagle’s medium (DMEM) (Invitrogen, Grand Island, NY) containing 10% fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin at 37°C in 5% CO₂.
Phage display, isolation, and sequencing of phage DNA

The biopanning procedure was performed as described previously [12]. Briefly, we utilized the M13-phage display 12-peptide library constructed using Phage Display Peptide Library Kit (New England Biolabs, Ipswich, MA). MMNK-1 cells were used as absorber cells for whole-cell subtractive screening, and RBE cells were used as the target cells. Biopanning was performed for a total of three rounds for enrichment of peptides binding selectively and efficiently to CCA. Phage display, isolation, and sequencing of phage DNA were performed as described previously [10, 11].

Peptide preparation

Custom peptides COP35 “TPVLETPKLLLW”, a control peptide “HAKSPEMCTFVG”, which has almost the same net hydrophobic/hydrophilic and charge properties as COP35, and trans-acting activator of transcription (TAT) peptide “GRKKRRQRRRPPQ” were purchased from SIGMA Lifescience Custom Peptide Service (SIGMA Genosys, Hokkaido, Japan). Synthetic peptides were HPLC-purified (>95%) with N-terminal biotinylation or N-hydroxy-succinimidy1 (NHS)-fluorescein conjugation.

Evaluation of phage clones for their ability to bind to human cancer cells

The evaluation of binding activity of selected phage clones to human cell lines was performed as described previously [11]. RBE cells were cultured and plated into 96-well plates (1 × 10^4 cells/well) the day before use. The cells were washed and fixed in
4% paraformaldehyde in PBS for 20 minutes. $1 \times 10^{10}$ pfu per well of each selected phage clone was added to the cells at 4°C, unbounded phage were removed by washing cells with PBS, and bound phage were detected by cell-based enzyme-linked immunosorbent assay (ELISA).

Fluorescence microscopy of living cells with synthesized NHS-fluorescein-labeled peptides

Cells were cultured overnight in eight-well chamber slides, and were washed three times with PBS containing 10% FBS. The cells were then incubated with 1.7 mg/ml NHS-fluorescein-labeled peptide (Sigma Genosys, Hokkaido, Japan) for 2 hours at 37°C. After 2 hours, the medium was discarded and the cells were washed again with PBS containing 10% FBS, and then stained with medium containing 4',6-diamidino-2-phenylindole (DAPI) for nuclear counterstaining (Invitrogen, Grand Island, NY), and the samples were imaged using a fluorescence microscope.

Fluorescence microscopy of NHS-fluorescein-labeled peptides binding to human resected tissue and fixed RBE cells

Frozen sections from human resected tissues and RBE cells were stained with NHS-fluorescein-labeled COP35 or control peptide. Optimal Cutting Temperature (OCT) compound (Tissue-Tek; Sakura Finetek, Torrance, CA)-embedded frozen sections (10 μm thick) were incubated with 100 μM NHS-fluorescein-labeled peptide (green) for 2 hours at room temperature. Sections were counterstained with DAPI for nuclear counterstaining.
counterstaining (Invitrogen, Grand Island, NY), and the sections were imaged using a fluorescence microscope. For triple staining of frozen sections, they were incubated with 100 \( \mu \text{M} \) NHS-fluorescein-labeled peptide (green), and anti-CHC mouse monoclonal antibody with Alexa-Fluor\(^\text{TM} 647\)-conjugated secondary antibody (blue) (1:500 dilution) (Cell Signaling Technology, Danvers, MA), and anti-GRP78 rabbit polyclonal antibody with tri-methylrhodamine (TMR)-conjugated secondary antibody (red) (1:20 dilution) (DAKO, Glostrup, Denmark) for 2 hours at room temperature and the sections were imaged using a fluorescence microscope. The RBE cells fixed in 4% paraformaldehyde and permeabilized with 100% methanol were incubated with anti-CHC mouse monoclonal antibody with fluorescein isothiocyanate (FITC)-conjugated secondary antibody (green) (1:40 dilution) (DAKO, Glostrup, Denmark) and anti-GRP78 rabbit polyclonal antibody with tri-methylrhodamine (TMR)-conjugated secondary antibody (red) (1:20 dilution) (DAKO, Glostrup, Denmark). The sample slides were imaged using a fluorescence microscope.

**Evaluating the effect of clathrin depletion on COP-35 cellular binding and uptake in living RBE cells**

The clathrin-dependent endocytosis inhibitor, chlorpromazine hydrochloride, was purchased from SIGMA-ALDRICH (St. Louis, MO, USA). \( 1 \times 10^5 \) RBE cells/ml were incubated with 100 \( \mu \text{M} \) NHS-fluorescein-labeled COP35 or a control peptide in the presence or absence of 5 \( \mu \text{g/ml} \) chlorpromazine hydrochloride for 2 hours. Then, green fluorescence signal was observed by fluorescence microscopy.
Evaluation of fluorescence intensity of COP35

For the COP35 binding to frozen sections, the fluorescence signal intensity of COP35 result of 3(+) is defined as strong complete submembranous signals and/or uniform intense intracellular signals, 2(+) is defined as weak complete submembranous signals and/or uniform intense intracellular signals, 1(+) is defined as weak, incomplete submembranous or partial intracellular signals in any proportion of tumor cells, and 0 is defined as there being no specific fluorescence signal.

