Author Summary

Viruses hijack host cells and utilize host-derived proteins for viral propagation. In the case of hepatitis C virus (HCV), many host factors have been identified that are required for genome replication; however, only a little is known about cellular proteins that interact with HCV proteins and are important for the viral assembly process. The C-terminal half of nonstructural protein 2 (NS2), and the N-terminal third of NS3, form the NS2-3 protease that cleaves the NS2/3 junction. NS2 also plays a key role in the viral assembly process independently of the protease activity. We performed split-ubiquitin yeast two-hybrid screening and identified signal peptidase complex subunit 1 (SPCS1), which is a subunit of the microsomal signal peptidase complex. In this study, we provide evidence that SPCS1 interacts with both NS2 and E2, resulting in E2-SPCS1-NS2 complex formation, and has a critical role in the assembly of infectious HCV particles. To our knowledge, SPCS1 is the first NS2-interacting cellular factor that is involved in regulation of the HCV lifecycle.

responsible for the cleavage of signal peptides of many secreted or membrane-associated proteins. We show that SPCS1 is a novel host factor that participates in the assembly process of HCV through an interaction with NS2 and E2.

Results

SPCS1 is a novel host protein that interacts with HCV NS2 protein

To gain a better understanding of the functional role of NS2 in the HCV lifecycle, we screened a human liver cDNA library by employing a split-ubiquitin membrane yeast two-hybrid system with the use of NS2 as a bait. It is known that the split ubiquitin-based two-hybrid system makes it possible to study protein-protein interactions between integral membrane proteins at the natural sites of interactions in cells [26]. From the screening, several positive clones were identified from the 13 million transformants, and the nucleotide sequences of the clones were determined. A BLAST search revealed that one of the positive clones encodes a full-length coding region of signal peptidase complex subunit 1 (SPCS1). SPCS1 is a component of the microsomal signal peptidase complex which consists of five different subunit proteins in mammalian cells [27]. Although catalytic activity for SPCS1 has not been indicated to date, a yeast homolog of this subunit is involved in efficient membrane protein processing as a component of the signal peptidase complex [28].

To determine the specific interaction of NS2 with SPCS1 in mammalian cells, FLAG-tagged NS2 (FLAG-NS2; Fig. 1A) was co-expressed in 293T cells with myc-tagged SPCS1 (SPCS1-myc; Fig. 1A), followed by co-immunoprecipitation and immunoblotting. SPCS1 was shown to be co-immunoprecipitated with NS2 (Fig. 1B). Co-immunoprecipitation of SPCS1-myc with NS2 was also observed in the lysate of Huh-7 cells infected with cell culture-produced HCV (HCVcc) derived from JFH-1 isolate [29] (Fig. 1C). To determine the region of SPCS1 responsible for the interaction with NS2, deletion mutants of myc-tagged SPCS1 were constructed (Fig. 1A) and co-expressed with FLAG-tagged NS2. Since the expression of C-terminal deletion mutants, d3 and d4, was difficult to detect (Fig. 1D), N-terminal deletions (d1 and d2) as well as wild-type SPCS1 were subjected to immunoprecipitation analysis. SPCS1-myc, -d1, and -d2 were co-immunoprecipitated with NS2 (Fig. 1E), suggesting that the SPCS1 region spanning amino acids (aa) 43 to 102 is involved in its interaction with NS2. Next, to identify the NS2 region responsible for its interaction with SPCS1, deletion mutants for FLAG-NS2 (Fig. 1A) were co-expressed with SPCS1-myc-d2 in cells, followed by being immunoprecipitated with anti-myc antibody. SPCS1 was co-immunoprecipitated with the NS2 deletions, except for a mutant lacking transmembrane (TM) 2 and TM3 (dTM23) domains (Fig. 1F). These finding suggests that the TM3 region of NS2 is involved in the interaction with SPCS1.

To investigate SPCS1-NS2 interaction *in situ*, the proximity ligation assay (PLA) [30], which is based on antibodies tagged with circular DNA probes, was used. Only when the antibodies are in close proximity, the probes can be ligated together and subsequently be amplified with a polymerase. We were able to detect PLA signal predominantly in the cytoplasm of the cells expressing FLAG-NS2 and SPCS1-myc-d2 tagged with V5 at N-terminus (Fig. 1G). By contrast, the PLA signal was not observed in the context of NS2-Core co-expression. We further analyzed the SPCS1-NS2 interaction by the monomeric Kusabira-Green (mKG) system [31], which is based on fusion proteins with complementary fragments (mKG-N and mKG-C) of the monomeric coral fluorescent reporter protein. When the mKG fragments are in close proximity due to the protein-protein interaction, the mKG fragments form a beta-barrel structure and emit green fluorescence. Co-expression of SPCS1-mKG-N and NS2-mKG-C fusion proteins in cells reconstituted green cellular fluorescence as shown in Fig. 1H. Thus, these results represented structures with SPCS1 and NS2 in close proximity, and strongly suggest their physical interaction in cells.

SPCS1 participates in the propagation of infectious HCV particles

To investigate the role(s) of endogenous SPCS1 in the propagation of HCV, four small interfering RNAs (siRNAs) for SPCS1 with different target sequences or scrambled control siRNA were transfected into Huh7.5.1 cells, followed by infection with HCVcc. Among the four SPCS1-siRNAs, the highest knockdown level was observed by siRNA #2. siRNAs #3 and #4 showed moderate reductions of SPCS1 expression, and only a marginal effect was obtained from siRNA #1 (Fig. 2A). As indicated in Fig. 2B, the infectious viral titer in the culture supernatant was significantly reduced by the knockdown of SPCS1. It should be noted that the infectious titers correlated well with the expression levels of endogenous SPCS1. siRNA #2 reduced the HCV titer to ~5% of the control level in Huh7.5.1 cells. To rule out the possibility of off-target effect of SPCS1-siRNA on HCV propagation, we also used "C911" mismatch control siRNAs in which bases 9 through 11 of siRNAs are replaced with their complements but other parts of antisense- and sense-strand sequences are kept intact. These mismatch designed-control siRNAs have been shown to reduce the down-regulation of the targeted mRNA, but maintains the off-target effects of the original siRNA [32]. The C911 controls against SPCS1-siRNA #2, #3, and #4 (C911-#2, -#3, and -#4) showed little effect on knockdown of SPCS1 as well as propagation of HCV (Fig. S1A and B).

We further determined the loss- and gain-of-function of SPCS1 on HCV propagation in an SPCS1-knockdown cell line. To this end, Huh-7 cells were transfected with a plasmid encoding a short hairpin RNA (shRNA) targeted to SPCS1 and were selected with hygromycin B, resulting in clone KD#31 where little or no expression of SPCS1 was detectable (Fig. 2C). KD#31 cells and parental Huh-7 cells were transfected with an RNA polymerase I (pol)-driven full-genome HCV plasmid [33] in the presence or

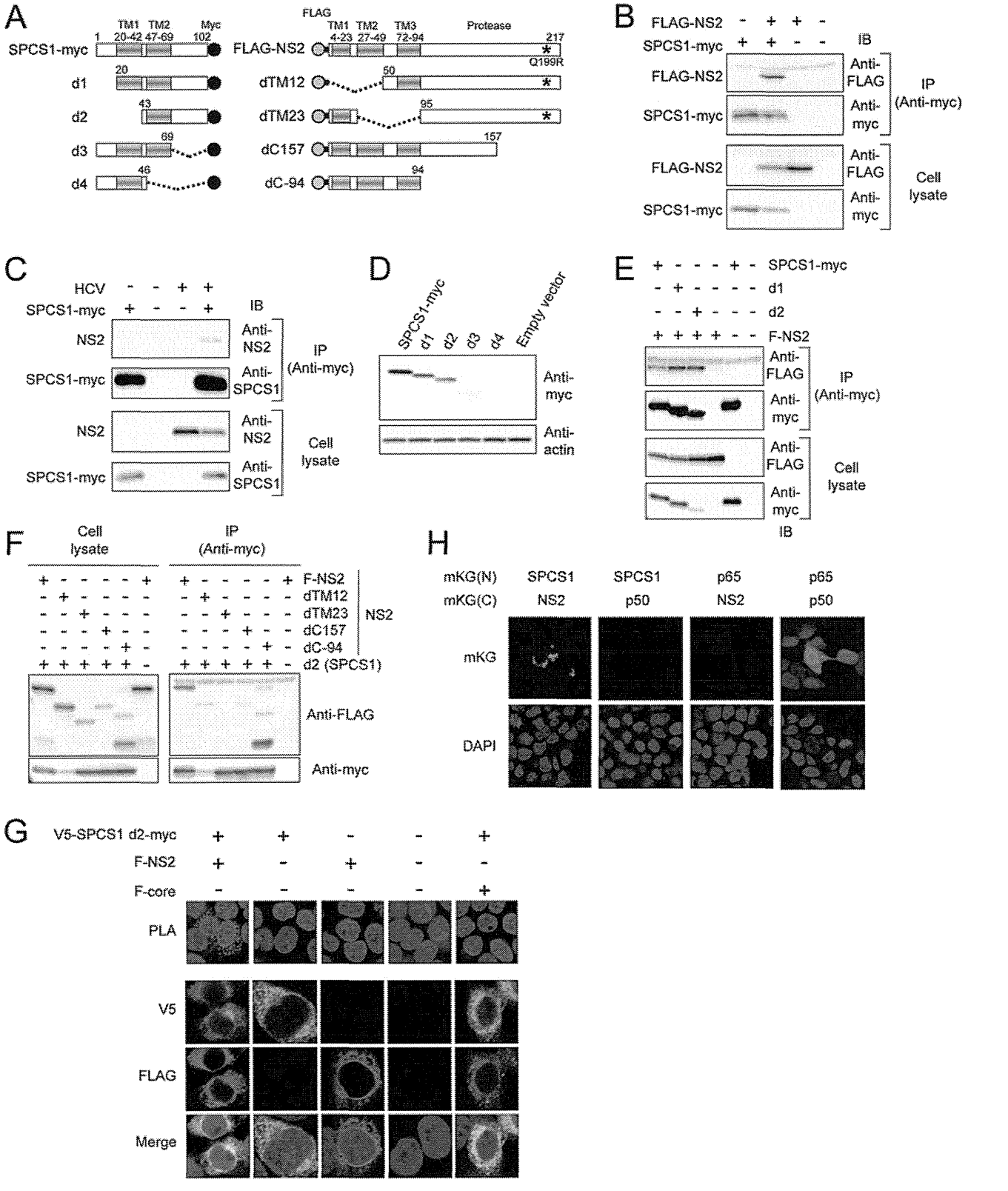

Figure 1. Interaction of HCV NS2 protein with SPCS1 in mammalian cells. (A) Expression constructs of SPCS1-myc and FLAG-NS2 used in this study. TM regions are represented as gray. Myc-tag regions are depicted by the black circles. Gray circles and bold lines indicated FLAG-tag and spacer (GGGGS) sequences, respectively. Adaptive mutations are indicated as asterisks. Positions of the aa resides are indicated above the boxes. (B) 293T cells were co-transfected with a FLAG-tagged NS2 expression plasmid in the presence of a SPCS1-myc expression plasmid. Cell lysates of the transfected cells were immunoprecipitated with anti-myc antibody. The resulting precipitates and whole cell lysates used in immunoprecipitation (IP) were examined by immunoblotting using anti-FLAG- or anti-myc antibody. An empty plasmid was used as a negative control. (C) HCVcc infected

Huh-7 cells were transfected with a SPCS1-myc expression plasmid. Cell lysates of the transfected cells were immunoprecipitated with anti-myc antibody. The resulting precipitates and whole cell lysates used in immunoprecipitation (IP) were examined by immunoblotting using anti-NS2 or anti-SPCS1 antibody. (D) Expression of SPCS1-myc and its deletion mutants. 293T cells were transfected with indicated plasmids. The cell lysates were examined by immunoblotting using anti-myc or anti-actin antibody. (E) Cells were co-transfected with indicated plasmids, and then lysates of transfected cells were immunoprecipitated with anti-myc antibody. The resulting precipitates and whole cell lysates used in IP were examined by immunoblotting using anti-FLAG- or anti-myc antibody. (F) Lysates of the transfected cells were immunoprecipitated with anti-myc antibody. The resulting precipitates (right panel) and whole cell lysates used in IP (left panel) were examined by immunoblotting using anti-FLAG or anti-myc antibody. (G) 293T cells were transfected with indicated plasmids. 2 days posttransfection, cells were fixed and permeabilized with Triton X-100, then subjected to in situ PLA (Upper) or immunofluorescence staining (Lower) using anti-FLAG and anti-V5 antibodies. (H) Detection of the SPCS1-NS2 interaction in transfected cells using the mKG system. 293T cells were transfected by indicated pair of mKG fusion constructs. Twenty-four hours after transfection, cell were fixed and stained with DAPI, and observed under a confocal microscope.
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absence of an expression plasmid for shRNA-resistant SPCS1 (SPCS1- sh^r). Western blotting confirmed the expression levels of SPCS1 in cells (Fig. 2D). As expected, viral production in the culture supernatants of the transfected cells was significantly impaired in SPCS1-knockdown cells compared with parental Huh-7 cells (Fig. 2E white bars). Expression of SPCS1- sh^r in KD#31 cells recovered virus production in the supernatant to a level similar to that in the parental cells. Expression of SPCS1-sh^r in parental Huh-7 cells did not significantly enhance virus production. Taken together, these results demonstrate that SPCS1 has an important role in HCV propagation, and that the endogenous expression level of SPCS1 is sufficient for the efficient propagation of HCV.

A typical feature of the *Flaviviridae* family is that their precursor polyprotein is processed into individual mature proteins mediated by host ER-resident peptidase(s) and viral-encoded protease(s). We therefore next examined the role of SPCS1 in the propagation of Japanese encephalitis virus (JEV), another member of the *Flaviviridae* family. SPCS1 siRNAs or control siRNA were transfected into Huh7.5.1 cells followed by infection with JEV or HCVcc. Although knockdown of SPCS1 severely impaired HCV production (Fig. 3A), the propagation of JEV was not affected under the SPCS1-knockdown condition (Fig. 3B). Expression of the viral proteins as well as knockdown of SPCS1 were confirmed (Fig. 3C). This suggests that SPCS1 is not a broadly active modulator of the flavivirus lifecycle, but rather is involved specifically in the production of certain virus(es) such as HCV.