Evaluation of cell growth

To gauge toxicological side effects of the iteratively produced peptides, cell viability was evaluated by MTS assay. RBE cells were seeded in 96-well plates at $5 \times 10^3$ cells/well. The culture medium was replaced with 120 $\mu$l of medium containing 20 $\mu$l of CellTiter 96 AQueous One solution reagent (Promega, Madison, WI), and the culture plates was incubated at 37°C for 2 hours. One hundred $\mu$l of the medium were transferred to a new 96-well plate, and the quantity of the formazan product was determined by measuring the absorbance at 490 nm.

Peptide precipitation

RBE cells were lysed in 1 ml of NP-40 buffer (0.25% or 1% Nonidet P-40, 142.5 mM KCl, 5 mM MgCl2, 10 mM HEPES [pH 7.6], 0.2 mM PMSF, 1 mM EDTA) with proteinase inhibitor cocktail Complete Mini (Roche-diagnostics, Basel, Switzerland) [22].
The lysate was mechanically dislodged from the plate. The lysate from one dish was incubated on ice, and centrifuged at 15000g for 15 minutes. The supernatant was precipitated with 40 \( \mu l \) of streptavidin-conjugated agarose beads (Invitrogen, Grand Island, NY) and 20 \( \mu l \) of diluted biotinylated-peptide and incubated for 1 hour at 4°C. After incubation, the streptavidin-conjugated agarose beads were washed with lysis buffer 4 times and centrifuged for 1 minute, and the supernatant was discarded. The precipitated proteins were subjected to SDS-PAGE, and protein bands were excised from Coomassie brilliant blue-stained gel. The excised proteins were identified by mass spectrometry (nano LC-ESI-Q-TOF MS/MS) and then searched for in the NCBI nr protein database using their tandem mass spectra and the MASCOT algorithm (Matrix Science).

**Immunoprecipitation**

RBE cell lysate was prepared as peptide precipitation. The supernatant was precipitated with 40 \( \mu l \) of protein A-conjugated agarose beads (Invitrogen, Grand Island, NY) and 20 \( \mu g \) of specific antibodies including anti-Myc rabbit polyclonal antibody (negative control for rabbit polyclonal antibody) (sc-789; Santa Cruz Biotechnology, Santa Cruz, CA), anti-GRP-78 rabbit polyclonal antibody (positive control) (ab21685; Abcam, Cambridge, UK), anti-Flag mouse monoclonal antibody (negative control for mouse monoclonal antibody) (M2; Sigma–Aldrich, St. Louis, MO), or anti-CHC mouse monoclonal antibody (610499; BD, San Diego, CA) and incubated for 1 hour at 4°C. The precipitated proteins were subjected to SDS-PAGE and then immunoblotting as described
previously [22].

**Expression plasmids and siRNAs**

CHC and GRP78 expression plasmids were cloned into the Hind III site of pcDNA3 (Invitrogen, Grand Island, NY) by polymerase chain reaction (PCR) using primer sets of GCAAGCTTGCCATGGCCCAGATTCTGCCAA and AGAAGCTTCACATGCTGTACCCAAAGCCAG, or into the KpnI and XhoI sites of pcDNA3 by PCR using primer sets of ATGGTACCACCATGAAGCTCTCCCTGGTGG and ATCTCGAGCTACAACTCATCTTTTTCTGCT from human expressed sequence tag (EST) clones (Clone id: 6045540 and 10004803, respectively) purchased from Openbiosystems (Huntsville, AL, USA). The plasmids were sequenced to ensure that the correct sequences were inserted. CHC- and GRP78-specific Trilencer-27 siRNA kits were purchased from OriGene Technologies (Rockville, MD, USA).

**Transfection of expression plasmids or siRNAs**

$1 \times 10^4$ RBE cells/100 $\mu$l well were transfected with 0.34 $\mu$g of CHC and/or GRP78 expression plasmids or empty plasmid alone (negative control) by Lipofectamine 2000 (Invitrogen, Grand Island, NY) in accordance with the manufacturer's instructions. $1 \times 10^4$ RBE cells/100 $\mu$l well were transfected with 1.67 pmol of CHC and/or GRP78 specific siRNAs or universal scrambled negative control (USNC) siRNA by Lipofectamine 2000 in accordance with manufacturer's instructions.
Immunohistochemistry

Immunohistochemistry was performed as described previously [11]. Anti-CHC rabbit polyclonal antibody (ab24578; Abcam, Cambridge, UK) or anti-GRP78 rabbit polyclonal antibody (ab21685; Abcam, Cambridge, UK) was diluted 1:100 in blocking buffer and exposed to the tissues overnight at 4°C.