Knockdown of SPCS1 exhibits no influence on the processing of HCV proteins and the secretion of host-cell proteins

Since SPCS1 is a component of the signal peptidase complex, which plays a role in proteolytic processing of membrane proteins at the ER, it may be that SPCS1 is involved in processing HCV

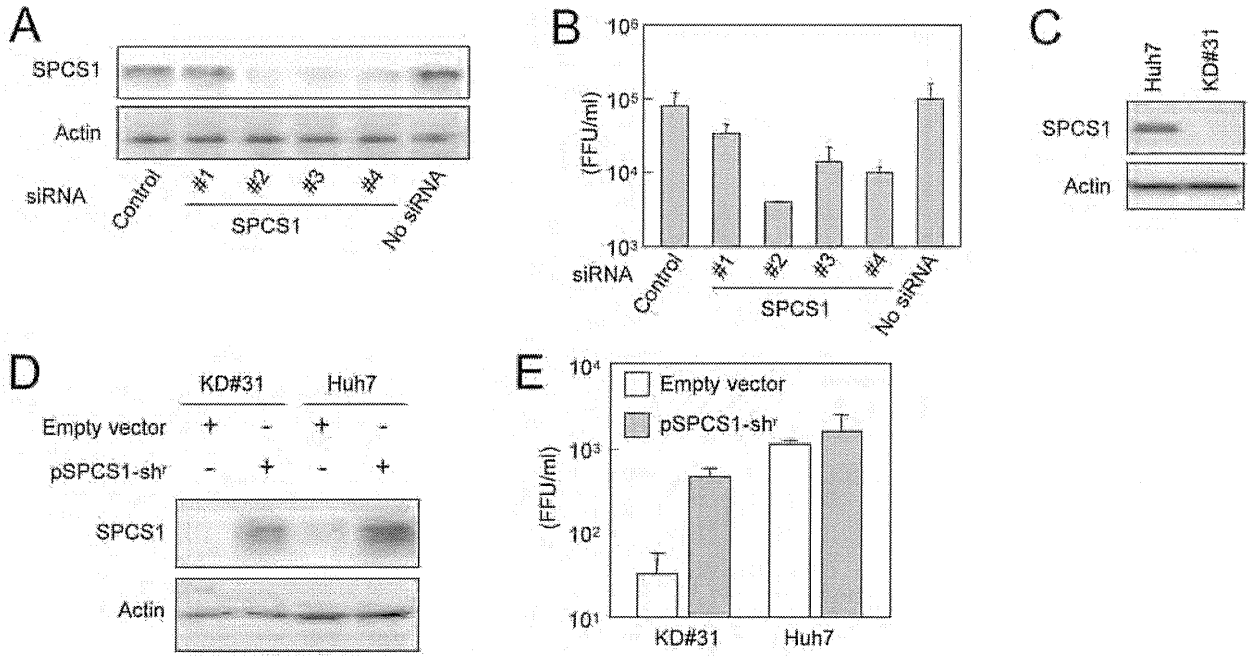

Figure 2. Effect of SPCS1 knockdown on the production of HCV. (A) Huh7.5.1 cells were transfected with four different siRNAs targeted for SPCS1 or control siRNA at a final concentration of 15 nM, and infected with HCVcc at a multiplicity of infection (MOI) of 0.05 at 24 h post-transfection. Expression levels of endogenous SPCS1 and actin in the cells were examined by immunoblotting using anti-SPCS1 and anti-actin antibodies at 3 days post-infection. (B) Infectious titers of HCVcc in the supernatant of cells infected as above were determined at 3 days postinfection. (C) Huh-7 cells were transfected with pSilencer-SPCS1, and hygromycin B-resistant cells were selected. The SPCS1-knockdown cell line established (KD#31) and parental Huh-7 cells were subjected to immunoblotting to confirm SPCS1 knockdown. (D) KD#31 cells or parental Huh-7 cells were transfected with RNA pol I-driven full-length HCV plasmid in the presence or absence of shRNA-resistant SPCS1 expression plasmid. Expression levels of SPCS1 and actin in the cells at 5 days post-transfection were examined by immunoblotting using anti-SPCS1 and anti-actin antibodies. (E) Infectious titers of HCVcc in the supernatants of transfected SPCS1-knockdown cells or parental Huh-7 cells at 5 days post-transfection were determined.
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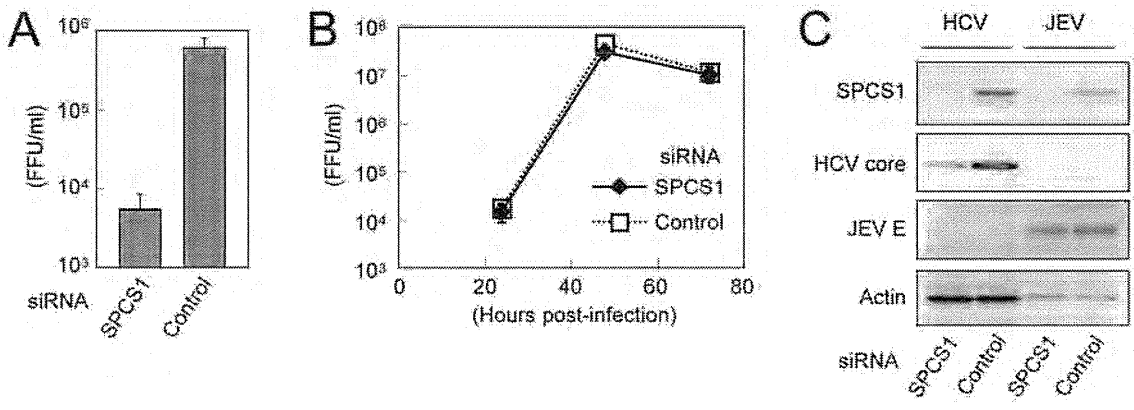

Figure 3. Effect of SPCS1 knockdown on the propagation of JEV. Huh7.5.1 cells were transfected with SPCS1 siRNA or control siRNA at a final concentration of 10 nM, and infected with JEV or HCVcc at an MOI of 0.05 at 24 h post-transfection. (A) Infectious titers of HCVcc in the supernatant at 3 days post-infection were determined. (B) Infectious titers of JEV in the supernatant at indicated time points were determined. (C) Expression levels of endogenous SPCS1 and actin as well as viral proteins in the cells were determined by immunoblotting using anti-SPCS1, anti-actin, anti-HCV core, and anti-JEV antibodies 3 days post-infection.
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proteins via interacting with ER membranes. To address this, the effect of SPCS1 knockdown on the processing of HCV precursor polyproteins in cells transiently expressing the viral Core-NS2 region was analyzed. Western blotting indicated that properly processed core and NS2 were observed in KD#31 cells as well as Huh-7 cells (Fig. 4A). No band corresponding to the unprocessed precursor polyprotein was detected in either cell line (data not shown). We also examined the effect of SPCS1 knockdown on the cleavage of the NS2/3 junction mediated by NS2/3 protease. Processed NS2 was detected in both cell lines with and without SPCS1 knockdown, which were transfected with wild-type or protease-deficient NS2-3 expression plasmids (Fig. 4B & C).

Signal peptidase plays a key role in the initial step of the protein secretion pathway by removing the signal peptide and releasing the substrate protein from the ER membrane. It is now accepted that the secretion pathways of very-low density lipoprotein or apolipoprotein E (apoE) are involved in the formation of infectious HCV particles and their release from cells [34,35]. ApoE is synthesized as a pre-apoE. After cleavage of its signal peptide in the ER, the protein is trafficked to the Golgi and trans-Golgi network before being transported to the plasma membrane and secreted. As shown in Fig. 4D, the secreted levels of apoE from Huh-7 cells with knocked-down of SPCS1 were comparable to those from control cells. In addition, the level of albumin, an abundant secreted protein from hepatocytes, in the culture supernatants of the cells was not influenced by SPCS1 knockdown (Fig. 4E). These data suggest that the knockdown of SPCS1 has no influence on the processing of viral and host secretory proteins by signal peptidase and HCV NS2/3 protease.

SPCS1 is involved in the assembly process of HCV particles but not in viral entry into cells and RNA replication

To further address the molecular mechanism(s) of the HCV lifecycle mediated by SPCS1, we examined the effect of SPCS1 knockdown on viral entry and genome replication using single-round infectious trans-complemented HCV particles (HCVtcp) [33], of which the packaged genome is a subgenomic replicon containing a luciferase reporter gene. This assay system allows us to evaluate viral entry and replication without the influence of reinfection. Despite efficient knockdown of SPCS1 (Fig. 5A), luciferase activity expressed from HCVtcp in SPCS1-knockdown cells was comparable to that in control or non-siRNA-transfected cells (Fig. 5B), suggesting that SPCS1 is not involved in viral entry into cells and subgenomic RNA replication. As a positive control, knockdown of claudin-1, a cell surface protein required for HCV entry, reduced the luciferase activity. We also examined the effect of SPCS1 knockdown on full-genome replication using HCVcc-infected cells. Despite efficient knockdown of SPCS1, expression of HCV proteins was comparable to that in control cells (Fig. 5C). By contrast, knockdown of PI4 Kinase (PI4K), which is required for replication of HCV genome, led to decrease in expression of HCV proteins. As cells that had already been infected with HCV were used, knockdown of claudin-1 had no effect on HCV protein levels. These data suggest that SPCS1 is not involved in viral entry into cells and the viral genome replication. We also observed properly processed Core, E2, NS2 and NS5B in SPCS1-knockdown cells in consistent with the result as shown in Fig. 4A, indicating no effect of SPCS1 on HCV polyprotein processing.

Next, to investigate whether SPCS1 is involved in the assembly or release of infectious particles, SPCS1-shRNA plasmid along with a pol I-driven full-genome HCV plasmid [33] were transfected into CD81-negative Huh7-25 cells, which can produce infectious HCV upon introduction of the viral genome, but are not permissive to HCV infection [36]. It is therefore possible to examine viral assembly and the release process without viral reinfection. The infectivity within the transfected cells as well as supernatants was determined 5 days post-transfection. Interestingly, both intra- and extracellular viral titers were markedly reduced by SPCS1 knockdown (Fig. 5C).

Taken together, in the HCV lifecycle, SPCS1 is most likely involved in the assembly of infectious particles rather than cell entry, RNA replication, or release from cells.

Role of SPCS1 in complex formation between NS2 and E2

It has been shown that HCV NS2 interacts with the viral structural and NS proteins in virus-producing cells [18–21], and that some of the interactions, especially the NS2-E2 interaction, are important for the assembly of infectious HCV particles. However, the functional role of NS2 in the HCV assembly process has not been fully elucidated. To test whether SPCS1 is involved in the interaction between NS2 and E2, cells were co-transfected