Evaluation of immunoreactivity of CHC and GRP78

For the protein expression in human sections, evaluation of immunoreactivity of anti-CHC and anti-GRP78 antibodies was as follows: 3(+) is defined as strong complete submembranous and uniform intense intracellular staining, 2(+) is defined as weak complete submembranous staining or uniform intense intracellular staining, 1(+) is defined as weak, incomplete submembranous or partial intracellular staining in any proportion of tumor cells, and 0 is defined as there being no specific staining.

Statistics

Results are presented as the mean and standard deviation. Levels of significance were evaluated using Student’s t test. A p-value <0.05 was considered statistically significant. Correlation was measured using Pearson’s product-moment correlation coefficient.
RESULTS

Identification of peptide motifs binding to human cholangiocarcinoma RBE cells

In vitro biopanning was performed as described previously with slight
modifications [10-12]. Briefly, following subtractive clearance of the library using the normal cell line MMNK-1, three consecutive rounds of in vitro biopanning were performed on the target human ICC RBE cells. After removal of unbound phage, the cell-associated phage were recovered from each round of biopanning by lysing the cells and pooled as candidate phage clones. Approximately $1 \times 10^{11}$ clones were screened through this iterative biopanning procedure. Finally, forty clones were selected and their affinity was evaluated by cell-based ELISA (Fig. 1A). We selected a single phage clone, #35, expressing the sequence “TPVLETPKLLLW”, which exhibited higher affinity to RBE cells than the other clones at the concentrations tested (Fig. 1A, #35). We defined the peptide as CCA-binding oligo-peptide #35 (COP35).

**Binding of COP35 to human CCA cell lines**

To evaluate the affinity and specificity of COP35 to several cancer cell lines, binding assays were performed in a variety of cell lines including ICC cell lines RBE, IHGGK, and HuH-28, the ECC cell line TFK-1, the hepatocellular carcinoma cell line Hep3B, and the normal cholangiocyte cell line MMNK-1. COP35 demonstrated significantly higher affinity to cancerous cell lines, RBE, HuH-28, TFK-1, IHGGK, and Hep3B, than to normal cholangiocyte cell line MMNK-1 (Fig. 1B).

**Fluorescence microscopy analysis of COP35 binding to RBE cells**

To confirm the binding and specificity of COP35 to CCA cell lines, we utilized NHS-fluorescein-labeled COP35 for fluorescence microscopy. Fluorescence signal was
observed in the ICC cell line RBE cells incubated with COP35 (Fig. 2A, upper left panel), whereas no significant fluorescence was observed in the cholangiocyte cell line MMNK-1 cells incubated with COP35 (Fig. 2A, lower left panel). Furthermore, no significant fluorescence was observed in RBE or MMNK-1 cells when a control peptide “HAKSPEMCTFVG”, which retains the overall net hydrophobic/hydrophilic and charge properties, was used as a negative control (Fig. 2A, upper and lower central panels). Fluorescence was observed in both RBE and MMNK-1 cells incubated with trans-acting activator of transcription (TAT) peptide “GRKKRRQRRRPPQ” as a cell-penetrating positive control peptide (Fig. 2A, upper and lower right panels) [23].

**Evaluation of COP35 binding to clinically resected CCA samples**

To test whether COP35 retained its capacity to bind to cells from samples from primary isolated CCA samples, eighteen CCA cases and nontumorous liver and biliary tissues of the same samples were stained with the NHS-fluorescein-labeled COP35 peptide. The median age of the patients was 64.7 y/o (range: 34 to 77 years old), and 10 patients were male and 8 patients were female. The tumor histology is presented in Table 1. Representative figures are shown (Fig. 2B). Fluorescence was observed in the CCA samples including both ICC (Fig. 2B, left top panel, Case 1) and ECC (Fig. 2B, central top panel, Case 16) with COP35, whereas no specific fluorescence was observed in these CCA tissues with the control peptide (Fig. 2B, left and central middle panels, Case 1 and Case 16). Signals were hard to detect in nontumorous tissue sections in Case 1 with either COP35 or the control peptide (Fig. 2B, right top and middle panels, Case 1). Parallel
hematoxylin and eosin staining images are presented (Fig. 2B, bottom panels).

**Enhancement of the tumor inhibitory effect of 5-fluorouracil by COP35 against RBE cells**

To evaluate whether COP35 could enhance the anti-tumor activity of 5-fluorouracil (5-FU) on RBE cells, tumor inhibitory effect was quantified in the presence of COP35 or control peptide (Fig. 2C). We next evaluated the effect on cell growth of 5-FU against RBE cells in the presence of COP35 or the control peptide by MTS assay (Fig. 2D). COP35 and 5-FU were added together and cell viability quantified after 36 or 48 hours of incubation. COP35 significantly enhanced the tumor inhibitory effect of 10 μg/ml 5-FU against RBE cells when it was incubated with 500 μM COP35 following both 36 and 48 hours of incubation (Fig. 2D). The COP35 peptide alone demonstrated no tumor inhibitory effect (Fig. 4A).