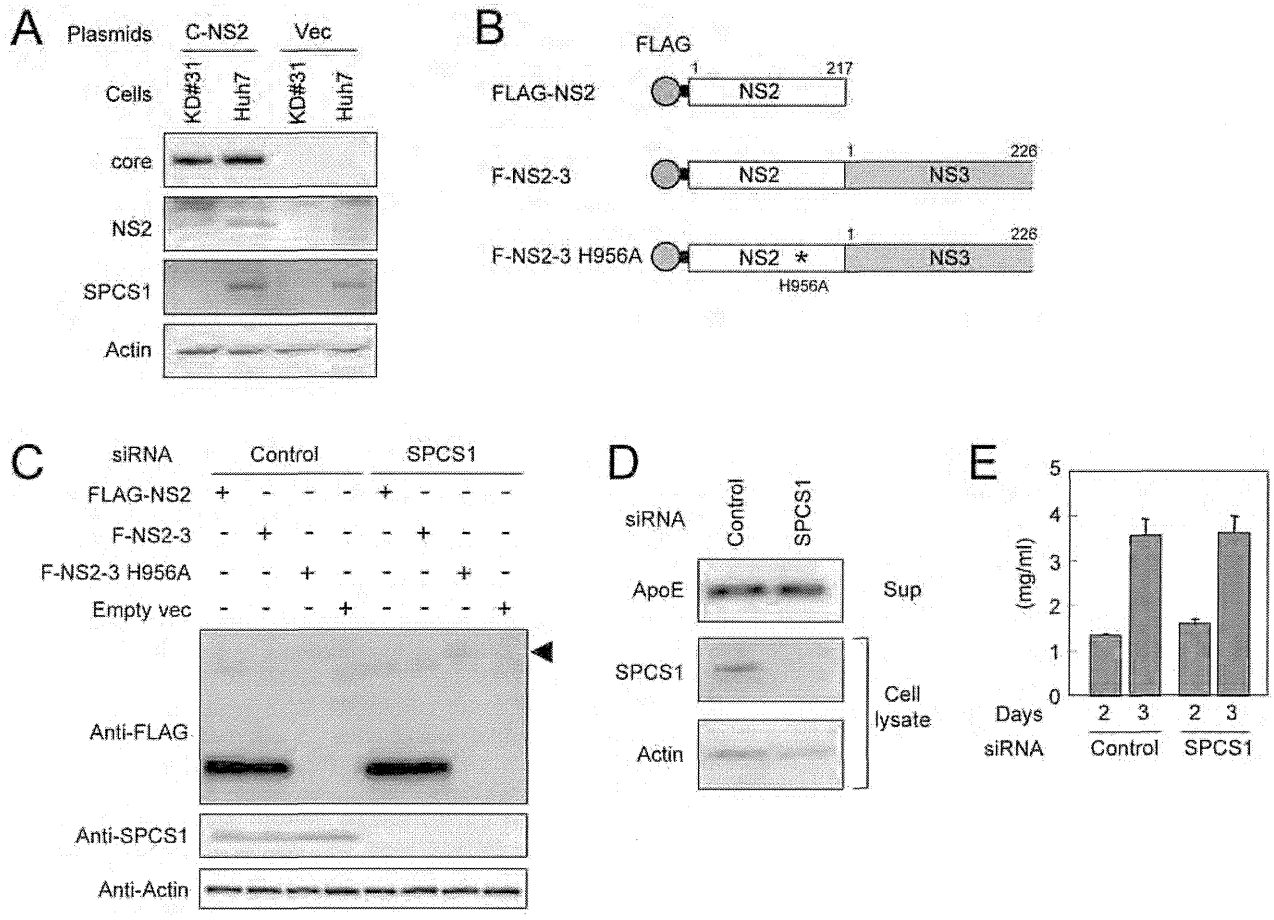

Figure 4. Effect of SPCS1 knockdown on the processing of HCV structural proteins and secretion of host proteins. (A) Core-NS2 polyprotein was expressed in KD#31 cells or parental Huh-7 cells. Core, NS2, SPCS1, and actin were detected by immunoblotting 2 days post-transfection. (B) Expression constructs of NS2 and NS2/3 proteins. His to Ala substitution mutation at aa 956 in NS2 is indicated by an asterisk. Gray circles and bold lines indicate FLAG-tag and the spacer sequences, respectively. Positions of the aa residues are indicated above the boxes. (C) Effect of SPCS1 knockdown on processing at the NS2/3 junction. Huh-7 cells were transfected with SPCS1 siRNA or control siRNA at a final concentration of 30 nM, and then transfected with plasmids for FLAG-NS2, F-NS2-3, or F-NS2-3 with a protease-inactive mutation (H956A). NS2 in cell lysates was detected by anti-FLAG antibody 2 days post-transfection. Arrowhead indicates unprocessed NS2-3 polyproteins. (D) Effect of SPCS1 knockdown on the secretion of apoE. Huh7.5.1 cells were transfected with SPCS1 siRNAs or control siRNA at a final concentration of 20 nM, and apoE in the supernatant and SPCS1 and actin in the cells were detected 3 days post-transfection. (E) Effect of SPCS1 knockdown on the secretion of albumin. Huh7.5.1 cells were transfected with SPCS1 siRNA or control siRNA, and albumin in the culture supernatants at 2 and 3 days post-transfection was measured by ELISA.
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with expression plasmids for E2, FLAG-NS2, and SPCS1-myc. E2 and NS2 were co-immunoprecipitated with SPCS1-myc, and E2 and SPCS1-myc were co-immunoprecipitated with FLAG-NS2 (Fig. 6A), suggesting the formation of an E2-NS2-SPCS1 complex in cells. To investigate the interaction of SPCS1 with E2 in the absence of NS2, HCV Core-p7 polyprotein or E2 protein were co-expressed with SPCS1-myc in cells, followed by immunoprecipitation with anti-myc antibody. As shown in Fig. 6B and Fig. S2, E2 was co-immunoprecipitated with SPCS1-myc. The interaction between SPCS1 and E2 was further analyzed *in situ* by PLA and mKG system. Specific signals indicating formation of the SPCS1-E2 complex were detected in both assays (Fig. S3), suggesting physical interaction between SPCS1 and E2 in cells.

We further determined the region of SPCS1 responsible for the interaction with E2 by co-immunoprecipitation assays. Full-length and deletion mutant d2 of SPCS1 (Fig. 1A) were similarly co-immunoprecipitated with E2, while only a limited amount of d1 mutant SPCS1 (Fig. 1A) was co-precipitated (Fig. 6C). It may be that the aa 43–102 region of SPCS1, which was identified as the region involved in the NS2 interaction (Fig. 1D), is important for its interaction with E2, and that deletion of the N-terminal cytoplasmic region leads to misfolding of the protein and subsequent inaccessibility to E2.

Finally, to understand the significance of SPCS1 in the NS2-E2 interaction, Huh7.5.1 cells with or without SPCS1 knockdown by siRNA were transfected with expression plasmids for Core-p7 and FLAG-NS2, followed by co-immunoprecipitation with anti-FLAG antibody. As shown in Fig. 6D, the NS2-E2 interaction was considerably impaired in the SPCS1-knockdown cells as compared to that in the control cells. A similar result was obtained in the stable SPCS1-knockdown cell line (Fig. 6E). In contrast, in that cell line, the interaction of NS2 with NS3 was not impaired by SPCS1 knockdown (Fig. 6E).

These results, together with the above findings, suggest that SPCS1 is required for or facilitates the formation of the membrane-associated NS2-E2 complex, which participates in the proper assembly of infectious particles.

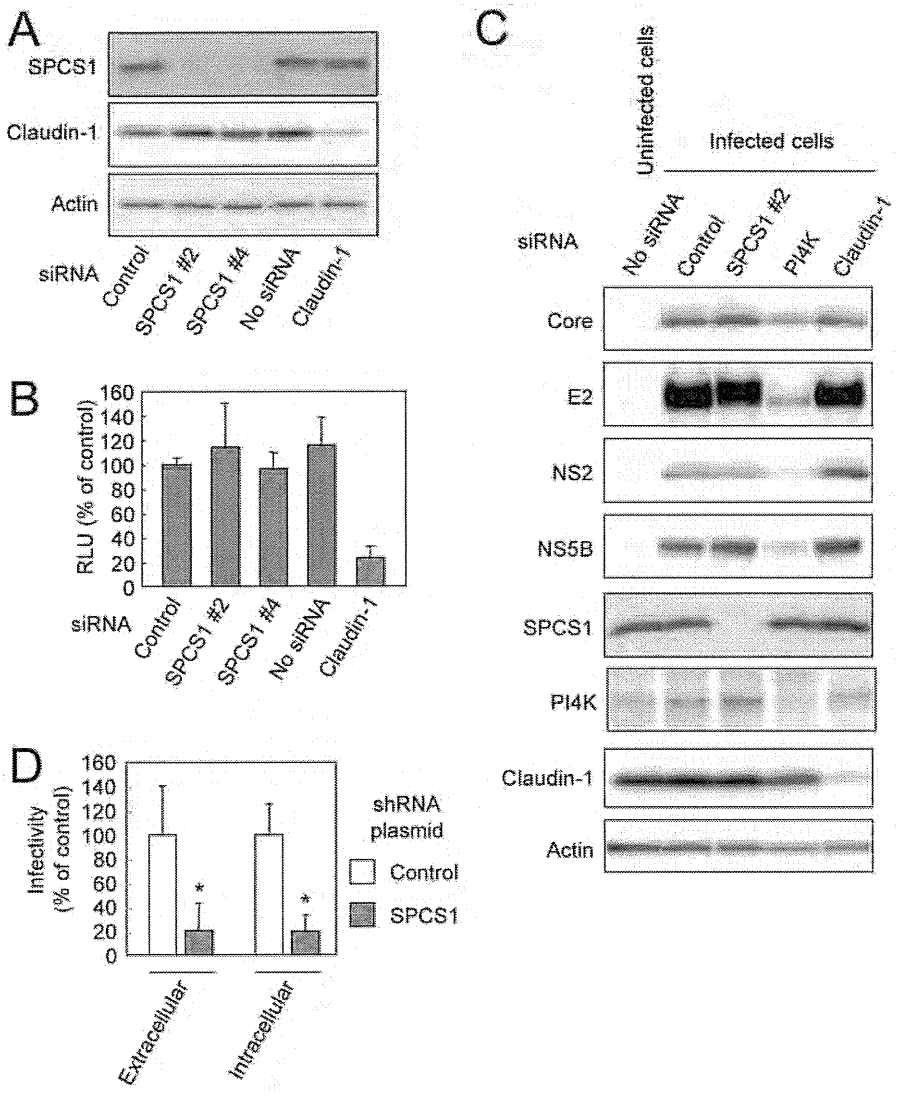

Figure 5. Effect of SPCS1 knockdown on entry into cells, genome replication, and assembly or release of infectious virus. (A) Huh7.5.1 cells were transfected with siRNA for SPCS1 or claudin1, or control siRNA at a final concentration of 30 nM. Expression levels of endogenous SPCS1, claudin-1, and actin in the cells at 2 days post-transfection were examined by immunoblotting using anti-SPCS1, anti-actin, and anti-claudin-1 antibodies. (B) Huh7.5.1 cells transfected with indicated siRNAs were infected with HCVtcp at 2 days post-transfection. Luciferase activity in the cells was subsequently determined at 2 days post-infection. Data are averages of triplicate values with error bars showing standard deviations. (C) Effect of SPCS1 knockdown on replication of HCV genome. HCV-infected Huh-7 cells transfected with siRNA for SPCS1, PI4K or claudin1, or control siRNA at a final concentration of 30 nM. Expression levels of HCV proteins as well as endogenous SPCS1, PI4K, claudin-1, and actin in the cells at 3 days post-transfection were examined by immunoblotting. (D) HCV infectivity in Huh7.5.1 cells inoculated with culture supernatant and cell lysate from Huh7-25 cells transfected with pSilencer-SPCS1 or control vector along with pHH/JFH1am at 5 days post-transfection. Statistical differences between Control and SPCS1 knockdown were evaluated using Student's t-test. *$p<0.005$ vs. Control.
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Discussion

In this study, we identified SPCS1 as a novel host factor that interacts with HCV NS2, and showed that SPCS1 participates in HCV assembly through complex formation with NS2 and E2. In general, viruses require host cell-derived factors for proceeding and regulating each step in their lifecycle. Although a number of host factors involved in genome replication and cell entry of HCV have been reported, only a few for viral assembly have been identified to date. To our knowledge, this is the first study to identify an NS2-interacting host protein that plays a role in the production of infectious HCV particles.

NS2 is a hydrophobic protein containing TM segments in the N-terminal region. The C-terminal half of NS2 and the N-terminal third of NS3 form the protease, which is a prerequisite for NS2-NS3 cleavage. In addition, it is now accepted that this protein is essential for particle production [4–6,12]. However, the mechanism of how NS2 is involved in the assembly process of HCV has been unclear.

So far, two studies have screened for HCV NS2 binding proteins by yeast two-hybrid analysis [37,38]. Erdtmann et al. reported that no specific interaction was detected by a conventional yeast hybrid screening system using full-length NS2 as a bait, probably due to hampered translocation of the bait to the

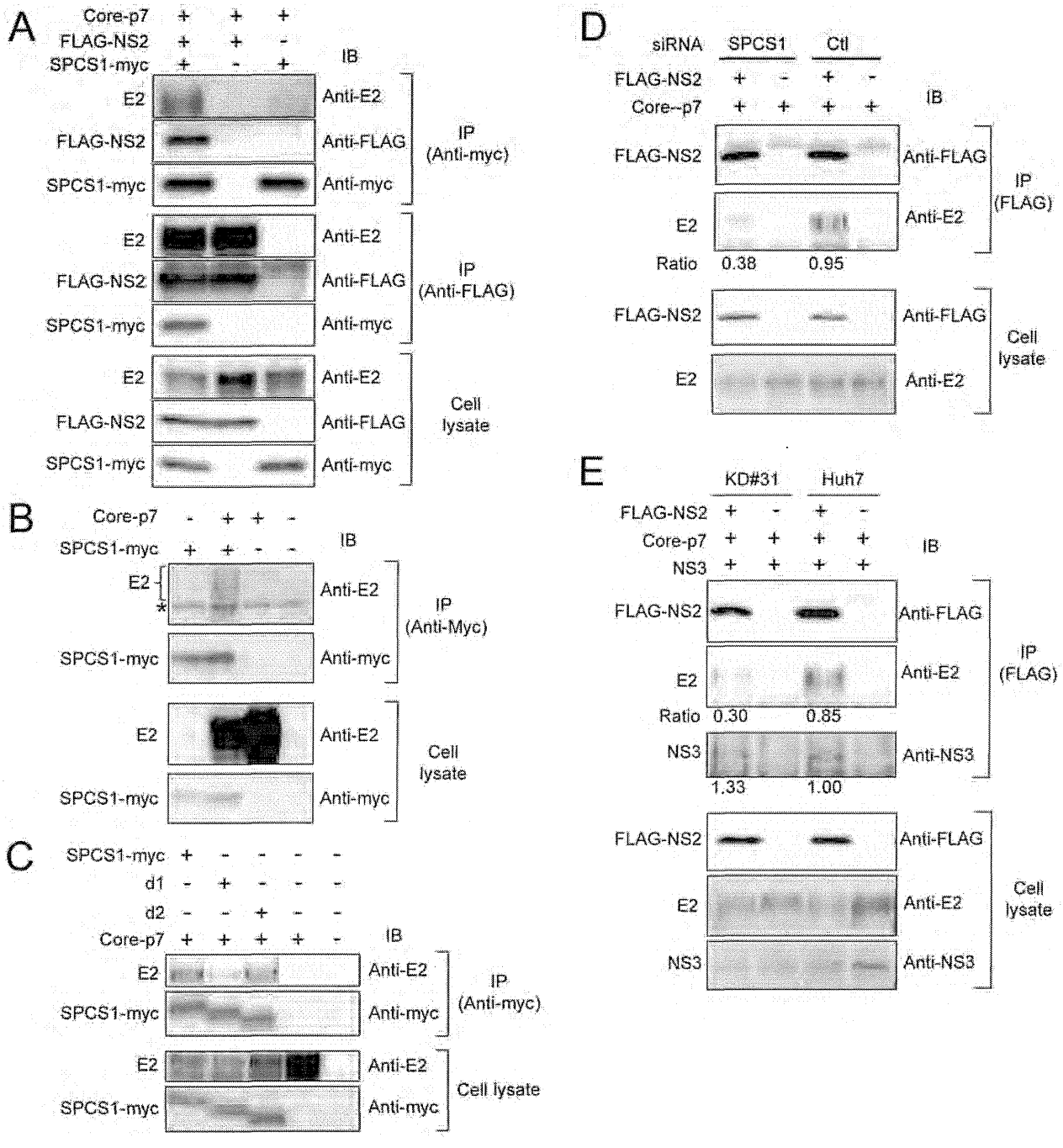

Figure 6. SPCS1 forms a complex with NS2 and E2. (A) Lysates of cells, which were co-transfected with Core-p7, FLAG-NS2, and SPCS1-myc expression plasmids, were immunoprecipitated with anti-myc or anti-FLAG antibody. The resulting precipitates and whole cell lysates used in IP were examined by immunoblotting using anti-E2, anti-FLAG, or anti-myc antibody. An empty plasmid was used as a negative control. (B) Cells were transfected with Core-p7 expression plasmid in the presence or absence of SPCS1-myc expression plasmid. The cell lysates of the transfected cells were immunoprecipitated with anti-myc antibody. The resulting precipitates and whole cell lysates used in IP were examined by immunoblotting using anti-E2 or anti-myc antibody. An empty plasmid was used as a negative control. The bands corresponding to immunoglobulin heavy chain are marked by an asterisk. (C) Cells were co-transfected with Core-p7 and SPCS1-myc expression plasmids. The cell lysates of the transfected cells were immunoprecipitated with anti-myc antibody. The resulting precipitates and whole cell lysates used in IP were examined by immunoblotting using anti-E2 or anti-myc antibody. (D) Huh7.5.1 cells were transfected with SPCS1 siRNA or control siRNA at a final concentration of 20 nM. After 24 h, Huh7.5.1 cells were then co-transfected with FLAG-NS2 and Core-p7 expression plasmids. The lysates of transfected cells were immunoprecipitated with anti-FLAG antibody, followed by immunoblotting with anti-FLAG and anti-E2 antibodies. Immunoblot analysis of whole cell lysates was also performed. Intensity of E2 bands was quantified, and the ratio of immunoprecipitated E2 to E2 in cell lysate was shown. Similar results were obtained in 2 independent experiments. (E) KD#31 cells and parental Huh-7 cells were co-transfected with FLAG-NS2, Core-p7, and NS3 expression plasmids. The lysates of transfected cells were immunoprecipitated with anti-FLAG antibody followed by immunoblotting with anti-FLAG, anti-E2, and anti-NS3 antibodies. Immunoblot analysis of whole cell lysates was also performed. The ratio of immunoprecipitated E2 or NS3 to E2 or NS3 in cell lysate, respectively, were shown.

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nucleus [37]. They further screened a human liver cDNA library using NS2 with deletion of the N-terminal TM domain, and CIDE-B protein, a member of the CIDE family of apoptosis-inducing factors, was identified. However, whether CIDE-B is involved in the HCV lifecycle and/or viral pathogenesis is unclear. de Chassey et al. reported several cellular proteins as potential NS2 binding proteins using NS2 with N-terminal deletion as a bait [38]. Involvement of these proteins in the HCV lifecycle is also unclear. In our study, to screen for NS2-binding partners using full-length NS2 as a bait, we utilized a split-ubiquitin yeast two-hybrid system that allows for the identification of interactions between full-length integral membrane proteins or between a full-length membrane-associated protein and a soluble protein [39]. SPCS1 was identified as a positive clone of an NS2-binding protein, but proteins that have been reported to interact with NS2 were not selected from our screening.

SPCS1 is a component of the signal peptidase complex that processes membrane-associated and secreted proteins in cells. The mammalian signal peptidase complex consists of five subunits, SPCS1, SPCS2, SPCS3, SEC11A, and SEC11C [27]. Among them, the functional role of SPCS1 is still unclear, and SPCS1 is considered unlikely to function as a catalytic subunit according to membrane topology [40]. The yeast homolog of SPCS1, Spc1p, is also known to be nonessential for cell growth and enzyme activity [28,41]. Interestingly, these findings are consistent with the results obtained in this study. Knockdown of SPCS1 did not impair processing of HCV structural proteins (Fig. 4A) or secretion of apoE and albumin (Fig. 4B and C), which are regulated by ER membrane-associated signal peptidase activity. The propagation of JEV, whose structural protein regions are cleaved by signal peptidase, was also not affected by the knockdown of SPCS1 (Fig. 3B). SPCS1, SPCS2, and SPCS3 are among the host factors that function in HCV production identified from genome-wide siRNA screening [42]. It seemed that knockdown of SPCS1 had a higher impact on the later stage of viral infection compared to either SPCS2 or SPCS3, which are possibly involved in the catalytic activity of the signal peptidase.

Further analyses to address the mechanistic implication of SPCS1 on the HCV lifecycle revealed that SPCS1 knockdown impaired the assembly of infectious viruses in the cells, but not cell entry, RNA replication, or release from the cells (Fig. 5). We thus considered the possibility that the SPCS1-NS2 interaction is important for the role of NS2 in viral assembly. Several studies have reported that HCV NS2 is associated biochemically or genetically with viral structural proteins as well as NS proteins [10,18–25]. As an intriguing model, it has been proposed that NS2 functions as a key organizer of HCV assembly and plays a key role in recruiting viral envelope proteins and NS protein(s) such as NS3 to the assembly sites in close proximity to lipid droplets [21]. The interaction of NS2 with E2 has been shown by use of an HCV genome encoding tagged-NS2 protein in virion-producing cells. Furthermore, the selection of an assembly-deficient NS2 mutation located within its TM3 for pseudoreversion leads to a rescue mutation in the TM domain of E2, suggesting an in-membrane interaction between NS2 and E2 [21]. Another study identified two classes of NS2 mutations with defects in virus assembly; one class leads to reduced interaction with NS3, and the other, located in the TM3 domain, maintains its interaction with NS3 but shows impaired interaction between NS2 and E1-E2 [20]. However, the precise details of the NS2-E2 interaction, such as direct protein-protein binding or participating host factors, are unknown. Our results provide evidence that SPCS1 has an important role in the formation of the NS2-E2 complex by its interaction with both NS2 and E2, most likely via their transmembrane domains, including TM3 of NS2. As knockdown of SPCS1 reduced the interaction of NS2 and E2 as shown in Fig. 6D and E, it may be that SPCS1 contributes to NS2-E2 complex formation or to stabilizing the complex. Based on data obtained in this study, we propose a model of the formation of an E2-SPCS1-NS2 complex at the ER membrane (Fig. 7).

In summary, we identified SPCS1 as a novel NS2-binding host factor required for HCV assembly by split-ubiquitin membrane yeast two-hybrid screening. Our data demonstrate that SPCS1 plays a key role in the E2-NS2 interaction via formation of an E2-SPCS1-NS2 complex. These findings provide clues for understanding the molecular mechanism of assembly and formation of infectious HCV particles.

Materials and Methods

Split ubiquitin-based yeast two-hybrid screen

A split-ubiquitin membrane yeast two-hybrid screen was performed to identify possible NS2 binding partners. This screening system (DUALmembrane system; Dualsystems Biotech, Schlieren, Switzerland) is based on an adaptation of the ubiquitin-based split protein sensor [26]. The full-length HCV NS2 gene derived from the JFH-1 strain [29] was cloned into pBT3-SUC bait vector to obtain bait protein fused to the C-terminal half of ubiquitin (NS2-Cub) along with a transcription factor. Prey proteins generated from a human liver cDNA library (Dualsystems Biotech) were expressed as a fusion to the N-terminal half of ubiquitin (NubG). Complex formation between NS2-Cub and NubG-protein from the library leads to cleavage at the C-terminus of reconstituted ubiquitin by ubiquitin-specific protease(s) with consequent translocation of the transcription factor into the nucleus. Library plasmids were recovered from positive transformants, followed by determining the nucleotide sequences of inserted cDNAs, which were identified using the BLAST algorithm with the GenBank database.

Cell culture

Human embryonic kidney 293T cells, and human hepatoma Huh-7 cells and its derivative cell lines Huh7.5.1 [43] and Huh7-25 [36], were maintained in Dulbecco's modified Eagle medium supplemented with nonessential amino acids, 100 U of penicillin/ml, 100 μg of streptomycin/ml, and 10% fetal bovine serum (FBS) at 37°C in a 5% CO_2 incubator.

Plasmids

Plasmids pCAGC-NS2/JFH1am and pHHJFH1am were previously described [33]. The plasmid pCAGC-p7/JFHam, having

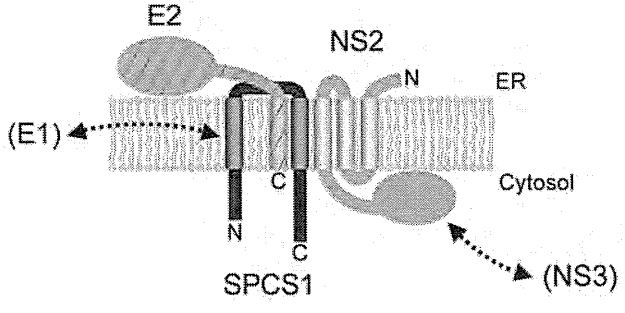

Figure 7. A proposed model for a complex consisting of NS2, SPCS1 and E2 associated with ER membranes.
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adaptive mutations in E2 (N417S) and p7 (N765D) in pCAG/C-p7 [44], was constructed by oligonucleotide-directed mutagenesis.

To generate the NS2 expression plasmid pCAG F-NS2 and the NS2-deletion mutants, cDNAs encoding the full-length or parts of NS2 possessing the FLAG-tag and spacer sequences (MDYKDDDDKGGGGS) were amplified from pCAGC-NS2/JFH1am by PCR. The resultant fragments were cloned into pCAGGS. For the NS2-NS3 expression plasmid pEF F-NS2-3, a cDNA encoding the entire NS2 and the N-terminal 226 amino acids of NS3 with the N-terminal FLAG-tag sequence as above was amplified by PCR and was inserted into pEF1/myc-His (Invitrogen, Carlsbad, CA). The plasmid pEF F-NS2-3 H956A, having a defective mutation in the protease active site within NS2, was constructed by oligonucleotide-directed mutagenesis.

To generate the NS3 expression plasmid pCAGN-HANS3JFH1, a cDNA encoding NS3 with an HA tag at the N terminus, which was amplified by PCR with pHHJFHam as a template, was inserted downstream of the CAG promoter of pCAGGS.

To generate the SPCS1-expressing plasmid pCAG-SPCS1-myc and its deletion mutants, cDNAs encoding all of or parts of SPCS1 with the Myc tag sequence (EQKLISEEDL) at the C-terminus, which was amplified by PCR, was inserted into pCAGGS. pSilencer-shSPCS1 carrying a shRNA targeted to SPCS1 under the control of the U6 promoter was constructed by cloning the oligonucleotide pair 5′- GATCCGCAATAGTTGGATTTATCT TTCAAGAGAAGATAAATCCAACTATTGCTTTTTTGGA AA-3′ and 5′- AGCTTTTCCAAAAAAGCAATAGTTGGATT-TATCTTCTCTTGAAAGATAAATCCAACTATTGCG-3′ between the BamHI and HindIII sites of pSilencer 2.1-U6 hygro (Ambion, Austin, TX). To generate a construct expressing shRNA-resistant SPCS1 pSPCS1-sh^r, a cDNA fragment coding for SPCS1, in which the 6 bp within the shRNA targeting region (5′-GCAATAGTTGGATTTATCT-3′) was replaced with GCT ATTGTCGGCTTCATAT that causes no aa change, was amplified by PCR. The resulting fragment was confirmed by sequencing and then cloned into pCAGGS.

Full-length SPCS1 and N-terminal region of NS2 (aa 1–94) were amplified by PCR and cloned onto EcoRI and HindIII sites of phmKGN-MN and phmKGC-MN, which encode the mKG fragments (CoralHue Fluo-chase Kit; MBL, Nagoya, Japan), designated as pSPCS1-mKG(N) and pNS2-mKG(C), respectively. Transmembrane domain of the E1 to E2 was also amplified by PCR and cloned onto EcoRI and HindIII sites of phmKGC-MN. To avoid the cleavage of E2-mKG(C) fusion protein in the cells, last alanine of the E2 protein was deleted. Positive control plasmids for mKG system, pCONT-1 and pCONT-2, which encode p65 partial domain from NF-κB complex fused to mKG(N) and p50 partial domain from NF-κB complex fused to mKG(C) respectively, were supplied from MBL. For PLA experiments, cDNA for SPCS1 d2-myc with the V5 tag at the N-terminus was amplified by PCR, and inserted into pCAGGS. For expression of HCV E2, cDNA from E1 signal to the last codon of the transmembrane domain of the E2, in which part of the hypervariable region-1 (aa 394–400) were replaced with FLAG-tag and spacer sequences (DYKDDDDKGGG), was amplified by PCR, and inserted into pCAGGS. For expression of FLAG-core, cDNAs encoding Core (aa 1–152) possessing the FLAG-tag and spacer sequences (MDYKDDDDKGGGGS) were amplified from pCAGC191 [45] by PCR. The resultant fragments were cloned into pCAGGS.

DNA transfection

Monolayers of 293T cells were transfected with plasmid DNA using FuGENE 6 transfection reagent (Roche, Basel, Switzerland) in accordance with the manufacturer's instructions. Huh-7, Huh7.5.1, and Huh7-25 cells were transfected with plasmid DNA using TransIT LT1 transfection reagent (Mirus, Madison, WI).

PLA

The assay was performed in a humid chamber at 37°C according to the manufacturer's instructions (Olink Bioscience, Uppsala, Sweden). Transfected 293T cells were grown on glass coverslips. Two days after transfection, cells were fixed with 4% paraformaldehyde in phosphate-buffered saline (PBS) for 20 min, then blocked and permeabilized with 0.3% Triton X-100 in a nonfat milk solution (Block Ace; Snow Brand Milk Products Co., Sapporo, Japan) for 60 min at room temperature. Then the samples were incubated with a mixture of mouse anti-FLAG monoclonal antibody M2 and rabbit anti-V5 polyclonal antibody for 60 min, washed three times, and incubated with plus and minus PLA probes. After washing, the ligation mixture containing connector oligonucleotide was added for 30 min. The washing step was repeated, and amplification mixture containing fluorescently labeled DNA probe was added for 100 min. Finally, the samples were washed and mounted with DAPI mounting medium. The signal representing interaction was analyzed by Leica TCS SPE confocal microscope.

mKG system

The assay was performed according to the manufacturer's instructions (CoralHue Fluo-chase Kit; MBL). 293T cells were transfected by a pair of mKG fusion constructs. Twenty-four hours after transfection, cell were fixed and stained with DAPI. The signal representing interaction was analyzed by Leica TCS SPE confocal microscope.

Gene silencing by siRNA

The siRNAs were purchased from Sigma-Aldrich (St. Louis, MO) and were introduced into the cells at a final concentration of 10 to 30 nM using Lipofectamine RNAiMAX (Invitrogen). Target sequences of the siRNAs were as follows: SPCS1 #1 (5′-CAGUUCGGGUGGACUGUCU-3′), SPCS1 #2 (5′-GCAAUA GUUGGAUUUAUCU-3′), SPCS1 #3 (5′-GAUGUUUCAGG-GAAUUAUU-3′), SPCS1 #4 (5′-GUUAUGGCCGGAUUUG-CUU-3′), claudin-1 (5′-CAGUCAAUGCCAGGUACGA-3′), PI4K (5′-GCAAUGUGCUUCGCGAGAA-3′) and scrambled negative control (5′-GCAAGGGAAACCGUGUAAU-3′). Additional control siRNAs for SPCS1 were as follows: C911-#2 (5′-GCAAUAGUaccAUUUAUCU-3′), C911-#3 (5′-GAUGUUU-CuccGAAUUAUU-3′) and C911-#4 (5′-GUUAUGGCgccAUU UGCUU-3′). Bases 9 through 11 of the siRNAs replaced with their complements were shown in lower cases.