**Identification of the COP35 binding partners**

To identify putative binding partners for COP35, RBE cells were lysed with detergent concentrations of 0.25% or 1% NP-40 buffer and precipitated using biotinylated COP35 with streptavidin-conjugated agarose beads (Fig. 3A, left panel). As shown in the left panel of Figure 3A, a sharp band was found at approximately 190-kDa regardless of which buffer was used (Fig. 3A, left panel, arrowhead with band Q). Since the band lysed with 0.25% NP-40 buffer was clearer than that with 1.0% NP-40 buffer, we used 0.25% NP-40 buffer for the later analysis. In the peptide precipitation assay, as
we decreased the concentration of COP35 in 0.25% NP-40 buffer, while we found only an approximately 190-kDa band precipitated with 20 μ mol COP35 in lysis buffer (Fig. 3A, central panel, arrowhead with band Q), another band was found to appear around 80-kDa precipitated with 4.0-2.0 μ mol COP35 in lysis buffer (Fig. 3A, central panel, arrowhead with band R). The band disappeared at concentrations below 0.2 μ mol COP35 in lysis buffer (Fig. 3A, central panel, arrowhead with band R). We applied liquid chromatography-mass spectrometry (nano LC-ESI-Q-TOF MS/MS) analysis to identify both “Q” and “R” bands. A search for its tandem mass spectra in the NCBI nr protein database using MASCOT identified these two bands, “Q” as the clathrin heavy chain (CHC) with ion score 75 (Fig. 3A, upper right panel), and “R” as GRP78/BiP with ion score 120 (Fig. 3A, lower right panel). For further confirmation, RBE cell lysate was precipitated with COP35 or the control peptide (Fig. 3B). The precipitated proteins were subjected to SDS-PAGE (Fig. 3B, left panel) following immunoblotting analysis with detection using anti-CHC monoclonal antibody (Fig. 3B, central panel, arrowhead with CHC) and anti-GRP78 monoclonal antibody (Fig. 3B, right panel, arrowhead with GRP78). A band of molecular weight ~ 190-kDa was recognized by an anti-CHC monoclonal antibody (Fig. 3B, central panel, arrowhead with CHC). The CHC band disappeared with a decrease of COP35 titration, whereas no signal was detected in the control peptide precipitation. In addition to the CHC band, a band of around 80-kDa recognized by anti-GRP78 monoclonal antibody appeared (Fig. 3B, right panel, arrowhead with GRP78). The GRP78 band was most intense at 4.0 μ mol concentration in lysis buffer and disappeared at lower COP35 concentration, which was consistent with
SDS-PAGE data (Fig. 3A, central panel, arrowhead with band R). Next, we confirmed the interaction between CHC and GRP78 by immunoprecipitation (Fig. 3C) and dual immunofluorescence staining of CHC and GRP78 in RBE cells (Fig. 3D). Endogenous GRP78 was found to be co-precipitated with anti-CHC monoclonal antibody (Fig. 3C, α CHC). As controls, the precipitate with anti-GRP78 polyclonal antibody was also detected by anti-GRP78 monoclonal antibody, whereas the precipitate with anti-Myc polyclonal antibody or anti-Flag monoclonal antibody was not detected by anti-GRP78 monoclonal antibody (Fig. 3C). In dual immunofluorescence microscopy, GRP78 clearly co-localized with CHC (Fig. 3D, arrowheads). The green CHC signals were partially merged with GRP78 signals, and both appeared to be located in perinuclear cytoplasm and cellular periphery in RBE cells (Fig. 3D, Merge and Merge (high power), arrowheads). In human resected tumors, we performed triple immunohistochemical staining for tissues from CCA patients using NHS-fluorescein-labeled COP35 (green), anti-CHC mouse monoclonal antibody with Alexa-Fluor™ 647-conjugated secondary antibody (blue), and anti-GRP78 rabbit polyclonal antibody with TMR-conjugated secondary antibody (red). We found substantial colocalization between the COP35 and CHC fluorescence signals (blue-green) (Fig. 3E, lower central panel, arrowheads). We also noticed some partial colocalization between COP35 and GRP78 (yellow) (Fig. 3E, upper right panel, arrowheads) and these three fluorescence signals were merged at the cellular periphery (green-yellow) (Fig. 3E, lower right panel, arrowheads).

**Effect of cellular clathrin depletion on COP35 binding and internalization**
To examine whether clathrin-mediated endocytosis is required for COP35-mediated cellular binding and internalization, experiments were performed in cells depleted of clathrin through treatment with chlorpromazine. RBE cells were incubated with 100 μM NHS-fluorescein-labeled COP35 (Fig. 3F, upper panels, COP35) or a control peptide (Fig. 3F, lower panels, Control) with or without 5 μg/ml chlorpromazine hydrochloride for 2 hours. As expected, we observed strong intercellular COP35 fluorescence in RBE cells incubated with vehicle saline alone (Fig. 3F, upper left panel, Chlorpromazine (-)), while the signals were substantially decreased in cells incubated with chlorpromazine hydrochloride (Fig. 3F, upper right panel; Chlorpromazine (+)). No significant fluorescence of control peptide was observed in RBE cells when incubated with either vehicle saline alone or chlorpromazine hydrochloride (Fig. 3F, lower panels).