Establishment of a stable cell line expressing the shRNA

Huh-7 cells were transfected with pSilencer-SPCS1, and drug-resistant clones were selected by treatment with hygromycin B (Wako, Tokyo, Japan) at a final concentration of 500 μg/ml for 4 weeks.

Virus

HCVtcp and HCVcc derived from JFH-1 having adaptive mutations in E2 (N417S), p7 (N765D), and NS2 (Q1012R) were generated as described previously [33]. The rAT strain of JEV [46] was used to generate virus stock.

Antibodies

Mouse monoclonal antibodies against actin (AC-15) and FLAG (M2) were obtained from Sigma-Aldrich (St. Louis, MO). Mouse

monoclonal antibodies against flavivirus group antigen (D1-4G2) were obtained from Millipore (Billerica, MA). Rabbit polyclonal antibodies against FLAG and V5 were obtained from Sigma-Aldrich. Rabbit polyclonal antibodies against SPCS1, claudin-1, PI4K and myc were obtained from Proteintech (Chicago, IL), Life Technologies (Carlsbad, CA), Cell Signaling (Danvers, MA) and Santa Cruz Biotechnology (Santa Cruz, CA), respectively. An anti-apoE goat polyclonal antibody was obtained from Millipore. Rabbit polyclonal antibodies against NS2 and NS3 were generated with synthetic peptides as antigens. Mouse monoclonal antibodies against HCV Core (2H9) and E2 (8D10-3) and rabbit polyclonal antibodies against NS5A and JEV are described elsewhere [47].

Titration

To determine the titers of HCVcc, Huh7.5.1 cells in 96-well plates were incubated with serially-diluted virus samples and then replaced with media containing 10% FBS and 0.8% carboxymethyl cellulose. Following incubation for 72 h, the monolayers were fixed and immunostained with the anti-NS5A antibody, followed by an Alexa Fluor 488-conjugated anti-rabbit secondary antibody (Invitrogen). Stained foci were counted and used to calculate the titers of focus-forming units (FFU)/ml. For intracellular infectivity of HCVcc, the pellets of infected cells were resuspended in culture medium and were lysed by four freeze-thaw cycles. After centrifugation for 5 min at 4,000 rpm, supernatants were collected and used for virus titration as above. For titration of JEV, Huh7.5.1 cells were incubated with serially-diluted virus samples and then replaced with media containing 10% FBS and 0.8% carboxymethyl cellulose. After a 24 h incubation, the monolayers were fixed and immunostained with a mouse monoclonal anti-flavivirus group antibody (D1-4G2), followed by an Alexa Fluor 488-conjugated anti-mouse secondary antibody (Invitrogen).

Immunoprecipitation

Transfected cells were washed with ice-cold PBS, and suspended in lysis buffer (20 mM Tris-HCl [pH 7.4] containing 135 mM NaCl, 1% TritonX-100, and 10% glycerol) supplemented with 50 mM NaF, 5 mM Na_3VO_4, and complete protease inhibitor cocktail, EDTA free (Roche). Cell lysates were sonicated for 10 min and then incubated for 30 min at 4°C, followed by centrifugation at 14,000× *g* for 10 min. The supernatants were immunoprecipitated with anti-Myc-agarose beads (sc-40, Santa Cruz Biotechnology) or anti-FLAG antibody in the presence of Dynabeads Protein G (Invitrogen). The immunocomplexes were precipitated with the beads by centrifugation at 800× *g* for 30 s, or by applying a magnetic field, and then were washed four times with the lysis buffer. The proteins binding to the beads were boiled with SDS sample buffer and then subjected to SDS–polyacrylamide gel electrophoresis (PAGE).

Immunoblotting

Transfected cells were washed with PBS and lysed with 50 mM Tris-HCl, pH 7.4, 300 mM NaCl, 1% Triton X-100. Lysates were then sonicated for 10 min and added to the same volume of SDS sample buffer. The protein samples were boiled for 10 min, separated by SDS-PAGE, and transferred to polyvinylidene difluoride membranes (Millipore). After blocking, the membranes were probed with the primary antibodies, followed by incubation with peroxidase-conjugated secondary antibody. Antigen-antibody complexes were visualized by an enhanced chemiluminescence detection system (Super Signal West Pico Chemiluminescent Substrate; PIERCE, Rockford, IL) according to the manufacturer's protocol and were detected by an LAS-3000 image analyzer system (Fujifilm, Tokyo, Japan).

Albumin measurement

To determine the human albumin level secreted from cells, culture supernatants were collected and passed through a 0.45-μm pore filter to remove cellular debris. The amounts of human albumin were quantified using a human albumin ELISA kit (Bethyl Laboratories, Montgomery, TX) according to the manufacturer's protocol.

Supporting Information

Figure S1 Effects of SPCS1-siRNAs and the C911 mismatch control siRNAs on the expression of SPCS1 and production of HCV. (A) Huh7.5.1 cells were transfected with either siRNAs targeted for SPCS1 (SPCS1-#2, -#3, and -#4), scrambled control siRNA (Scrambled) or C911 siRNA in which bases 9 through 11 of each SPCS1 siRNA were replaced with their complements (C911-#2, -#3, and -#4) at a final concentration of 15 nM, and were infected with HCVcc at a multiplicity of infection (MOI) of 0.05 at 24 h post-transfection. Expression levels of endogenous SPCS1 and actin in the cells were examined by immunoblotting using anti-SPCS1 and anti-actin antibodies at 3 days post-infection. (B) Infectious titers of HCVcc in the supernatant of the infected cells were determined at 3 days postinfection.
(TIF)

Figure S2 293T cells were transfected with E2 expression plasmid in the presence or absence of SPCS1-myc expression plasmid. The cell lysates of the transfected cells were immunoprecipitated with anti-myc antibody. The resulting precipitates and whole cell lysates used in IP were examined by immunoblotting using anti-E2 or anti-myc antibody. An empty plasmid was used as a negative control.
(TIF)

Figure S3 Interaction of HCV E2 with SPCS1 in mammalian cells. (A) 293T cells were transfected with indicated plasmids. 2 days posttransfection, cells were fixed and permeabilized with Triton X-100, then subjected to in situ PLA (Upper) or immunofluorescence staining (Lower) using anti-FLAG and anti-V5 antibodies. (B) Detection of the SPCS1-E2 interaction in transfected cells using the mKG system. 293T cells were transfected by indicated pair of mKG fusion constructs. Twenty-four hours after transfection, cell were fixed and stained with DAPI, and observed under a confocal microscope.
(TIF)

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Author Contributions

Conceived and designed the experiments: RS TS. Performed the experiments: RS MM. Analyzed the data: RS KW HA TS. Contributed reagents/materials/analysis tools: YM TW. Wrote the paper: RS TS.

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Specific inhibition of hepatitis C virus entry into host hepatocytes by fungi-derived sulochrin and its derivatives

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Compound

ABSTRACT

Hepatitis C virus (HCV) is a major causative agent of hepatocellular carcinoma. Although various classes of anti-HCV agents have been under clinical development, most of these agents target RNA replication in the HCV life cycle. To achieve a more effective multidrug treatment, the development of new, less expensive anti-HCV agents that target a different step in the HCV life cycle is needed. We prepared an in-house natural product library consisting of compounds derived from fungal strains isolated from seaweeds, mosses, and other plants. A cell-based functional screening of the library identified sulochrin as a compound that decreased HCV infectivity in a multi-round HCV infection assay. Sulochrin inhibited HCV infection in a dose-dependent manner without any apparent cytotoxicity up to 50 μM. HCV pseudoparticle and trans-complemented particle assays suggested that this compound inhibited the entry step in the HCV life cycle. Sulochrin showed anti-HCV activities to multiple HCV genotypes 1a, 1b, and 2a. Co-treatment of sulochrin with interferon or a protease inhibitor telaprevir synergistically augmented their anti-HCV effects. Derivative analysis revealed anti-HCV compounds with higher potencies (IC_{50} < 5 μM). This is the first report showing an antiviral activity of methoxybenzoate derivatives. Thus, sulochrin derivatives are anti-HCV lead compounds with a new mode of action.

1. Introduction

Hepatitis C virus (HCV) infection is a major causative agent of chronic liver diseases such as liver cirrhosis and hepatocellular carcinoma [1]. The standard anti-HCV therapy has been a co-treatment with pegylated-interferon (IFN)α and ribavirin, but this therapy is limited by less efficacy to certain HCV genotypes, poor tolerability, serious side effects, and high cost [2,3]. In addition to the newly approved protease inhibitors, telaprevir and boceprevir, a variety of anti-HCV candidates are under clinical development. Although these drugs improve the virological response rate, the emergence of drug-resistant virus is expected to be a significant problem. Moreover, these compounds are expensive due to their complex structure and the many steps required for their total synthesis. To overcome the drug-resistant virus and achieve a long-term antiviral effect, multidrug treatment is essential. Thus, the development of drugs targeting a different step in the HCV life cycle and presumably requiring low cost is urgently needed.

HCV propagates in hepatocytes through its viral life cycle including: attachment and entry (defined as the early step in this study); translation, polyprotein processing, and RNA replication (the middle step); and assembly, trafficking, budding, and release (the late step) (Supplementary Fig. S1). The middle step has been extensively analysed, especially after the establishment of the HCV replicon system [4]. The early step can be analysed with HCV pseudoparticle (HCVpp) [5,6], which is a murine leukemia virus- or human immunodeficiency virus-based pseudovirus carrying HCV E1 and E2 as envelope proteins. The HCV-producing cell culture system (HCVcc) is used for analyzing the whole life cycle [7–9]. In addition, the HCV trans-complemented particle (HCVtcp) system carrying an HCV subgenomic replicon RNA packaged in HCV E1 and E2-containing particles can evaluate the life cycle from the early to the middle step [10]. The majority of anti-HCV agents currently under clinical development, such as inhibitors of protease, polymerase, NS5A, and cellular cyclophilin, inhibit polyprotein processing and/or RNA replication. A desirable approach

Abbreviations: HCV, hepatitis C virus; IFN, interferon; HCVpp, HCV pseudoparticle; HCVcc, HCV derived from cell culture; HCVtcp, HCV trans-complemented particle; MOI, multiplicity of infection; HBs, HBV envelope protein; CsA, cyclosporin A; VSV, vesicular stomatitis virus.

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to achieving efficient multidrug therapy is to identify new antiviral drugs targeting different steps in the viral life cycle. A combination of drugs with different targets can greatly decrease the emergence of drug-resistant virus.

Natural products generally contain more characteristics of high chemical diversity than combinatorial chemical collections, and therefore have a wider range of physiological activities [11,12]. They offer major opportunities for finding novel lead structures that are active in a biological assay. Moreover, biologically active natural products are generally small molecules with drug-like properties, and thus development costs of producing orally active agents tend to be lower than that derived from combinatorial chemistry [13]. In addition, there is a wide variety of natural compounds reported to possess antiviral activity [14,15]. In the present study, we have taken advantage of the potential of natural products by screening a natural product library derived from fungal extracts with a cell-based assay that supports the whole life cycle of HCV.

2. Materials and methods

2.1. Cell culture

Huh-7.5.1 [8] and HepaRG cells [16] were cultured as described previously.

2.2. Natural product library and reagents

Natural products were extracted essentially as previously described [17]. Culture broths of fungal strains isolated from seaweeds, mosses, and other plants were extracted with CH_2Cl_2. The crude extracts were separated by silica gel column chromatography to purify compounds. The chemical structure of each compound was determined by NMR and mass spectrometry analyses. Thus, we prepared an in-house natural product library consisting of approximately 300 isolated compounds.

Cyclosporin A was purchased from Sigma. Bafilomycin A1 and chlorpromazine were purchased from Wako. Heparin was obtained from Mochida Pharmaceutical. IFNα was purchased from Schering-Plough.

2.3. Compound screening

Huh-7.5.1 cells were treated with HCV J6/JFH1 at a multiplicity of infection (MOI) of 0.15 for 4 h. The cells were washed and then cultured with growth medium treated with 10 μM of each compound for 72 h. The infectivity of HCV in the medium was quantified. Cell viability at 72 h post-treatment was simultaneously measured. Compounds that decreased the cell viability to less than 50% of that without treatment were eliminated for further evaluations. Normalised infectivity was calculated as HCV infectivity divided by cell viability. Compounds reducing the normalised infectivity to less than 40% were selected as initial hits. The initial hits were further evaluated for data reproduction and dose-dependency.

2.4. HCVcc assay

HCVcc was recovered from the medium of Huh-7.5.1 cells transfected with HCV J6/JFH-1 RNA as described [7]. HCVcc was infected into Huh-7.5.1 cells at 0.15 MOI for 4 h. After washing out the inoculated virus, the cells were cultured with normal growth medium in the presence or absence of compounds for 72 h. The infectivity of HCV and the amount of HCV core protein in the medium were quantified by infectious focus formation assay and chemiluminescent enzyme immunoassay (Lumipulse II HCV core assay, ortho clinical diagnostics), respectively [7,18].

2.5. Immunoblot analysis

Immunoblot analysis was performed as described previously [19]. The anti-HCV core antibody (2H9) was used as a primary antibody with 1:1000 dilution [7].

2.6. MTT assay

The viability of cells was quantified by using a Cell Proliferation Kit II XTT (Roche Diagnostics) as described previously [20].

2.7. HCV replicon assay

Huh-7.5.1 cells were transfected with an HCV subgenome replicon RNA (SGR-JFH1/Luc) for 4 h and then incubated with or without compounds for 48 h [21]. The cells were lysed with 1xPLB (Promega), and the luciferase activity was determined with a luciferase assay system (Promega) according to the manufacturer's protocol [22].

2.8. HCVpp assay

HCVpp was recovered from the medium of 293T cells transfected with expression plasmids for HCV JFH-1 E1E2, MLV Gag-Pol, and luciferase, which were kindly provided from Dr. Francois-Loic Cosset at Universite de Lyon [5]. Vesicular stomatitis virus pseudoparticles (VSVpp) was similarly recovered with transfection by replacing HCV E1E2 with VSV G.

Huh-7.5.1 cells were preincubated with compounds for 3 h and were then infected with HCVpp in the presence of compounds for 4 h. After washing out virus and compounds, cells were incubated for an additional 72 h before recovering the cell lysates and quantifying the luciferase activity.

2.9. HCVtcp assay

The HCVtcp assay was essentially performed as described [10]. Briefly, Huh-7 cells were transfected with expression plasmids for the HCV subgenomic replicon carrying the luciferase gene and for HCV core-NS2 based on genotype 1a (RMT) (kindly provided by Dr. Michinori Kohara at Tokyo Metropolitan Institute of Medical Science), 1b (Con1), and 2a (JFH-1) [4,10,23] to recover HCVtcp. HCVtcp can reproduce RNA replication as well as HCV-mediated entry into the cells [10].

2.10. Synergy analysis

To determine whether the effect of the drug combination was synergistic, additive, or antagonistic, MacSynergy (kindly provided by Mark Prichard), a mathematical model based on the Bliss independence theory, was used to analyse the experimental data shown in Fig. 3A. In this model, a theoretical additive effect with any given concentrations can be calculated by $Z = X + Y(1-X)$, where X and Y represent the inhibition produced by each drug alone, and Z represents the effect produced by the combination of two compounds if they were additive. The theoretical additive effects were compared to the actual experimental effects at various concentrations of the two compounds and were plotted as a three-dimensional differential surface that would appear as a horizontal plane at 0 if the combination were additive. Any peak above this plane (positive values) indicates synergy, whereas any depression below the plane (negative values) indicates antagonism. The 95% confidence interval of the experimental dose–response was considered to reveal only effects that were statistically significant.

3. Results

3.1. Screening of natural products possessing anti-HCV activity

We extracted culture broths of fungal strains isolated from seaweeds, mosses, and other plants and purified compounds as described in the Section 2 [17]. The chemical structure of each compound was determined by NMR and mass spectrometry analyses. Thus, we prepared an in-house natural product library consisting of approximately 300 isolated compounds. As shown in the Section 2, compounds reducing the normalised HCV infectivity to less than 40% as compared with DMSO were selected as primary hits. The primary hits were then validated by examining the reproducibility, dose-dependency, and cell viability in the HCVcc system. Sulochrin [methyl 2-(2,6-dihydroxy-4-methylbenzoyl)-5-hydroxy-3-methoxybenzoate] (Fig. 1A) was one of the compounds showing the highest anti-HCV activity, and the following analyses focus mainly on this compound.

3.2. Sulochrin decreased HCV infectivity in HCV cell culture assay

To characterise the anti-HCV activity of the compounds, Huh-7.5.1 cells were infected with HCV J6/JFH1 at an MOI of 0.15 and then cultured for 72 h in the presence or absence of compounds.

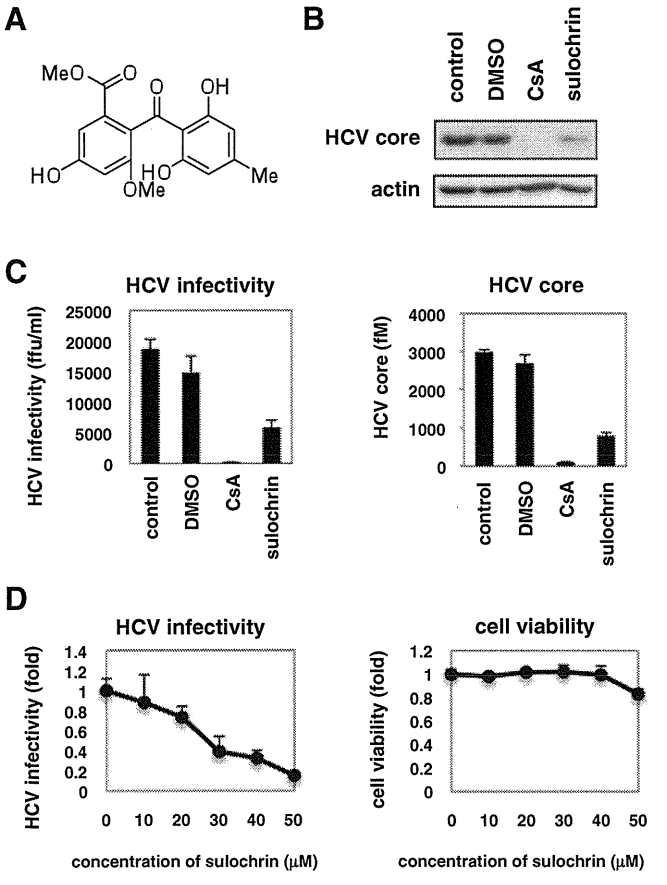


Fig. 1. Sulochrin decreased HCV production in a multi-round HCV infection assay. (A) Chemical structure of sulochrin. (B) Huh-7.5.1 cells were infected with HCV J6/JFH-1 at an MOI of 0.15 for 4 h and then incubated with or without 0.3% DMSO, 2 μM cyclosporin A (CsA), or 30 μM sulochrin for 72 h. The resultant medium was inoculated into naïve Huh-7.5.1 cells to detect intracellular HCV core and actin protein at 48 h postinoculation by immunoblot. (C) HCV infectivity (left) and HCV core protein (right) in the medium as prepared in (B) were quantified as shown in the Section 2. (D) HCV infectivity (left) determined as shown in (C) with varying concentrations (0–50 μM) of sulochrin. Cell viability was examined by MTT assay (right).

In this system, infectious HCV is secreted into the medium and then re-infects into uninfected cells to support the spread of HCV during a 72 h period (Section 2). Cell cultures were treated with sulochrin or cyclosporin A (CsA) as a positive control in this mul-

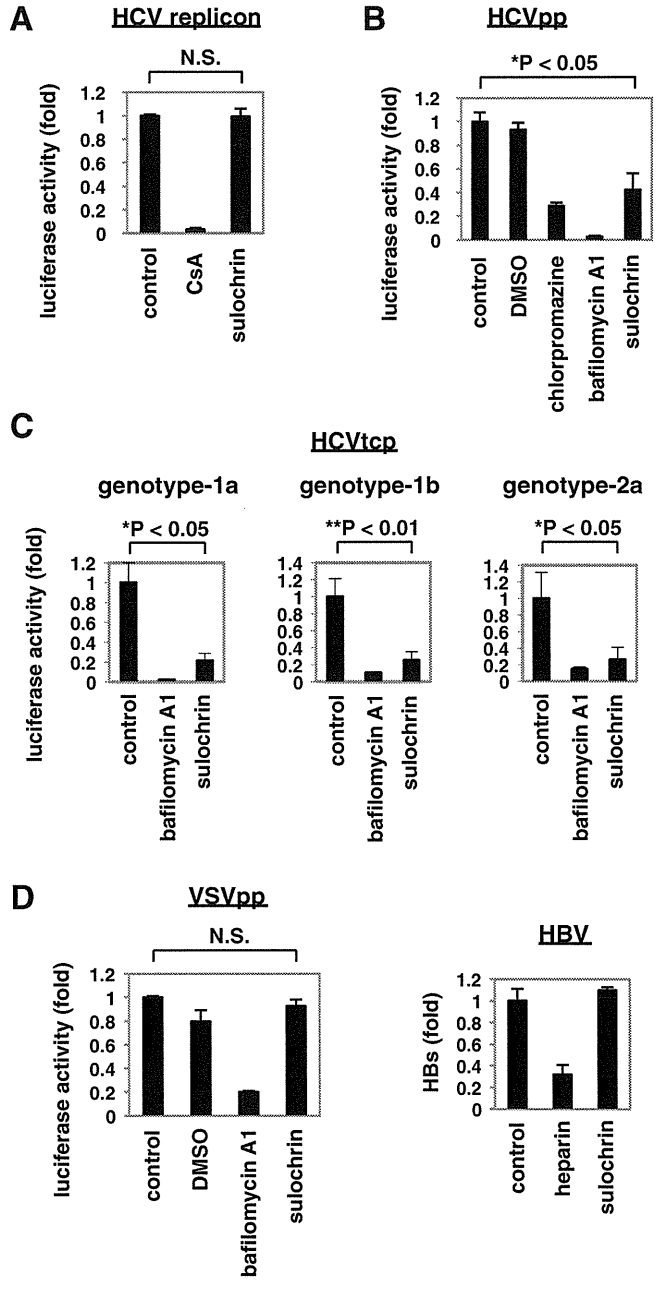


Fig. 2. Sulochrin blocked HCV entry. (A) Replicon assay. Huh-7.5.1 cells were transfected with an HCV subgenomic replicon RNA for 4 h followed by treatment with or without the indicated compounds for 48 h. Luciferase activity driven by the replication of the subgenomic replicon was quantified. (B and C) HCV pseudoparticle (HCVpp) and trans-complemented particle (HCVtcp) assay. Huh-7.5.1 cells were pretreated with the indicated compounds for 3 h and then infected with HCVpp (B) or HCVtcp (C) for 4 h. After washing out virus and compounds, cells were further incubated for 72 h and harvested for measuring luciferase activity driven by the infection of HCVpp or HCVtcp. HCVtcp assay was performed with HCV E1 and E2 derived from genotypes 1a (RMT), 1b (Con1), and 2a (JFH1). (D) Left, the pseudoparticle assay was performed as shown in (B) with VSV G instead of HCV E1 and E2. Right, HBV infection assay. HepaRG cells were pretreated with the indicated compounds for 3 h and then infected with HBV for 16 h. After washing out virus and compounds, cells were incubated for an additional 12 days. HBV infection was evaluated by measuring HBs secretion from the infected cells. Heparin was used as a positive control that inhibits HBV entry.

ti-round infection system. To examine the level of infectious HCV particles produced from the cells, the resultant medium was inoculated into naive Huh-7.5.1 cells to detect HCV core protein in the cells. As shown in Fig. 1B, intracellular production of HCV core but not that of actin was reduced in the cells inoculated with sulochrin- and CsA-treated medium (Fig. 1B). Quantitative analysis showed that sulochrin decreased HCV infectivity and HCV core protein in the medium to 1/3–1/4 of the untreated levels (Fig. 1C). Reduction of HCV infectivity by sulochrin was dose-dependent without serious cytotoxicity up to 50 μM (Fig. 1D).

3.3. Sulochrin blocked HCV entry

We investigated the step in the HCV life cycle that was inhibited by sulochrin. The middle step of the life cycle including translation and RNA replication was evaluated with the transient replication assay by using the HCV subgenomic replicon. Sulochrin had little effect on the replicon activity at doses up to 50 μM (Fig. 2A). In the HCVpp system, which reproduced the early step of HCV infection including entry, sulochrin significantly inhibited HCVpp infection (Fig. 2B). Sulochrin also inhibited the infection of HCVtcp, which reproduced both the viral entry and RNA replication, further supporting that this compound targeted the entry step (Fig. 2C). In contrast, VSV G-mediated viral entry efficiency was not altered by sulochrin treatment (Fig. 2D). Additionally, HBV entry was not inhibited by the presence of sulochrin (Fig. 2D). These data suggest that the inhibitory activity of sulochrin on viral entry is specific to HCV. The anti-HCV entry activity of sulochrin was conserved among different HCV genotypes, 1a (RMT), 1b (Con1), and 2a (JFH-1) [4,10,23] (Fig. 2C).

3.4. Synergistic effect of cotreatment of sulochrin with IFNα or telaprevir

We examined the anti-HCV activity of sulochrin co-administered with clinically available anti-HCV agents, IFNα and a prote-