Effect of overexpression, siRNA-mediated silencing of CHC and/or GRP78, or clathrin depletion on 5-FU-mediated tumor inhibition in combination with COP35

To examine whether the enhancement of the 5-FU-mediated tumor inhibitory effect by COP35 depends on CHC and/or GRP78, we evaluated the tumor inhibitory effect of 5-FU with overexpression or siRNA-mediated knockdown of the COP35 binding partners CHC and/or GRP78 in RBE cells (Fig. 4A and B). Furthermore, we evaluated the tumor inhibitory effect of 5-FU in the presence or absence of chlorpromazine (Fig. 4C). We found that the significant difference in tumor inhibitory effect observed between COP35 and control peptide in RBE cells incubated together with
5-FU was enhanced by overexpression of CHC and/or GRP78 (Fig. 4A). Overexpression of CHC and/or GRP78 in transfected RBE cells was confirmed by Western blotting (Fig. 4A, insets). Furthermore, we found a loss of effect of COP35 in enhancing the tumor inhibitory effect of 5-FU following the specific knockdown of CHC and/or GRP78 using siRNAs (Fig. 4B). Reduced expression of CHC and/or GRP78 was confirmed by Western blotting (Fig. 4B, insets). Furthermore, we found that the significant difference in tumor inhibitory effects observed between COP35 and control peptide in RBE cells incubated with 5-FU was abolished when RBE cells were incubated with 5 $\mu$ g/ml chlorpromazine hydrochloride to deplete clathrin (Fig. 4C).

**Evaluating the expression of CHC and GRP78 in CCA specimens**

We confirmed expression of both CHC and GRP78 by immunohistochemistry in formalin-fixed paraffin-embedded human CCA specimens (Fig. 5A). We evaluated the immunoreactivity of anti-CHC and anti-GRP78 antibodies in eighteen cases (the same patient group as for when we evaluated COP35 binding to clinically resected CCA samples (Table 1)). Representative figures are shown (Fig. 5A). Evaluations of the immunoreactivity of CHC and GRP78 are presented in Table 1, and plotted in Figures 5B and C. Expression of CHC and GRP78 was found to be higher in ICC (Fig. 5A, ICC (Case 1)) and ECC (Fig. 5, ECC (Case 16)) than in nontumorous bile duct epithelium (Fig. 5A, Normal (Case 1)). Parallel hematoxylin and eosin images are presented (Fig. 5A, bottom panels). Since there were some normal biliary epithelia in tumor-free tissues in pathological specimens of Case 1 to Case 16, we were able to quantify the
immunoreactivities of CHC and GRP78 in tumor and nontumorous tissues, which were plotted (Fig. 5B and C). We found that the arithmetic mean (M) immunoreactivities of CHC (M=2.4) and GRP78 (M=1.3) in tumor tissues were significantly higher than those of CHC (M=1.1) and GRP78 (M=0.062) in nontumorous tissues with paired t-test probabilities **p<0.01 (Fig. 5B and C).

Correlation between COP35 fluorescence intensity and immunoreactivity of CHC and GRP78

Since COP35 bound to both CHC and GRP78, we examined whether COP35 fluorescence intensity positively correlated with the immunoreactivity of CHC and GRP78 in the same patient samples presented in Table 1. We found that COP35 fluorescence intensity was statistically correlated with the immunoreactivity of CHC and GRP78 with Pearson’s product-moment correlation coefficient R=0.706 with p-value=0.00154, and R=0.531 with p-value=0.0282, respectively (Fig. 5D and E).

DISCUSSION

CCA is known to have a poor prognosis carcinoma compared to many other malignant tumors [1-4]. Novel therapeutics are urgently required to effectively treat CCA. Peptide-presenting phage display libraries are powerful tools for iteratively producing ligands that can bind to specific targets [9-12]. In this study, we utilized a phage display
library to identify a novel peptide, defined as COP35. COP35 selectively bound to CCA derived from clinically resected specimens from patients as well as CCA cell lines (Fig. 1, 2A and B). Therefore, we consider that COP35 binds to a CCA-specific target ligand. In addition, COP35 was found to enhance the tumor inhibitory effect of 5-FU (Fig. 2C and D).

Using liquid chromatography-mass spectrometry (nano LC-ESI-Q-TOF MS/MS), we identified the clathrin heavy chain (CHC) as a COP35 binding partner (Fig. 3A). The molecular weight of CHC is 192-kDa, which is consistent with our SDS-PAGE results and following immunoblotting detected with anti-CHC monoclonal antibody (Fig. 3A and B). Clathrin is the major protein component of a major class of coated vesicles, and plays an important role in endocytosis [24-26], a pathway known to be involved in pathogen internalization [27, 28]. We therefore speculated that COP35 is internalized via a clathrin-dependent endocytic pathway by direct or indirect interaction with CHC in living cells. Using TAT peptide as a cell-penetrating positive control peptide for peptide internalization, fluorescence was detected ubiquitously in all cells, while fluorescence signal from COP35 was specifically detected in RBE cells and not MMNK-1 cells (Fig. 2A). Thus, it is suggested that the internalization of COP35 in RBE cells may occur in a different way from that for cell-penetrating peptide. Since it was reported that endocytosis might be accelerated in CCA cells because of their motility and high-energy demand [29], we examined the effect of an inhibitor of clathrin-mediated endocytosis, chlorpromazine, to investigate whether COP35 is actually internalized into CCA cells via clathrin-mediated endocytosis. We found that depletion of clathrin using chlorpromazine
inhibited the COP35 internalization in RBE cells (Fig. 3F). The result supports our hypothesis that COP35 is internalized via clathrin-mediated endocytosis. It was also suggested that CHC is up-regulated in hepatocellular carcinoma tissues [30]. Consistent with this, our data suggest that CHC expression in CCA lesions was higher than that in normal bile duct epithelium by immunohistochemical staining of formalin-fixed and paraffin-embedded tissues (Table 1) (Fig. 5A, upper panels, and B). Thus, it was suggested that CHC could be an attractive target of COP35.

Notably, as we decreased the concentration of COP35, another clear band became apparent around 80-kDa precipitated with CHC (Fig. 3A, central panel, arrowhead with band R). The 80-kDa protein was determined to be a glucose-regulated protein of 78-kDa (GRP78, also referred to as BiP) (Fig. 3A, right panel, band R). GRP78 is a member of the heat shock protein 70 family that functions as a chaperone critical for folding, maturation, and transport of polypeptides and proteins, which is expressed on the cell surface where it functions as a receptor for a wide variety of ligands [31, 32]. GRP78 is also important in the unfolded protein response that ameliorates stress conditions, such as glucose starvation and hypoxia, which are characteristic of malignant tumors, and serves to protect tumor cells against cell death [33, 34]. GRP78 has been reported to be strongly expressed in gastric and prostate cancer, and correlate with their aggressive behavior and poor prognosis [35, 36]. The induction of GRP78 by unfolded protein response during endoplasmic reticulum stress is reported to be required for pathophysiologic conditions, such as tumor proliferation, survival, and angiogenesis [37]. Consistent with this, our findings indicated that GRP78 was highly expressed in CCA.
cells (Table 1) (Fig. 5A, middle panels, and C). The interaction between CHC and GRP78 is likely to affect the tumor inhibitory effect of 5-FU. We found that COP35 enhanced the tumor inhibitory effect of 5-FU (Fig. 2C and D), and siRNA-mediated knockdown of CHC and/or GRP78 and chlorpromazine treatment of RBE cells resulted in abolishment of the enhancement of the 5-FU tumor inhibitory effect of COP35 (Fig. 4B and C), while overexpression of CHC and/or GRP78 in RBE cells resulted in an enhanced 5-FU mediated tumor inhibitory effect of COP35 (Fig. 4A). In addition, the ability of COP35 to bind to clinical samples was statistically correlated with the expression of CHC and GRP78 (Fig. 5D and E). Thus, it was suggested that both CHC and GRP78 are important molecules for the function of COP35 in enhancing the tumor inhibitory effect of 5-FU.

As shown in Figure 3, while high concentration (20.0 μ mol) of COP35 bound only to CHC, the lower concentration (4.0-2.0 μ mol) of COP35 bound to CHC accompanied by GRP78 (Fig. 3A, central panel, and B). We speculate that COP35 could directly bind to CHC, which may interact with a surface receptor protein GRP78. The hypothesis was also confirmed by further evidence that GRP78 was co-precipitated with CHC by immunoprecipitation, and appeared to co-localize with CHC by immunofluorescence microscopy (Fig. 3C, D and E). However, we noted the limitation of our study to explain this finding that COP35 interacts with CHC at high concentration and GRP78 at lower concentration, which may reflect a key function of COP35 on enhancement of the tumor inhibitory effect of 5-FU. We speculated that higher concentration of COP35 might induce a conformational change in CHC that reduces the power of binding between CHC and GRP78 under our experimental conditions.
Additional studies will be required in order to fully elucidate the mechanism by which COP35 enhances the tumor inhibitory effect of 5-FU prior to clinical studies. It has been reported that a number of prognostic and predictive gene mutations such as k-ras, p53, and Raf/Mek/Erk in tumor can correlate with sensitivity and/or resistance to chemotherapies [38]. In patients, germline pharmacogenetic mutations or polymorphisms can influence chemotherapeutic toxicity [38]. We speculate that metabolism and degradation by nonspecific peptidases and proteases, or clathrin-dependent endocytosis of macrophages, may be different for each patient. Here, we present data suggesting that tumor expression levels of CHC and GRP78 could be important factors for gauging the likely efficacy of 5-FU in combination therapies of COP35 and 5-FU.

IN MEMORIAM

Our colleague, a surgeon, Dr. Fukuto Maruta, died prior to publication of this study. This paper is dedicated to his memory.