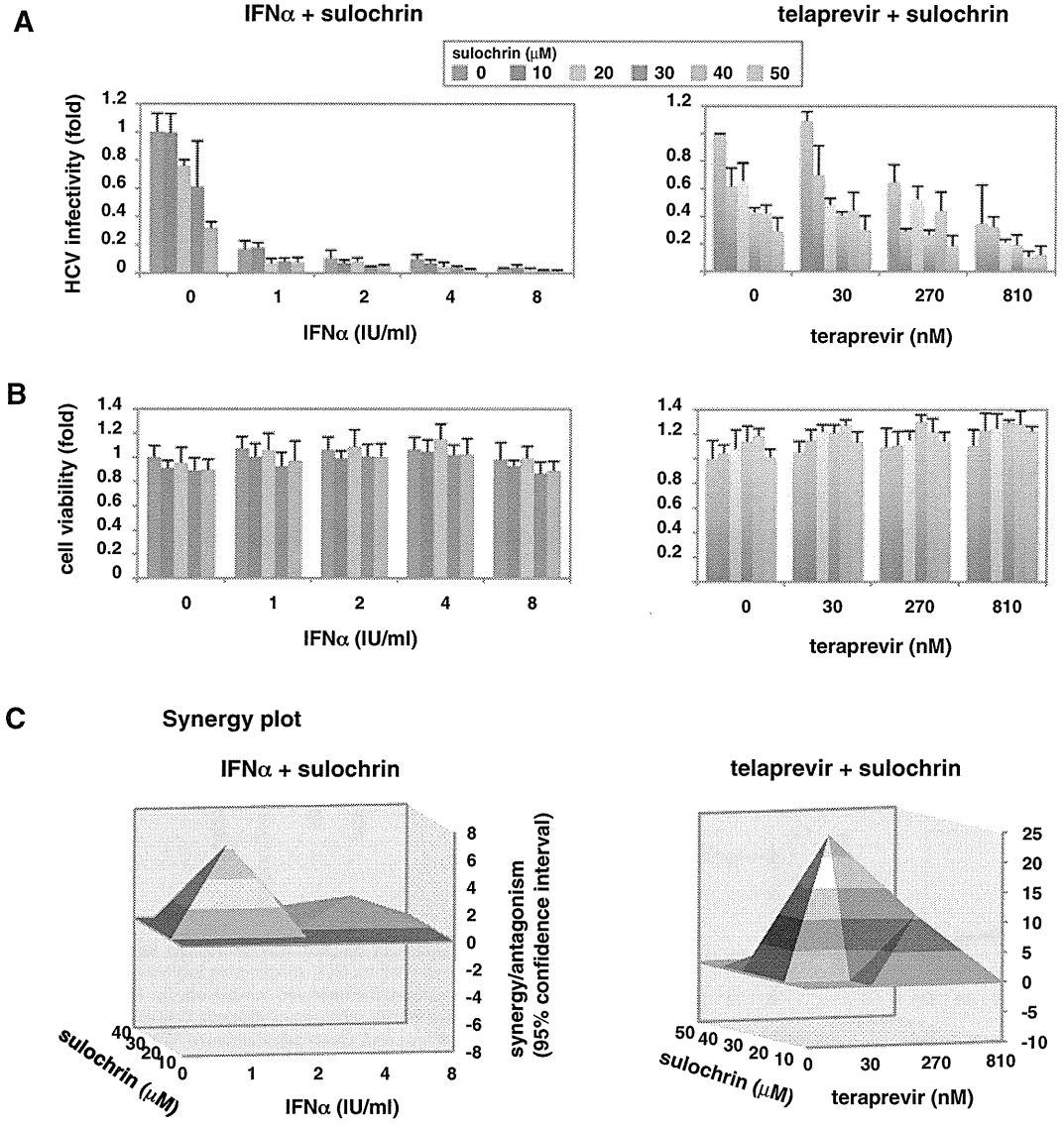


Fig. 3. Cotreatment of sulochrin with IFNα or telaprevir. (A, B) Huh-7.5.1 cells infected with HCV were treated with the indicated concentrations of sulochrin with IFNα (left) or telaprevir (right) to determine HCV infectivity in the medium (A) as shown in Fig. 1C. Cell viability was also quantified (B). (C) Synergy analysis. The results of the combinations shown in (A) were analysed with a mathematical model, MacSynergy, as described in the Section 2. The three-dimensional surface plot represents the difference between actual experimental effects and theoretical additive effects of the combination treatment (95% confidence interval). The theoretical additive effects are shown as the zero plane (dark gray) across the *z*-axis. A positive value in the *z*-axis as a peak above the plane indicates synergy, and a negative value with a valley below the plane indicates antagonism. Sulochrin in combination with IFNα (left) or telaprevir (right) produced synergistic antiviral effects that were greater than the theoretical additive effects.

ase inhibitor telaprevir. As shown in Fig. 3, addition of sulochrin with IFNα or telaprevir led to a further decrease in HCV infectivity (Fig. 3A) without significantly enhancing cytotoxicity (Fig. 3B) at any given concentrations. Thus, the combination of sulochrin and IFNα or telaprevir always resulted in a greater reduction in HCV infectivity as compared with that achieved by either agent alone. Synergy/antagonism analysis with the Bliss independence model showed that the experimental anti-HCV activity in combination with sulochrin and IFNα or telaprevir showed a peak above the zero plane in the *z*-axis, which shows the calculated theoretical additive effect (Fig. 3C). Any peak above the zero plane indicates more than an additive effect, namely, synergy (Section 2). The data clearly indicate that sulochrin had a synergistic anti-HCV effect with both IFNα and telaprevir.

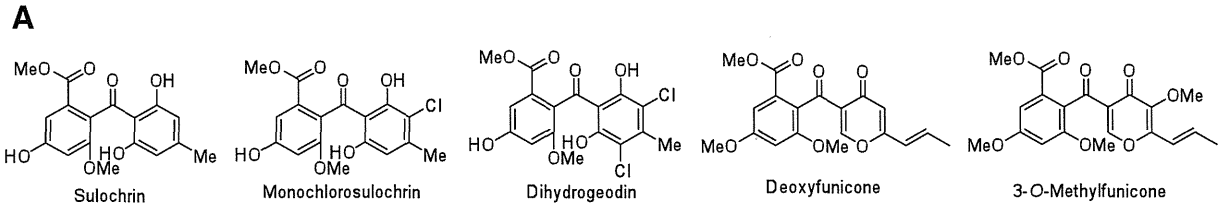
3.5. Derivative analysis of sulochrin

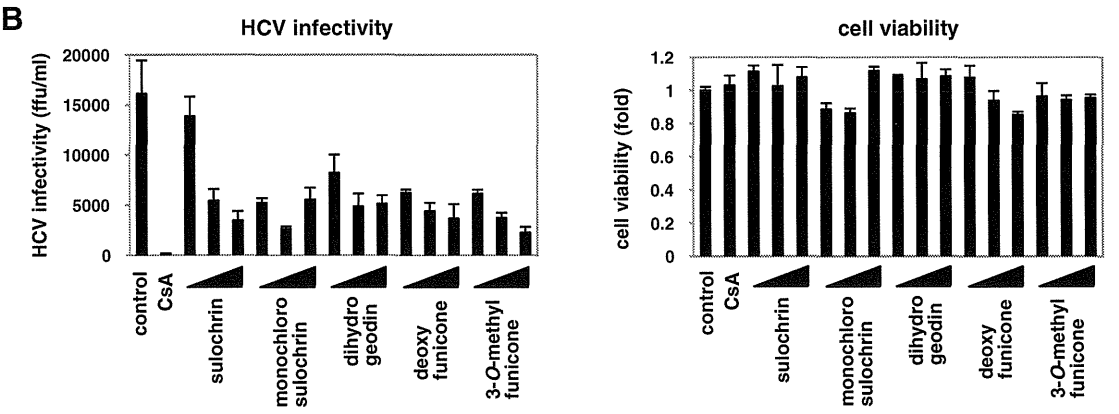
We examined the anti-HCV activity of a series of sulochrin derivatives (Fig. 4A) in the HCVcc system. Monochlorosulochrin and dihydrogeodin, mono- or dichloro-substituted derivatives of sulochrin, possessed even higher anti-HCV activity than sulochrin (Fig. 4B and C). Deoxyfunicone, of which one aromatic ring was replaced by a 4-pyrone ring, had approximately 5-fold greater HCV inhibitory activity as compared with sulochrin (Fig. 4B and C). An additional compound, 3-*O*-methylfunicone, also possessed anti-HCV activity (Fig. 4B and C). These data suggest that the 1,3-dihydroxy-5-methylbenzene moiety of sulochrin is important for anti-HCV activity. Furthermore, funicone derivatives as well as sulochrin derivatives are likely to be lead compounds for a new class of anti-HCV agents.

4. Discussion

In the present study, we prepared a natural product library consisting of approximately 300 isolated compounds derived from fungi extract [17]. Among these compounds, we focused on sulochrin, which reduced HCV infectivity in the HCVcc system. Sulochrin suppressed the viral entry efficiencies both in the HCVpp and the HCVtcp systems, suggesting that this compound blocked HCV envelope-mediated entry. HCV was reported to enter host cells through clathrin-dependent endocytosis after engagement to host receptors [24–27]. Sulochrin is not likely to be a general inhibitor of clathrin-dependent endocytosis, but rather is specific for HCV entry, as it did not affect the entry of other viruses such as VSVpp and HBV, which were reported to enter by clathrin-dependent manners [28,29].

Sulochrin inhibits eosinophil degranulation, activation, and chemotaxis [30,31]. It also inhibits VEGF-induced tube formation of human umbilical vein endothelial cells [32]. In addition, 3-*O*-methylfunicone, a sulochrin derivative possessing anti-HCV activity, has an anti-tumor activity [33]. It is unknown if these activities of the compounds are related to their anti-HCV activity. The establishment of drug-resistant virus and the identification of the target molecule are in progress to reveal the mechanism of action of sulochrin and its derivatives. However, the present study is the





C

IC_{50}s and CC_{50}s

compound	IC_{50} (μM)	CC_{50} (μM)
sulochrin	24.4 ± 2.0	> 50
monochlorosulochrin	4.3 ± 1.1	> 50
dihydrogeodin	10.3 ± 0.3	> 50
deoxyfunicone	4.6 ± 1.1	> 50
3-*O*-methylfunicone	6.2 ± 2.3	> 50

Fig. 4. Derivative analysis of sulochrin. (A) Chemical structures of sulochrin derivatives examined in this study, monochlorosulochrin, dihydrogeodin, deoxyfunicone, 3-*O*-methyfunicone, as well as sulochrin. (B) Anti-HCV effects of the sulochrin derivatives (10, 30, and 50 μM) were investigated as shown in Fig. 1C. (C) The IC_{50} and CC_{50} values of the sulochrin derivatives are shown.

first report to demonstrate the antiviral activity of these compounds. It is important to note that sulochrin inhibited the entry of HCV genotype 1a and b, which are the dominant genotypes in North America, Europe, and East Asia, indicating that this compound has potential clinical applications. Promising applications of entry inhibitors include the prevention of HCV recurrence in patients after liver transplantation. In patients with HCV-related end-stage liver diseases undergoing liver transplantation, re-infection of the graft is universal and characterised by accelerated progression of liver diseases. Entry inhibitors may be effective especially in these conditions under robust re-infection of HCV into hepatocytes. In the present study, we showed that co-treatment of sulochrin with IFNα and a protease inhibitor, teleprevir, synergistically augmented the anti-HCV effects of these approved drugs. These results suggest the possibility that co-treatment with sulochrin and probably its effective derivatives helps to inhibit the spread of HCV infection. We also identified the chemical structure and the derivatives of sulochrin as lead compounds for anti-HCV agents. Further derivatives analysis may identify more preferable anti-HCV agents.

In conclusion, our results demonstrate that sulochrin and its derivatives are potent and selective inhibitors of HCV infection in cell culture. Although further studies including an analysis of mode of action and pharmacological properties *in vivo* are required, this class of compounds should be pursued for its clinical potential in the treatment of HCV infection.

Acknowledgments

Huh-7.5.1 cells were kindly provided by Dr. Francis Chisari at The Scripps Research Institute. The expression plasmids for producing HCVpp were a generous gift from Dr. Francois-Loic Cosset at Universite de Lyon. The expression plasmid for HCV E1E2 of genotype 1a (RMT) was kindly provided by Dr. Michinori Kohara at Tokyo Metropolitan Institute of Medical Science. We thank all of the members of the Department of Virology II, National Institute of Infectious Diseases, for their helpful discussions. This study was supported by grants-in-aid from the Ministry of Health, Labour, and Welfare, Japan, from the Ministry of Education, Culture, Sports, Science, and Technology, Japan, and from the Japan Society for the Promotion of Science.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.bbrc.2013.09.100.

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Total Synthesis and Anti-Hepatitis C Virus Activity of MA026

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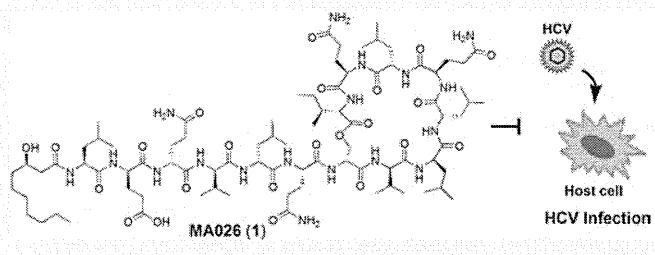
Supporting Information

ABSTRACT: The first total synthesis of MA026 and the identification of its candidate target protein for anti-hepatitis C virus activity are presented. MA026, a novel lipocyclodepsipeptide isolated from the fermentation broth of *Pseudomonas* sp. RtIB026, consists of a cyclodepsipeptide, a chain peptide, and an N-terminal (*R*)-3-hydroxydecanoic acid. The first subunit, side chain **2**, was prepared by coupling fatty acid moiety **4** with tripeptide **5**. The key macrocyclization of the decadepsipeptide at L-Leu[10]-D-Gln[11] provided the second subunit, cyclodepsipeptide **3**. Late-stage condensation of the two key subunits and final deprotection afforded MA026. This convergent, flexible, solution-phase synthesis will be invaluable in generating MA026 derivatives for future structure–activity relationship studies. An infectious hepatitis C virus (HCV) cell culture assay revealed that MA026 suppresses HCV infection into host hepatocytes by inhibiting the entry process in a dose-dependent manner. Phage display screening followed by surface plasmon resonance (SPR) binding analyses identified claudin-1, an HCV entry receptor, as a candidate target protein of MA026.



INTRODUCTION

MA026 (**1**) (Figure 1),[1] a novel lipocyclodepsipeptide, exhibits antiviral activity against hepatitis C virus (HCV). HCV, a member of the *Flaviviridae* family, is a major causative agent of chronic liver diseases such as liver cirrhosis and hepatocellular carcinoma[2] and is thought to affect more than 170 million individuals worldwide, resulting in approximately 280 000 deaths per year.[3] Unfortunately, antiviral treatments consisting of PEGylated interferon (IFN) in combination with ribavirin and newly approved protease inhibitors are limited by serious adverse effects. The emergence of drug-resistant viruses and the high cost of current treatment regimens has led to an urgent search for alternative approaches to prevent HCV infection.[4] The life cycle of HCV includes entry into the host cell (entry process), uncoating of the viral genome, translation of viral proteins, viral genome replication, and the assembly and release of viral particles.[5] The recent development of an HCV cell culture system facilitated the elucidation of the viral replication machinery.[6] Identification of anti-HCV compounds, such as MA026, may be important in establishing novel strategies to inhibit HCV infection.

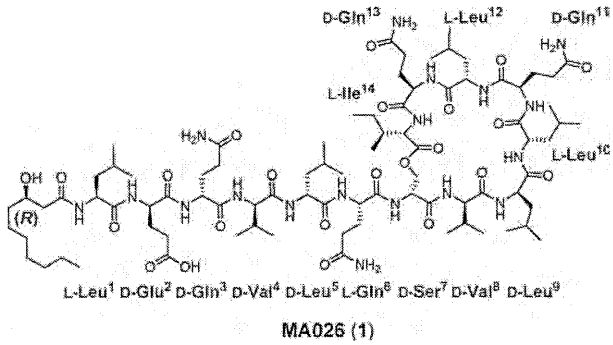


Figure 1. Chemical structure of MA026 (**1**).