ACKNOWLEDGEMENTS

We thank M. Narita, Y. Shimojo, and H. Kawate for their technical assistance. This work was supported by Grants-in-Aid for Scientific Research from the Japan Society for the Promotion of Science (19591581, 20591588) and by grants from the Japan Research Foundation for Clinical Pharmacology and the Public Trust Surgery Research Fund (to S.M.), and in part by Grants-in-Aid for Research on Measures for Intractable
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FIGURE LEGENDS

Figure 1. Evaluation of selected phage specificity

(A) The affinities of 40 candidate clones were evaluated by cell-ELISA. Absorbance is indicated on the left. Values represent the mean and SD from triplicate cultures. Clone #35 was selected for further studies. (B) The binding of clone #35 was assessed in a variety of cell lines including ICC cell lines RBE, IHGGK, and HuH-28, the ECC cell line TFK-1, the hepatocellular carcinoma cell line Hep3B, and the normal cholangiocyte cell line MMNK-1. Plaque forming units (pfu) are indicated on the left. Values are the mean and SD from triplicate culture plates. *p<0.01.
Figure 2. Fluorescence microscopy with NHS-fluorescein-labeled COP35 and MTS assay of RBE cells incubated with 5-FU and COP35

(A) Human cholangiocarcinoma RBE cells (upper panels) and human cholangiocyte MMNK-1 cells (lower panels) were stained with NHS-fluorescein-labeled COP35 (left panels, COP35), a control peptide (central panels, Control), or trans-acting activator of transcription (TAT) peptide (right panels, TAT). One hundred μM NHS-fluorescein-labeled peptides were incubated with RBE or MMNK-1 cells for 2 hours. Cell nuclei were counterstained with DAPI for nuclear counterstaining. Bar is 25 μm. (B) Fluorescence microscopy of frozen sections from cholangiocarcinoma and nontumorous liver tissue with NHS-fluorescein-labeled COP35. The sections were incubated with 100 μM NHS-fluorescein-labeled peptide for 2 hours at room temperature. Sections were counterstained with DAPI for nuclear counterstaining. Representative ICC (Case 1 in Table 1), ECC (Case 16 in Table 1), and nontumorous normal bile duct epithelium of CCA (Case 1 in Table 1) are presented. Parallel hematoxylin and eosin staining images are shown (bottom panels). Bar is 100 μm. (C) Tumor inhibitory effect of 5-FU with COP35 in RBE cells. RBE cells were incubated with 50 μM (upper panels) or 500 μM (lower panels) COP35 or control peptide with 1 μg/ml or 10 μg/ml 5-FU for 48 hours. The bar is 50 μm. (D) MTS assay of RBE cells. RBE cells were plated in 96-well plates at 5 × 10³ cells/well for 24 hours before the MTS assay. After 24 hours, cells were incubated with COP35 or the control peptide, and 1 μg/ml or 10 μg/ml 5-FU. After incubation for 36 and 48 hours, the growth inhibitory
effect on the RBE cells was assessed. Values are the mean and SD results from triplicate cultures. *p<0.05, **p<0.01.

Figure 3. Identification of COP35-binding molecules

(A) RBE cells were lysed with different detergent concentrations of 0.25% or 1% NP-40 buffer and precipitated with the biotinylated COP35, the control peptide, or no peptide with streptavidin-conjugated agarose beads. Then, the precipitates were subjected to SDS-PAGE. An approximately 190-kDa band was precipitated with COP35 (left panel, arrowhead with band Q). RBE cells were lysed with 0.25% NP-40 buffer and precipitated with the titrated concentration of biotinylated COP35 with streptavidin-conjugated agarose beads. Then, the precipitates were subjected to SDS-PAGE. Another approximately 80-kDa band appeared with 4.0 and 2.0 μ mol COP35 in lysis buffer (central panel, arrowhead with band R). Spectra of liquid chromatography-mass spectrometry (nano LC-ESI-Q-TOF MS/MS) analysis of band Q and band R are shown in upper and lower right panels, respectively. (B) RBE cells were lysed with 0.25% NP-40 buffer and precipitated with the indicated concentration of biotinylated COP35 or control peptide with streptavidin-conjugated agarose beads. Then, the precipitates were subjected to SDS-PAGE (left panel) followed by immunoblotting with anti-CHC monoclonal antibody (central panel) and anti-GRP78 monoclonal antibody (left panel).