MA026 (**1**) was isolated from the fermentation broth of *Pseudomonas* sp. RtIB026 found in the digestive tract of rainbow trout (*Oncorhynchus mykiss*).[1] Rainbow trout, an important aquaculture species, is known to be highly susceptible to infectious hematopoietic necrosis virus (IHNV).[7] IHNV, a member of the genus *Novirhabdovirus* in the Rhabdoviridae family, is a causative agent of infectious hematopoietic necrosis (IHN), which is one of the most serious infectious diseases of salmonids.[8] An outbreak of IHNV in rainbow trout aquaculture can cause extensive economic loss.[9] For this reason, surveys were conducted on farmed rainbow trout that identified individual fish resistant to IHNV infection. Our previous studies revealed that rainbow trout with

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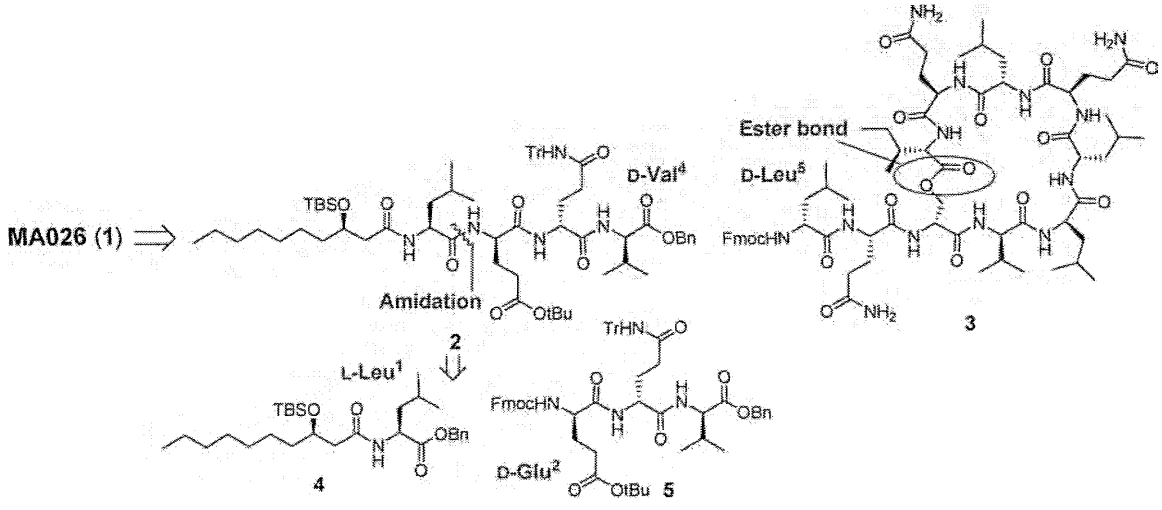
Scheme 1. Retrosynthetic Analysis of MA026 (1)



resistance to IHNV infection live in symbiosis with *Pseudomonas* sp. RtIB026 in their digestive tracts.[1] Anti-IHNV bioassay-guided fractionation of organic extracts from the culture fluid of *Pseudomonas* sp. RtIB026 resulted in the isolation of a new lipocyclodepsipeptide, designated MA026, as a principal active constituent.

The structure of MA026 was established in 2002[1] by amino acid composition analyses and NMR analyses with chemical modifications. MA026 was found to consist of a cyclodepsipeptide composed of eight amino acids, a chain peptide composed of six amino acids, and an N-terminal (*R*)-3-hydroxydecanoic acid. In total, MA026 contains 14 amino acids, nine of which possess the D configuration, as shown by HPLC analyses using Marfey's reagent. The amino acid sequence was determined by MS/MS analyses and comparison of partial peptide segments obtained by degradation of the natural product with synthetic peptides. The cyclodepsipeptide comprises a 25-membered ring in which the carboxylic group of L-Ile[14] forms a lactone bond with the hydroxy group of D-Ser.[7] To date, a wide range of lipocyclodepsipeptides have been identified,[10] including xantholysin A, an analogue of MA026.[11] In terms of sequence, xantholysin A differs from MA026 by two amino acids, namely, Gln[10]-Leu[11] in xantholysin A versus L-Leu[10]-D-Gln[11] in MA026. However, absolute configurations at all stereogenic centers in xantholysin A have yet to be determined.

In common with a number of lipocyclodepsipeptides, MA026 possesses a complex structure and interesting biological activity. In particular, MA026 displays anti-HCV activity that could be used to develop a novel antiviral drug. However, in order to reveal the mechanism of this anti-HCV activity, it is essential to develop a flexible chemical synthesis of MA026 to facilitate chemical modification of its structure. Herein we describe the first total synthesis of MA026 (**1**). Using a HCV cell culture assay, we have clarified that MA026 inhibits the HCV entry process into a hepatocyte cell line. Moreover, phage display screening and surface plasmon resonance (SPR) binding analyses suggested that MA026 might interact with claudin-1 (CLDN1), a cellular entry receptor of HCV.

■ RESULTS AND DISCUSSION

Retrosynthetic Analysis. MA026 (**1**) was divided into two key segments to maximize the convergency of the synthesis: side chain **2** and cyclodepsipeptide **3** (Scheme 1). The cyclodepsipeptide contains a lactone bond composed of the carboxylic group of L-Ile[14] and the hydroxy group of D-Ser.[7] We envisaged a potential exchange of an ester bond with an amide bond by attack of a free N-terminal amine located proximal to the ester linkage.[12] To prevent such an exchange, it is necessary to maintain a sufficient distance between the ester bond and the N-terminus of the cyclodepsipeptide. Therefore, **3** should contain the cyclodepsipeptide plus an additional two amino acids, with the coupling site of **2** and **3** chosen to be D-Val[4]-D-Leu[5]. The side chain **2** was separated between L-Leu[1] and D-Glu[2] to give fatty acid moiety **4** and tripeptide **5**.

Key to the synthesis of cyclodepsipeptide **3** was the macrocyclization of a decapeptide (Scheme 2). Because it is more difficult to construct an ester bond than an amide bond,[13] we decided to disconnect the macrocycle at an amide bond and construct an ester bond in the early stage of the synthesis. The macrocyclization site was chosen at L-Leu[10]-D-Gln[11] considering the steric hindrance due to the isopropyl group of Val or the isobutyl group of Leu. The macrocyclization substrate, decadepsipeptide **6**, was to be prepared by the joining of hexadepsipeptide **7** with two dipeptides.

In the course of the construction of several peptide fragments, selective protection and deprotection of specific functional groups are critical. The Fmoc group was employed to protect the N-terminal amines of cyclodepsipeptide **3** and tripeptide **5**. The orthogonal Boc group was used to protect the N-terminal amines of other peptides. We also introduced a trityl (Tr) protecting group for the side-chain amides of D-Gln[3] and L-Gln[6] to maintain the solubility of the peptides in several organic solvents. In particular, the Tr group plays a significant role in affording solubility for peptides in aprotic solvents such as THF. During the preparation of Tr-protected Gln, an amine was protected with an Alloc group, as this protective group could be selectively removed using a palladium catalyst without affecting the Tr group.

Synthesis of Side Chain 2. We began our synthetic efforts by targeting fatty acid moiety **4** (Scheme 3). Protection of alcohol **8**[14] with a *tert*-butyldimethylsilyl (TBS) group afforded (*R*)-3-hydroxycarboximide **9** in 97% yield. The chiral auxiliary of **9** was hydrolyzed (58% yield), and the resulting carboxylic acid was then coupled with TsOH·L-Leu-OBn to provide fatty acid moiety **4** in 66% yield.

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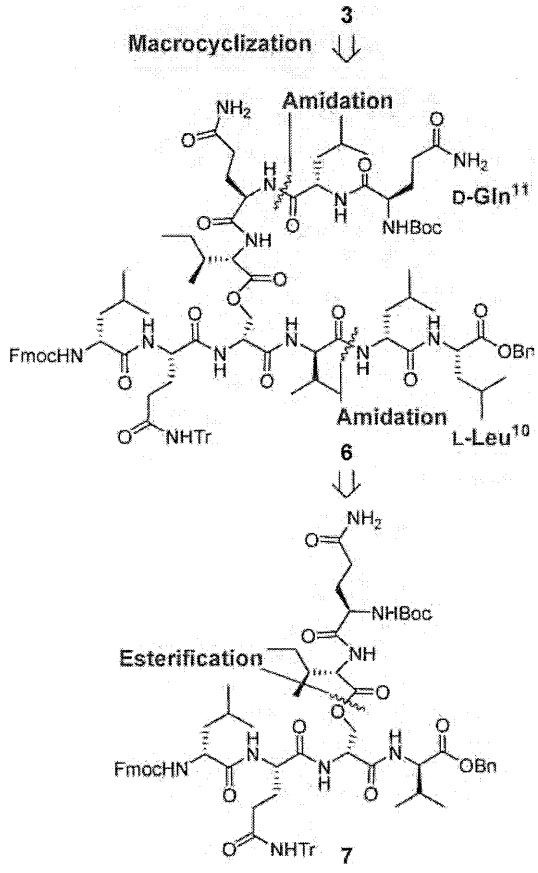
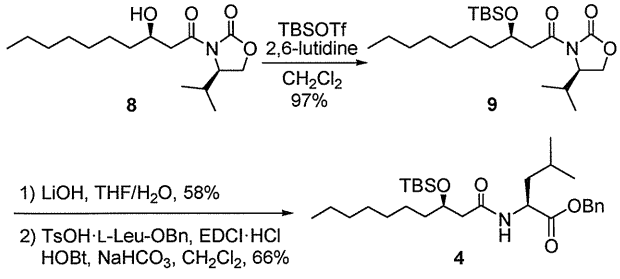
Scheme 2. Retrosynthetic Analysis of Cyclodepsipeptide 3



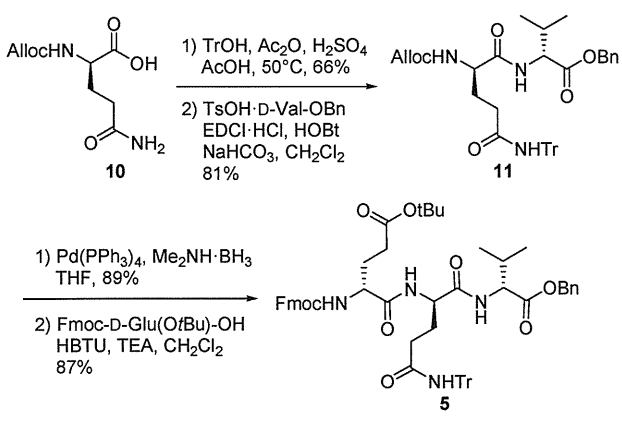
Scheme 3. Synthesis of Fatty Acid Moiety 4



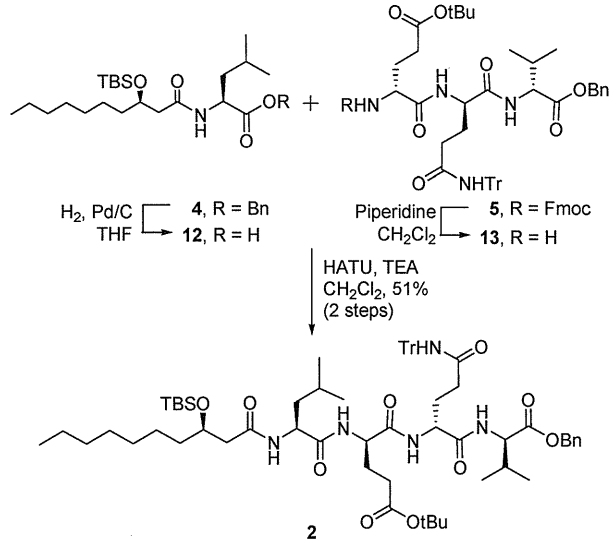
Tripeptide **5** was assembled as follows (Scheme 4). Alloc-D-Gln-OH (**10**) was treated with trityl alcohol and acetic anhydride under acidic conditions[15] to give the side-chain-protected residue in 66% yield. Subsequent condensation of this product with TsOH·D-Val-OBn provided dipeptide **11** in 81% yield. The Alloc group of **11** was then removed in the presence of a palladium catalyst and dimethylamine borane[16] (89% yield), and the resulting amine residue was coupled with Fmoc-D-Glu(O*t*Bu)-OH to afford **5** in 87% yield.

With fatty acid moiety **4** and tripeptide **5** in hand, we tried to link them together to obtain side chain **2** (Scheme 5).

Scheme 4. Preparation of Tripeptide 5



Scheme 5. Synthesis of Side Chain 2



Hydrogenolysis of the benzyl ester in **4** gave carboxylic acid **12**, and cleavage of the Fmoc group in **5** by treatment with piperidine provided amine **13**.[17] Condensation of **12** with **13** in the presence of 2-(1*H*-7-azabenzotriazol)-1-yl-1,1,3,3-tetramethyluronium hexafluorophosphate (HATU) and triethylamine (TEA) afforded side chain **2** in 51% yield over the two steps.

Synthesis of Cyclodepsipeptide 3. The synthesis of the other key subunit, cyclodepsipeptide **3**, started with the construction of hexadepsipeptide **7**, an intermediate leading to the macrocyclization substrate, decadepsipeptide **6** (Scheme 6). To assemble **7** efficiently, three dipeptides were prepared as follows. Alloc-L-Gln-OH (**14**)[18] was treated with benzyl bromide and 1,8-diazabicycloundec-7-ene (DBU) to give the benzyl ester in 92% yield. Subsequent side-chain protection with a Tr group (86% yield) and removal of the Alloc group were performed by the same procedure as described earlier to give amine residue **15** in 94% yield. Condensation of **15** with Fmoc-D-Leu (93% yield) followed by hydrogenolysis of the benzyl ester afforded the corresponding dipeptide carboxylic acid **16** in 98% yield. Boc-D-Ser[19] and D-Val-OBn were coupled (92% yield), and cleavage of the carbamate linkage under acidic conditions furnished the corresponding dipeptide amine **17** in quantitative yield. Condensation of Boc-D-Gln with L-Ile-OBn (95% yield) and subsequent benzyl ester hydrogenolysis provided the corresponding dipeptide carboxylic acid **18** in 92% yield. Coupling of **16** with **17** in the presence of *O*-(benzotriazol-1-yl)-*N*,*N*,*N*′,*N*′-tetramethyluronium hexafluorophosphate (HBTU) and TEA afforded tetrapeptide **19** in 90% yield. The key esterification of the hindered alcohol of **19** with dipeptide carboxylic acid **18** was problematic. A wide range of procedures were examined, including the use of 1-(3-dimethylaminopropyl)-3-ethylcarbodiimide hydrochloride

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