Abbreviations: P, precipitation; CBB, Coomassie brilliant blue; CHC: clathrin heavy chain. (C) RBE cells were lysed with 0.25% NP-40 buffer and precipitated with anti-Myc polyclonal antibody (negative control), anti-GRP-78 polyclonal antibody (positive
control), anti-Flag monoclonal antibody (negative control), or anti-CHC monoclonal antibody. The precipitates were subjected to immunoblotting with anti-GRP78 monoclonal antibody. (D) Dual immunofluorescence microscopy of RBE cells. RBE cells were stained with anti-CHC mouse monoclonal antibody with FITC-conjugated secondary antibody (upper left panel, CHC, green) and anti-GRP78 rabbit polyclonal antibody with tri-methylrhodamine (TMR)-conjugated secondary antibody (upper central panel, GRP78, red), and were observed using a fluorescence microscope. Merged images and high-power view of merged images of square field are shown (upper right panel, Merge; lower right panel, Merge (High power)). The yellow merged signals were observed (arrowheads). Single staining controls stained with anti-CHC mouse monoclonal antibody with FITC-conjugated secondary antibody (lower left panel, CHC, green) or anti-GRP78 rabbit polyclonal antibodies with TMR-conjugated secondary antibody (lower central panel, GRP78, red) are shown. Bar is 10 μm. (E) Triple immunofluorescence microscopy for tissues from CCA patients using NHS-fluorescein-labeled COP35 (upper left panel, COP35, green), anti-CHC mouse monoclonal antibody with Alexa-Fluor™ 647-conjugated secondary antibody (lower left panel, CHC, blue), and anti-GRP78 rabbit polyclonal antibody with TMR-conjugated secondary antibody (upper central panel, GRP78, red). Merged images with yellow, blue-green, and yellow-green are shown (upper right panel, Merge (green+red); lower central panel, Merge (blue +green); and lower right panel, Merge (green+red+blue), respectively). Bar is 10 μm. (F) Effect of an inhibitor of clathrin-mediated endocytosis, chlorpromazine, on COP35 internalization. RBE cells were incubated with 100 μM
NHS-fluorescein-labeled COP35 (upper panels, COP35) or a control peptide (lower panels, Control), and with (right panels, Chlorpromazine (+)) or without (left panels, Chlorpromazine (-)) 5 μg/ml chlorpromazine hydrochloride for 2 hours. Bar is 25 μm.

Figure 4. MTS assay to evaluate whether COP35 enhances the tumor inhibitory effect of 5-FU on RBE cells

(A) RBE cells transfected with CHC and/or GRP78 expression plasmids or a vector plasmid (pcDNA3) were incubated with 500 μM COP35 or control peptide together with 10 μg/ml 5-FU for 48 hours. (B) RBE cells transfected with CHC and/or GRP78 specific knockdown siRNAs or universal scrambled negative control (USNC) siRNA were incubated with 500 μM COP35 or control peptide together with 10 μg/ml 5-FU for 48 hours. Expression levels of CHC and/or GRP78 were confirmed by Western blotting (A and B insets, respectively). (C) RBE cells were incubated with 500 μM COP35 or control peptide together with 10 μg/ml 5-FU in the presence or absence of an inhibitor of clathrin-mediated endocytosis, chlorpromazine hydrochloride (5 μg/ml) for 48 hours. Values are the mean and SD results from triplicate cultures. *p<0.05, **p<0.01.

Figure 5. Expression of the CHC and GRP78 in cholangiocarcinoma

(A) ICC and ECC in formalin-fixed paraffin-embedded specimens were immunostained with anti-CHC polyclonal antibody (top panels) or anti-GRP78 polyclonal antibody (middle panels) or stained with hematoxylin and eosin (bottom panels). Details are summarized in Table 1. Representative ICC (Case 1 in Table 1), ECC (Case 16 Table 1),
and nontumorous bile duct normal epithelium of CCA (Case 1 in Table 1) are presented (Normal epithelium). The bar is 100 μ m. (B and C) Differences between immunoreactivity in tumorous tissues and nontumorous tissues. The evaluated immunoreactivities of CHC and GRP78 in tumorous tissues and nontumorous tissues are plotted. The arithmetic means (M) of evaluated immunoreactivities of CHC (M=2.4) and GRP78 (M=1.3) in tumor tissues are significantly higher than those of CHC (M=1.1) and GRP78 (M=0.062) in nontumorous tissues with paired t-test probabilities p<0.01. (D and E) Correlations between COP35 fluorescence intensity and immunoreactivity of CHC and GRP78. Evaluated COP35-fluorescence intensity is on the x-axis and evaluated immunoreactivity of CHC or GRP78 is on the y-axis. Evaluated COP35-fluorescence intensity is statistically correlated with the evaluated immunoreactivity of CHC and GRP78 with Pearson’s product-moment correlation coefficient R=0.706 with p-value=0.00154, and R=0.531 with p-value=0.0282, respectively.
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Table 1. Clinicopathological data, fluorescence signal intensity of COP35 and immunoreactivity of CHC and GRP78 in 18 CCA.

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Footnote: Age(y/o): age (years old) at surgery. Gender, female (F) and male (M); Location, intrahepatic (I), extrahepatic (E); Histology, well-differentiated adenocarcinoma (wel), moderately differentiated adenocarcinoma (mod) and poorly differentiated adenocarcinoma (por) in intrahepatic cholangiocarcinoma, and tubular adenocarcinoma (tub) or papillary adenocarcinoma (pap) in carcinoma of the extrahepatic bile ducts, tumorous tissue (T), nontumorous tissue (NT). *There is no nontumorous tissue.
Molecular Cancer Research

COP35, a cholangiocarcinoma-binding oligo-peptide, interacts with the clathrin heavy chain accompanied by GRP78

Hiroe Kitahara, Junya Masumoto, Alan L Parker, et al.

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